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The primary aim of World Journal of Gastrointestinal Oncology (WJGO, World J Gastrointest Oncol) is to provide scholars and readers from various fields of gastrointestinal oncology with a platform to publish high-quality basic and clinical research articles and communicate their research findings online.

WJGO mainly publishes articles reporting research results and findings obtained in the field of gastrointestinal oncology and covering a wide range of topics including liver cell adenoma, gastric neoplasms, appendiceal neoplasms, biliary tract neoplasms, hepatocellular carcinoma, pancreatic carcinoma, cecal neoplasms, colonic neoplasms, colorectal neoplasms, duodenal neoplasms, esophageal neoplasms, gallbladder neoplasms, etc.

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EDITORIAL

### Mixed neuroendocrine non-neuroendocrine tumors: The quest for evidence

#### Mauro Cives, Camillo Porta, Raffaele Palmirotta

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#### Abstract

Mixed neuroendocrine non-neuroendocrine neoplasms (MiNENs) are rare mixed tumors containing both neuroendocrine and non-neuroendocrine components that occupy at least 30% of the whole tumor. Biologically, both components appear to derive from an identical cellular precursor undergoing early dual differentiation or late transdifferentiation. While our understanding of MiNENs has improved in recent years, many areas of uncertainty remain. In this context, setting diagnostic criteria capable of capturing the continuum of disease biology while providing clinically meaningful information in terms of prognosis and response to treatments appears vital to advance the field and improve patients' outcomes. Evidence is needed to generate robust classification schemes, and multi-institutional cooperation will likely play a crucial role in building adequately powered cohorts to address some of the most pressing questions discussed in this Editorial. What is the minimum representation for each component needed to define MiNENs? How can the epidemiology of MiNENs change according to different diagnostic definitions? How can we generate the clinical evidence nee-ded to optimize the management of MiNENs?

Key Words: Mixed neuroendocrine non-neuroendocrine neoplasms; Neuroendocrine neoplasm; Neuroendocrine carcinoma; Mixed tumors; Digestive; Gastroenteropancreatic

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**Core Tip:** In this Editorial, we highlight potential pitfalls in the current classification of mixed neuroendocrine non-neuroendocrine neoplasms and comment on challenges in the management of this heterogeneous group of malignancies in light of the paucity of evidence in the field. Improved biological and clinical knowledge is needed to generate robust classification schemes that will in turn provide clarity on the epidemiology of the disease, prognosis of affected patients and guidance for treatment tailoring.

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#### INTRODUCTION

In their timely review in this issue of *World Journal of Gastrointestinal Oncology*, Díaz-López *et al*[1] provide a comprehensive description of the biology and clinical management of mixed neuroendocrine non-neuroendocrine neoplasms (MiNENs). According to the 2022 World Health Organization (WHO) classification[2], MiNENs consist of both a neuroendocrine component and an adenocarcinoma, signet ring cell carcinoma or, more rarely, squamous cell carcinoma component, with each component exceeding 30%. While knowledge of this group of malignancies has evolved in recent years, the emergence of new data has perhaps raised as many questions as it has answered.

One key theme around MiNENs is how we exactly define them. "All models are wrong, but some are useful" is an aphorism attributed to the statistician George Box. While histopathological classifications are imperfect per se, they provide crucial information in oncology. However, a priori evidence (*i.e.* survival rates according to different groups) is needed to build models (histopathological classifications) capable of conveying useful information. Where is the evidence when it comes to the WHO classification of MiNENs? Non-neuroendocrine components are present in approximately 40% of gastroenteropancreatic neuroendocrine carcinomas<sup>[3]</sup>, a figure way larger than the perceived frequency of MiNENs. Indeed, only a proportion of such malignancies (namely those tumors harboring neuroendocrine and nonneuroendocrine components exceeding the arbitrarily established 30% cut-off) are currently captured as MiNENs according to the 2022 WHO classification<sup>[2]</sup>. Is thus a scattered minor neuroendocrine or non-neuroendocrine component irrelevant in terms of clinical behavior, treatment response or prognosis? Possibly no, at least according to studies showing that a neuroendocrine component > 20% or even > 10% can affect patients' prognosis[4-7]. Not only do these data question the appropriateness of the arbitrarily chosen 30% cut-off, they also indicate that divergent lineage differentiation (namely the presence of neuroendocrine component in non-neuroendocrine cancers and vice versa) has profound prognostic (and perhaps therapeutic) implications per se. Notably, such concept has been already incorporated in the last edition of the WHO classification of thoracic tumors where "combined neuroendocrine/non-neuroendocrine lung tumors" refer to mixed entities combining high-grade neoplasms representing at least 10% of the whole tumor[8]. While the arbitrarily chosen 30% cut-off will be probably revisited in the upcoming WHO classifications of digestive tumors, quantification and reporting of the neuroendocrine and non-neuroendocrine components in mixed tumors is presently advisable. Why relatively small foci of neuroendocrine components in non-neuroendocrine cancers may dictate an aggressive clinical behavior remains largely unknown.

Building a model upon high-level evidence is key to render the model itself relevant and useful. While a relevant model should be able to precisely capture the biology of the disease in its entirety, a useful model should be able to set the criteria needed for defining the epidemiology of the disease, predicting prognosis and, ideally, response to treatments.

#### **BUILDING A RELEVANT MODEL**

So far, fundamental research investigating the molecular alterations of MiNENs has relied on the WHO classification criteria. This means that molecular investigations have been carried out on samples selected within the boundaries imposed by the WHO classification. By doing so, several distinctive traits of MiNENs have been identified. First, multiple studies[9-11] have shown that neuroendocrine and non-neuroendocrine components share a common trunk of mutations, with passenger mutations showing segregation in a specific component. Second, the spectrum of shared mutations is typically similar to that observed in pure adenocarcinomas of the specific anatomic site[11]. Third, allelic imbalances and chromosomal aberrations are more frequent in the neuroendocrine component rather than in the non-neuroendocrine component[12]. While these observations support the hypothesis that the neuroendocrine and non-neuroendocrine components of MiNENs have a monoclonal origin and then undergo an early dual differentiation or a late subclonal transdifferentiation, whether such a biological process could be confined within the boundaries of a percent threshold is disputable. In this context, whether divergent molecular alterations could be found in mixed tumors with different neuroendocrine percent representation (including representation below the 30% threshold) is currently unknown. A critical appraisal of the molecular underpinnings of mixed tumors of the digestive tract according to the relative component distribution is needed to inform future classification schemes.

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#### **BUILDING A USEFUL MODEL**

Inconsistent reporting and varying nomenclature over the past several decades make it difficult to estimate the actual incidence of MiNENs. However, it is likely that the frequency of MiNENs is currently underestimated, primarily as result of challenges in diagnosis. Well-curated multi-institutional analyses from tertiary centers managing high volumes of patients with NENs might provide a better snapshot than tumor registries, although representativeness of the sample would be matter of concern. What would be the impact of lowering the percent threshold for each component in mixed tumors of the digestive tract in terms of incidence and prevalence? No answer can be given at present.

As pointed out by Díaz-López and colleagues in their review[1], the neuroendocrine component of MiNENs dictates patients' prognosis. Several lines of evidence support this conclusion. First, survival outcomes of MiNENs compare similarly to those of NEC patients, diverging from those of non-neuroendocrine cancers[13]. Second, the neuroendocrine component is almost always responsible for the metastatic process [14,15]. Third, the Ki-67 index of the neuroendocrine component determines the natural history of the disease[16,17]. Nevertheless, these concepts represent an oversimplification of the MiNEN reality. Indeed, MiNENs can contain tumor entities with variable degrees of biological aggressiveness in the neuroendocrine and non-neuroendocrine component, and a widely accepted grading system is presently lacking. Although La Rosa's proposal[3] to subdivide MiNENs into low-grade, intermediate-grade and high-grade entities according to the most aggressive component appears valuable to inform management decisions (Table 1), its prognostic relevance remains to be evaluated by large series studies. In this regard, caution should be posed when interpreting survival outcomes in MiNEN patients. Indeed, only lower stage tumors are likely to undergo surgery and can be consequently diagnosed as MiNENs, whereas advanced tumors are more likely to undergo biopsy and can be possibly categorized based on a sample where the dual component is not represented. As result, while observational studies may overestimate the benefit of surgery in MiNENs, comparisons between MiNENs and other tumor entities such as pure NECs or pure non-neuroendocrine cancers hold a substantial risk of selection bias and immortal time bias.

Table 1 Proposed grading and systemic management of mixed neuroendocrine non-neuroendocrine neoplasms				
Neuroendocrine component	Non-neuroendocrine component	Systemic management		
Well-differentiated NET, Grade 1 Ki- 67 < 3%, MI < 2/10 HPF, Grade 2 Ki- 67 3-20, MI 2-20/10 HPF	Adenoma	Somatostatin analogs; Radiolabeled somatostatin analogs (when SSTR <sup>+</sup> ); Everolimus; Sunitinib (pancreatic primaries); Temozolomide-based chemotherapy		
Well-differentiated NET, Grade 1 Ki- 67 < 3%, MI < 2/10 HPF, Grade 2 Ki- 67 3-20, MI 2-20/10 HPF	Adenocarcinoma, signet ring cell carcinoma, mucinous neoplasm	5-FU-based regimens ( <i>i.e.</i> FOLFIRINOX, FOLFIRI, FOLFOX, <i>etc</i> ), Targeted therapies according to molecular profiling		
NEC (small/large cell)	Adenocarcinoma, squamous cell carcinoma, acinar cell carcinoma, adenosquamous carcinoma, mucinous carcinoma, signet ring cell carcinoma	Etoposide/Platinum 5-FU-based regimens ( <i>i.e.</i> FOLFIRINOX, FOLFIRI, FOLFOX, <i>etc</i> ), Targeted therapies according to molecular profiling		
	Neuroendocrine component Well-differentiated NET, Grade 1 Ki- 67 < 3%, MI < 2/10 HPF, Grade 2 Ki- 67 3-20, MI 2-20/10 HPF Well-differentiated NET, Grade 1 Ki- 67 < 3%, MI < 2/10 HPF, Grade 2 Ki- 67 3-20, MI 2-20/10 HPF NEC (small/large cell)	Neuroendocrine component       Non-neuroendocrine component         Well-differentiated NET, Grade 1 Ki- 67 < 3%, MI < 2/10 HPF, Grade 2 Ki- 67 3-20, MI 2-20/10 HPF       Adenoma         Well-differentiated NET, Grade 1 Ki- 67 < 3%, MI < 2/10 HPF, Grade 2 Ki- 67 3-20, MI 2-20/10 HPF       Adenocarcinoma, signet ring cell carcinoma, mucinous neoplasm         NEC (small/large cell)       Adenocarcinoma, squamous cell carcinoma, acinar cell carcinoma, adenosquamous carcinoma, mucinous carcinoma, signet ring cell carcinoma		

HPF: High power field; MI: Mitotic index; NEC: Neuroendocrine carcinoma; NET: Neuroendocrine tumor.

Evidence on MiNEN treatment is very limited, and guidelines[18] often extrapolate data from neuroendocrine and non-neuroendocrine space. In most institutions, when a poorly differentiated neuroendocrine component is present, the etoposide/platinum regimen is recommended; on the other hand, when the non-neuroendocrine component is the most aggressive one, 5-FU-based combinations are preferred[19]. Whether etoposide/platinum combination is the most effective option for the upfront treatment of high-grade NENs has been recently questioned[20], and prospective evidence, possibly generated by using innovative clinical trial designs<sup>[21]</sup>, is needed to guide the management of patients with MiNEN.

#### CONCLUSION

The frequency of MiNENs appears very low at present, but future changes to the WHO classification as well as improved recognition of these entities among both pathologists and clinicians might change the epidemiology of the disease, allowing a better understanding of their biology, natural history and clinical management. While the need of the hour is how we exactly define MiNENs, questing for high-level evidence through collaborative studies will certainly be instrumental to improve patients' outcomes.

#### FOOTNOTES

Author contributions: Cives M, Porta C and Palmirotta R contributed to this paper; Palmirotta R designed the overall concept and outline



of the manuscript; Cives M and Palmirotta R contributed to the discussion and design of the manuscript; Cives M, Porta C and Palmirotta R contributed to the writing and editing of the manuscript, and review of literature.

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EDITORIAL

## Is nutritional status a new indicator to use in clinical practice for colorectal cancer patients?

Rossana Berardi, Rebecca Chiariotti, Giulia Mentrasti

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#### Abstract

In this editorial we comment on the interesting article by Liu *et al*. The topic of discussion is the need for a cost-effective and easy-to-use scoring system for predicting the prognosis of colorectal cancer patients. In this context, nutritional assessment plays a crucial role in the multimodal evaluation of patients. In particular, the controlling nutritional status score was found to be an effective tool in the clinical decision-making process, in order to customize treatment strategies and to improve patient outcomes.

Key Words: Controlling nutritional status score; Colorectal cancer; Nutritional status; Clinical outcome; Nutritional biomarkers; Tailored-medicine; Personalized therapies

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Core Tip: The controlling nutritional status (CONUT) score is significantly associated with the prognosis of colorectal cancer patients, as supported by a large body of literature. Compared with other nutritional scores, the CONUT score may be introduced in clinical practice as an optimal prognostic nutritional index to predict patient outcome.

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#### INTRODUCTION

Colorectal cancer (CRC) represents a significant global health and financial burden, and is currently ranked the third most common cancer in the world and the second leading cause of cancer-related death[1] in both sexes. Over a million new cases of CRC have been diagnosed globally every year in the past decade[2].

Cancer patients usually experience malnutrition and weight loss, especially those with gastrointestinal tumors. Previous studies have shown that malnutrition and cachexia are responsible for 20% of cancer-related deaths, rather than cancer itself[3].

Malnutrition is linked to an increased risk of postoperative complications and to prolonged hospitalization, with a considerable burden in terms of health care costs[4]. Besides, a compromised nutritional status reduces patient's tolerance to radiation and chemotherapy, resulting in a poor response to treatment and worse prognosis[5]. Thus, nutritional assessment of CRC patients should become a part of routine clinical practice to determine its impact on treatment efficacy and survival[6,7].

Patients with good nutritional status at diagnosis and during treatments are expected to have a better quality of life and longer survival[8], but it has also been postulated that nutritional status may impact the activity of immune cells against cancer in patients receiving treatments with chemotherapy, targeted therapy or immune checkpoint inhibitors (ICIs)[4]. The matter of discussion is how systemic inflammation and body composition (BC) influence prognosis, and the identification of nutritional and immunological signatures able to predict clinical outcome and response to therapies, with the aim of better stratification of patients and personalized treatments.

#### Systemic inflammation status

Tumor growth has been essentially linked to cancer-associated systemic inflammatory response. A consistent body of literature has identified several circulating inflammatory indicators as potentially helpful for prognosis prediction. Serum markers associated with inflammation can be divided into two categories: Upregulated in disease progression (neutrophils, platelets, monocytes, and C-reactive protein), and downregulated in disease progression (lymphocytes and albumin). Their combination can be used as inflammation-related markers.

In this regard, Yamamoto *et al*[9] reviewed the prognostic impact of inflammation-related markers in CRC and their use in clinical practice.

They divided the markers into five groups: Neutrophil-related markers, albumin-related markers, monocyte-related markers, C-reactive protein-related markers[10] and platelet-related markers. The most relevant in CRC are reported in the Table 1.

#### Nutritional status and body composition

In the issue of the *World Journal of Gastrointestinal Oncology* Liu *et al*[6], published a valuable paper. This case control study highlights the role of preoperative nutritional status as an independent prognostic factor to predict the outcome of CRC patients who underwent potentially curative resection. In particular, the study addresses the role of the Controlling Nutritional Status (CONUT) score, an immune-nutritional screening tool based on serum albumin, total cholesterol, and lymphocyte count, in predicting CRC patients' prognosis[11]. According to the study, a pre-operative CONUT score  $\geq$  5, characterizing patients with moderate or severe malnutrition, was independently associated with poorer overall survival (OS) and relapse-free survival (RFS) compared to those with a CONUT score  $\leq$  4, who showed significantly longer RFS and OS (Table 2).

Recent studies have confirmed that the CONUT score is an easy-to-use parameter to prognosticate cancer response during treatment[12-14]. A review published by Chen *et al*[7] including 62 studies involving a total of 25224 patients showed the value of the CONUT score, assessed before surgical or medical treatment. A high CONUT was correlated with shorter OS, cancer-specific survival, progression and recurrence-free survival, disease-free survival and a higher incidence of postoperative complications and mortality.

#### WHAT IS INNOVATIVE ABOUT CONUT COMPARED TO OTHER SCORES?

The CONUT score is a cost-effective immuno-metabolic tool evaluated from three peripheral blood parameters routinely assessed in clinical practice. Compared to the abovementioned biomarkers, derived from a maximum of two serum markers, the CONUT score provides a more comprehensive representation of both the nutritional and immunological status of patients[14].

Albumin, the main component of serum proteins, is highly correlated with body cell mass and inflammation. The presence of an ongoing inflammatory response contributes to sarcopenia, with repercussions on patients' prognosis[15]. The albumin level reflects nutritional and metabolic status in cancer patients.

Lymphopenia is independently associated with poorer survival outcomes in cancer patients, as the lymphocyte count suggests the grade of immunological and systemic inflammatory response in these patients[16,17].

The neutrophil-to-lymphocyte ratio (NLR) describes tumor inflammation. According to many studies, a high NLR is linked to poor survival in different solid tumors, including colon cancer[18,19].

Lymphocytes and the NLR play a crucial role in cancer immune evasion and surveillance, in addition to the tumor microenvironment, and this seems to be related to response to immunotherapy[20].

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#### Table 1 Most frequently reported inflammation-related biomarkers for the prediction of prognosis in colorectal cancer patients as shown in previous reports[9]

Inflammation-related biomarkers			
Neutrophil-related markers	NLR: Low NLR was related to better CSS and DFS, with different cut-off values depending on the study: The smallest was 2, while the largest was 5		
Albumin-related markers	GPS that includes serum CRP levels and serum albumin levels: High GPS indicated systemic inflammation (elevated CRP) and low nutritional state (hypoalbuminemia), that was associated with lower CSS and DFS		
Monocyte-related markers	Monocyte count: Elevated monocyte count was significantly associated with poor OS and DFS, with variable cut off values depending on the study. LMR: Low LMR was independently associated with worse OS and DFS. The cutoff value depended on the study		
C-reactive protein-related markers	CAR: Elevated CAR was significantly associated with worse OS and RFS in patients who underwent curative resection. The cutoff value varied between 0.025 and 0.22 according to the study. LCR: Low LCR (cut off between 12980 and 6000 depending on the study) was most significantly and independently correlated with worse OS and DFS. CLR: Was reported as an independent and significant indicator of poor long-term outcomes in patients with CRCm after hepatic resection, with a cutoff level of $62.8 \times 10^{-6}$ [10]		
Platelet-related markers	PLR: High PLT reflects both an increase in PLT count and a decrease in lymphocyte count and was negatively related to OS in previous reports on colorectal cancer. The cutoff value varied among studies from 150 to 246.36		

CSS: Cancer-specific survival; DFS: Disease-free survival; GPS: Glasgow prognostic score; CRP: C-reactive protein; OS: Overall survival; LMR: Lymphocyte-monocyte ratio; CAR: C-reactive protein-albumin ratio; LCR: Lymphocyte-C-reactive protein ratio; CLR: C-reactive protein-lymphocyte ratio; CRCm: Metastatic colorectal cancer; PLR: Platelet-lymphocyte ratio; PLT: Platelet.

Table 2 Definition of controlling nutritional status score				
Variable	Normal	Light	Moderate	Severe
Albumin (g/dL)	3.5-4.5	3.0-3.49	2.5-2.9	< 2.5
Albumin score	0	2	4	6
Total lymphocyte count (mm <sup>3</sup> )	≥ 1600	1200-1599	800-1199	< 800
Total lymphocyte count score	0	1	2	3
Total cholesterol (mg/dL)	< 180	140-180	100-139	< 100
Total cholesterol score	0	1	2	3
CONUT score	0-1	2-4	5-8	9-12
Assessment	Normal	Light	Moderate	Severe

Low controlling nutritional status (CONUT) score includes: Normal (0-1) and light (2-4) subgroups. High CONUT score includes: Moderate (5-8) and severe (9-12) subgroups[6]. CONUT: Controlling nutritional status.

With regard to the CONUT score, high serum cholesterol levels have been shown to enhance the anticancer activity of natural killer cells in mice[21], and in solid cancers treated with ICIs, high cholesterol has been demonstrated to correlate with better clinical outcomes<sup>[22]</sup>.

Another element worth mentioning is the relationship between the CONUT score and BC.

In the study of Liu *et al*[6], no significant association was observed between body mass index (BMI) and the CONUT score. BMI is a crude measure, does not adequately discriminate the percentage of fat-free mass and does not rule out sarcopenia in cancer patients.

By contrast, in their study an inverse correlation between the CONUT score and skeletal muscle mass index (SMI) was shown (Liu et al[6], Figure 4C). The incidence of sarcopenia was higher in the high CONUT group. Moreover, comparing the time-dependent curves of CONUT + tumor-node-metastasis (TNM) stage and SMI + TNM stage, they showed concordance in both 3-year OS (Liu et al[6], Figure 4A) and 3-year RFS (Liu et al[6], Figure 4B), suggesting that the CONUT score is as reliable as SMI in predicting the postoperative prognosis of CRC. This association likely relies on both the CONUT score and SMI reflecting the body protein reserves.

#### **KEY POINTS**

The SMI was obtained by dividing the skeletal muscle area (SMA) (cm<sup>2</sup>) by the square of height (m). The SMA was evaluated in a cross-section of the third lumbar vertebrae on CT, by measuring the areas of psoas major, paraspinal



muscles, transverse abdominis, external oblique, internal oblique, and rectus abdominis muscles. Sarcopenia was defined as SMI < 40.8  $(cm^2/m^2)$  in men and SMI < 34.9  $(cm^2/m^2)$  in women.

Sarcopenia is a multifactorial condition that is frequently seen in cancer patients. It is characterized by a degenerative and systemic loss of skeletal muscle mass (SMM) and function[23].

Previous studies have demonstrated that a decreased SMM in cancer patients, as well as proven sarcopenia/cachexia, have negative effects on response to treatments, both in surgical and oncological treatments [24,25].

In addition, a SMM assessed by CT seems to be associated with increased chemotherapy and radiotherapy toxicity[26].

Several studies in advanced tumors treated with ICIs have confirmed the key prognostic role of SMM and the importance of patients' assessment, at baseline and during treatment, to actively assess the efficacy and tolerance of immunotherapy[27].

One of the potential limitations of the paper written by Liu *et al*[6] is that the authors focused on the CONUT score, neglecting other nutritional markers, such as the NLR, Glasgow prognostic score (GPS/modified GPS, (mGPS)) and prognostic nutritional index, which have been largely validated in previous studies[9]. However, their choice to focus on the CONUT score could be justified considering that it represents a more comprehensive prognostic indicator, as it combines nutritional parameters (albumin, and cholesterol) with immunologic status (including lymphocyte count), whose interplay validated by a body of literature, is significant in prognosis[7].

Nutritional assessment has an essential role in gastrointestinal tumors, particularly in CRC, that has generally a low survival rate due to its high prevalence, delayed diagnosis and elevated rate of local recurrence or metastasis, despite continuous therapeutic progress.

A multidisciplinary team-based approach has improved clinical outcomes, but substantial disparities between patients are still often observed in terms of disease presentation, response to treatments and prognosis. Therefore, it is necessary to identify new biological indicators to improve the accuracy of prognostic prediction and patient outcome[25,28].

In this context, nutritional evaluation could have a key role, representing a cost-effective and modifiable chance of therapeutic intervention for clinicians. In fact, various effective nutritional assessment tools have already been described, especially in the pre-operative setting, but there is no gold standard and they have not been routinely implemented in clinical practice[29,30].

Shan et al<sup>[25]</sup> suggested a prognostic model based on multiple parameters such as psoas muscle index in stage II-III CRC patients, highlighting how the presence of sarcopenia before adjuvant chemotherapy affects RFS and OS[25].

A recent study by Wang et al[31] including 5014 CRC patients indicated white blood cells, neutrophils, monocytes, eosinophils, alkaline phosphatase, and lactate dehydrogenase levels as additional indicators to be included in the CONUT scoring system, to provide a more accurate assessment of the clinical prognosis for patients with CRC.

Considering the concordance between the CONUT score and SMI, both resonating with TNM staging in CRC patients undergoing surgery, the two indicators could be combined in an innovative prognostic index to better stratify patients before and during treatments. In this regard, in the pre- and post-operative setting it could help in selecting patients with an increased risk of relapse, who would benefit from a more intensive adjuvant and neo-adjuvant treatment, from those who do not require oncological therapy after curative resection. The role of the CONUT score together with TNM stage in predicting the risk of relapse in the study by Liu et al[6], suggests that the data recently observed on circulating tumor DNA in the adjuvant setting of CRC could be replicated with nutritional and metabolic tools in the future[32].

Therefore, in the era of immuno-oncology a new body of research is attempting to clarify the mechanism of resistance to immunotherapy in proficient mismatch repair CRC patients to enhance sensitivity to ICIs[8]. Ongoing clinical trials are focusing on this matter especially in the peri-operative setting[32]. Given its immune-metabolic dimension and the relationship to immunotherapy outcome[33], the CONUT score could also be considered in this setting as a stratification factor to evaluate patients.

#### CONCLUSION

The role of the CONUT score, as an independent prognostic factor in patients undergoing surgery for CRC and in advanced disease, is well established. Based on the abovementioned evidence and the valuable findings of Liu et al[6], use of the CONUT score should also be encouraged and considered in clinical practice due to its affordability[34]. Further studies are needed to validate the relevance of this promising score in the clinical decision-making process, and to suggest when early nutritional interventions are indicated; thus, implementing personalized oncology from a supportive care perspective[8].

#### FOOTNOTES

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EDITORIAL

### Gene targets with therapeutic potential in hepatocellular carcinoma

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#### Abstract

Hepatocellular carcinoma (HCC) is the third leading cause of cancer-related deaths worldwide. Major treatments include liver transplantation, resection, and chemotherapy, but the 5-year recurrence rate remains high. Late diagnosis often prevents surgical intervention, contributing to poor patient survival rates. Carcinogenesis in HCC involves genetic alterations that drive the transformation of normal cells into malignant ones. Enhancer of zeste homolog 2 (EZH2), a key regulator of cell cycle progression, is frequently upregulated in HCC and is associated with advanced stages and poor prognosis, making it a potential biomarker. Additionally, signal transducer and activator of transcription 3, which binds to EZH2, affects disease staging and outcomes. Targeting EZH2 presents a promising therapeutic strategy. On the other hand, abnormal lipid metabolism is a hallmark of HCC and impacts prognosis. Fatty acid binding protein 5 is highly expressed in HCC tissues and correlates with key oncogenes, suggesting its potential as a biomarker. Other genes such as guanine monophosphate synthase, cell division cycle associated 5, and epidermal growth factor receptor provide insights into the molecular mechanisms of HCC, offering potential as biomarkers and therapeutic targets.

**Key Words:** Hepatocellular carcinoma; Enhancer of zeste homolog 2; Target genes; Biomarkers; Potential therapeutic

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**Core Tip:** Hepatocellular carcinoma (HCC) is one of the leading causes of cancer-related deaths due to late diagnosis and high recurrence rates. Key biomarkers such as enhancer of zeste homolog 2 and fatty acid binding protein 5, along with other genetic biomarkers provide insights into HCC progression and potential therapeutic targets.

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#### INTRODUCTION

Hepatocellular carcinoma (HCC) is the most common form of primary liver cancer, accounting for 80% of all cases[1,2]. HCC imposes a substantial health and economic burden worldwide, especially in Asia[3]. Moreover, HCC is the third leading cause of cancer-related deaths globally, with a 5-year survival rate around 18%[3]. In 2020, there were about 906000 new cases and 830000 deaths from HCC, with Asia bearing 80% of the global disease burden[4]. Various treatments are available for managing HCC, including transcatheter arterial chemoembolization, liver transplantation (LT) or resection, transarterial radioembolization, radiofrequency ablation, and targeted systemic chemotherapy[5]. While surgical treatment is often viewed as the standard curative option for early-stage HCC[6-8], it is not a complete solution since the majority of patients are diagnosed at a more advanced stage with poor prognoses. Despite various treatment efforts, the 5-year recurrence rate remains high at approximately 70% following surgery[9]. Consequently, there is a critical need for more effective treatments to enhance the long-term survival of HCC patients.

Indeed, HCC is prevalent and frequently linked to a poor prognosis for patients[2]. The disease's incidence and mortality rates have been rising globally, particularly in regions such as eastern and southeastern Asia and Africa[10]. Chronic infections with hepatitis B virus (HBV) and hepatitis C virus (HCV) are well-established primary contributors to liver cirrhosis and HCC. Furthermore, exposure to aflatoxin B1 and long-term alcohol abuse are notable risk factors for the development of HCC[11,12]. Despite advancements in surgical techniques that have improved overall survival (OS) rates among patients with HCC, the 5-year OS remains low at 15%, and cancer-specific survival is less than 20%[13]. This is likely because many patients are not eligible for surgical resection or LT, primarily due to late diagnosis[14]. Furthermore, the disease is marked by a significant recurrence rate, with more than 40%-70% of patients experiencing a relapse within 5 years of surgical intervention[15]. The process of cancer development is generally understood to be a multistep phenomenon, driven by the accumulation of genetic changes that activate multiple signaling pathways, and ultimately leading to the transformation of normal cells into cancerous ones[16].

Genetics plays a crucial role in understanding the structure and function of organisms and have been widely applied in clinical diagnosis, drug development, and disease prediction[17-19]. Genes that play a role in DNA replication and maintaining proper sister chromatid cohesion are crucial for cell division, and any disruptions in these processes can greatly influence the onset and progression of malignant diseases[20]. In HCC, the genes related to this condition, along with their interacting counterparts, create a network of gene interactions[21]. Several molecules in this network are integral to the development and progression of HCC. For example, genes such as signal transducer and activator of transcription 3 (STAT3) and centrosomal protein of 55 kDa (CEP55) are involved in cell migration and invasion[22,23]. Additionally, EZH2, the catalytic subunit of polycomb repressive complex 2, is functionally associated with cell cycle regulation. Abnormal regulation of EZH2 can accelerate cell proliferation and extend cell survival, which may contribute to the onset and progression of cancer[24]. Study indicates that EZH2 is overexpressed in other cancers, including breast and prostate cancers, and its presence is linked to advanced disease and unfavorable outcomes[25].

The correlation between EZH2 and lymph node metastasis is more pronounced in EZH2-expressing tumor cells within lymph nodes compared to their matched primary tumor cells[25]. This suggests that elevated EZH2 expression is linked to higher tumor grade and increased likelihood of lymph node metastasis[25]. EZH2 also interacts with CEP55, worsening the prognosis in HCC[22]. Moreover, STAT3 causes carcinogenesis by binding to and being activated by EZH2 [26,27]. STAT3 and EZH2 are both promising molecular biomarkers for tumor progression and are associated with poor prognosis[25]. Their activation shows a strong correlation with tumor-node-metastasis (TNM) stage and patient survival, indicating that the combined expression of STAT3 and EZH2 may aid in determining the clinical TNM stage and predicting disease outcomes. STAT3 can be downregulated by EZH2 knockdown, making EZH2 a potential therapeutic target and biomarker for HCC diagnosis and prognosis[25].

Given the liver's crucial role in lipid metabolism, including the synthesis of most of the body's cholesterol and fatty acids[28,29], disrupted lipid metabolism is a key feature of metabolic reprogramming in HCC and significantly impacts its prognosis[30]. In HCC, this disruption is characterized by alterations in lipid oxidation processes, increased cholesterol esterification, elevated endogenous lipid synthesis, and changes in lipid uptake and efflux[30]. These changes closely correlate with tumor survival, growth, proliferation, and metastasis[30]. It is notable that FABP5 is highly expressed in human HCC tissues and cell lines compared with normal liver tissues and hepatocytes. FABP5, a specific isoform of FABPs, binds various long-chain fatty acids and retinoids. It is involved in transporting lipids to cellular compartments for membrane synthesis, storage, trafficking, and transcriptional regulation[31,32]. FABP5 increases the activity of the nuclear receptor peroxisome proliferator-activated receptor  $\beta/\delta$ , which drives cell migration, growth, and survival, thus

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displaying tumor-promoting properties[33]. High FABP5 expression correlates with cancer hallmarks and oncogenes such as polo like kinase 1 and baculoviral IAP repeat containing, which are master regulators in cell cycle progression and inhibition of cell death[32]. Positive FABP5 expression is associated with worse prognoses and higher recurrence rates[32]. Together, these data strongly suggest that both EZH2 and FABP5 may be useful as markers and novel therapeutic targets for treating HCC, providing valuable insights for potential therapeutic development.

#### OTHER POTENTIAL THERAPEUTIC GENE TARGET FOR HCC

The pathomechanism of liver cancer involves a complex interplay of various risk factors, including race, age, HBV, and HCV, which all contribute to abnormal gene expression linked to the onset and progression of HCC. Current research is focused on identifying key genes crucial for the initiation as well as the progression of HCC as a potential treatment strategy. With the advancement of genomics, numerous gene sequencing data have been stored in public databases, providing valuable resources for bioinformatic mining of gene expression profiles related to cancer[34]. In 2017, Zhang et al[35] identified key genes and pathways related to HCC through bioinformatic analysis of differentially expressed genes (DEGs) between HCC samples and normal samples. In HCC, 10 deregulated genes include: KRAS proto-oncogene, GTPase (KRAS), epidermal growth factor receptor (EGFR), B-cell lymphoma 2, acetyl-CoA carboxylase alpha, cluster of differentiation 8A, guanine monophosphate synthase (GMPS), transforming growth factor beta 1, STAT3, human epidermal growth factor receptor 2. Among these, albumin combined with bilirubin (albumin-bilirubin grade) displayed higher prognostic value. GMPS, essential for the synthesis of purines, has been recognized as a significant target for repression by p53, and its upregulation disrupts the tumor-suppressive p53 network in liver cancer, making GMPS a potential therapeutic target. EGFR overexpression contributes to HCC progression by enhancing cell proliferation, migration, and invasion, establishing it as an effective drug target and prognostic biomarker.

On the other hand, in 2021, Li and Xu<sup>[36]</sup> identified six genes that serve as potential therapeutic targets for HCC. Among these, cell division cycle associated 5 (CDCA5) plays a crucial role in the accurate separation of sister chromatids during the S and G2/M phases of the cell cycle[37,38]. Overexpression of CDCA5 has been clinically associated with a poor prognosis in HCC patients<sup>[39]</sup>. Opa interacting protein 5 (OIP5) regulates HCC growth and metastasis through the AKT/mammalian target of rapamycin signaling pathways<sup>[40]</sup>. DNA topoisomerase 2 alpha (TOP2A) is highly expressed in HCC tumors and is associated with shorter patient survival and increased resistance to chemotherapy[41]. Protein regulator of cytokinesis 1 (PRC1) overexpression enhances chemoresistance and inhibits apoptosis in HCC patients undergoing chemotherapy[42]. Abnormal spindle-like microcephaly-associated protein (ASPM) overexpression serves as a marker for increased metastatic potential and poor prognosis in HCC[43]. Additionally, nucleolar and spindleassociated protein 1 (NUSAP1) overexpression is associated with significantly lower survival rates in patients with HCC [44], with microRNA 193a-5p implicated in hepatocarcinogenesis suppression by regulating NUSAP1 Levels. Cyclin A2 (CCNA2) and kinesin family member 20A (KIF20A) also demonstrate elevated expression levels in HCC tissues compared to normal tissues[45].

In 2018, Hu et al [46] identified 56 upregulated and 8 downregulated DEGs in HCC. Their analysis revealed significant enrichment of genes involved in cell cycle arrest, transcription regulation, protein amino acid phosphorylation, cell cycle, and apoptosis. They proposed JUN, early growth response protein 1 (EGR1), MYC, and cyclin-dependent kinase inhibitor 1A (CDKN1A) as potential diagnostic and therapeutic molecular biomarkers for HCC. c-JUN prevents apoptosis by antagonizing p53 activity, contributing to early-stage HCC[47]. EGR1 contributes to HCC radio resistance by upregulating autophagy-related 4B, yet paradoxically, its upregulation by beta-lapachone inhibits hepatoma cell progression and metastasis[48]. MYC controls various cellular processes, including cell cycle progression, proliferation, and apoptosis, with miR-320a acting as a tumor suppressor by targeting MYC in HCC[49]. CDKN1A, a prominent cell cycle inhibitor, arrests cell cycle progression at the G1/S and G2/M transitions by blocking the activity of CDK4/6-cyclin D and CDK2cyclin E complexes[28,50]. In summary, ongoing research continues to uncover crucial genes and pathways involved in HCC, offering new insights into potential therapeutic targets and prognostic biomarkers.

#### CONCLUSION

In conclusion, both EZH2 and FABP5 serve as biomarkers for poor outcomes in HCC and show potential as therapeutic targets for patients with this disease. Additionally, other markers such as GMPS, CDCA5, EGFR, OIP5, TOP2A, PRC1, ASPM, NUSAP1, CCNA2, JUN, EGR1, MYC, and CDKN1A contribute to a detailed understanding of the molecular mechanisms underlying HCC occurrence and progression. These molecules hold promise as both biomarkers and therapeutic targets.

#### FOOTNOTES

Author contributions: Shodry S wrote the original manuscript; Hasan YTN and Ahdi IR supervised the project; Ulhaq ZS conceived the study, wrote the original draft and revised the manuscript, and supervised the study; Ulhaq ZS was the main contributor to this manuscript.

Conflict-of-interest statement: The authors have no conflicts of interest to declare.



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EDITORIAL

## Estimating prognosis of gastric neuroendocrine neoplasms using machine learning: A step towards precision medicine

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#### Abstract

Survival rates following radical surgery for gastric neuroendocrine neoplasms (g-NENs) are low, with high recurrence rates. This fact impacts patient prognosis and complicates postoperative management. Traditional prognostic models, including the Cox proportional hazards (CoxPH) model, have shown limited predictive power for postoperative survival in gastrointestinal neuroectodermal tumor patients. Machine learning methods offer a unique opportunity to analyze complex relationships within datasets, providing tools and methodologies to assess large volumes of high-dimensional, multimodal data generated by biological sciences. These methods show promise in predicting outcomes across various medical disciplines. In the context of g-NENs, utilizing machine learning to predict survival outcomes holds potential for personalized postoperative management strategies. This editorial reviews a study exploring the advantages and effectiveness of the random survival forest (RSF) model, using the lymph node ratio (LNR), in predicting disease-specific survival (DSS) in postoperative g-NEN patients stratified into low-risk and high-risk groups. The findings demonstrate that the RSF model, incorporating LNR, outperformed the CoxPH model in predicting DSS and constitutes an important step towards precision medicine.

Key Words: Machine learning; Artificial intelligence; Gastric neuroendocrine neoplasm; Random survival forest model; Disease-specific survival

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**Core Tip:** Liu *et al*'s study addresses a critical issue in determining the postoperative prognosis of gastric neuroendocrine tumors by identifying the significance of lymph node ratio. Moreover, the random survival forest model, a machine-learning approach, surpasses traditional Cox proportional hazards models by enhancing predictive accuracy, clinical utility, and overall performance. This model's ability to stratify patient risks and personalize survival predictions can aid in formulating targeted postoperative strategies, thus realizing an important aspect of personalized "precision medicine".

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#### INTRODUCTION

Liu et al[1] published a study titled "Combining lymph node ratio to develop prognostic models for postoperative gastric neuroendocrine neoplasm patients". Their study utilized machine learning techniques to identify risk factors associated with disease-specific survival (DSS) in postoperative gastric neuroendocrine neoplasm (g-NEN) patients, and succeeded in constructing an efficient and precise prognostic model based on lymph node ratio (LNR), defined as the ratio of the number of positive lymph nodes to the number examined. It also shows off one of the most promising features of artificial intelligence or machine learning, its capacity to identify patterns from multidimensional data sets such as those found in medicine. They researched a field that is in sore need of a reliable prognostic model to guide postoperative management. g-NENs represent a rare and challenging type of gastric malignancy in oncology. These neoplasms are classified into three types: Well-differentiated neuroendocrine tumors (NETs), poorly differentiated neuroendocrine carcinomas (NEC), and mixed neuroendocrine-non-NETs. While gastric NETs typically exhibit an indolent growth pattern and are often benign, gastric NECs (g-NECs) are highly malignant, aggressive, and associated with a poor prognosis[2], showing lower postoperative survival rates and higher recurrence rates[3,4]. Currently, there are no highly effective treatment options for NENs. Various clinical characteristics significantly influence the prognosis of NEN patients [5-7]. In resected g-NECs, the presence of more than two metastatic lymph nodes, metastatic disease in over 10% of resected lymph nodes, and involvement of station 2 lymph nodes have all been demonstrated as significant prognostic indicators associated with poorer outcomes[8]. Due to its incorporation of the number of lymph nodes examined during surgery, LNR turns out to be a more advantageous parameter for prognostic estimation in such patients. Indeed, many studies have shown that the prognostic value of LNR exceeds that of the absolute number of involved lymph nodes[9] for various types of cancer. The present editorial explores the promise of machine learning as a pathway toward precision medicine, particularly in its capacity to predict postoperative outcomes for NEN patients. The advent of such artificial intelligence techniques offers unique opportunities to identify subtle patterns and factors that traditional prognostic methods might overlook[10,11].

#### MACHINE LEARNING IN G-NEN RESEARCH

Machine learning models can analyze complex relationships within datasets and has shown promise in predicting various medical outcomes[10]. In the context of g-NENs, machine learning has the potential to predict postoperative prognosis and tailor personalized postoperative management strategies.

Traditionally, predictive models such as the Cox proportional hazards (CoxPH) model have been employed [12,13]. However, their limitations have spurred the exploration of innovative approaches[11,14]. Liu et al's study critically compared the performance of the random survival forest (RSF) and CoxPH models in predicting DSS for patients after g-NEN surgery[1]. This greater certainty regarding outcomes allow physicians to tailor the postoperative management strategies for their patients, avoiding the pitfalls and discomfort that can be inherent to end-of-life treatment.

Inspired by a comprehensive cohort consisting of 286 patients from the Surveillance, Epidemiology, and End Results (SEER) database and 92 g-NEN patients from the First Affiliated Hospital of Soochow University, Liu et al[1] constructed a RSF model using 14 key features. These features encompass demographic, clinicopathologic, and tumor-specific factors. The RSF model underwent rigorous evaluation in terms of discrimination, calibration, clinical utility, and overall performance, and its performance was compared with that of traditional models.

This study analyzed data from 7685 patients in the SEER database from 2000 to 2019, of which 286 met the inclusion criteria. Included patients had primary g-NEN, underwent curative surgery, and had complete pathological information. The exclusion criteria (n = 7399) included: (1) Cases without histopathological evidence; (2) History of other malignancies; (3) Cases lacking detailed clinical data such as differentiation grade, tumor size, or tumor node metastasis (TNM) stage; (4) Cases without information on survival duration or those who died within one month; (5) Cases that did not undergo surgery or had only local surgery; and (6) Cases without information on the number of examined lymph nodes and positive lymph nodes. Patients from the SEER database were randomly divided into a training set and an internal validation set at a ratio of 8:2. The external test cohort consisted of 92 patients from the First Affiliated Hospital of Soochow University, covering the period from 2011 to 2020.





Figure 1 Construction of random survival forest model and Cox proportional hazards model. g-NEN: Gastric neuroendocrine neoplasm; AJCC: American Joint Committee on Cancer; LNR: Lymph node ratio; C-index: Concordance Index; AUC: Area under the curve; DCA: Decision curve analysis; RSF: Random survival forest; CoxPH: Cox proportional hazards.

Both RSF and CoxPH models were constructed. For the CoxPH model, univariate and multivariate regression analyses identified primary site, histologic type, size, M stage, and LNR as independent risk factors. These selected independent risk factors were then used to develop the CoxPH model, which was visualized using a nomogram. The RSF model, utilizing random forest techniques such as feature and sample bootstrapping, demonstrated faster training times and reduced estimation bias. This model was built using 14 factors: Sex, age at diagnosis, race, marital status, primary site, differentiation grade, tumor size, American Joint Committee on Cancer (AJCC) T stage, AJCC N stage, AJCC M stage, LNR, surgery at the primary site, radiotherapy, and chemotherapy. Optuna was used to determine the optimal hyperparameters for the RSF model: 330 estimators, a minimum of 5 samples per split, and a minimum of 1 sample per leaf. Shapley additive explanations (SHAP) plots were used to interpret the RSF model. Patients were then assigned risk scores and divided into low-risk, medium-risk, and high-risk groups, providing valuable insights for identifying highrisk populations and facilitating timely clinical interventions. Kaplan-Meier analysis confirmed the stratification for all cohorts (P < 0.0001) (Figure 1). Additionally, individualized survival predictions were made, allowing for a clear prediction of the impact of all admission variables on each patient's prognosis.

The performance of the 8<sup>th</sup> edition AJCC TNM staging system, CoxPH model, and RSF model was evaluated using the C-index, areas under the receiver operating characteristic curves (AUCs), calibration curves, and decision curve analysis (DCA). The RSF model was further interpreted using SHAP values. In an external test set, the RSF model outperformed the 8th AJCC TNM staging system and the CoxPH model, with C-index values of 0.769, 0.744, and 0.723, respectively.

The 1-, 3-, and 5-year AUCs for the 8th AJCC TNM staging system were 0.690, 0.769, and 0.770, respectively. For the CoxPH model, the AUCs were 0.786, 0.834, and 0.810. The RSF model achieved AUCs of 0.803, 0.895, and 0.869 at 1, 3, and 5 years, respectively. DCA indicated that the RSF model had a higher net benefit compared to the other models (Table 1).

SHAP analysis indicated that histologic type was the most significant variable in the RSF model, followed by LNR, T stage, and M stage. Elevated LNR levels were linked to worse patient outcomes.

The study's limitations include selection bias from its retrospective design and the SEER database's primary focus on the United States population, which may not generalize to Asian, especially Chinese, populations. Additionally, the lack of multi-center external validation reduces the robustness of the findings.

In the study by Song *et al*[12], a survival nomogram for g-NECs was constructed. Yang *et al*[15] developed a prognostic nomogram for g-NEN patients using computed tomography radiomic features. However, both studies failed to demonstrate that LNR is an independent risk factor. Padwal et al[16] and Jiang et al[17] employed machine learning to build prognostic models for pancreatic NEN patients, while Liu et al[1] were the first to use a random forest survival model for g-NENs. This study, through multivariable regression analysis, identified LNR as an independent risk factor, providing higher statistical power and significance.

#### CONCLUSION

The RSF model has become a key tool for precise postoperative prognostic estimation and optimized management of g-NENs, showing advantages over traditional models. Its capability to stratify risks and predict individual survival marks a new era of personalized prediction and optimized prognostic strategies. Artificial intelligence, particularly machine learning algorithms, holds great promise in transforming the diagnosis, treatment, and prognosis of gastric diseases by analyzing extensive medical data to identify patterns and anomalies. We predict that artificial intelligence's role in personalized, prognosis-based management in gastric diseases will be crucial, aiding healthcare professionals in selecting



#### Table 1 Performance of the Cox proportional hazards model and the random survival forest model

Madal	Cohort	C-index	AUC		
wodei			1-year	3-year	5-year
CoxPH	Training	0.834 (0.789-0.879)	0.848 (0.763-0.930)	0.881 (0.831-0.932)	0.875 (0.822-0.927)
	Internal	0.871 (0.802-0.940)	0.843 (0.717-0.969)	0.948 (0.892-1.000)	0.990 (0.969-1.000)
	External	0.744 (0.665-0.822)	0.786 (0.622-0.889)	0.834 (0.735-0.934)	0.810 (0.688-0.931)
RSF	Training	0.940 (0.924-0.956)	0.962 (0.938-0.989)	0.979 (0.963-0.995)	0.971 (0.951-0.992)
	Internal	0.870 (0.818-0.921)	0.867 (0.761-0.973)	0.955 (0.899-1.000)	0.986 (0.960-1.000)
	External	0.769 (0.691-0.846)	0.803 (0.608-0.891)	0.895 (0.814-0.976)	0.869 (0.769-0.970)

CoxPH: Cox proportional hazards; RSF: Random survival forest; AUC: Area under receiver operating characteristic curve; C-index: Concordance Index.

the right intervention for each patient. The RSF model is expected to redefine g-NEN prognosis and guide more precise, individualized patient management.

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#### FOOTNOTES

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EDITORIAL

## Exploring Xiaojianzhong decoction's potential in gastric cancer treatment: Integrative insights and experimental validation

Chun-Han Cheng, Wen-Rui Hao, Tzu-Hurng Cheng

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#### Abstract

Gastric cancer (GC) remains a formidable global health concern with significant morbidity and mortality rates, despite the fact that numerous advances have been made to improve conventional therapies. Xiaojianzhong decoction (XJZ), a traditional Chinese medicine, has garnered academic attention as a multicomponent, multitarget approach to managing GC. The present editorial explores the potential of XJZ in the treatment of GC through a comprehensive analysis of network pharmacology and experimental validation. Network pharmacology was used to identify key molecular targets of XJZ, including interleukin 6, prostaglandin-endoperoxide synthase 2, and matrix metalloproteinase 9, and in vitro experiments were used to confirm the efficacy of XJZ in inhibiting cell proliferation, inducing apoptosis, and modulating gene expression associated with GC progression. This editorial highlights XJZ as a promising therapeutic strategy for GC and indicates a need for further clinical exploration and validation of its efficacy.

Key Words: Xiaojianzhong decoction; Gastric cancer; Network pharmacology; Traditional Chinese medicine; Experimental validation

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**Core Tip:** This editorial integrates network pharmacology insights with rigorous experimental validation to highlight the potential of Xiaojianzhong decoction as a multifaceted therapeutic approach for gastric cancer.

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#### INTRODUCTION

Gastric cancer (GC) remains a formidable global health challenge because of its high morbidity and mortality rates. The effectiveness of conventional treatments, such as those involving surgery, chemotherapy, and molecular targeting agents, is often limited because of the treatments' severe adverse effects and the emergence of drug resistance. Consequently, traditional Chinese medicine (TCM) has increasingly gained attention as a complementary approach to managing GC; it offers a holistic approach to treatment that contrasts with the reductionist approach of conventional medicine. In TCM, health and disease are viewed through the lens of syndrome differentiation, which involves identifying patterns of disharmony within the body's organ systems. In the context of GC, relevant TCM syndromes include spleen qi deficiency, damp-heat in the stomach, and blood stasis. These syndromes correspond to specific symptoms and underlying imbalances that contribute to the development and progression of gastric malignancies. For example, spleen qi deficiency is characterized by symptoms such as fatigue, poor appetite, and abdominal distention, which are common in patients with GC. Spleen qi deficiency is believed to weaken the digestive system, leading to the accumulation of dampness and the subsequent development of phlegm and blood stasis, which creates an internal environment conducive to tumor growth[1].

Xiaojianzhong (XJZ) decoction, a classical TCM formulation, was reported to produce promising results in the treatment of GC[1]. XJZ is traditionally used to treat spleen qi deficiency with cold in the middle jiao, a condition that manifests as abdominal pain, loose stools, and a preference for warmth and pressure on the abdomen. XJZ comprises a synergistic combination of herbs, with each playing a unique role in restoring balance. The key ingredients of XJZ are *Bai Shao* (*Paeonia lactiflora*), *Gui Zhi* (*Cinnamonum cassia*), *Zhi Gan Cao* (*Glycyrrhiza uralensis*), *Sheng Jiang* (*Zingiber officinale*), *Da Zao* (*Ziziphus jujuba*), and *Yi Tang* (*Saccharum Granorum*)[1]. *Bai Shao* and *Gui Zhi* are the core ingredients of the formula, working together to harmonize the interior and alleviate pain by warming and nourishing the spleen and stomach. *Zhi Gan Cao* and *Sheng Jiang* support the digestive system, enhancing the body's ability to absorb nutrients and expel dampness. *Da Zao* and *Yi Tang* have nourishing and strengthening effects, replenishing the qi and blood[1].

The components of XJZ have been studied for their potential anticancer effects from a modern pharmacological perspective. *Bai Shao* was discovered to exert anti-inflammatory and antiproliferative effects, which may help inhibit the growth of gastric tumors by modulating immune responses and mitigating oxidative stress. *Gui Zhi*, known for its warming properties, was demonstrated to enhance blood circulation and reduce inflammation, potentially counteracting the hypoxic and acidic microenvironment that supports cancer cell survival. *Zhi Gan Cao*, a widely studied herb in TCM, contains glycyrrhizin, a compound that exerts anticancer activities by inducing apoptosis and inhibiting proliferation of various cancer cell lines[2].

Recent research has provided further insights into the mechanisms underlying the efficacy of XJZ in treating GC. Studies utilizing network pharmacology and experimental validation have elucidated the multicomponent, multitarget activities of this decoction. For instance, XJZ was discovered to alleviate aspirin-induced gastric mucosal injury through the phosphoinositide 3-kinase (PI3K)/AKT/mammalian target of rapamycin (mTOR)/Unc-51-like autophagy-activating kinase 1 (ULK1) pathway and the AMP-activated protein kinase/ULK1 pathway, both of which are crucial in regulating cell survival, autophagy, and metabolism[2]. This suggests that XJZ not only protects the gastric mucosa from damage but also modulates key signaling pathways involved in cancer progression. XJZ was also revealed to prevent the growth of gastric precancerous lesions by inhibiting autophagy and glycolysis – pathways often hijacked by cancer cells to support their growth under nutrient-limiting conditions – in gastric mucosal cells[3]. Moreover, the ability of the decoction to activate the p62/Keap1/nuclear factor erythroid 2-related factor 2 signaling pathway and inhibit ferroptosis underscores its potential in GC treatment[4]. Ferroptosis, a type of regulated cell death driven by iron-dependent lipid peroxidation, has been implicated in cancer development and resistance to therapy. By inhibiting this pathway, XJZ may protect cells from oxidative stress and inflammation, both of which are key drivers of gastric carcinogenesis[4].

In generally, XJZ exemplifies the holistic approach of many forms of TCM in treating complex diseases such as GC. Its traditional use for addressing spleen qi deficiency and related syndromes aligns with the modern understanding of its pharmacological activities, which include anti-inflammatory, antiproliferative, and cytoprotective effects[1,3]. These findings highlight the potential of XJZ as an adjunct to conventional GC therapies and as a multifaceted strategy that targets the disease from both a symptomatic and mechanistic standpoint. As researchers continue to explore the integration of TCM with modern medicine, formulations such as XJZ may play an increasingly pivotal role in the comprehensive management of GC[5].

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#### NETWORK PHARMACOLOGY INSIGHTS

Network pharmacology has emerged as a crucial approach for deciphering the complex mechanisms through which XJZ treats GC. By integrating computational analysis with extensive data available from databases, researchers have elucidated the active ingredients in XJZ and their molecular targets, thereby uncovering its broad therapeutic potential in treating GC. XJZ is a formulation composed of several herbs (Table 1), each of which contributes unique active compounds that collectively influence various biological pathways related to GC[1]. The key constituents of XJZ are paeoniflorin from P. lactiflora, cinnamaldehyde from C. cassia, and glycyrrhizic acid from G. uralensis. These compounds modulate critical processes such as inflammation, cell proliferation, and metastasis. Paeoniflorin inhibits the nuclear factor kappa-light-chain-enhancer of the activated B cells signaling pathway, thereby reducing inflammation and enhancing the sensitivity of GC cells to chemotherapy[6]. Cinnamaldehyde targets the PI3K/AKT signaling pathway, which is central to tumor growth and survival<sup>[2]</sup>. Glycyrrhizic acid, known for its anti-inflammatory properties, modulates the Toll-like receptor 4 pathway, thereby reducing the levels of proinflammatory cytokines and ameliorating gastric mucosal injury[4,7].

Network pharmacology studies have identified genes encoding interleukin (IL)-6, prostaglandin-endoperoxide synthase 2, matrix metalloproteinase (MMP) 9, and MMP2 as the primary targets of XJZ. IL-6, a proinflammatory and protumor cytokine, is a vital target in GC treatment. Prostaglandin-endoperoxide synthase 2 facilitates cancer progression by contributing to inflammation and angiogenesis within the tumor microenvironment[8-12]. MMP9 and MMP2 enable cancer cell invasion and metastasis by degrading extracellular matrix components [3,13]. These network pharmacological insights highlight the holistic therapeutic potential of XJZ. Unlike conventional treatments that often target single mechanisms, XJZ involves multiple targets, offering a comprehensive approach to managing GC by addressing its complexity and heterogeneity. This multitarget approach is particularly advantageous for preventing resistance and addressing the multifactorial nature of GC[1]. Moreover, the network pharmacological approach provides a deeper understanding of the interactions and pathways through which XJZ exerts its effects. This thorough analysis supports the optimization of XJZ formulations and the identification of potential biomarkers for evaluating treatment efficacy and patient responses. Network pharmacology can considerably enhance the understanding of the mechanisms of action of XJZ in GC treatment and supports its integration into contemporary GC management strategies[2,3].

#### IN VITRO EXPERIMENTAL VALIDATION

The results of *in vitro* experiments on XJZ further indicate its therapeutic potential against GC, complementing the insights gained through network pharmacological analysis. XJZ significantly inhibits the proliferation of various GC cell lines, including MKN-45, AGS, and SGC-7901, in a dose-dependent manner. These cell lines represent different subtypes and stages of GC, suggesting that the decoction exerts broad anticancer activities across different GC contexts. Control experiments were performed on normal gastric epithelial cell lines, such as GES-1, to assess the specificity and potential toxicity of the components of XJZ. The results confirmed that XJZ preferentially targets cancerous cells, indicating its potential as a selective therapeutic agent<sup>[2]</sup>. Further experiments revealed that XJZ induces apoptosis and causes cell cycle arrest at the  $G_0/G_1$  phase in GC cell lines, which is crucial for tumor suppression because it prevents cancer cells from proliferating and facilitates programmed cell death. These effects were consistently observed across the GC cell lines that were used, suggesting that the mechanisms of XJZ are not specific to a particular GC subtype[3]. Molecular assays provided deeper insights into the effects of XJZ on gene expression within GC cells. Notably, XJZ treatment resulted in the downregulation of oncogenic markers such as IL-6 and MMP9, which are associated with tumor growth, inflammation, and metastasis. Furthermore, protective factors such as heme oxygenase 1 (HMOX1) were upregulated, reflecting a shift toward a more regulated and less malignant cellular environment. HMOX1, known for its cytoprotective and antiinflammatory properties, contributes significantly to the overall anticancer effects of XJZ[4,13]. To enhance the generalizability of these findings, additional experiments were conducted on a broader range of GC cell lines, including MGC-803 and BGC-823. The consistent antiproliferative, proapoptotic, and gene regulatory effects observed across these diverse cell lines underscore the potential of XJZ as a broad-spectrum therapeutic agent against GC[14,15].

Overall, these in vitro experiments have robustly substantiated the therapeutic potential of XJZ in GC treatment. The dose-dependent inhibition of GC cell proliferation, induction of apoptosis, cell cycle arrest, and significant alterations in gene expression profiles collectively validate the multifaceted mechanisms through which XJZ exerts its anticancer effects. These findings highlight the importance of integrating experimental validation with network pharmacology to fully understand and optimize the therapeutic applications of traditional formulations such as XJZ in modern oncology [11,16].

#### IMMUNE MODULATION BY XJZ IN THE TUMOR MICROENVIRONMENT

XJZ has garnered attention for its potential to modulate the tumor microenvironment of GC. The tumor microenvironment, comprising a complex network of cancer cells, immune cells, stromal cells, and signaling molecules, plays a pivotal role in cancer progression, metastasis, and response to therapy [1,16]. In addition to exerting direct cytotoxic effects on GC cells, XJZ modulates the immune response within the tumor microenvironment, which is crucial for effective anticancer therapy [1,3]. Studies have highlighted the ability of XJZ to modulate immune responses in GC. For example, research reported that XJZ can enhance the activity of cytotoxic T lymphocytes while reducing the immunosup-



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Table 1 Key components of Xiaojianzhong decoction and their pharmacological activities in gastric cancer treatment <sup>1</sup>				
Component	Herb source	Pharmacological activity	Ref.	
Cinnamaldehyde	Cinnamomum cassia	Exhibits anti-inflammatory and antiulcer effects by modulating NF-kB and MAPK pathways. Prevents <i>Helicobacter pylori</i> infection and enhances mucosal healing	Chen et al[1], 2024; Li et al[7], 2024; Han et al[17], 2023	
Galangin	Alpinia officinarum	Protects gastric mucosa by mediating the TLR4/NF-ĸB and transient receptor potential vanilloid 1 signaling pathways, promoting healing of gastric lesions	Lin et al <mark>[12]</mark> , 2023; Lin et al[18], 2024	
Gingerol	Zingiber officinale	Possesses anti-inflammatory and antioxidant properties. Protects gastric mucosa by inhibiting lipid peroxidation and cytokine production	al-Yahya <i>et al</i> [8], 1989; Gumbarewicz <i>et al</i> [9], 2022	
Glycyrrhizin	Glycyrrhiza uralensis	Modulates immune responses, reduces oxidative stress, and prevents gastric ulcer formation, playing a role in the suppression of gastric cancer cell proliferation	Yang et al[10], 2017; Chen et al [13], 2024	
Liquiritigenin	Glycyrrhiza uralensis	Protects against gastric mucosal injury by activating the PI3K/AKT pathway. Exhibits antiulcerative and anticancer properties through antiapoptotic and anti-inflammatory mechanisms	Yang et al[10], 2017; Guo et al [11], 2024	
Paeoniflorin	Paeonia lactiflora	Inhibits multidrug resistance in gastric cancer cells by suppressing NF-κB activation. Modulates autophagy and exerts protective effects against gastric mucosal injury	Chen et al[1], 2024; Asai et al[5], 2011; Fang et al[6], 2012	
Honey	Natural source	Demonstrates gastroprotective effects through antioxidant activity. Promotes mucosal healing and reduces inflammation in gastric lesions	Chen <i>et al</i> [2], 2023; Zheng <i>et al</i> [16], 2024	

<sup>1</sup>Key components of Xiaojianzhong decoction (XJZ) and their pharmacological activities in gastric cancer treatment.

The table highlights the primary herbal components of XJZ, their active constituents, and the associated pharmacological activities that contribute to gastric cancer treatment, including modulation of key signaling pathways, inhibition of cancer cell proliferation, induction of apoptosis, and enhancement of gastric mucosal protection. The information is synthesized from studies that explore both the network pharmacology and experimental validations of XJZ in gastric cancer contexts.

pressive effects of regulatory T cells within the tumor microenvironment. This dual action not only supports the body's natural immune response against cancer cells but also helps overcome the immune evasion strategies employed by tumors[16]. Furthermore, XJZ was indicated to modulate key signaling pathways involved in immune regulation, such as the PI3K/AKT and mTOR pathways, which are critical for maintaining immune cell homeostasis and function[2]. By influencing these pathways, XJZ may strengthen the efficacy of immune-based therapies, making it a valuable adjunct to conventional treatments<sup>[1]</sup>.

Although in vitro studies have provided substantial evidence of the immunomodulatory and anticancer properties of XJZ, comprehensive *in vivo* studies are required to validate these findings. Animal models of GC can be employed to evaluate the effects of XJZ on both the immune microenvironment and tumor progression. Studies employing such models should focus on assessing the direct cytotoxic effects of XJZ on GC cells and its ability to modulate immune responses within the tumor microenvironment in a living organism[1,3]. Future research should also investigate the potential synergistic effects of XJZ when it is combined with other immunotherapies or conventional chemotherapies. Understanding the interactions between XJZ and existing treatments could pave the way for more effective and personalized therapeutic strategies for GC[15]. Overall, although XJZ has been demonstrated to act as a potent immunomodulator in the tumor microenvironment of GC, comprehensive in vivo studies are required to fully evaluate its therapeutic potential and optimize its use in clinical settings. Such research will be crucial for establishing XJZ as a cornerstone in the fight against GC and establishing its potential to improve patient outcomes through a multifaceted approach to tumor suppression.

#### CLINICAL IMPLICATIONS AND FUTURE DIRECTIONS

XJZ has received considerable recognition for its holistic anticancer effects, particularly against GC. Conventional monotherapies target specific molecular pathways; XJZ likely has higher efficacy because of the synergistic interactions among multiple bioactive compounds within the decoction (Table 1). Network pharmacology has revealed that XJZ influences a broad spectrum of molecular targets involved in GC progression, including key signaling pathways such as PI3K/AKT/mTOR and AMP-activated protein kinase/ULK1, which are critical for regulating cell proliferation, apoptosis, autophagy, and glycolysis[2,13]. This network-based interaction suggests that the therapeutic effects of XJZ are likely due to the synergistic activity of its constituents, which work together to disrupt cancer cell survival and growth more effectively than any individual component could. Furthermore, the p62/Keap1/nuclear factor erythroid 2-related factor 2 signaling pathway, which plays a prominent role in mitigating oxidative stress and ferroptosis in GC cells, is another crucial target of XJZ. The ability of XJZ to activate this pathway highlights its potential for protecting cells from



oxidative damage, which is often implicated in cancer progression[4]. This multifaceted mechanism of action reinforces the idea that XJZ exerts its anticancer effects through a network of interactions rather than through the isolated actions of individual compounds. In addition to directly targeting cancer cells, XJZ may modulate the tumor immune microenvironment, which could further enhance its anticancer efficacy. The tumor microenvironment is a complex ecosystem that comprises cancer cells, various immune cells, stromal cells, and signaling molecules. The effects of XJZ on this microenvironment, particularly through the regulation of immune responses, may contribute to its ability to suppress tumor growth and improve overall treatment outcomes[16]. By modulating immune pathways, XJZ might bolster the body's natural ability for immune surveillance and attacking cancer cells, with this involving a dual mechanism of action: Direct cytotoxicity against cancer cells and indirect immune system modulation to promote anticancer activity. Integrating network pharmacology data with experimental outcomes reveals the potential of XJZ as a complementary or alternative therapy in the management of GC. In vitro studies have robustly demonstrated the ability of XJZ to inhibit GC cell proliferation and induce apoptosis through various molecular pathways, suggesting that XJZ could effectively supplement conventional treatments by targeting multiple pathways simultaneously. This multifaceted approach may reduce side effects and overcome drug resistance[1,2,16].

However, translating these promising preclinical findings into clinical practice requires careful consideration and further research. Rigorous clinical trials must be conducted to validate the efficacy and safety of XJZ in human patients, with such trials focusing on optimal dosing regimens, pharmacokinetic profiles, and potential interactions with conventional cancer therapies to ensure therapeutic synergy without adverse effects [1,14]. Moreover, identifying biomarkers that predict patient responses to XJZ could facilitate the development of personalized treatment approaches, enabling clinicians to tailor therapies to patients' genetic and molecular profiles and thereby maximize efficacy while minimizing toxicity. Longitudinal studies are also warranted to assess the long-term effects of XJZ on patients with GC, including the potential benefits and risks associated with its prolonged use[15]. Future research should delve deeper into the precise molecular mechanisms that mediate the effects of XJZ, particularly its effects on various cellular processes and its interactions with other therapeutic agents. Elucidating these mechanisms would improve the understanding of the therapeutic potential of XJZ and guide future drug development efforts. Moreover, exploring different treatment combinations and protocols is essential to optimizing therapeutic strategies and improving patient outcomes. Although preclinical evidence strongly supports the efficacy of XJZ as a treatment for GC, substantial additional efforts are required to translate these findings into clinical practice. XJZ presents a unique opportunity for bridging TCM and modern oncology and may reshape the landscape of cancer treatment with a more personalized and comprehensive approach to GC management[1,16].

#### CONCLUSION

XJZ has a rich history in TCM and has been validated through modern scientific methodologies as a promising therapeutic option for GC. Network pharmacology has unveiled the intricate mechanisms responsible for the efficacy of XJZ, highlighting its ability to modulate critical pathways involved in GC progression. Network pharmacology has identified key molecular targets and pathways affected by XJZ, including inflammation, cell proliferation, and metastasis, which are crucial in the context of cancer<sup>[1]</sup>. Experimental validation has reinforced these findings, demonstrating the potential of XJZ to inhibit cell proliferation, induce apoptosis, and alter gene expression profiles in GC cells. Studies have indicated that XJZ can inhibit GC cell growth in a dose-dependent manner, induce cell cycle arrest at the  $G_0/G_1$  phase, and downregulate oncogenic markers such as IL-6 and MMP9 while upregulating protective factors such as HMOX1[2, 3]. Moving forward, integrating XJZ into clinical practice holds considerable potential for enhancing current GC treatment paradigms. Its multicomponent, multitarget approach addresses the limitations of conventional therapies, such as adverse side effects and drug resistance. This holistic alternative offers a more comprehensive treatment strategy by targeting multiple pathways and processes involved in cancer progression[4]. However, in-depth clinical studies are imperative to validate these preclinical findings and determine optimal dosing regimens. Rigorous clinical trials will be crucial for establishing the safety, efficacy, and pharmacokinetic profile of XJZ in human patients. Elucidating potential drug interactions and optimizing personalized treatment protocols will also be vital steps toward integrating XJZ into conventional oncological practice. In conclusion, XJZ represents a convergence of ancient wisdom and modern scientific rigor, presenting a compelling avenue for advancing personalized and integrative approaches to GC therapy. By bridging TCM and contemporary oncology, XJZ paves the way for innovative strategies that prioritize efficacy, safety, and patientcentered care in the management of GC. Such integration holds promise for improving treatment outcomes and quality of life for patients with GC, exemplifying the potential benefits of combining traditional and modern medical practices.

#### FOOTNOTES

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EDITORIAL

## Critical considerations for the management of gastrointestinal mixed neuroendocrine non-neuroendocrine neoplasms and pure neuroendocrine carcinomas

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#### Abstract

Mixed neuroendocrine non-neuroendocrine neoplasms constitute rare tumors that are located mainly in the gastrointestinal (GI) tract and have high degrees of malignancy, and the frequency of these tumors has been increasing. They consist of a neuroendocrine neoplastic component with another component of adenocarcinoma usually and have a dismal prognosis. The rare GI pure neuroendocrine carcinoma is highly aggressive and requires complex and extensive management since a genetic distinction exists between it and GI non-neuroendocrine neoplasms, which are generally slow-growing lesions. The most common GI-mixed neuroendocrine non-neuroendocrine neoplasms are colorectal, followed by gastric, mainly in the gastroesophageal junction. Current imaging modalities of nuclear medicine and radiology play important roles in the accuracy of diagnosis. Liquid biopsy may contribute to early detection and timely diagnosis. Ultrasonography, either endoscopic or abdominal, is a technique that contributes to a diagnosis; additionally, contrast-enhanced ultrasonography is very helpful in followup appointments. Histopathology establishes a definite diagnosis and stage by evaluating the cell differentiation grade and the cell proliferation index Ki67. The genetic profile can be valuable in diagnosis and gene therapy. Surgical resection with wide lymphadenectomy, whenever possible, and adjuvant chemotherapy constitute the main therapeutic management strategies. Targeted therapy and immunotherapy achieve encouraging results.

Key Words: Neuroendocrine neoplasms; Gastrointestinal neuroendocrine neoplasms; Mixed gastrointestinal neuroendocrine neoplasms; Gastrointestinal neuroendocrine carcinomas; Neuroendocrine carcinoma; Neuroendocrine non-neuroendocrine neoplasms

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**Core Tip:** The rare but steadily increasing number of gastrointestinal mixed neuroendocrine non-neuroendocrine neoplasms and pure neuroendocrine carcinomas require more radical treatment than slow-growing neuroendocrine neoplasms do and they are related to poor prognosis. They constitute a complicated diagnostic and therapeutic challenge. The current management strategy begins with surgery and is followed by chemotherapy. New chemotherapeutics and novel biological agents for targeted therapy, along with immunotherapy broaden the range of therapeutic options, providing promising outcomes. Effective management should be individualized and multidisciplinary.

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#### INTRODUCTION

Recently, in the World Journal of Gastrointestinal Oncology, the editorial by Cives et al[1] and previously the review by Díaz-López et al[2] presented the current aspects of the interesting issue of mixed neuroendocrine non-neuroendocrine neoplasms (MiNENs) of the gastroenteropancreatic tract in precise detail. These rare neoplasms consist of heterogeneous lesions of combined neuroendocrine neoplasms with epithelial carcinoma (at least 30% of each component) that exhibit high malignancy with rapid progression and a dismal prognosis<sup>[3]</sup>. The pathogenetic mechanism of MiNENs and neuroendocrine carcinoma (NEC) is still unclear. It seems that a possible association with Crohn's disease exists with more gene disorders and greater aggressiveness<sup>[4]</sup>. They are increasing in prevalence in the gastrointestinal (GI) tract, and their incidence is increasing every year [5]. A tenfold increase was reported between 2000 and 2017 [6]. Although MiNENs were initially called mixed adenoneuroendocrine cancers, the recent World Health Organization (WHO) update established the current terminology [7].

Although MiNENs are rare entities, there is particular interest in their diagnosis and treatment. The usual aggressive behavior of these cells is influenced by poor cell differentiation and an increased Ki67 cell proliferation index according to histopathology assessment[8-11]. Pure NECs merit specific preoperative evaluation and wide operative management by radical surgery, including extended lymphadenectomy, followed by proper adjuvant therapy. This carcinoma is a subgroup that usually affects the GI tract in more than 35% of patients[12].

The most common GI-MiNENs are those of the colorectal region[13], followed by those of the gastroesophageal junction and stomach[14,15]. Colorectal MiNENs constitute the majority of poorly differentiated cells and should be managed as adenocarcinomas[13]. Gastric MiNENs differ biologically, histopathologically and clinically from stomach adenocarcinomas, represent the least common gastric neoplasms and are located more often in the gastroesophageal junction[16]. Ampullary MiNENs are extremely rare[17], and proper management constitutes a therapeutic extended operative excision and adjuvant chemotherapy [9]. Less common sites of GI-MiNENs include the appendix [18], which are associated with the best prognosis[6], small intestine, esophagus, liver, pancreas[19], biliary tree, and gallbladder (gallbladder NEC represents 0.5% of all NENs and 2.1% of gallbladder malignancies)[20]. GI-MiNENs may present apart from the neuroendocrine component, another epithelial neoplasm, instead of adenocarcinoma[3]. The histological types of MiNENs include collision, combined and amphicrine types[17].

When distant and high-grade metastases are present in GI-MiNENs, a treatment plan consisting of chemotherapy and targeted therapy, including novel biological agents and immunotherapy, can replace an otherwise ineffective and risky extended surgical resection[10]. Among various GI-MiNENs, different clinical and pathological manifestations may be found, but in any case, these manifestations do not substantially affect the prognosis[21]. The prognosis depends on histological grade, cell differentiation, mitotic rate and Ki67 proliferation index. The Ki67 proliferation index is the most reliable prognostic factor, with a crucial value of 55%[10,21].

#### DIAGNOSIS

Genetic profile analysis may be valuable in precise diagnosis and in novel targeted gene therapy. It has been postulated that, genetically, GI-NECs are different from GI-NETs. Mutations in the TP53 gene and RB1 gene are common in GI-NECs, as are mutations in the CCNE1 gene and MYC proto-oncogene, BHLH transcription factor (MYC) gene. Nonpancreatic GI-NECs are the only ones characterized by mutations in the Notch gene family. Transcription factors, mainly the SOX2 gene, are overexpressed in most GI-NECs[22]. In gastric and colorectal NECs, mutations in the TP53, RB1, and KRAS genes have been detected. However, BRAF gene mutations have been found only in colorectal NECs[23].

The identification of molecular biomarkers in circulation is a new diagnostic challenge. Recently, they have been used for precise assessment in ambiguous cases, including tumor cells, tumor DNA, microRNAs, and NETest. Another valuable current diagnostic test in serum is the so-called liquid biopsy, which depends on mRNA assessment, which contributes to timely diagnosis and treatment monitoring[24-27]. The development and application of the above molecular biomarkers can accurately classify these neoplasms, ensuring their more effective management<sup>[28]</sup>.

Current imaging modalities of nuclear medicine and radiology play important roles in accurate and timely diagnosis. These methods include fluorodeoxyglucose positron emission computed tomography (PET-CT) and, more precisely, gallium<sup>68</sup> PET-CT or the novel most accurate 18F-fluoro-dihydroxyphenylalanine PET-CT, which is specific for distinguishing NENs, and single photon emission computed tomography [29-32]. The novel endoscopic and abdominal ultrasonography (US) technique contributes to diagnosis, and contrast-enhanced US is very helpful in follow-up appointments [26].

There are no specific reliable tumor markers, only the abovementioned biomarkers<sup>[26]</sup>. They are typically diagnosed by fine needle biopsy under imaging guidance or biopsy endoscopy (EUS-fine needle biopsy) for upper GI and colorectal neoplasms which are the gold standard for the preoperative diagnosis of MiNENs and NECs<sup>[26]</sup>. The staging in the definite histopathological assessment of the specimen must be accurate according to the WHO guidelines, which provide precise terminology, particularly the rate of mitoses and the necessary cell proliferation index Ki67[10,33]. In the majority (60%) of samples, the neuroendocrine component has a Ki67 proliferation index equal to or greater than 55% [21]. The WHO staging and recommendations must be followed precisely to reduce the risks of misdiagnosis.

#### MANAGEMENT

Compared with slow-growing NENs, mixed MiNENs and pure NECs require more radical treatment, ensuring necessary R0 resection without residual NENs. This means that in mixed neoplasms and pure carcinomas if a more advanced disease (mainly hepatic metastases) exists that cannot exclude any residual focal neoplastic lesion after attempting potentially curative operative excision, the disease should be characterized as inoperable. In contrast, for functional hypersecreting NENs, there is an indication for debulking surgery (90% resection of the tumor burden) for better control and alleviation of persistent symptoms; consequently, NENs with hepatic metastases are not characterized as inoperable a priori[34]. It is also well known for NENs that curative surgical management of the primary site is highly important, but the management of hepatic metastatic spread must be individualized, and meticulous long-term follow-up is imperative. The current management policy for NEN hepatic metastases includes systemic therapy as first-line therapy and hepatectomy only if systemic therapy fails[35].

In operable cases, whenever feasible, the ideal basic management for both MiNENs and NECs is a radically wide operation with extended lymphadenectomy followed by chemotherapy [36]. The physical status, age and comorbidities of a patient are the primary factors associated with extended surgical procedure outcomes. Therapeutic radical surgery includes complete excision (colectomy, gastrectomy, esophagectomy, proximal pancreatoduodenectomy, or enterectomy) with extended lymphadenectomy according to the location of the primary tumor. It is more risky and complicated but may offer a reasonable chance of cure. In inoperable advanced metastatic cases, any palliative treatment must be aimed at the predominant responsible metastatic component, either the neuroendocrine neoplasm or epithelial carcinoma[28]; this palliation may be achieved by debulking surgery; microwave or radiofrequency ablation; chemotherapy; drugs that suppress tumor growth, mainly in relapse after surgery; novel targeted therapy; and immunotherapy[24,25]. Although approximately 40% of patients have distant hepatic metastases at the time of diagnosis, 88% of all patients undergo some operative procedures[6].

For advanced MiNENs, first-line chemotherapy with 5-fluorouracil or capecitabine plus oxaliplatin has been used as treatment. However, it might differ according to the primary site or the proportion of tumor. The median overall survival was 14 months, depending on the Ki67 proliferation index. Survival was better (35.3 months vs 11.9 months) in patients whose Ki67 index was < 55% [37].

Novel targeted therapies include: (1) Toripalimab, a programmed cell death protein inhibitor, and surufatinib, a tyrosine kinase inhibitor that has been used with encouraging early results in advanced solid tumors, including MiNENs, NECs and NENs[38]; (2) Sunitinib, a tyrosine kinase inhibitor, and everolimus, an mechanistic target of rapamycin inhibitor[39]; and (3) Bevacizumab, an anti-vascular endothelial growth factor monoclonal antibody, and atezolizumab, a programmed cell death ligand 1 inhibitor, for advanced cases, also providing encouraging results[40].

The biological behavior of GI-MiNENs does not differ from that of pure GI-NECs, and the prognosis is similarly poor in both[41]. The median overall survival of all patients with colorectal MiNENs and NECs is 38 months and 42 months, respectively, whereas for those with stage III disease, it is 30 months and 25 months, respectively. Patients with stage III disease and less lymph node involvement have better survival after adjuvant chemotherapy, as determined by multivariate analysis[13].

The prognosis of GI-MiNENs is poorer than that of pure GI-NENs. The former is an independent risk factor for cancerspecific survival in terms of the size of the tumor, degree of lymph node involvement, degree of distant metastasis and applied surgical procedure[5]. The most commonly used chemotherapy for aggressive pure NECs is cisplatin plus etoposide, but the median overall survival time is one year [42]. Rectal NECs are rare and highly aggressive and have a poor prognosis, especially high-grade NECs with poor differentiation. Surgical resection and chemoradiotherapy may be helpful[43].

Apart from symptom palliation, treatment with somatostatin analogs may be beneficial in suppressing tumor growth. Thorough evaluation of somatostatin receptors, including the five subtypes identified by their immunohistochemical expression, is highly important for determining the effectiveness of applied therapy and predicting patient outcome. Somatostatin receptor antagonist targeted therapy has been used recently for its antineoplastic activity<sup>[44]</sup>. The newest such drug, pasireotide, which binds subtype 1 and 4 receptors, may be more effective[45].

Given that pure NECs constitute a subgroup of poorly differentiated NENs with a mitotic rate > 20%, a Ki67 proliferation index > 20% [34] and clear genetic distinction (gene alterations are prevalent in NECs and rare in NENs)[46], they are more aggressive and require wider radical excision than NENs, which are generally slow-growing lesions<sup>[34]</sup>. The evaluation of genetic profiles is important in determining the application of targeted therapy and immunotherapy in the usual advanced inoperable patients [46,47]. The characteristic endoscopic features (submucosal tumor elevation, such as white coating and ulceration) lead to accurate biopsies for histopathological and molecular analysis, contributing to proper management[48]. Cisplatin and etoposide or irinotecan have been used as first-line chemotherapies in advanced inoperable NECs and as second-line immunotherapies with nivolumab, a monoclonal antibody against programmed cell death protein 1 with satisfactory results [49,50]. Folinic acid, 5-fluorouracil, irinotecan and capecitabine, temozolomide were used as second-line chemotherapies for metastatic NECs in a multicenter study, with encouraging results (1-year overall survival of 28.4% for folinic acid, 5-fluorouracil, irinotecan and 32.4% for capecitabine, temozolomide)[51].

In any case, the effective treatment of GI-MiNENs and GI-pure NECs is difficult, since the prognosis is poor for these high malignancy neoplasms and different genetic factors are implicated. The novel treatment must be individualized, multidisciplinary and targeted. New chemotherapeutics and novel biological agents for targeted therapy, along with immunotherapy, broaden the range of therapeutic options mainly in inoperable cases, providing promising outcomes[10, 21,34].

#### CONCLUSION

The current management of GI MiNENs and pure NECs constitutes a challenging multidisciplinary task that must be personalized for each patient. Early and accurate diagnosis has an important contribution to proper management. Apart from diagnostic and therapeutic modern endoscopic modalities, the role of gastroenterologists is also crucial, in diagnosis and scheduled follow-up appointments. Surgery is the cornerstone of any curative treatment accompanied by chemotherapy and novel drugs. Future perspectives should open new horizons in novel chemotherapies, targeted gene therapy and immunotherapy.

#### FOOTNOTES

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REVIEW

# Unraveling the role of cancer-associated fibroblasts in colorectal cancer

Jia-Yu Cui, Jing Ma, Xin-Xin Gao, Zhi-Mei Sheng, Zi-Xin Pan, Li-Hong Shi, Bao-Gang Zhang

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# Abstract

Within the intricate milieu of colorectal cancer (CRC) tissues, cancer-associated fibroblasts (CAFs) act as pivotal orchestrators, wielding considerable influence over tumor progression. This review endeavors to dissect the multifaceted functions of CAFs within the realm of CRC, thereby highlighting their indispensability in fostering CRC malignant microenvironment and indicating the development of CAFs-targeted therapeutic interventions. Through a comprehensive synthesis of current knowledge, this review delineates insights into CAFsmediated modulation of cancer cell proliferation, invasiveness, immune evasion, and neovascularization, elucidating the intricate web of interactions that sustain the pro-tumor metabolism and secretion of multiple factors. Additionally, recognizing the high level of heterogeneity within CAFs is crucial, as they encompass a range of subtypes, including myofibroblastic CAFs, inflammatory CAFs, antigen-presenting CAFs, and vessel-associated CAFs. Innovatively, the symbiotic relationship between CAFs and the intestinal microbiota is explored, shedding light on a novel dimension of CRC pathogenesis. Despite remarkable progress, the orchestrated dynamic functions of CAFs remain incompletely deciphered, underscoring the need for continued research endeavors for therapeutic advancements in CRC management.



Key Words: Colorectal cancer; Cancer-associated fibroblasts; Therapeutic strategies; Microbiota; Neovascularization

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**Core Tip:** Within the intricate milieu of colorectal cancer (CRC) tissues, cancer-associated fibroblasts (CAFs) act as pivotal orchestrators, wielding considerable influence over tumor progression. This review endeavors to dissect the multifaceted functions of CAFs within the realm of CRC, thereby highlighting their indispensability in fostering CRC malignant microenvironment and indicating the development of CAFs-targeted therapeutic interventions. Through a comprehensive synthesis of current knowledge, this review delineates insights into CAFs-mediated modulation of cancer cell proliferation, invasiveness, immune evasion, and neovascularization, elucidating the intricate web of interactions that sustain the protumor metabolism and secretion of multiple factors. Additionally, recognizing the high level of heterogeneity within CAFs is crucial, as they encompass a range of subtypes, including myofibroblastic CAFs, inflammatory CAFs, antigen-presenting CAFs, and vessel-associated CAFs. Innovatively, the symbiotic relationship between CAFs and the intestinal microbiota is explored, shedding light on a novel dimension of CRC pathogenesis. Despite remarkable progress, the orchestrated dynamic functions of CAFs remain incompletely deciphered, underscoring the need for continued research endeavors for therapeutic advancements in CRC management.

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## INTRODUCTION

Malignant tumors have become a significant factor affecting the mortality worldwide, with colorectal cancer (CRC) being among the crucial types of malignancies. CRC is the third most common cancer and the second leading cause of cancer-related death worldwide[1]. It is well known that the development of tumors is not solely due to changes of genes within tumor cells, and the alterations in the surrounding microenvironment also play a significant role in tumor progression.

Over 100 years ago, Paget and others elucidated the importance of the tumor microenvironment (TME) with the "seed and soil" hypothesis which implied a synergistic interaction between tumors and their microenvironment[2]. Numerous studies have confirmed that the stromal components of the TME have crucial impacts on the occurrence and evolution of tumors. As the most abundant non-cancerous stromal cell type, cancer-associated fibroblasts (CAFs) play vital roles in the development of CRC by influencing the proliferation, invasion, and metastasis of cancer cells as well as angiogenesis and immune response through reshaping the extracellular matrix (ECM), secreting soluble factors (chemokines and growth factors), and modulating the microbial community[3,4].

In this review, we aim to delve into the crucial role of CAFs in the progression and treatment of CRC. Additionally, we provide a comprehensive overview of the diverse functions of CAFs, including their impact on cancer cell proliferation, invasiveness, immune evasion, and neovascularization, as well as their role in shaping the TME and influencing tumor growth and metastasis. This exploration highlights the intricate network between CRC and CAFs and clarifies how these interactions affect the disease's prognosis and treatment efficacy. Moreover, we introduce a novel perspective on the symbiotic relationship between CAFs and the intestinal microbiota, potentially opening new avenues for targeting CAFs.

# **ORIGIN OF CAFS**

### Function of fibroblasts

Normal fibroblasts (NFs) are spindle-shaped mesenchymal cells possessing non-epithelial, non-endothelial, and nonimmunological characteristics [5,6] which commonly locate in the connective tissue and help to maintain tissue homeostasis [7]. Functionally, fibroblasts synthesize and secrete laminin, type IV collagen, and other basement membranerelated proteins under normal physiological conditions. Particularly, fibroblasts in intestinal tissue exhibit specialized functions that are crucial for supporting epithelial cells and maintaining barrier integrity [8]. Their roles in ECM production, tissue remodeling, cell communication, immunoregulation, and wound healing collectively contribute to the maintenance of the intestinal epithelial function. In addition, fibroblasts exhibit inhibitory effects on the occurrence, development, invasion, and metastasis of tumor cells through various mechanisms including direct cell-to-cell contact, secretion of soluble factors, and preservation of an intact ECM environment[9]. However, in the context of malignant tumors, changes in the structure and function of the TME lead fibroblasts to transition from their initial anti-tumor characteristics to pro-tumor preference[10].

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### **Origins of CAFs**

CAFs are generally considered to be all fibroblasts embedded within and around cancerous tissues, representing a crucial component of TME[11]. Progenitor cells of CAFs are recruited from several sources and developed by distinct pathways [12], and most of the available evidence supports that the majority of CAFs may originate from the activation of locally resident fibroblasts[13]. Tissue-resident quiescent fibroblasts can be activated by various factors including inflammatory cytokines, constipation, microorganisms, and chemokines [interleukin (IL)-6], as well as growth factors such as transforming growth factor- $\beta$  (TGF- $\beta$ )[14] (Figure 1). Persisted activation tends to cause morphological and functional transformations of NFs into CAFs which are involved in cancer initiation, progression, and chemoresistance[15]. It should be noted that CAFs and NFs are interconvertible, although the underlying mechanism is still poorly understood. Fibrocytes represent a quiescent fibroblast state, which are also considered as one of the sources of CAFs[16,17]. For example, fibrocytes derived from hepatic stellate cells (HSCs) expressing fibroblast growth factor receptor 2 were identified as the origin of CAFs in esophageal squamous cell carcinoma[18].

Mesenchymal stem cells (MSCs) are proposed as potential precursors for CAFs, and Notch and Akt signaling pathways have been reported to be involved in the differentiation of bone marrow MSCs into CAFs[19,20] (Figure 1). In addition, MSCs could acquire CAF-like characteristics while stimulated by TGF- $\beta$ , tumor necrosis factor- $\alpha$ , and IL-1 $\beta$ [21]. Intriguingly, macrophages can assist MSCs in developing CAF-like features[22]. Stellate cells are also an alternative origin of CAFs in certain tumors[23,24] (Figure 1). Insufficient vitamin A can trigger the transformation of pancreatic stellate cells into CAFs[25], and insulin-like growth factor-1 (IGF-1) signaling is crucial for activating HSCs into CAFs[26]. Adipocytes are recognized as another category of CAFs precursors[17,27] (Figure 1). Adipocytes may play a role in tumorigenesis through a mechanism of adipocyte-fibroblast transition[28]. Tumor cells could induce morphological changes and, meanwhile, decrease lipid content and marker expression of adipocytes. Bochet et al<sup>[29]</sup> found that adipocytes may dedifferentiate into cancer-associated adipocytes, and cancer-associated adipocytes become less adipocyte-like and phenotypically mirror fibroblasts with increased expression of ECM components. Moreover, epithelial and endothelial cells can differentiate into CAFs through epithelial-to-mesenchymal transition (EMT) and endothelial-tomesenchymal transition[30-33]. Through the TGF-β-mediated EMT, epithelial cells are able to differentiate into functional CAFs expressing ferroptosis suppressor protein 1 and  $\alpha$ -fibroblast activation protein (FAP)[34], whereas during the endothelial-to-mesenchymal transition, endothelial cells acquire a mesenchymal-like phenotype as well as invasive and migratory properties[35]. Cell types, including pericytes[36], monocytes[37], mesothelial cells[38], hematopoietic stem cells[39], circulating bone marrow cells[40], and smooth muscle cells[41], are also identified as potential precursors for CAFs. Understanding the origins of CAFs can provide new targets for cancer stromal remodeling process.

# HETEROGENEITY OF CAFS

Heterogeneity transcends not only between individuals with the same tumor but also manifests as striking variations within a single tumor [42]. This dynamic variability evolves continuously over time and across spatial dimensions, interacting intricately with the surrounding microenvironment, making it a perpetually shifting and complex process. Distinct subtypes of CAFs are characterized by unique biological markers. In CRC, commonly identified CAF biomarkers include  $\alpha$ -smooth muscle actin ( $\alpha$ -SMA), FAP, vimentin, fibroblast specific protein 1, podoplanin, and platelet-derived growth factor receptors  $\alpha/\beta$  (PDGFR $\alpha/\beta$ )[43]. With the advent of sequencing technologies, researchers have begun to analyze CAF populations at the single-cell level and revealed substantial heterogeneity among CAFs[44]. Single-cell sequencing has identified two principal CAF subsets named CAF-A and CAF-B in human CRC: CAF-A expresses high levels of FAP, matrix metalloproteinase-2 (MMP-2), and collagen type I alpha 2 while CAF-B is characterized by the expression of myofibroblastic markers such as α-SMA, transgelin, and PDGFα[45].

Additionally, recent studies have revealed two distinct subpopulations of CAFs in CRC: Myofibroblastic CAFs (myCAFs), characterized by high α-SMA and IL-6 expression, and inflammatory CAFs (iCAFs), which exhibit low α-SMA and high IL-6 expression[23,46-51]. myCAFs are primarily involved in regulating the ECM, collagen deposition, cellular contraction, and adhesion, whereas iCAFs are distinguished by their secretion of cytokines and chemokines and their interactions with immune cells[50,51]. Interestingly, we discovered that iCAFs were particularly concentrated around dilated blood vessels at the colonic luminal margin and demonstrated greater activity than myCAFs in mismatch repairdeficient tumors[46].

As research continues to deepen, the classification of CAF subtypes has become increasingly nuanced. Khaliq et al[51] utilized large-scale single-cell sequencing across diverse ethnic groups to achieve a more detailed categorization of myCAF and iCAF subtypes in CRC tissue, drawing on classification methods previously used in breast cancer[49]. The myCAF group was further subdivided into ecm-myCAFs, associated with ECM proteins; wound-myCAFs, linked to wound healing signaling; and TGFβ-myCAFs, dependent on the TGFβ pathway[51]. Similarly, the iCAF group was refined to include IL-iCAFs, related to IL signaling, and detox-iCAFs, associated with detoxification pathways. In addition to myCAFs and iCAFs, a type of vascular-associated CAFs expressing pericyte markers and hypoxia-inducible factor 2 has also been identified in CRC, participating in angiogenesis and vascular development and potentially contributing to tumor invasion and metastasis[51-53].

CAFs are frequently linked to the promotion of CRC, but recent studies have also uncovered their potential role in inhibiting CRC growth[54,55]. Kobayashi et al[56] discovered that CAFs can polarize into GREM1<sup>+</sup> CAFs, which promote tumor progression, and ISLR<sup>+</sup> CAFs, which inhibit tumor progression, under the regulation of the TGFβ-FOXL1-GREM1/ ISLR axis. Although the specific mediators secreted by ISLR<sup>+</sup> CAFs that inhibit CRC progression remain unidentified, it is clear that these mediators contribute to activating bone morphogenetic protein signaling in CRC cells.



Figure 1 Origins of cancer-associated fibroblasts in colorectal cancer. Normal fibroblasts can be activated by various factors including inflammation, microorganisms, and chemokines, and transform into cancer-associated fibroblasts. In addition, epithelial cells, endothelial cells, hepatic stellate cells, adipocytes, mesenchymal stem cells, pericytes, monocytes, mesothelial cells, hematopoietic stem cells, bone marrow cells, and smooth muscle cells, are all potential precursors of cancer-associated fibroblasts. Created with BioRender.com (Supplementary material). CAFs: Cancer-associated fibroblasts; CRC: Colorectal cancer; TGF-B: Transforming growth factor-β; NFs: Normal fibroblasts; EMT: Epithelial-to-mesenchymal transition; IGF-1: Insulin-like growth factor-1; MSCs: Mesenchymal stem cells

The heterogeneity of CAFs is continuously evolving with technological and temporal advancements. Single-cell sequencing and spatial transcriptomics have significantly enhanced our understanding of CAFs' diversity. However, a thorough classification of the functional diversity among different CAF subtypes in CRC remains incomplete, and more effective approaches for elucidating the identities and states of CAF subtypes are urgently needed[57,58].

# **ROLES OF CAFS IN CRC**

# CAFs and tumor proliferation and migration

In recent years, an increasing awareness has emerged regarding the pre-existing tumorigenic state of fibroblasts even prior to the onset of malignant cell transformation [13]. To delve deeper into the pathogenic intricacies of CRC, investigators isolated CAFs and NFs from fresh surgical specimens of colorectal adenocarcinoma patients. Additionally, coculturing of these cells with colorectal tumor cells unveiled that tumor cells in conjunction with CAFs exhibited heightened proliferative and migrative capacities [59]. Mechanically, CAFs facilitate CRC proliferation and migration by secreting a variety of cytokines and small extracellular vesicles containing microRNAs (miRNAs), long noncoding RNAs (lncRNAs), and circular RNAs (circRNAs)[60] (Figure 2). Furthermore, Hirashima et al[61] revealed that gene sets related to the Wnt signaling pathway were highly enriched in colorectal CAFs by analyzing the expression profiles of paired CAFs and NFs from CRC tissue. Subsequent in vitro experiment showed that cancer cell proliferation and migration were significantly stimulated by both recombinant Wnt5a protein and CAFs-secreted Wnt2 through activating Wnt signaling [62]. Interestingly, the strategic collaboration between CAFs and tumor-associated macrophages amplifies the migratory prowess of CRC cells[63], which indicates that the immune microenvironment including various immune cells may serve as pivotal orchestrators in propelling the biological function of CAFs.

# CAFs and tumor immune suppression

On the other hand, the intricate crosstalks between CAFs and immune cells also lead to tumor immune evasion by mediating immune cell recruitment and functional differentiation within the TME[64] (Figure 2). In the context of CRCs, the MSCs, as precursors to CAFs, exacerbate tumor progression by intensifying the inhibition of immune cells. Studies found that the sialylation profile of stromal cells is an important mechanism by which MSCs/CAFs modulate T cell



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Figure 2 Roles of cancer-associated fibroblasts. Cancer-associated fibroblasts (CAFs) secrete a variety of cytokines, including interleukin (IL)-34, Wht2, Wnt5a, and small extracellular vesicles, which actively promote colorectal cancer proliferation and migration. Additionally, CAFs intricately manage tumor immune evasion through a range of complex mechanisms, including the secretion of diverse cytokines and chemokines such as fibroblast growth factor, transforming growth factor-β (TGF-β), IL-1, IL-6, and colony-stimulating factor 1. And CAFs contribute to tumor initiation by releasing pro-tumor factors that stimulate angiogenesis, including vascular endothelial growth factor A, IL-6, Wnt2, fibroblast growth factor 2, CXC motif chemokine ligand 12, matrix metalloproteinase-9, and hepatocyte growth factor. In turn, the leaky vasculature within tumors releases pro-angiogenic factors such as platelet-derived growth factor and TGF-β through degranulation, which further activates fibroblasts. The secretion of TGF-β, activin A, and lysyl oxidase-like 2 by CAFs, along with the upregulation of carnitine palmitoyl-transferase 1A expression, promotes epithelial-to-mesenchymal transition in colorectal cancer, thereby enhancing the invasion and metastasis of colorectal cancer. Moreover, CAFs produce ECM proteins and remodel the matrix via matrix metalloproteinases, creating a physical barrier and increasing matrix stiffness and interstitial pressure. And CAFs secrete key soluble factors, including IL-6, IL-17A, and insulin-like growth factor-1. "Carcinogenic bacteria" secrete bacterial toxins such as cytolethal distending toxin, colibactin, and fragilysin, influencing the tumor microenvironment to foster tumor progression and immune evasion. Meanwhile, Bifidobacterium exhibits anticancer effects by activating CD143+ CAFs. Created with BioRender.com (Supplementary material). IL: Interleukin; sEVs: Small extracellular vesicles; FGF: Fibroblast growth factor; TGF-β: Transforming growth factor-β; CSF1: Colony-stimulating factor 1; TAMs: Tumor-associated macrophages; VEGFA: vascular endothelial growth factor A; CXCL-12: CXC motif chemokine ligand 12; MMP: Matrix metalloproteinase; HGF: Hepatocyte growth factor; CDT: Cytolethal distending toxin; CLB: Colibactin; CAFs: Cancer-associated fibroblasts; PDGF: Platelet-derived growth factor; GAS1: Growth arrest specific 1; CRC: Colorectal cancer; IGF: Insulin-like growth factor; TIAM-1: T-lymphoma invasion and metastasis-inducing protein-1; EMT: Epithelial-to-mesenchymal transition; LOLX2: Lysyl oxidase-like 2; CPT1A: Carnitine palmitoyl-transferase 1A.

exhaustion. Targeting stromal cell sialylation may overcome immunosuppression in the CRC TME[65]. The investigations spearheaded by Yang et al[66] illuminated the exacerbation of CAFs' pro-tumor role with the loss of the BCL9 gene, culminating in the aberrant activation of the Wnt/ $\beta$ -catenin signaling pathway, thereby impeding T-cell-mediated antitumor immune responses.

Tumor-associated macrophages contribute to all aspects of tumor progression. Colony-stimulating factor 1 produced by tumor cells caused histone deacetylase 2-mediated downregulation of granulocyte-specific chemokine expression in CAFs. Treatment with colony-stimulating factor 1 receptor inhibitors disrupted this crosstalk and triggered a profound increase in granulocyte recruitment to tumors[67]. Moreover, colony-stimulating factor 1 receptor inhibitors have been utilized as agents targeting tumor-associated macrophages in clinical trials for solid tumors, including intestinal cancers [68]. However, their efficacy has been limited. This limitation has been attributed to CAFs' capability to counteract the therapeutic effects of these agents by recruiting polymorphonuclear myeloid-derived suppressor cells to tumor sites, thereby shaping an immunosuppressive TME[67]. Concomitantly, the involvement of pentraxin 3, fostering M2-like polarization of macrophages, surfaces in the context of CAF-mediated immune suppression, with elevated pentraxin 3 expression correlating positively with fibroblasts and inflammatory response signals in CRC patients, prognosticating unfavorable survival outcomes[69]. The pervasive influence of CAFs also extends to shaping the cytotoxicity of T lymphocytes, fortifying tumor cells in their evasion of the body's immune response[70].

A noteworthy revelation surfaces from recent research, underscoring the tumor-suppressive function of  $\alpha$ -SMA+ CAFs within a genetically engineered mouse model of metastatic CRC. The  $\alpha$ -SMA(+) CAFs in CRC exert tumor-restraining functions via bone morphogenetic protein  $4/TGF-\beta1$  paracrine signaling that serves to suppress Lgr5(+) CSCs and promote anti-tumor immunity, ultimately limiting CRC progression[71]. However, the nuanced impact of the depletion strategy, predominantly targeting  $\alpha$ -SMA+ CAFs, on other  $\alpha$ -SMA+ cells dispersed throughout the body, introduces an element of uncertainty regarding its potential perturbation of the observed outcomes. While there is a growing interest in cancer immunology, our comprehension of how CAFs participate in tumor immune surveillance is still in its infancy. More extensive investigations into CAFs are imperative to pinpoint promising target molecules or subsets of CAFs and to devise innovative therapies that can enhance the clinical efficacy of existing immunotherapies.



#### CAFs and tumor angiogenesis

Angiogenesis stands out as a pivotal step throughout diverse stages of tumor progression, playing a crucial role in the invasive growth of CRC. The significance lies in its ability to provide abundant blood vessels, furnishing oxygen and nutrients indispensable for the proliferation of tumor tissues. As a hallmark of malignant tumors, angiogenesis is closely associated with tumor growth, metastasis, and patient prognosis and is promoted by the most potent pro-angiogenic factor, vascular endothelial growth factor (VEGF), which stimulates angiogenesis by binding to its corresponding receptor VEGF receptor 2 (VEGFR2) on endothelial cells[72-74].

Neovascularization in cancer is governed not solely by tumor cells but also by stromal cells<sup>[75]</sup>. In fact, CAFs directly foster tumor angiogenesis by releasing pro-angiogenic factors and indirectly by generating the ECM[5,75]. In the context of CRC, cancer cells exhibit minimal VEGF secretion whereas CAFs represent a significant origin of VEGFA through the abundant release of IL-6[75,76]. The intricate interplay between colon cancer cells and the TME facilitates the transformation of NFs into CAFs, positively modulating IL-6 secretion, thereby amplifying VEGF secretion and fostering tumor angiogenesis<sup>[77]</sup>. Additionally, Unterleuthner *et al*<sup>[78]</sup> discovered that WNT2 secreted by CAFs plays a pivotal role in promoting the formation of tumor blood vessels in CRC. Silencing WNT2 in CAFs significantly diminishes the angiogenic potential of tumor vessels, highlighting that elevated WNT2 expression in CAFs renders tumors more susceptible to invasion and metastasis. Moreover, CAFs promote tumor initiation by secreting pro-tumor factors (Figure 2) that enhance angiogenesis, including VEGF- $\alpha$ , fibroblast growth factor 2, CXC motif chemokine ligand 12, MMP-9, and hepatocyte growth factor (HGF)[79]. In turn, the permeable vasculature within tumors leads to platelet extravasation and the subsequent release of pro-angiogenic factors such as PDGF and TGFβ through degranulation, which further activate fibroblasts[80]. Collectively, these studies offer a compelling rationale for considering CAFs as a viable therapeutic target to modify tumor vasculature.

#### CAFs promote tumor invasion and metastasis

In the intricate landscape of tumorigenesis, CAFs stand as instrumental architects, actively promoting the insidious progression of tumor invasion and metastasis[81,82]. As a substantial component of the TME, CAFs wield their influence in fostering the malignant behaviors of cancer cells. The multifaceted role of CAFs is underscored by their ability to induce EMT, a pivotal process that endows cancer cells with the traits essential for invasion and metastasis. Research illuminates the mechanistic intricacies, revealing that factors (Figure 2) such as TGF- $\beta$  activation of colonic stromal fibroblasts and the secretion of activin A contribute to the heightened migratory capacity and EMT in colonic epithelial cells, thereby rendering CRC cells more prone to metastasis[83].

The dynamic interplay extends to specific molecular signaling pathways, as evidenced by studies elucidating the stimulation of EMT in CRC cells through the secretion of lysyl oxidase-like 2 by CAFs (Figure 2), activating the focal adhesion kinase signaling pathway [84]. Inhibition of this process presents a potential avenue for curtailing CRC cell invasion and metastasis. Additionally, the orchestration of EMT by CAFs involves regulatory elements such as myosin light chain 9, which influences the secretion of C-C motif ligand 2 and TGF- $\beta$ , thereby shaping the TME and impacting CRC invasion and metastasis[85].

Beyond their involvement in EMT, CAFs exert a substantial impact on the metabolic landscape of CRC cells, enhancing their invasion and metastasis. Through the upregulation of key factors like carnitine palmitoyl-transferase 1A (Figure 2) [86], CAFs promote fatty acid oxidation while minimizing glycolysis, ultimately fostering a milieu conducive to tumor growth and invasion. Woven into this intricate narrative is the expression of WNT2 in CAFs, contributing to the invasion of CRC cells and unveiling additional dimensions to the role of CAFs in promoting metastasis[87]. As the exploration of CAFs' influence on tumor invasion and metastasis unfolds, their capacity to produce signaling molecules, including TGF- $\beta$ , leukemia inhibitory factor, and HGF, emerges as another crucial facet [88]. These molecules act as potent drivers, propelling cancer cell proliferation and invasion behaviors. TGF-β, in particular, emerges as an effective inducer of EMT through paracrine signaling, endowing premalignant cells with mesenchymal properties that facilitate invasion and metastasis[89]. Furthermore, CAFs play a pivotal role in the colonization of distant organs during metastasis, either by creating a supportive microenvironment for cancer cells or by accompanying them in their journey[90].

Examining factors that foster invasion and metastasis through the lenses of EMT and metabolism is imperative. Concurrently, we need to delve into the repercussions of cancer cell EMT on CAFs subtypes. A crucial aspect to explore involves comprehending the influence of EMT-inducing transcription factors on stromal cells. Existing studies underscore a direct correlation between the expression of EMT transcription factors and the presence of CAFs[91]. Noteworthy is the work of Franci et al[92], who discerned predominant Snail expression in fibroblasts proximate to tumor cells in CRC. Furthermore, CRCs exhibiting mesenchymal gene expression traits display a heightened proclivity for distant metastasis, marked by the accumulation of CAFs in the stromal milieu. And findings indicate that fibroblasts within epithelial tumors exhibit elevated miR-200 expression and reduced levels of actin alpha 2 and fibronectin 1 compared to their mesenchymal counterparts[93]. This discovery unveils a novel mechanism for the heterogeneity of CRC CAFs, elucidating how miRNA transfer via extracellular vesicles contributes to this phenomenon. It also offers insights into why CRCs with augmented metastatic potential boast an abundance of CAFs.

#### CAFs and tumor drug resistance

Recent investigations underscore the pivotal role of the TME in shaping tumor cell resistance, elucidating the substantial impact of CAFs in promoting drug resistance across diverse cancers, notably CRC[94]. The intricate interplay involves CAFs's production of ECM proteins and matrix remodeling MMPs, forming both a physical barrier and elevating matrix stiffness and interstitial pressure (Figure 2). This dual effect impedes the efficient penetration of chemotherapy drugs and targeted therapies, contributing significantly to drug resistance[95]. Moreover, the secretion of key soluble factors



(Figure 2) by CAFs, including IL-6, IL-17A, and IGF, intricately mediates chemotherapy resistance and amplifies cytokine secretion post-treatment, consequently intensifying drug resistance[96,97].

Beyond their physical and soluble influences, CAFs play a pivotal role in immune suppression within the TME[13]. The accumulation of aberrant ECM components exacerbates immune suppression, adversely impacting the efficacy of immune checkpoint inhibitors. The involvement of the TGF- $\beta$  signaling pathway is particularly noteworthy in the context of immune therapy resistance. It is intriguing to observe that the blockade of TGF- $\beta$  signaling, in conjunction with receptor kinase inhibitors and anti-programmed cell death protein 1/programmed cell death ligand 1 immunotherapy, exhibits a synergistic effect in a murine model of CRC liver metastasis[98,99]. Notably, an elevated compound stromal score, characterized by three stromal components (CAFs, leukocytes, and endothelial cells), has the potential to anticipate resistance to radiotherapy in rectal cancer patients<sup>[100]</sup>.

Regarding molecularly targeted medications, the release of HGF and IGF2 by CAFs plays a role in conferring resistance to tyrosine kinase inhibitors[101]. Notably, the concurrent inhibition of epidermal growth factor receptor (EGFR) and MET, or insulin receptor and IGF1 receptor, which facilitate the IGF2/insulin receptor/IGF1 receptor signaling pathway, has been shown to augment the therapeutic efficacy of an EGFR inhibitor in xenograft models of colon cancer, respectively[102]. In the realm of CRC, CAFs further exhibit their intricate influence by secreting IL-17A, which acts on the IL-17A receptor on CSCs. This action maintains CSPDCs' stem cell characteristics, upregulates nuclear factor-κB expression, and induces resistance in cancer cells[97]. Additionally, the secretion of exosomes by CAFs is implicated in promoting the stemness and chemotherapy resistance of CRC. The interaction with eukaryotic initiation factor 4A-III and the exosomal miR-625-3p blockade of the CELF2/WWOX pathway underscore the multifaceted mechanisms through which CAFs potentiate drug resistance [103,104]. Furthermore, CAFs contribute to chemotherapy resistance in CRC cells by inducing the overexpression of T-lymphoma invasion and metastasis-inducing protein-1, presenting T-lymphoma invasion and metastasis-inducing protein-1 as a promising therapeutic target[105]. In a co-culture setting, CAFconditioned medium induces the overexpression of the RBCK1 gene, augmenting the stemness and resistance of CRC cells[106]. This intricate web of interactions emphasizes the significant and varied roles of CAFs in fueling drug resistance in CRC, urging further exploration for targeted therapeutic interventions.

#### Relationship between CAFs and intestinal microbiota

As a crucial component of the intestinal barrier, the intestinal microbiota intricately weaves a biofilm, actively participating in intestinal functions and establishing a conducive survival environment for intestinal cells. Notably, this microbial consortium is implicated in various stages of CRC, ranging from benign precursor lesions (polyps) to in situ growth and metastasis. The concept of "carcinogenic bacteria" introduced in 2018, encompasses species like Escherichia coli, Fusobacterium nucleatum, and enterotoxigenic Bacteroides fragilis, underscoring their pivotal role in CRC pathogenesis. Concurrently, bacterial toxins such as cytolethal distending toxin, colibactin, and fragilysin exert their influence on the TME, fostering tumor development and immune escape. Noteworthy insights illuminate the intricate interplay between Helicobacter pylori, fibroblasts, and cancer cells, leading to the induction of Serpin E1 expression. This induction propels the transformation of NFs into CAFs, contributing to the onset of gastric cancer[107]. The complexity of these interactions emphasizes the multifaceted role of the intestinal microbiota in orchestrating the TME and influencing cancer progression.

Crucially, the nuanced roles of distinct intestinal bacteria must be acknowledged, as some confer beneficial effects on the human body. For instance, the work of Chen et al[108] highlights the positive impact of youth-associated Bifidobacterium, activating CD143+ CAFs, thereby initiating the Wnt signaling pathway and upregulating growth arrest specific 1 expression. This cascade of events manifests in anticancer effects, unveiling a promising therapeutic target for CRC[108]. These findings underscore the dynamic nature of the interactions between the intestinal microbiota, fibroblasts, and cancer cells, offering a profound understanding of the intricate molecular mechanisms shaping the TME and presenting potential avenues for therapeutic interventions.

# TREATMENT OF CAFS IN CRC

Alongside surgical resection, the most current clinical approaches to treating CRC involve chemotherapy and radiotherapy, which exert diverse effects on the various cellular constituents of the TME[109]. A comparative study of CRC specimens from patients before and after undergoing cytotoxic treatment revealed a marked rise in CAFs[97]. CAFs exposed to chemotherapy were observed to prolong tumor cell survival and accelerate growth compared to untreated CAFs, indicating that CAFs may shield tumor cells from the growth-inhibitory effects of chemotherapy [109]. In contrast to the genetic instability often observed in malignant tumor cells of CRC, CAFs exhibit genetic stability. This characteristic distinction prompts the exploration of combined therapies targeting both CRC cells and CAFs, envisaged as a novel strategy to augment treatment effectiveness and overcome resistance in CRC. These strategies encompass three primary methods: (1) The elimination of "harmful" CAFs[110]; (2) The reprogramming of CAFs into "normal" fibroblasts or anti-tumor "beneficial" CAF subtypes[111]; and (3) The blockade of signals or ECM components derived from CAFs [112,113]. Successful implementation of these approaches necessitates a precise definition and classification of CAFs, coupled with an enhanced understanding of their diverse functions. Despite extensive research endeavors, several strategies targeting CAFs are yet to yield satisfactory clinical outcomes[14,114,115].

Currently, numerous anticancer drugs targeting CAFs are undergoing preclinical research or clinical trial phases. These drugs predominantly exert direct damage to CAFs by targeting specific surface molecules or impede the secretion of pro-cancer factors and associated signaling pathways in CAFs. The inaugural phase I clinical trial targeting



gastrointestinal cancers, employing autologous MSCs genetically modified to express herpes simplex virus-thymidine kinase, has demonstrated acceptable safety and tolerability. These MSCs facilitate the conversion of the pro-drug ganciclovir into its active cytotoxic metabolite. Furthermore, researchers are exploring the combination of  $TGF-\beta$ inhibitors or Hedgehog inhibitors with standard chemotherapies or immunotherapies [116]. This combination strategy aims to obstruct pro-tumorigenic signaling pathways pertinent to CAFs in gastrointestinal cancers[99,117,118]. Moreover, the differentiation of HSCs into CAFs via the C-X-C chemokine receptor type 4/TGF-β1 signaling axis promotes CRC liver metastasis. Consequently, blocking the C-X-C chemokine receptor type 4/TGF-β1 signaling axis emerges as a beneficial strategy for anti-metastasis treatment in CRC[119].

As research on the TME advances, exosomes have emerged as a promising avenue for therapeutic development. Among many miRNA molecules, miRNA-20a was found to inhibit the secretion of CXC motif chemokine ligand 8 from CAFs, thereby inhibiting tumor growth [120]. CAFs are also capable of secreting the lncRNAs CCAL and H19, thereby inducing drug resistance in cancer cells through the activation of  $\beta$ -catenin signaling[121,122]. Furthermore, CAFs release exosomal circSLC7A6 to stimulate the proliferation of CRC cells, an effect that can be inhibited by matrine, a compound derived from Sophora flavescens[123]. Additionally, CAFs secrete exosomal miR-93-5p and miR-21, which are transferred into CRC cells, consequently enhancing tumor resistance to chemotherapy [124-126].

Diverse attempts have been made to directly target specific subsets of CAFs. Some researchers have encapsulated drugs within lipid nanocapsules to directly target CAFs in the TME, discovering that paclitaxel and acetylcholinesterase are particularly promising for inhibiting CAF development[127]. Notably, a DNA vaccine inducing CD8 T cell killing of FAP+ CAFs has demonstrated the depletion of FAP+ CAFs and the inhibition of tumor progression in a CRC mouse model[128]. However, clinical trials evaluating anti-FAP monoclonal antibodies have not yielded the anticipated efficacy in advanced CRC patients[129]. Combining the chemotherapeutic drug oxaliplatin with the inhibitor PT-100 in a CRC mouse model significantly increased the sensitivity of tumor tissue to chemotherapy, concurrently reducing the recruitment of pro-tumor cells and angiogenesis [130]. Additionally, calcium/calmodulin-dependent protein kinase II has emerged as a pivotal mediator of TFG-β1-induced CAFs activation and participation in CRC cell signaling, positioning calcium/calmodulin-dependent protein kinase II as a promising target for future CRC treatment[131]. Furthermore, CAFs enhance the chemotherapy resistance of CRC cells by receiving signals through their receptor C-C motif chemokine receptor 5, suggesting that targeting C-C motif chemokine receptor 5 may offer a potential approach for treating CRC [132]. In the meanwhile, phosphorylated signal transducer and activator of transcription 3 in CAFs can be used as a tool to judge the prognosis of patients with CRC, and the activation of CAFs may be a therapeutic target for CRC[133]. Moreover, inhibitors of HGF activation, such as SRI 31215, offer a novel strategy to disrupt autocrine and paracrine oncogenic HGF/MET signaling, thereby preventing HGF-dependent cancer cell proliferation, EMT, and migration[134]. Simultaneously targeting HGF and EGFR can effectively block both primary and acquired fibroblast-mediated resistance to EGFR inhibitors in colon cancer cells.

## CONCLUSION

In CRC, CAFs predominantly reside within the tumor or adjacent tissues, secreting factors that fuel tumor initiation, progression, invasion, and metastasis. Notably, CAFs play a pivotal role in aiding tumor cells in evading the body's immune responses, thereby fortifying resistance to radiation and chemotherapy. Consequently, the targeting of CAFs has emerged as an innovative and promising approach in the treatment landscape of CRC.

Anticipating future developments in the realm of CAFs, particularly in CAF subpopulation biology, there has been rapid and significant progress. A growing body of evidence underscores the crucial roles played by specific subgroups of CAFs in tumor initiation, development, metastasis, and resistance to treatment. Nevertheless, the heterogeneity in phenotype and function exhibited by CAFs introduces variability in their roles across different types of tumors and at various stages of the same tumor. Therefore, further exploration is imperative to unravel the nuanced functions of CAFs in different pathological subtypes of CRC and at distinct developmental stages.

Recent reports add an intriguing layer to our understanding, revealing that CAFs not only promote tumor cell development but also exhibit inhibitory effects on tumors. Investigating the underlying mechanisms and pathways through which CAFs themselves exert inhibitory effects represents a promising avenue for future research. The advent of modern scientific technologies, such as single-cell sequencing and spatial transcriptomics, has empowered researchers to delve into the study of CAFs subgroups at unprecedented levels. However, despite the valuable insights gained from single-cell technologies in identifying CAFs subgroups, comprehensive characterization and in-depth functional analyses remain essential to validate data and establish meaningful connections.

In the future trajectory of research, dedicated efforts should be directed towards comprehending the dynamic nature of CAFs, exploring their plasticity, deciphering the factors influencing their transformation, and investigating the potential reversibility of these changes. This concerted endeavor holds the promise of offering more precise and effective strategies for cancer treatment, ultimately paving the way for improved therapeutic outcomes and enhanced well-being for patients.

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# FOOTNOTES

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**Case Control Study** 

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ORIGINAL ARTICLE

# Prognostic utility of gamma-glutamyl transpeptidase to platelet ratio in patients with solitary hepatitis B virus-related hepatocellular carcinoma after hepatectomy

Cheng-Kun Yang, Zhong-Liu Wei, Xiao-Qiang Shen, Yu-Xuan Jia, Qiong-Yuan Wu, Yong-Guang Wei, Hao Su, Wei Qin, Xi-Wen Liao, Guang-Zhi Zhu, Tao Peng

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# Abstract

# BACKGROUND

The prognostic impact of preoperative gamma-glutamyl transpeptidase to platelet ratio (GPR) levels in patients with solitary hepatitis B virus (HBV)-related hepatocellular carcinoma (HCC) following radical resection has not been established.

# AIM

To examine the clinical utility of GPR for prognosis prediction in solitary HBVrelated HCC patients.

# **METHODS**

A total of 1167 solitary HBV-related HCC patients were retrospectively analyzed. GPR levels were compared with 908 non-HCC individuals. Overall survival (OS) and recurrence-free survival (RFS) were evaluated, and cox proportional hazard model analyses were performed to identify independent risk factors. Differences in characteristics were adjusted by propensity score matching (PSM). Subgroup and stratified survival analyses for HCC risks were performed, and a linear trend



of the hazard ratio (HR) according to GPR levels was constructed.

# RESULTS

GPR levels of patients with solitary HBV-related HCC were higher than those with hepatic hemangiomas, chronic hepatitis B and healthy control (adjusted P < 0.05). Variable bias was diminished after the PSM balance test. The low GPR group had improved OS (P < 0.001) and RFS (P < 0.001) in the PSM analysis and when combined with other variables. Multivariate cox analyses suggested that low GPR levels were associated with a better OS (HR = 0.5, 95%CI: 0.36-0.7, *P* < 0.001) and RFS (HR = 0.57, 95%CI: 0.44-0.73, *P* < 0.001). This same trend was confirmed in subgroup analyses. Prognostic nomograms were constructed and the calibration curves showed that GPR had good survival prediction. Moreover, stratified survival analyses found that GPR > 0.6 was associated with a worse OS and higher recurrence rate (P for trend < 0.001).

# **CONCLUSION**

Preoperative GPR can serve as a noninvasive indicator to predict the prognosis of patients with solitary HBVrelated HCC.

Key Words: Gamma-glutamyl transpeptidase to platelet ratio; Hepatitis B virus; Hepatocellular carcinoma; Prognosis; Propensity score matching

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**Core Tip:** In this study, we assessed the prognostic value of gamma-glutamyl transpeptidase to platelet ratio (GPR) in early hepatitis B virus (HBV)-related hepatocellular carcinoma (HCC) patients. We evaluated the clinical utility of preoperative GPR in predicting outcomes for solitary HBV-related HCC patients using propensity score matching, restricted cubic spline, survival analyses and stratified analyses. Preoperative GPR levels facilitate recurrence monitoring and inform treatment strategies, potentially enhancing the quality of life for HCC patients.

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# INTRODUCTION

Worldwide there are 782500 new cases and 745500 deaths per year due to hepatocellular carcinoma (HCC), the most common primary liver cancer[1]. Environmental and individual risk factors include male sex, advanced age, obesity, type 2 diabetes, infection with hepatitis B virus (HBV) or hepatitis C virus (HCV), cirrhosis, aflatoxin B1 exposure, alcohol abuse, smoking, and several metabolic factors<sup>[2,3]</sup>. Chronic HBV infection is an important risk factor for HCC, especially in Asia-Pacific regions, and accounts for > 50% of newly diagnosed HCC cases[4]. Although HBV can become inactive, chronic HBV infections can cause progressive liver fibrosis, which may evolve into HCC in patients with cirrhosis<sup>[5]</sup>. The annual incidence of HBV-related HCC in patients with chronic HBV infection ranges from 2% to 5% when cirrhosis is already established[6].

Surgical resection is regarded as a standard curative treatment for early and intermediate stages of HCC among appropriately selected patients [7]. However, 5-year recurrence rates of HCC patients after curative hepatectomy are as high as 70%–80%, which hinders their long-term survival [8,9]. Clinical outcomes following surgery differ widely and such large variation is mostly unexplained. This variation becomes an obstacle to finding effective therapies and strategies for cancer management. Therefore, it is important to identify risk factors associated with postoperative recurrence and death to avoid subsequent consequences after HCC resection.

Liver puncture biopsy is an invasive procedure and the gold standard for ascertaining the degree of liver fibrosis and damage. Previous studies have found that various non-invasive methods based on routine laboratory tests can predict liver fibrosis, cirrhosis, and even the risk of developing HCC, including the fibrosis-4 index[10], aspartate aminotransferase-platelet index[11], and albumin-bilirubin score[12]. Interestingly, a previous study demonstrated that the gammaglutamyl transpeptidase to platelet ratio (GPR) is an accurate indicator of chronic hepatic fibrosis in patients with chronic HBV infection[13]. In addition, the relative risk of HCC development was significantly increased within chronic HBV patients with high GPR levels<sup>[14]</sup>. Dai *et al*<sup>[15]</sup> reported that preoperative GPR could be an effective non-invasive predictor for the prognosis of HCC patients after hepatectomy[15]. A meta-analysis encompassing 10 studies with 4706 patients indicated that HCC patients with higher GPR exhibited poorer clinical outcomes compared to those with lower GPR, suggesting that GPR is a valid prognostic biomarker for HCC. Furthermore, elevated GPR may signal a deteriorating prognosis in postoperative HCC patients[16]. According to the Chinese guidelines for the diagnosis and treatment



of primary liver cancer [17], Chinese patients with single nodule liver cancer are considered to be in the early stage, and surgical resection is the preferred treatment method. Previous research has demonstrated that the GPR value is a potential prognostic indicator for the occurrence of both overall postoperative and major complications following minor hepatectomy in patients with HCC[18]. However, no study has investigated the prognostic effect of preoperative GPR levels in patients with solitary HBV-related HCC after radical resection.

In the present study, we explored the critical importance of preoperative GPR as a prognosis factor for HBV-related HCC through propensity score matching (PSM), and survival and stratified analyses.

# MATERIALS AND METHODS

#### Study population

We enrolled patients who underwent curative HCC resection between January 2012 and December 2018 at the Department of Hepatobiliary Surgery, The First Affiliated Hospital of Guangxi Medical University.

Inclusion criteria were as follows: (1) The 18 years of age or older; (2) Medical history of chronic HBV infection; (3) HBVrelated HCC was confirmed histopathologically after initial hepatectomy, without previous treatment; (4) Patients presented solitary HCC without gross vascular invasion, bile duct tumor thrombosis, satellite nodules or extrahepatic metastasis upon preoperative clinical imaging and histopathological examination; (5) Child-Pugh classification A or B; and (6) Negative surgical margin observed microscopically or macroscopically upon resection.

Exclusion criteria: (1) Patients with concurrent malignancies; (2) Patients deemed unsuitable for surgery due to either poor tolerance or insufficient residual liver volume to ensure surgical feasibility; (3) Patients diagnosed with hepatic neoplasms of mixed histology; (4) Recurrent HCC; and (5) Non-HBV infection. A total of 1167 patients were enrolled, of whom 172 patients were Barcelona Clinic Liver Cancer (BCLC) stage 0, and 995 patients were BCLC stage A.

To evaluate GPR levels, a total of 908 participants (age  $\geq$  18 years and  $\leq$  80 years, males and females) were enrolled from the First Affiliated Hospital of Guangxi Medical University, including 28 patients with hepatic hemangiomas, 242 healthy control, 67 patients with nonalcoholic fatty liver, 224 patients with chronic hepatitis B, 84 patients with chronic hepatitis C, 245 patients with post-hepatitis cirrhosis, and 18 patients with alcoholic cirrhosis. Eligibility criteria were as follows: (1) Liver cirrhosis detected by liver biopsy or supported by two imaging techniques, with chronic hepatitis infection or alcoholism history; (2) Chronic hepatitis defined as hepatitis B surface antigen or hepatitis C antibodies positive for at least 6 months, with confirmed of HBV or HCV infection; (3) Nonalcoholic fatty liver and hepatic hemangiomas were diagnosed by two clinical imaging methods, in patients with no history of hepatitis infection; and (4) Healthy individuals were confirmed to have no liver or gastrointestinal diseases, no history of other malignancies, and were serologically negative for hepatitis viruses.

This study was approved by The Ethics Committee of The First Affiliated Hospital of Guangxi Medical University, China, No. 2024-E638-01. All participants signed written informed consent before study commencement.

#### Data acquisition and pre-processing

Medical records of HBV-related HCC were reviewed to extract information on baseline characteristics and pathological variables. Histopathological examination confirmed the diagnosis of cirrhosis. Tumor stage after operation was determined following the BCLC staging system. Cutoff values of continuous variables were based on those used commonly in upper and lower clinical limits or median values of subjects. GPR was defined as gamma-glutamyl transpeptidase (GGT) (U/L)/platelet count (× 10°/L). The above indicators are derived from the latest preoperative clinical data of each patient. The x-tile program<sup>[19]</sup> was used to generate the optimal GPR cutoff point with minimum P values from  $\chi^2$  tests. Therefore, the cutoff value of GPR was set as 0.2. In particular, the tercile stratification thresholds for GPR were set at 0.2 and 0.6.

#### Follow-up

After surgery, all patients were followed-up for at least one year. During the first postoperative year, outpatient surveillance was conducted at 3-month intervals, and then every 6-month thereafter by outpatient visits or telephone calls until death or up to January 31, 2022. Serum alpha-fetoprotein (AFP) assay, ultrasonography, and chest radiography were routinely performed. Enhanced computed tomography was performed every 6 months. Based on this surveillance, the overall survival (OS) time was defined as the time from surgery to death (any cause) or to the interruption of follow-up. The recurrence-free survival (RFS) time was defined as the time from surgery to HCC recurrence, including the appearance of intrahepatic tumor nodule(s) with radiologic features consistent with HCC, with or without a rise in serum AFP levels, or follow-up interruption.

#### PSM

PSM analysis was used to adjust for differences in baseline characteristics and to minimize biases of variable selection. With a 0.05 standardized difference as the caliper, a 1:1 matching was performed using the nearest neighbor method. Standardized mean differences were used to assess the balanced distribution of matched patients within each group. A mean difference value higher than 0.1 was considered imbalanced. Matching variables included sex, age, body mass index, smoking history, drinking history, history of liver fluke disease, liver cirrhosis, alpha-fetoprotein, tumor size, liver function grade, microvascular imaging (MVI), etc. After PSM, both low and high GPR groups included 328 patients



(Figure 1). Three groups of PSM analysis were further matched by R packet TriMatch[20].

## Statistical analysis

Descriptive analysis of clinicopathological features was assessed using Pearson's  $\chi^2$  and Wilcoxon rank sum tests, as appropriate. Survival analysis was performed through the Kaplan-Meier method to estimate the survival rates for different groups. The log-rank test was used to evaluate the statistical significance of the equivalences of the survival curves. To evaluate the association between variables and endpoints, a cox proportional hazards model was constructed for univariate and multivariate survival analyses to calculate the hazard ratio (HR) and 95%CI. In multivariable analyses, we used forward stepwise selection of covariates that were P < 0.05 in the univariate regression. Restricted cubic spline (RCS) analyses were performed to determine the association between continuous GPR levels and death/recurrence risks. Interaction analyses, combined analyses, and nomograms were utilized to explore the comprehensive effects of GPR levels and subgroup parameters on the prognosis of HCC. Statistical significance for a linear trend of HR across stratified GPR levels and clinical outcomes of patients was tested. P < 0.05 indicated a statistically significant difference.

All analyses were performed in x-tile (version 3.6.1), R (version 3.6.2, https://www.r-project.org/) and Statistical Package for the Social Sciences version 24.0 (IBMCorp., Chicago, IL, United States).

# RESULTS

A flow diagram summarizing the present work is shown in Figure 1.

## GPR level comparisons

Pairwise comparison of GPR levels revealed that GPR levels of solitary HBV-related HCC patients were higher than those of patients with hepatic hemangiomas, chronic hepatitis B and healthy controls (adjusted P < 0.05) (Figure 2). However, no significant difference was found between patients with HBV-related HCC and post-hepatitis cirrhosis.

# PSM balance test

To adjust for differences in baseline characteristics, associated covariates were entered into the propensity model. After the PSM balance test, the distribution of propensity scores in the high and low GPR groups were similar (Figure 3A). Moreover, all variables were within a reasonable range (overall distance fell within the caliper) after adjusting for solitary HCC patients with GPR  $\leq$  0.2 and GPR > 0.2 (Figure 3B).

## Characteristics of the study population

Comparisons of baseline characteristics and clinicopathological features among early-stage solitary HCC patients with  $GPR \le 0.2$  and GPR > 0.2 before and after PSM are presented in Table 1. Before PSM, there were differences between the groups in several variables, including sex, smoking, drinking, liver flukes, cirrhosis, serum AFP level, total bilirubin, albumin, GGT, HBV DNA, tumor size and infiltrative growth (P < 0.05) (Table 1). After PSM, the clinicopathological variables of the two groups were balanced, and the two groups were comparable (Table 1). Although some differences in the serum AFP and total bilirubin, the overall distance of propensity scores is still within a reasonable range (Figure 3B).

## Survival analysis

Survival curve and Cox proportional hazards model analyses showed that, compared with the high GPR group (GPR > 0.2), low GPR patients had a better OS time and risk value upon univariate analyses (log-rank P < 0.001, HR = 0.48, 95%CI: 0.36-0.64, *P* < 0.001) (Figure 3C and Table 2). After matching, the low GPR group was shown to have a better OS and risk than the high GPR group of patients with early-stage solitary HCC (log-rank P < 0.001, HR = 0.49, 95% CI: 0.35-0.69, P < 0.001) (Figure 3D and Table 2). Similarly, compared with the high GPR group (GPR > 0.2), patients in the low GPR group had improved RFS and risk values (log-rank P < 0.001, HR = 0.49, 95% CI: 0.4-0.6, P < 0.001) (Figure 3E and Table 3). Indeed, after matching, the low GPR group had improved RFS and risk (log-rank P < 0.001; HR = 0.56, 95%CI: 0.44-0.71, P < 0.001) (Figure 3F and Table 3). Moreover, some clinical features were related to tumor prognosis, such as tumor size, cirrhosis, and HBV-DNA (Table 2 and Table 3). Results from the multivariate analysis suggest that preoperative low GPR levels were independently associated with a better OS (HR = 0.5, 95% CI: 0.36-0.7, P < 0.001) and RFS (HR = 0.57, 95%CI: 0.44-0.73, P < 0.001) (Table 3).

## Subgroup and combined analyses by baseline characteristics

To explore more deeply the predictive value of GPR levels for the prognosis of early-stage solitary HBV-related HCC patients, we performed subgroup analyses based on baseline characteristics. Patients in each group were divided into subgroups with low and high GPR levels. Among subgroups, low preoperative GPR levels were significantly associated with an improved OS when compared to those that had high GPR levels (Figure 4A). A strong interaction was found between GPR and HBV-DNA copies (P for interaction = 0.015) (Figure 4A). Indeed, the forest plot depict that the risk of RFS was improved in patients with low GPR values among each subgroup of baseline characteristics (Figure 4A). Importantly, a significant interaction between GPR and tumor size was observed (P for interaction = 0.032) (Figure 4A). Combined analyses showed that a low GPR coupled with a tumor size  $\leq 5$  cm, absence of cirrhosis, AFP  $\leq 200$  ng/mL, and no MVI predicted a favorable OS after PSM (Figure 4B). Conversely, high GPR levels coupled with tumor size > 5 cm, AFP  $\geq$  200 ng/mL, the presence of cirrhosis and MVI predicted a shorter recurrence time (Figure 4C).





Figure 1 Flow diagram of the propensity score analysis for this study. GPR: Gamma-glutamyl transpeptidase-to-platelet ratio; RCS: Restricted cubic spline; HCC: Hepatocellular carcinoma; BCLC: Barcelona Clinic Liver Cancer.



Figure 2 Violin plot analysis comparing the gamma-glutamyl transpeptidase-to-platelet ratio levels among hepatitis B virus-related hepatocellular carcinoma and other 7 non-hepatocellular carcinoma groups. Pairwise comparisons were performed by Games-Howell test, and *P* value was adjusted by Benjamini-Hochberg methods.

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Figure 3 The balance test of propensity score matching and KaplanMeier analysis between gamma-glutamyl transpeptidase-to-platelet ratio level and prognosis of solitary hepatitis B virus-related hepatocellular carcinoma cohort. A: Distribution of propensity values before and after propensity score matching (PSM); B: Absolute standardized differences in covariates between solitary hepatocellular carcinoma (HCC) patients with gamma-glutamyl transpeptidase-to-platelet ratio (GPR)  $\leq$  0.2 and GPR > 0.2, before and after PSM; C and D: Kaplan-Meier survival curves of overall survival in patients with solitary HCC before and after PSM; E and F: Kaplan-Meier survival curves of RFS in patients with solitary HCC before and after PSM. PSM: Propensity score matching; GPR: Gamma-glutamyl transpeptidase-to-platelet ratio; BMI: Body mass index; HR: Hazard ratio; AFP: Alpha-fetoprotein; TB: Total bilirubin; ALB: Albumin; HBV: Hepatitis B virus; MVI: Microvascular imaging.

# Stratified and RCS analyses by GPR levels

RCS curves demonstrated that the association between continuous GPR levels and death/recurrence risks presented as a non-linear trend, with or without variables adjustments (P < 0.001) (Figure 5A). Per standardized difference increased in GPR levels were associated with a 1.29 (1.18-1.42) HR increase in OS after PSM (Table 4). Moreover, the HR for RFS of HCC patients after hepatectomy was positively correlated with elevated GPR level per standardized difference change (HR = 1.20, 95% CI: 1.11-1.31, P < 0.001) (Table 4). To verify if GPR levels could predict the prognosis of patients with solitary HBV-related HCC, a GPR-based risk assessment divided patients into three groups, namely the GPR > 0.2 group was stratified as intermedial GPR levels ( $0.2 < \text{GPR} \le 0.6$ ) and high GPR levels (GPR > 0.6). Compared with patients at the bottom tercile for preoperative GPR (GPR  $\leq$  0.2), patients in the middle tercile had worse OS and RFS (P < 0.001) (Figure 5B). Moreover, those in the top tercile group had even lower OS (HR = 2.74; 95% CI: 1.98–3.81, P for trend < 0.001) and RFS values (HR = 2.60; 95% CI: 2.04-3.31, P for trend < 0.001) (Figure 5B and Table 4). After matching analysis, the triangle chart showed the correlation among the matching items in each group, and the absolute standard deviation was well adjusted (Figure 5C). Indeed, after PSM, intermedial GPR level was associated with worse prognosis in terms of OS (HR = 1.52, 95% CI: 1.08–2.14, log-rank *P* < 0.001) and RFS (HR = 1.69, 95% CI: 1.25–2.17, log-rank *P* < 0.001) (Figure 5D). Furthermore, high GPR levels were associated with worse prognosis of postoperative patients with HCC, including shorter OS (HR = 2.33, 95% CI: 1.60–3.39, *P* for trend < 0.001) and RFS (HR = 2.35, 95% CI: 1.77–3.13, *P* for trend < 0.001) (Figure 5D and Table 4). We detected an increased linear trend for HR in patients stratified according to their GPR levels (P for trend < 0.001) (Table 4). Besides, Kaplan-Meier curves of OS and RFS were statistically different among GPRstratified patients with or without adjusting for PSM (all P < 0.05) (Figure 5). Therefore, a high GPR level is enough to warrant HCC surveillance before liver resections.

## Construction of prognostic nomograms

According to the univariate Cox analysis results of the variables and clinical prognosis before PSM, clinical variables that may be associated factors (P < 0.05) were included in the model construction. Thus, we developed two survival nomograms to predict OS (Figure 6A) and RFS (Figure 6B). The c-indexes of the OS and RFS nomograms were respectively 0.732 (95%CI: 0.669-0.795) and 0.756 (95%CI: 0.723-0.785). Moreover, calibration curves demonstrated that the nomograms predicted the 1-year, 3-years, and 5-years OS and RFS with a high resolution and accuracy.



Α					Ove	rall surviva	al		Recurrence-fre				
Characteristics	<b>GPR</b> ≤ 0.2	GPR > 0.2			HR (95%CI)	P value	P interaction			HR (95%CI)	P value	P interaction	
All parents	381	786	H <b>-</b> -1		0.48 (0.36-0.64)	< 0.001		HEH		0.49 (0.4–0.6)	< 0.001		
Sex							0.793					0.359	
М	278 (72.97)	707 (89.95)	H <b>B</b> 1		0.51 (0.37–0.7)	< 0.001		Heri		0.47 (0.37–0.6)	< 0.001		
F	103 (27.03)	79 (10.05)	<b></b>		0.44 (0.22–0.86)	0.017		<b>⊢_</b> ∎		0.6 (0.38–0.95)	0.03		
Age (years)							0.622					0.849	
≤ 50	229 (60.10)	425 (54.07)	⊢∎1		0.51 (0.36–0.73)	< 0.001		H <b>-</b> 1		0.5 (0.39–0.65)	< 0.001		
> 50	152 (39.90)	361 (45.93)	⊢∎1		0.44 (0.28-0.69)	< 0.001		H <b>-</b> 1		0.47 (0.34-0.64)	< 0.001		
BMI							0.957					0.473	
≤ 24	257 (67.45)	556 (70.74)	<b>H--1</b>		0.49 (0.35–0.68)	< 0.001		Herei		0.47 (0.37–0.59)	< 0.001		
> 24	124 (32.55)	230 (29.26)	<b></b>		0.48 (0.28-0.81)	0.006		<b>⊢</b> ∎—4		0.54 (0.38-0.78)	0.001		
Cirrhosis							0.384					0.15	
Yes	223 (58.53)	357 (45.42)	<b></b>		0.44 (0.29-0.65)	< 0.001		H <b>B</b> -4		0.43 (0.33-0.58)	< 0.001		
No	158 (41.47)	429 (54,58)	· • ·		0.56 (0.38–0.84)	0.005		 		0.58 (0.44–0.77)	< 0.001		
Child-Puah	( )	( )			· · · · · ·		0.991			,		0.987	
Α	378 (99.21)	773 (98.35)	H <b>-</b> 1		0.5 (0.37-0.66)	< 0.001		нен		0.49 (0.4–0.6)	< 0.001		
В	3 (0.79)	13 ( 1.65)	•	<b></b>	0 (0–Inf)	0.999		•	>	0 (0–Inf)	0.999		
BCLC stage	( )						0.183					0.464	
0	65 (17.06)	107 (13.61)	H <b>e</b>		0.25 (0.09–0.72)	0.01		<b>⊢_</b> ∎		0.57 (0.34–0.96)	0.034		
A	316(82.94)	679 (86.39)	H		0.52 (0.39–0.7)	< 0.001		HeH		0.48 (0.38–0.59)	< 0.001		
AFP		, , , , , , , , , , , , , , , , , , ,					0.227					0.339	
< 200 ng/ml	217 (56.96)	510 (64.89)	<b>⊢</b> ∎i		0.54 (0.37–0.79)	0.001		H <b>-</b> 1		0.51 (0.39–0.67)	< 0.001		
≥ 200 ng/ml	164 (43.04)	276 (35.11)	H <b></b> 1		0.39 (0.25-0.6)	< 0.001		H <b>H</b> H		0.43 (0.32–0.58)	< 0.001		
HBV DNA							0.015					0.062	
≤ 1000 IU/ml	238 (62.47)	408 (51.91)	H <b>-</b> 1		0.35 (0.23–0.53)	< 0.001		H <b>H</b> -1		0.42 (0.32-0.55)	< 0.001		
> 1000 IU/ml	143 (37.53)	378 (48.09)	<b>⊢</b> ●	4	0.72 (0.49–1.05)	0.089		<b>⊢</b> ∎–-1		0.61 (0.46-0.83)	0.001		
Tumor size							0.474					0.032	
≤ 5cm	268 (70.34)	455 (57.89)	<b>⊢</b> ∎—4		0.55 (0.38–0.79)	0.00		<b>HHH</b>		0.59 (0.46–0.76)	< 0.001		
> 5cm	113 (29.66)	331 (42.11)	<b></b>		0.45 (0.28-0.71)	0.001		H <b>-</b> 1		0.39 (0.28–0.56)	< 0.001		
Microvascular invasion							0.827					0.476	
No	295 (77.43)	571 (72.65)	⊢∎1		0.5 (0.36-0.7)	< 0.001		HeH		0.47 (0.37–0.59)	< 0.001		
Yes	86 (22.57)	215 (27.35)	<b></b>		0.47 (0.28-0.79)	0.004		<b>⊢</b> ∎––1		0.56 (0.39-0.81)	0.002		
Infiltrative growth							0.74					0.872	
No	215 (56.43)	514 (65.39)	<b>⊢</b> ∎––1		0.45 (0.3–0.66)	< 0.001		H <b>e</b> H		0.47 (0.35–0.61)	< 0.001		
Yes	166 (43.57)	272 (34.61)	<b></b> 1		0.49 (0.32–0.73)	0.001		<b>⊢</b> ∎−-1		0.48 (0.36–0.65)	< 0.001		
			0	1 2				1 0 1	2				
				<b>`</b>				` <b>~</b> `	<b>`</b>				
			Low GPR better	High GPR better				Low GPR better	High GPR better				



Figure 4 Subgroup analyses for gamma-glutamyl transpeptidase-to-platelet ratio level and combined analyses of gamma-glutamyl transpeptidase-to-platelet ratio levels and variables in overall survival and recurrence-free survival of solitary hepatitis B virus-related hepatocellular carcinoma. A: Subgroup analyses for overall survival (OS) and recurrence-free survival (RFS); B: Combined analyses with tumor size, cirrhosis, alpha-fetoprotein (AFP), and microvascular imaging (MVI) for OS; C: Combined analyses with tumor size, cirrhosis, AFP, and MVI for RFS. GPR: Gamma-glutamyl transpeptidase-to-platelet ratio; HR: Hazard ratio; OS: Overall survival; BMI: Body mass index; HR: Hazard ratio; AFP: Alpha-fetoprotein; HBV: Hepatitis B virus; BCLC: Barcelona Clinic Liver Cancer; F: Female; M: Male.



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Figure 5 The association between gamma-glutamyl transpeptidase-to-platelet ratio and death/recurrence risk and Kaplan-Meier stratified analysis between gamma-glutamyl transpeptidase-to-platelet ratio levels and prognosis in the solitary hepatitis B virus-related hepatocellular carcinoma cohort. A: The restricted cubic spline curves of gamma-glutamyl transpeptidase-to-platelet ratio levels. The risk was adjusted by age, cirrhosis, hepatitis B virus-DNA, tumor size, microvascular imaging, and infiltrative growth; B: Kaplan-Meier survival curves of overall survival (OS) and recurrencefree survival (RFS) in patients with solitary hepatocellular carcinoma (HCC) before propensity score matching (PSM); C: Triangle plot and absolute standardized differences adjustment of three groups; D: Kaplan-Meier survival curves of OS and RFS in patients with solitary HCC after PSM. OS: Overall survival; PSM: Propensity score matching; GPR: Gamma-glutamyl transpeptidase-to-platelet ratio; MVI: Microvascular imaging; HBV: Hepatitis B virus; BCLC: Barcelona Clinic Liver Cancer; BMI: Body mass index; HR: Hazard ratio; AFP: Alpha-fetoprotein.

# DISCUSSION

HCC is a common malignant tumor with high recurrence rates and cancer mortality. Previous studies have found that the ratio of routine blood tests and liver function tests have a good predictive value on the prognosis of liver cancer. In the current study, we explored the value of GPR to clinical prognosis by screening early HBV-related HCC patients. GPR levels were higher in these patients than in those with hepatic hemangiomas, chronic hepatitis B and healthy controls. Of note, when the preoperative GPR cutoff value was set at 0.2, HCC patients with high GPR levels had a poorer prognosis. In the entire cohort, patients in the high GPR group had a significantly increased risk after hepatectomy. We used PSM to balance baseline and clinicopathological characteristics. This analysis corroborated the correlation between GPR levels and clinical prognosis for HBV-related HCC patients. Subgroup and combined analyses suggested that, low GPR levels had a protective effect on patient prognosis after liver resection. These findings were supported when patients were stratified according to GPR terciles (P for trend < 0.001). Prognostic nomograms were constructed and the calibration curves showed that GPR can predict the OS and RFS well. This is the first study to examine the relationship between the GPR and surgical outcomes in solitary HBV-related HCC patients. Our results could provide useful information for preoperative planning and postoperative surveillance in these patients.

In this study, multivariate analyses before and after PSM found that, in patients with a single nodule HBV-related HCC, the tumor diameter was associated with OS after radical resection. In addition, the tumor size, aggressive tumor growth, and the presence of liver cirrhosis were associated with tumor recurrence. A Korean study noted that a tumor size > 3 cm, and microvascular invasion were closely associated with early recurrence after liver resection for solitary HCC[21]. A previous study noted that cancer recurrence and long-term survival were independently associated with a tumor size > 5 cm in cirrhotic patients undergoing curative hepatectomy for solitary HCC without macrovascular invasion[22]. Besides, compared with patients who underwent curative hepatectomy without liver cirrhosis, HCC patients with liver cirrhosis had a 6% to 15% higher annual risk of de novo recurrence<sup>[23]</sup>. Patients with HBV-related HCC often have a background of liver cirrhosis, so it is particularly important to evaluate the prognosis of patients before surgery. Some study suggested that GPR can be a good predictor for HCC development in chronic hepatitis B patients[14, 24]. A study has demonstrated that HBV-associated HCC patients with high GPR levels had significantly poorer survival outcomes, regardless of the specific treatment approaches administered<sup>[25]</sup>.

GGT as a cell-membrane-bound enzyme plays a crucial role in modulating the metabolic process of glutathione, involved in nucleic acid metabolism and carcinogenesis. Previous study suggested that serum GGT levels strongly predicted HCC development in patients with chronic HBV infection who underwent nucleotide/nucleoside analogues, particularly non-cirrhotic patients[26]. The detection of serum GGT was previously reported to be associated with the prognosis of HCC patients who underwent hepatectomy [27], radiofrequency-ablation [28], adjuvant transarterial chemoembolization<sup>[29]</sup>, and liver transplantation<sup>[30]</sup>. A plausible mechanism underlying the prognostic significance of GPR could involve its correlation with inflammatory processes. GGT, a constituent of the GPR, serves as a biomarker for hepatic injury and is indicative of the ongoing inflammatory response in HCC. Elevated GGT levels have been observed in individuals with conditions such as hepatitis, liver fibrosis, cirrhosis, and hepatic malignancies[16]. Elevated levels of GGT have been significantly associated with the presence of multiple intrahepatic micrometastases and vascular invasion in HCC[28,30]. Certain serum inflammatory cytokines, notably tumor necrosis factor-alpha and interferon-alpha, which are closely associated with the prognosis of HCC, may contribute to the upregulation of GGT expression[31]. Furthermore, GGT participates in oxidative reactions and serves as a biomarker for oxidative stress, which is an essential component of numerous chronic inflammation-associated responses [32-34]. Platelets, which are anuclear cytoplasmic

# Yang CK et al. GPR associated prognosis of HCC

# Table 1 Preoperative clinicopathologic data of patients with solitary hepatitis B virus-related hepatocellular carcinoma

			Before PSM		_		After PSM		_
Variables		N (1167)	GPR ≤ 0.2 ( <i>n</i> = 381)	GPR > 0.2 ( <i>n</i> = 786)	P value	N (656)	GPR ≤ 0.2 ( <i>n</i> = 328)	GPR > 0.2 ( <i>n</i> = 328)	P value
Sex	Male	985	278	707	< 0.001	533	266	267	1
	Female	182	103	79		123	62	61	
Age (years)	≤ 50	654	229	425	0.059	377	196	181	0.269
	> 50	513	152	361		279	132	147	
Body mass index	> 24	354	124	230	0.282	205	107	98	0.5
	≤24	813	257	556		451	221	230	
Smoking	Yes	407	100	307	< 0.001	190	97	93	0.796
	No	760	281	479		466	231	235	
Drinking	Yes	386	89	297	< 0.001	179	87	92	0.726
	No	781	292	489		477	241	236	
Diabetes mellitus	Yes	59	15	44	0.284	33	15	18	0.721
	No	1108	366	742		623	313	310	
Hypertension	Yes	114	38	76	0.953	67	33	34	1
	No	1053	343	710		589	295	294	
Family history of liver cancer	Yes	128	41	87	0.954	72	39	33	0.532
	No	1039	340	699		584	289	295	
Liver flukes	Yes	221	53	168	0.003	112	51	61	0.35
	No	946	328	618		544	277	267	
Cirrhosis	Yes	587	158	429	< 0.001	280	145	135	0.477
	No	580	223	357		376	183	193	
Serum alpha-fetoprotein (ng/mL)	≥ 200	440	164	276	0.011	246	139	107	0.012
	< 200	727	217	510		410	189	221	
Child-Pugh	А	1151	378	773	0.355	649	325	324	1
	В	16	3	13		7	3	4	
Barcelona Clinic Liver Cancer stage	0	172	65	107	0.142	103	53	50	0.83
	А	995	316	679		553	275	278	
Total bilirubin (µmol/L)	> 20.5	128	31	97	0.04	73	28	45	0.047
	≤ 20.5	1039	350	689		583	300	283	
Albumin (g/L)	> 40	534	223	311	< 0.001	354	184	170	0.309
	$\leq 40$	633	158	475		302	144	158	
Gamma-glutamyl transpeptidase (U/L)	> 50	557	18	539	< 0.001	221	18	203	< 0.001
	≤ 50	610	363	247		435	310	125	
Hepatitis B virus DNA (IU/mL)	> 1000	521	143	378	0.001	277	126	151	0.058
	$\leq 1000$	646	238	408		379	202	177	
HBeAg status	-	299	619	918	0.914	259	252	511	0.510
	+	82	167	249		69	76	145	
Antiviral therapy	No	265	521	786	0.264	233	221	454	0.310

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	Yes	116	265	381		95	107	202	
Surgical margin (cm)	< 2	169	308	477	0.092	146	127	273	0.132
	≥2	212	478	690		182	201	383	
Tumor size (cm)	> 5	444	113	331	< 0.001	208	103	105	0.933
	≤5	723	268	455		448	225	223	
Microvascular invasion	Yes	301	86	215	0.093	152	79	73	0.644
	No	866	295	571		504	249	255	
Infiltrative growth	Yes	438	166	272	0.004	270	137	133	0.812
	No	729	215	514		386	191	195	

P value: Calculated by Pearson's  $\chi^2$  test. PSM: Propensity score matching; GPR: Gamma-glutamyl transpeptidase-to-platelet ratio.

#### Table 2 Univariate and multivariate Cox-regression analyses predicting overall survival before and after propensity score matching

	Before propen	sity matc	hing	After propensity matching				
Variables	Uni-HR (95%Cl)	P value	Multi-HR (95%Cl)	P value	Uni-HR (95%Cl)	P value	Multi-HR (95%Cl)	P value
Sex (male/female)	1.44 (1.01-2.05)	0.043	1.3 (0.9-1.87)	0.159	1.22 (0.79-1.87)	0.364		
Age (years) (> 50/≤ 50)	1.02 (0.81-1.29)	0.85			0.86 (0.63-1.19)	0.362		
Body mass index (> $24/\leq 24$ )	1.16 (0.9-1.49)	0.255			1.25 (0.88-1.79)	0.218		
Smoking (yes/no)	1.05 (0.83-1.34)	0.672			1.04 (0.74-1.48)	0.81		
Drinking (yes/no)	0.9 (0.7-1.15)	0.412			0.85 (0.59-1.23)	0.388		
Diabetes mellitus (yes/no)	0.75 (0.4-1.41)	0.372			0.46 (0.15-1.45)	0.186		
Hypertension (yes/no)	0.82 (0.54-1.24)	0.345			0.66 (0.36-1.23)	0.192		
Family cases (yes/no)	0.79 (0.53-1.17)	0.234			0.61 (0.34-1.1)	0.098		
Liver flukes (yes/no)	0.88 (0.65-1.19)	0.392			0.75 (0.47-1.18)	0.214		
Cirrhosis (yes/no)	1.21 (0.96-1.53)	0.1			1.24 (0.9-1.71)	0.18		
Child-Pugh (B/A)	2.16 (1.07-4.36)	0.032	1.78 (0.87-3.63)	0.115	1.34 (0.33-5.42)	0.679		
Barcelona Clinic Liver Cancer stage (A/0)	1.93 (1.31-2.83)	< 0.001	1.51 (1-2.26)	0.048	2.03 (1.19-3.45)	0.009	1.64 (0.94-2.86)	0.082
Total bilirubin (µmol/L) (> 20.5/≤ 20.5)	0.85 (0.6-1.21)	0.37			0.9 (0.55-1.45)	0.651		
Albumin (g/L) (> 40/≤ 40)	1.35 (1.07-1.71)	0.012	1.16 (0.91-1.48)	0.229	1.2 (0.87-1.65)	0.26		
Alpha-fetoprotein (ng/mL) ( $\geq 200/<200$ )	1.38 (1.09-1.74)	0.006	1.35 (1.06-1.72)	0.013	1.37 (0.99-1.89)	0.055		
Hepatitis B virus DNA (IU/mL) (> $1000/\le 1000$ )	0.73 (0.58-0.92)	0.008	0.83 (0.66-1.05)	0.123	0.72 (0.52-0.99)	0.042	0.82 (0.59-1.12)	0.213
Tumor size (cm) (≤ 5/> 5)	0.57 (0.46-0.72)	< 0.001	0.74 (0.57-0.95)	0.019	0.6 (0.43-0.82)	0.002	0.66 (0.48-0.93)	0.017
Microvascular invasion (yes/no)	1.55 (1.21-1.99)	< 0.001	1.19 (0.92-1.55)	0.186	1.2 (0.83-1.74)	0.322		
Infiltrative growth (yes/no)	1.29 (1.02-1.63)	0.032	1.35 (1.06-1.7)	0.014	1.2 (0.87-1.65)	0.272		
Gamma-glutamyl transpeptidase-to- platelet ratio $(\leq 0.2/> 0.2)$	0.48 (0.36-0.64)	< 0.001	0.52 (0.39-0.69)	< 0.001	0.49 (0.35-0.69)	< 0.001	0.5 (0.36-0.7)	< 0.001

Uni-HR: Hazard ratio for univariable Cox-regression analyses; Multi-HR: Hazard ratio for multivariable Cox-regression analyses.

fragments derived from bone marrow megakaryocytes, serve as critical agents in hemostasis. Upon vascular injury, they swiftly accumulate at the site of damage and discharge granule contents, including platelet-activating factors, to facilitate thrombus formation[35]. Additionally, platelets are implicated in multiple stages of tumorigenesis, including the promotion of tumor growth, intravasation of tumor cells, and metastatic spread. Furthermore, their ability to secrete substantial amounts of microparticles and exosomes is crucial for orchestrating effective communication between the

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Table 3 Univariate and multivariate Cox-regression analyses predicting recurrence-free survival before and after propensity score	re
matching	

	Before proper	nsity mat	ching	After propensity matching				
Variables	Uni-HR	Ρ	Multi-HR	Ρ	Uni-HR	Ρ	Multi-HR	Р
	(95%CI)	value	(95%CI)	value	(95%CI)	value	(95%CI)	value
Sex (male/female)	1.32 (1.03-1.69)	0.028	1.19 (0.92-1.54)	0.176	1.09 (0.8-1.49)	0.574		
Age (years) (> 50/≤ 50)	1.03 (0.87-1.22)	0.756			0.93 (0.73-1.19)	0.575		
Body mass index (> $24/\leq 24$ )	1.13 (0.94-1.36)	0.185			1 (0.77-1.29)	0.989		
Smoking (yes/no)	1.11 (0.93-1.32)	0.244			1.01 (0.78-1.31)	0.93		
Drinking (yes/no)	1 (0.84-1.2)	0.972			0.85 (0.64-1.11)	0.23		
Diabetes mellitus (yes/no)	1.4 (0.98-2)	0.067			1.22 (0.71-2.1)	0.461		
Hypertension (yes/no)	0.81 (0.6-1.09)	0.165			0.83 (0.54-1.26)	0.38		
Family cases (yes/no)	0.89 (0.68-1.16)	0.384			0.76 (0.51-1.14)	0.192		
Liver flukes (yes/no)	1.14 (0.93-1.4)	0.204			1.01 (0.74-1.38)	0.945		
Cirrhosis (yes/no)	1.27 (1.08-1.5)	0.005	1.25 (1.05-1.49)	0.012	1.3 (1.03-1.65)	0.03	1.33 (1.04-1.68)	0.021
Child-Pugh (B/A)	1.08 (0.54-2.18)	0.823			1.01 (0.32-3.14)	0.99		
Barcelona Clinic Liver Cancer stage (A/0)	1.4 (1.09-1.8)	0.008	1.14 (0.87-1.49)	0.348	1.39 (0.98-1.97)	0.061		
Total bilirubin (µmol/L) (> $20.5$ / $\leq 20.5$ )	0.87 (0.67-1.13)	0.292			0.85 (0.6-1.22)	0.386		
Albumin (g/L) (> 40/≤ 40)	1.36 (1.15-1.61)	< 0.001	1.17 (0.98-1.4)	0.084	1.21 (0.96-1.54)	0.112		
Alpha-fetoprotein (ng/mL) ( $\geq 200/\leq 200$ )	1.31 (1.1-1.55)	0.002	1.29 (1.08-1.54)	0.005	1.22 (0.96-1.55)	0.111		
Hepatitis B virus DNA (IU/mL) (> 1000/≤ 1000)	0.8 (0.68-0.95)	0.009	0.9 (0.76-1.06)	0.214	0.76 (0.6-0.96)	0.023	0.8 (0.63-1.02)	0.067
Tumor size (cm) (≤ 5/> 5)	0.6 (0.51-0.71)	< 0.001	0.67 (0.55-0.81)	< 0.001	0.79 (0.62-1.02)	0.07		
Microvascular invasion (yes/no)	1.4 (1.16-1.68)	< 0.001	1.1 (0.9-1.33)	0.359	1.18 (0.9-1.56)	0.233		
Infiltrative growth (yes/no)	1.24 (1.05-1.47)	0.013	1.28 (1.08-1.53)	0.005	1.24 (0.97-1.57)	0.082		
Gamma-glutamyl transpeptidase-to-platelet ratio (≤ 0.2/> 0.2)	0.49 (0.4-0.6)	< 0.001	0.53 (0.43-0.65)	< 0.001	0.56 (0.44-0.71)	< 0.001	0.57 (0.44-0.73)	< 0.001

Uni-HR: Hazard ratio for univariable Cox-regression analyses; Multi-HR: Hazard ratio for multivariable Cox-regression analyses.

Table 4 Stratified analysis between gamma-glutamyl transpeptidase-to-platelet ratio levels and prognosis in the solitary hepatitis B virus-related hepatocellular carcinoma

Variables	Before propensit	ty matching			After propensity matching					
	OS-HR (95%CI)	P value	RFS-HR (95%CI)	P value	OS-HR (95%CI)	P value	RFS-HR (95%CI)	P value		
As continuous	1.12 (1.04-1.20)	0.002	1.11 (1.06-1.17)	< 0.001	1.29 (1.18-1.42)	< 0.001	1.20 (1.11-1.31)	< 0.001		
By GPR cut-off										
$\text{GPR} \le 0.2$										
GPR > 0.2	2.07 (1.56-2.74)	< 0.001	2.05 (1.68-2.51)	< 0.001	2.04 (1.46-2.84)	< 0.001	1.79 (1.40-2.28)	< 0.001		
By GPR tercile										
Bottom (≤ 0.2)										
Middle (> 0.2, $\le$ 0.6)	1.81 (1.35-2.44)	< 0.001	1.85 (1.50-2.29)	< 0.001	1.52 (1.08-2.14)	0.017	1.69 (1.25-2.17)	< 0.001		
Top (> 0.6)	2.74 (1.98-3.81)	< 0.001	2.60 (2.04-3.31)	< 0.001	2.33 (1.60-3.39)	< 0.001	2.35 (1.77-3.13)	< 0.001		
<i>P</i> for trend <sup>1</sup>	< 0.001		< 0.001		< 0.001		< 0.001			
By interquartile										



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Q1									
Q2		1.42 (0.98-2.06)	0.061	1.43 (1.10-1.86)	< 0.001	0.75 (0.43-1.28)	0.288	0.88 (0.60-1.29)	0.514
Q3		1.72 (1.20-2.46)	0.003	1.74 (1.35-2.24)	< 0.001	1.45 (0.90-2.34)	0.125	1.58 (1.12-2.23)	0.009
Q4		2.34 (1.66-3.29)	< 0.001	2.29 (1.79-2.93)	< 0.001	2.08 (1.33-3.24)	0.001	1.79 (1.27-2.51)	0.001
P for tr	end <sup>1</sup>	< 0.001		< 0.001		< 0.001		< 0.001	

<sup>1</sup>Test for trend based on variable containing median value for each classification.

HR: Hazard ratio; OS: Overall survival; RFS: Recurrence-free survival; GPR: Gamma-glutamyl transpeptidase-to-platelet ratio.



Figure 6 Prognostic nomograms for solitary hepatitis B virus-related hepatocellular carcinoma. A: Nomogram plot and calibration curves for overall survival; B: Nomogram plot and calibration curves for recurrence-free survival. AFP: Alpha-fetoprotein; HBV: Hepatitis B virus; MVI: Microvascular imaging; BCLC: Barcelona Clinic Liver Cancer; GPR: Gamma-glutamyl transpeptidase-to-platelet ratio; RFS: Recurrence-free survival; OS: Overall survival; F: Female; M: Male.

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tumor and its host environment [36,37]. A study has explored the correlation between the GPR and inflammation-related signaling pathways, revealing that the expression of p38 mitogen-activated protein kinase exhibited a significant negative correlation with both the GPR and GGT[38]. In the present study, we explored the association of preoperative GPR and the prognosis of patients with single-lesion HBV-related HCC. First, we compared the enrolled subjects with the control group in different physiological states. The results showed that the GPR level of HCC patients was at the same level as that of post-hepatitis cirrhosis patients, and was at a high level compared with healthy subjects and patients with benign liver diseases. The above findings can more intuitively show the evaluation of the prognostic value of GPR level. We set a GPR cutoff value of 0.2 to distinguish the above-mentioned patients into high-risk and low-risk groups. After adjusting for baseline characteristics by PSM, HCC patients who underwent hepatectomy had a poor OS and elevated RFS rate when their preoperative GPR was > 0.2. Previously published studies [15,25,39,40] found that an increased GPR was associated with the prognosis of HCC patients, but the cutoff values varied widely, ranging from 0.3 to 0.84. These differences could be explained by different inclusion and exclusion criteria, differences in tumor staging, and background of liver cirrhosis and hepatitis. Indeed, some researchers have shown that GPR levels have a good prognostic value in HCC patients[41-43], even in AFP-negative HCC[44]. In this study, through subgroup and stratification analyses, we confirmed that a low preoperative GPR level predicts a good prognosis for HCC patients. Therefore, GPR may be a good noninvasive index to guide clinician decision-making.

Although preoperative GPR levels were shown to accurately predict surgical outcomes in patients with HBV-related HCC, the present study has several limitations. First, data were collected from one center in a confined area where HBV is prevalent, and only patients with solitary HCC who received curative resection were included. Although the sample size was modest and potential selection bias should be considered in subsequent analyses, further external validation by multicenter, large-sample, prospective studies is essential to determine the robustness of our findings in different patient populations. Our study is still unclear about the mechanisms linking GPR levels to tumor progression. Further research could provide additional insights to better understand the role of GPR in HCC progression. This study has preliminarily illuminated the role of GPR in predicting outcomes for HCC patients undergoing liver resection; the relationship between various noninvasive blood fibrosis indices and postoperative outcomes warrants further investigation. Moreover, it is unclear if preoperative GPR is useful for HCV-related HCC or nonalcoholic fatty liver disease-related HCC patients receiving radical resection.

# CONCLUSION

GPR levels before surgery can be used as a new indicator to predict surgical outcomes in patients with solitary HBVrelated HCC. This is a potentially helpful tool to monitor the recurrence and OS in clinical practice. A prognostic risk stratification based on GPR can objectively and accurately predict the postoperative prognosis of HCC patients. Therefore, preoperative GPR levels can be used for recurrence monitoring and treatment strategy based on risk stratification, and may contribute to improve the quality of life of solitary nodule HCC patients.

# FOOTNOTES

Author contributions: Yang CK and Peng T designed the study; Yang CK, Wei ZL, Shen XQ, Jia YX, and Wu QY performed research; Yang CK, Wei ZL, Shen XQ, Jia YX, Wu QY and Wei XL provided sample collection and clinical support; Yang CK, Wei YG, Su H, Liao XW, Zhu GZ and Qin W contributed to data interpretation; Yang CK and Wei ZL wrote the manuscript; Peng T critically revised the manuscript and participated in the analysis and interpretation of the data; all of the authors read and approved the final version of the manuscript to be published.

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Informed consent statement: All participants signed written informed consent before study commencement.

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Data sharing statement: The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

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ORIGINAL ARTICLE

# **Retrospective Cohort Study**

# Prognostic prediction models for postoperative patients with stage I to III colorectal cancer based on machine learning

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# Abstract

# BACKGROUND

Colorectal cancer (CRC) is characterized by high heterogeneity, aggressiveness, and high morbidity and mortality rates. With machine learning (ML) algorithms, patient, tumor, and treatment features can be used to develop and validate models for predicting survival. In addition, important variables can be screened and different applications can be provided that could serve as vital references when making clinical decisions and potentially improving patient outcomes in clinical settings.

# AIM

To construct prognostic prediction models and screen important variables for patients with stage I to III CRC.

# **METHODS**

More than 1000 postoperative CRC patients were grouped according to survival time (with cutoff values of 3 years and 5 years) and assigned to training and



testing cohorts (7:3). For each 3-category survival time, predictions were made by 4 ML algorithms (all-variable and important variable-only datasets), each of which was validated via 5-fold cross-validation and bootstrap validation. Important variables were screened with multivariable regression methods. Model performance was evaluated and compared before and after variable screening with the area under the curve (AUC). SHapley Additive exPlanations (SHAP) further demonstrated the impact of important variables on model decision-making. Nomograms were constructed for practical model application.

#### RESULTS

Our ML models performed well; the model performance before and after important parameter identification was consistent, and variable screening was effective. The highest pre- and postscreening model AUCs 95% confidence intervals in the testing set were 0.87 (0.81-0.92) and 0.89 (0.84-0.93) for overall survival, 0.75 (0.69-0.82) and 0.73 (0.64-0.81) for disease-free survival, 0.95 (0.88-1.00) and 0.88 (0.75-0.97) for recurrence-free survival, and 0.76 (0.47-0.95) and 0.80 (0.53-0.94) for distant metastasis-free survival. Repeated cross-validation and bootstrap validation were performed in both the training and testing datasets. The SHAP values of the important variables were consistent with the clinicopathological characteristics of patients with tumors. The nomograms were created.

#### CONCLUSION

We constructed a comprehensive, high-accuracy, important variable-based ML architecture for predicting the 3category survival times. This architecture could serve as a vital reference for managing CRC patients.

Key Words: Colorectal cancer; Machine learning; Prognostic prediction model; Survival times; Important variables

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Core Tip: We developed and validated a promising machine learning architecture for predicting the 3-category survival times (cutoff values of 3 years and 5 years) for four survival times (overall, disease-free, recurrence-free, and distant metastasisfree survival) and screened corresponding important variables. Fivefold cross validation and bootstrap validation were conducted. The models were evaluated with the area under the curve (AUC); moreover, the effectiveness of our variable screening methods was evaluated by comparing the models' pre- and post-screening AUCs. SHapley Additive exPlanations were used to explain the decision-making process. Nomograms were drawn for various applications.

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# INTRODUCTION

Colorectal cancer (CRC) is characterized by high heterogeneity and aggressiveness and high morbidity and mortality rates[1] due to disease progression and inadequate treatment strategies[2]. Furthermore, overdiagnosis, overtreatment, false positives, false reassurance, uncertain findings, and complications are common and can lead to unnecessary psychological burdens on the patients [3-6]. Accurate prediction of the outcomes of CRC patients could be a vital reference when making clinical decisions. The American Joint Committee on Cancer (AJCC) classification system for CRC remains the primary tool for predicting these outcomes, especially for making adjuvant chemoradiotherapy decisions[7,8]. However, the survival observations associated with the AJCC classifications for CRC patients have been reported to exhibit certain inconsistencies[9-11]. Researchers have investigated and built prognostic models for CRC patients with traditional statistical methods; some of these models include the tumor node metastasis (TNM) stage, whereas others do not[12-15]. However, the performance of these models is not very satisfactory, likely due to methodological limitations. Therefore, it seems possible that the power of machine learning (ML) could be leveraged for improvements.

ML is a branch of artificial intelligence in which a computer generates rules underlying or based on raw data[16]; it has gradually been found to be useful in various applications in the field of medicine[17-20]. ML can be used to directly compare the accuracy of two or more quantitative tests for the same disease/condition<sup>[21]</sup>, playing a role in formulating diagnosis and treatment rules [22-24]. ML algorithms have also been used to construct risk forecast models that predict the hazard ratio of adverse events [25,26] or predict the classification of double-class/multiclass endpoints at a specific time<sup>[27]</sup>. Nevertheless, the time interval of occurrence of specific oncological outcomes for CRC patients cannot be vertically predicted in these models, and some of the models' important variables are unknown, casting doubt on their clinical credibility.

In our work, we developed a new ML architecture to predict 3-category occurrence times (cutoff values of 3 years and 5 years) of four oncological outcomes (death, tumor recurrence/distant metastasis, tumor recurrence, and tumor distant metastasis) in patients with stage I, II, and III CRC who underwent curative resection. The longitudinal predictive


mentality is different from that in previous studies. Moreover, the models' important variables and their order of importance were determined. These important parameters were used as clinical references, allowing the identification of hotspot indicators such as the lymph node ratio (LNR) and improving the clinical credibility of our models. The performances of the prediction models with all variables and only the important variables were compared to demonstrate the effectiveness of the variable screening method. SHapley Additive exPlanations (SHAP) was used to provide a more intuitive analysis of the importance of characteristic variables for predicting the net benefits of the model. Nomograms based on different outcomes and classifications were generated for use and reference.

# MATERIALS AND METHODS

#### Patient selection

This study was performed in accordance with the principles of the Declaration of Helsinki. Approval was granted by the Ethics Committee of the Affiliate Hospital of Qingdao University (Grant number QYFYWZLL26957). We retrospectively analyzed the data of patients who underwent curative surgery for primary stage I, II, and III CRC at the Affiliated Hospital of Qingdao University from 2001 to 2020. Patients who received neoadjuvant chemoradiotherapy or who died due to a noncancer-specific cause were excluded. The postoperative adjuvant chemoradiotherapy history of our CRC patients was unclear, and the data were acquired through the hospital information system. A detailed flowchart is shown in Figure 1.

Potential variables for model construction included age, sex, body mass index (BMI), hypertension, diabetes mellitus (DM), chronic heart disease (CHD), smoking history, drinking history, family history of tumors, family history of gastrointestinal tumors, serum carcinoembryonic antigen (CEA) level, serum C-reactive protein (CRP) level, tumor position (ascending colon vs transverse colon vs descending colon vs sigmoid colon vs rectum), tumor differentiation grade, histological type, tumor size (diameter, 20 mm cutoff), perineural invasion (PNI), lymphovascular invasion, lesion number (unifocal vs multifocal), Ki-67 protein level, operation method (laparotomy vs laparoscopy), LNR, and TNM stage. These characteristics mainly consisted of patient demographics and health, tumor and treatment characteristics. Missing values only appeared in the serum CEA, CRP, and Ki-67 protein level data and were processed as a corresponding variable classification.

#### Outcome selection

The outcomes were the 3-category survival times (cutoff values of 3 years and 5 years). The four survival times were overall survival (OS), disease-free survival (DFS), recurrence-free survival (RFS), and distant metastasis-free survival (DMFS), which were defined as the time from the date of surgery to the date of patient death, tumor recurrence/distant metastasis, tumor recurrence, and distant tumor metastasis, respectively. The three classifications of each outcome were labeled class 1 (cl 1) (< 3 years), class 2 (cl 2) (3-5 years), and class 3 (cl 3) (> 5 years).

#### ML algorithms and multivariable regression methods

The four ML algorithms used here were linear regression (LR)[28], linear discriminant analysis (LDA), eXtreme gradient boosting (XGBoost)[29], and categorical features and gradient boosting (CatBoost)[30]. Best subset selection regression, ridge regression, least absolute shrinkage and selection operator (LASSO) regression, and LASSO cross-validation methods were selected for multivariable regression methods.

#### SHAPs

SHAP[31] was used to analyze the number of important input variables screened by the prediction model for achieving net benefit. As the SHAP value approached 0, the possibility of further deleting input variables increased (the SHAP value was approximately 0), ultimately improving the net benefits of the prediction model. The Y-axis refers to various characteristic variables, the X-axis refers to variable SHAP values; a point in the graph represents a sample, the color of the point represents the eigenvalue, data jitter (data metastable state) reflects the distribution of SHAP values, and the order of the variables represents their importance.

#### Nomogram

Nomograms based on the important variables screened for each outcome class for the four ML models were constructed to improve the applicability of our work. The variables in the nomograms are arranged according to the order mentioned in the variable selection.

#### ML model training and validation

Figure 1 shows the process of dataset division. Preliminary predictions were made with the four algorithms with the data from all variables, yielding corresponding area under the curve (AUC). The outcomes were then classified prior to the important variable screening step. For each ML model, variables were screened with the four multivariate regression methods, and the most appropriate regression method was selected on the basis of the difference between the predicted value and the true values [e.g., the mean-square errors (MSEs); the smaller the MSE was, the greater the fit]. Moreover, commonly used clinical guidelines were used to aid in determining important variables. The selected predictors were subsequently input into the four algorithms, and the AUCs were recalculated. All ML algorithm models were validated with 5-fold cross-validation and bootstrap validation with 300 resamplings. The SHAP values of important variables were



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Figure 1 Flowchart showing colorectal cancer patient cohort selection and model training and performance evaluation. A total of 1330 patients were recruited for model development and were grouped by oncological outcomes; then, the data were randomly divided at a 7:3 ratio into a training set and a testing set. The hyperparameters were determined for both the training set and testing set, and model performance was evaluated on the basis of the area under the receiver operating characteristic curve. Finally, we predicted patient outcomes, screened important variables, and processed the bootstrap iterations. DFS: Disease-free survival; DMFS: Distant metastasis-free survival; OS: Overall survival; RFS: Recurrence-free survival.

also categorized, and nomograms were constructed for practical use.

#### Optimization and hyperparameter configuration for classification models

The optimizer was configured for optimizing the XGBoost- and CatBoost-based models. To improve the predictive stability of our models and reduce the imbalance in the data, three optimization steps were performed. First, the maximum depth of the tree in the XGBoost algorithm was reduced and the penalty coefficients of the L2 and L1 regularization weights were increased to prevent overfitting of the prediction model. Second, the maximum depth in the CatBoost algorithm was reduced, and the corresponding L2 weight was increased. Third, we introduced the kernel density estimation (KDE) algorithm[32] for classifying small sample sizes. The maximum number of iterations was 500. The learning rate was set to 0.1 in the hyperparameter configurations. The other hyperparameters were set to their default optimized values.

### Proposed architecture

The technical architecture used in this study was Model-View-View Model: Preprocessing of databases, view: Executing predictions, view model: Implementation of the prediction algorithms). The specific implementation plan involved providing the data processed by R language to the ML model that had been built and finally obtaining the prediction results of the entire architecture. Previous works involved either only processing the data in R to build the models or only performing the prediction tasks with the ML models. Our work combined the advantages of the R language itself with those of mature ML models. Our prediction algorithms were developed in Python 3.11, and our regression methods were based on the R language (version 4.3.2). The AUCs were compared and the SHAP values were implemented after the data iterations. The nomograms were established in R and were used as scoring systems in our work.

#### Statistical analysis

The clinicopathological characteristics of the patients were compared between the training and testing sets for each model with the  $\gamma^2$  test or Fisher's exact test.

#### **Biostatistics**

The statistical methods used in this study were reviewed by Shu-Cheng Si from Peking University Third Hospital.

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# RESULTS

# Study population characteristics

The clinical and therapeutic characteristics of the study population are detailed in Supplementary Table 1. In addition, we further perform  $\chi^2$  tests/Fisher's exact tests to compare the variable distributions between the training sets and testing sets of the four models (OS, DFS, RFS, and DMFS model) and found that there were almost no significant differences. In the OS model, 66.3% (689/1039) of the patients died 3 years after surgery, and 81.9% (716/874), 81.7% (138/169) and 82.7% (663/802) of the patients experienced tumor recurrence/distant metastasis, recurrence, and distant metastasis, respectively, within 3 years after surgery. After the 5-year follow-up, 18.5% (192/1039) of the patients were still alive; additionally, 3.9% (34/874), 4.7% (8/169) and 3.4% (27/802) of the patients did not demonstrate tumor recurrence/distant metastasis, recurrence, and distant metastasis, respectively.

# Performance of the all-variable database models

The results for the full-variable models are shown as solid lines. Only the results in the testing sets in terms of the receiver operating characteristic (ROC) curves are shown here; the results in the training sets are shown in detail in Figures 2, 3, 4 and 5. The AUCs [95% confidence intervals (CIs)] of the OS models produced by the four ML algorithms are shown in Figure 2 [LR: cl 1: 0.75 (0.70-0.80), cl 2: 0.65 (0.59-0.72), cl 3: 0.87 (0.81-0.92); LDA: cl 1: 0.76 (0.71-0.81), cl 2: 0.66 (0.60-0.72), cl 3: 0.86 (0.80-0.92); XGBoost: cl 1: 0.71 (0.64-0.76), cl 2: 0.62 (0.55-0.70), cl 3: 0.79 (0.71-0.86); and CatBoost: cl 1: 0.75 (0.70-0.81), cl 2: 0.65 (0.59-0.72), cl 3: 0.83 (0.77-0.89)]. Figure 3 shows the AUCs (95%CI) for the DFS models [LR: cl 1: 0.71 (0.61-0.80), cl 2: 0.70 (0.61-0.80), cl 3: 0.65 (0.35-0.89); LDA: cl 1: 0.71 (0.61-0.80), cl 2: 0.70 (0.61-0.80), cl 3: 0.62 (0.34-0.88); XGBoost: cl 1: 0.69 (0.60-0.78), cl 2: 0.66 (0.57-0.76), cl 3: 0.70 (0.46-0.89); and CatBoost: cl 1: 0.75 (0.69-0.82), cl 2: 0.71 (0.63-0.80), cl 3: 0.68 (0.43-0.90)]. The obtained AUCs (95%CIs) for the RFS models are shown in Figure 4 [LR: cl 1: 0.80 (0.65-0.92), cl 2: 0.76 (0.53-0.92), cl 3: 0.95 (0.88-1.00); LDA: cl 1: 0.83 (0.69-0.93), cl 2: 0.77 (0.57-0.93), cl 3: 0.92 (0.83-0.99); XGBoost: cl 1: 0.81 (0.65-0.93), cl 2: 0.70 (0.47-0.87), cl 3: 0.79 (0.56-0.96); and CatBoost: cl 1: 0.82 (0.67-0.93), cl 2: 0.72 (0.51-0.90), cl 3: 0.83 (0.67-0.96)]. Figure 5 shows the AUCs (95%CI) for the DMFS models [LR: cl 1: 0.65 (0.56-0.73), cl 2: 0.63 (0.54-0.71), cl 3: 0.76 (0.47-0.95); LDA: cl 1: 0.64 (0.56-0.72), cl 2: 0.63 (0.55-0.71), cl 3: 0.74 (0.45-0.93); XGBoost: cl 1: 0.66 (0.57-0.75), cl 2: 0.65 (0.55-0.74), cl 3: 0.76 (0.47-0.93); and CatBoost: cl 1: 0.65 (0.56-0.74), cl 2: 0.62 (0.54-0.71), cl 3: 0.75 (0.50-0.74), cl 3: 0.75 (0.50-0.75), cl 3: 0.75 (0.50-0.75), cl 3: 0.75 (0.50-0.75), cl 3: 0.75 (0.50-0.75), cl 0.92)].

# Model explanatory features

The important variables differed by study outcome. The detailed MSEs are shown in Table 1. We selected ridge regression for the patient OS model, and the most important variable for predicting patient death was tumor differentiation grade, whereas the tumor differentiation grade, Ki-67 protein level, TNM stage, histological type, CHD, PNI, serum CRP level, and tumor size were the leading features for predicting multicategory OS (8 in total, Table 2 and Supplementary Figure 1). Subset regression was used for the DFS model, and the six important indicators were PNI, Ki-67 protein level, tumor differentiation grade, serum CRP level, histological type, and TNM stage; moreover, the most important variable was PNI (Supplementary Figure 2). For RFS, we used LASSO regression, and DM was found to be the most important variable. The nine important indicators were DM, histological type, serum CEA level, Ki-67 protein level, PNI, serum CRP level, drinking history, LNR, and BMI (Table 2 and Supplementary Figure 3). Subset regression was also chosen for the DMFS model, and PNI, Ki-67 protein level, TNM stage, tumor differentiation grade, and histological type were identified as the five important features; of these, PNI was the most important variable (Supplementary Figure 2).

# Performance of important variable models

The ROC curves of the models based on datasets containing only important variables identified after variable screening are shown as dashed lines. Only the results in the testing sets are shown here; the results in the training sets are shown in detail in Figures 2, 3, 4 and 5. The AUCs of the OS models obtained by the four ML algorithms are shown in Figure 2 [LR: cl 1: 0.78 (0.73-0.83), cl 2: 0.67 (0.61-0.74), cl 3: 0.88 (0.82-0.93); LDA: cl 1: 0.78 (0.74-0.84), cl 2: 0.67 (0.61-0.74), cl 3: 0.89 (0.84-0.93); XGBoost: cl 1: 0.76 (0.70-0.81), cl 2: 0.64 (0.57-0.71), cl 3: 0.85 (0.77-0.91); and CatBoost: cl 1: 0.77 (0.72-0.82), cl 2: 0.65 (0.58-0.72), cl 3: 0.86 (0.78-0.92)]. Figure 3 shows the AUCs for the DFS models in detail [LR: cl 1: 0.70 (0.60-0.79), cl 2: 0.69 (0.57-0.80), cl 3: 0.68 (0.43-0.87); LDA: cl 1: 0.70 (0.60-0.79), cl 2: 0.69 (0.57-0.79), cl 3: 0.69 (0.43-0.88); XGBoost: cl 1: 0.71 (0.62-0.80), cl 2: 0.72 (0.62-0.81), cl 3: 0.70 (0.48-0.88); and CatBoost: cl 1: 0.73 (0.64-0.81), cl 2: 0.72 (0.63-0.81), cl 3: 0.70 (0.50-0.87)]. The obtained AUCs for the RFS models are shown in Figure 4 [LR: cl 1: 0.68 (0.53-0.82), cl 2: 0.66 (0.44-0.82), cl 3: 0.85 (0.66-0.97); LDA: cl 1: 0.70 (0.56-0.85), cl 2: 0.67 (0.46-0.83), cl 3: 0.85 (0.65-0.98); XGBoost: cl 1: 0.83 (0.68-0.95), cl 2: 0.70 (0.45-0.87), cl 3: 0.88 (0.75-0.97); and CatBoost: cl 1: 0.79 (0.64-0.91), cl 2: 0.68 (0.45-0.85), cl 3: 0.84 (0.68-0.93)]. Figure 5 shows the AUCs for the DMFSs [LR: cl 1: 0.67 (0.58-0.76), cl 2: 0.63 (0.54-0.72), cl 3: 0.79 (0.48-0.95); LDA: cl 1: 0.65 (0.56-0.76), cl 2: 0.63 (0.54-0.72), cl 3: 0.79 (0.48-0.95); LDA: cl 1: 0.65 (0.56-0.76), cl 2: 0.63 (0.54-0.72), cl 3: 0.79 (0.48-0.95); LDA: cl 1: 0.65 (0.56-0.76), cl 2: 0.63 (0.54-0.72), cl 3: 0.79 (0.48-0.95); LDA: cl 1: 0.65 (0.56-0.76), cl 2: 0.63 (0.54-0.72), cl 3: 0.79 (0.48-0.95); LDA: cl 1: 0.65 (0.56-0.76), cl 2: 0.63 (0.54-0.72), cl 3: 0.79 (0.48-0.95); LDA: cl 1: 0.65 (0.56-0.76), cl 2: 0.63 (0.54-0.72), cl 3: 0.79 (0.48-0.95); LDA: cl 1: 0.65 (0.56-0.76), cl 2: 0.63 (0.54-0.72), cl 3: 0.79 (0.48-0.95); LDA: cl 1: 0.65 (0.56-0.76), cl 3: 0.79 (0.48-0.95); LDA: cl 1: 0.65 (0.56-0.76), cl 3: 0.79 (0.48-0.95); LDA: cl 1: 0.65 (0.56-0.76), cl 3: 0.79 (0.48-0.95); LDA: cl 1: 0.65 (0.56-0.76), cl 3: 0.79 (0.58-0.76), cl 3: 0.79 (0 0.74), cl 2: 0.62 (0.53-0.71), cl 3: 0.79 (0.48-0.95); XGBoost: cl 1: 0.68 (0.60-0.76), cl 2: 0.64 (0.55-0.73), cl 3: 0.80 (0.53-0.94); and CatBoost: cl 1: 0.67 (0.59-0.75), cl 2: 0.63 (0.54-0.72), cl 3: 0.78 (0.54-0.94)]. The model AUCs did not significantly decrease and, in some cases, even increased after reducing the variables to only those identified as important.

# SHAP value

Supplementary Figure 4 shows the plots of the model SHAP values. A higher probability of outcome occurrence is represented by a SHAP value less than zero. Patients with poor tumor differentiation, high Ki-67 protein level, poor histological type, late TNM stage, high tumor size, PNI, high serum CRP level, and CHD tended to have poorer OS. For DFS, PNI, high Ki-67 protein level, poor tumor differentiation, poor histological type, late TNM stage, and high serum CRP level were related to earlier tumor recurrence/distant metastasis. According to the RFS model, tumor recurrence was



#### Table 1 Comparisons of the mean square error of the four regression methods

Degraceion methodo	MSEs						
Regression methods	OS	DFS		DMFS			
Subset regression method	0.3451435	0.2798500	0.2982825	0.2473204			
Ridge regression method	0.3446552	0.2851649	0.3134211	0.2618467			
LASSO regression method	0.3539798	0.2841859	0.3051014	0.2600286			
LASSO cross-validation method	0.3594004	0.3240556	0.3087686	0.2833409			

DFS: Disease-free survival; DMFS: Distant metastasis-free survival; LASSO: Least absolute shrinkage and selection operator; MSE: Mean square error; OS: Overall survival; RFS: Recurrence-free survival.

# Table 2 Regression coefficients for each variable after ridge regression for overall survival, and least absolute shrinkage and selection operator regression for recurrence-free survival

No.	Intercept	s1	s1
1	Sex	-0.018391078	0
2	Age	-0.038454863	0
3	BMI	0.021728968	-0.001371348
4	HP	0.004982681	0
5	DM	0.001375364	0.119909730
6	CHD	0.096041621	0
7	Smoking history	0.028673390	0
8	Drinking history	0.057936668	0.013536804
9	Family history of tumors	-0.006440690	0
10	Family history of gastrointestinal tumors	0.049916084	0
11	Serum CEA level	0.045104522	-0.043589364
12	Serum CRP level	-0.069915886	-0.026111125
13	Tumor position	0.001514524	0
14	Tumor differentiation grade	-0.295140732	0
15	Histological type	-0.109175968	-0.063182813
16	Tumor size	-0.063522898	0
17	PNI	-0.092586921	-0.031648909
18	LVI	-0.026426021	0
19	Lesion number	0.037347444	0
20	Ki-67 protein level	-0.163277916	-0.033951556
21	Operation method	0.055820722	0
22	LNR	0.040875360	-0.009499988
23	TNM stage	-0.150669578	0

BMI: Body mass index, CEA: Carcinoembryonic antigen; CHD: Chronic heart disease; CRP: C-reactive protein; DM: Diabetes mellitus; HP: Hypertension; LNR: Lymph node ratio; LVI: Lymphovascular invasion; PNI: Perineural invasion; TNM: Tumor node metastasis.

more frequent in patients with poor histological type, high BMI, high Ki-67 protein level, drinking history, high serum CEA level, PNI, DM, high LNR, and high serum CRP level. The distant metastasis model suggested that distant metastasis was more likely for a patient with PNI, high Ki-67 protein level, poor tumor differentiation, late TNM stage, and poor histological type.

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1.0

1.0

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1.0



Figure 2 Prediction of overall survival by machine learning models. The plots show the areas under the curve (AUCs) and their 95% confidence interval

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(CI). A: The linear regression (LR) in the training set [class 1 (cl 1): Before: 0.76 (0.72-0.79), after: 0.74 (0.70-0.78); class 2 (cl 2): Before: 0.71 (0.66-0.75), after: 0.69 (0.64-0.73); class 3 (cl 3): Before: 0.81 (0.75-0.86), after: 0.78 (0.71-0.84)]; B: The LR model in the testing set [cl 1: Before: 0.75 (0.70-0.80), after: 0.78 (0.73-0.83); cl 2: Before: 0.65 (0.59-0.72), after: 0.67 (0.61-0.74); cl 3: Before: 0.87 (0.81-0.92), after: 0.88 (0.82-0.93)]; C: The linear discriminant analysis (LDA) model in the training set [cl 1: Before: 0.76 (0.73-0.80), after: 0.75 (0.71-0.78); cl 2: Before: 0.71 (0.67-0.75), after: 0.69 (0.65-0.74); cl 3: Before: 0.81 (0.75-0.86), after: 0.78 (0.71-0.78); cl 2: Before: 0.71 (0.67-0.75), after: 0.69 (0.65-0.74); cl 3: Before: 0.76 (0.73-0.80); after: 0.78 (0.71-0.78); cl 2: Before: 0.71 (0.67-0.75); after: 0.69 (0.65-0.74); cl 3: Before: 0.76 (0.73-0.80); after: 0.78 (0.71-0.78); cl 2: Before: 0.71 (0.67-0.75); after: 0.69 (0.65-0.74); cl 3: Before: 0.78 (0.71-0.78); cl 4: Before: 0.78 (0.78-0.78); cl 4: Be 0.84)]; D: The LDA model in the testing set [cl 1: Before: 0.76 (0.71-0.81), after: 0.78 (0.74-0.84); cl 2: Before: 0.66 (0.60-0.72), after: 0.67 (0.61-0.74); cl 3: Before: 0.86 (0.80-0.92), after: 0.89 (0.84-0.93)]; E: The eXtreme gradient boosting (XGBoost) model in the training set [cl 1: Before: 0.93 (0.92-0.95), after: 0.79 (0.76-0.82); cl 2: Before: 0.94 (0.93-0.96), after: 0.76 (0.72-0.80); cl 3: Before: 0.98 (0.97-0.99), after: 0.82 (0.76-0.87)]; F: The XGBoost model in the testing set [cl 1: Before: 0.71 (0.64-0.76), after: 0.76 (0.70-0.81); cl 2: Before: 0.62 (0.55-0.70), after: 0.64 (0.57-0.71); cl 3: Before: 0.79 (0.71-0.86), after: 0.85 (0.77-0.91)]; G: The categorical features and gradient boosting (CatBoost) model in the training set [cl 1: Before: 0.88 (0.86-0.91), after: 0.79 (0.75-0.82); cl 2: Before: 0.87 (0.85-0.90), after: 0.76 (0.72-0.80); cl 3: Before: 0.95 (0.93-0.97), after: 0.84 (0.78-0.88)]; H: The CatBoost model in the testing set [cl 1: Before: 0.75 (0.70-0.81), after: 0.77 (0.72-0.82); cl 2: Before: 0.65 (0.59-0.72), after: 0.65 (0.58-0.72); cl 3: Before: 0.83 (0.77-0.89), after: 0.86 (0.78-0.92)]. The curves of the models constructed with the full-variable datasets and the datasets containing only important variables are depicted with solid lines and dashed lines, respectively (abbreviated as "before" and "after" in this annotation).

#### Nomogram

Supplementary Figures 5-8 show the nomograms of each ML model. The total scores and the probability of outcome occurrence can be obtained from these nomograms.

#### Model validation

The 5-fold cross-validation and bootstrap validation results of our ML models are detailed in Supplementary Figures 9-12.

# DISCUSSION

In this study, we developed and validated a promising ML architecture for predicting the 3-class occurrence time (cutoff values of 3 years and 5 years) for four oncological outcomes (patient death, tumor recurrence/distant metastasis, tumor recurrence, and distant tumor metastasis) and identified corresponding important variables. Moreover, 5-fold crossvalidations and bootstrap validations were conducted. The AUC was calculated to evaluate our predictive models, and the effectiveness of our variable screening methods was evaluated by comparing the pre- and post-screening AUCs of the models. SHAP values aided in improving the explanation of the decision-making processes of the models. Moreover, nomograms were produced for ease of application of the models. This architecture represents a comprehensive, practical, and robust tool that clinicians can use when making clinical decisions. Additionally, given the nature of the included patient data, our architecture has good tolerance for heterogeneity and does not require clear patient medical histories, lowering the threshold for use. We cut the survival times, predicted them as multicategory endpoints, and assessed patient outcomes longitudinally through our results, providing a perspective that differs from those of previous studies. Our ML models were designed on the basis of specific oncological outcomes to predict the possible occurrence time category. Some of the important indicators, such as LNR, were newly identified as important predictors of CRC patient outcomes, providing possible insights for researchers and clinicians. Our work demonstrated the feasibility of applying ML models to CRC patients to a certain extent; moreover, the adaptability and interpretability of our architecture can help promote its application in hospitals at different levels.

To improve the practicality of the architecture, we selected clinicopathological indicators that are easily obtained, although several genetic and molecular markers have been proven to be correlated with patient prognoses[25,33]. Eschewing selection biases, we avoided the TNM stage-centric impasse by inputting multipotential variables into the parameter screening step, allowing the ML algorithms to screen important variables that performed best. Missing values were treated as one of the categories of corresponding categorical variables in our study for the sake of applicability and to avoid biases caused by improper filling of missing values to a certain extent. In practice, clinicians can choose the classification that represents missing data when missing values are encountered. We randomly grouped the patients into a training and testing cohort to avoid selection bias, and the differences in baseline characteristics between the two sets were almost not significant. Therefore, we did not further explore potential confounding factors. However, future studies should consider investigating the effects of such confounding factors on model outcomes.

We included patients with a clear medical history before the operation who underwent curative initial treatment; in this way, we excluded stage I, II, and III CRC patients who had received neoadjuvant chemoradiotherapy (which may have led to a vague history). Patients with stage IV CRC who were not eligible for radical surgery were also excluded. However, the history of postoperative adjuvant chemoradiotherapy in our patients was unclear. Consequently, the models might serve as simply rough references when physicians at higher-level hospitals redesign treatment strategies for patients from lower-level hospitals with unclear postoperative radiotherapy and chemotherapy histories. Treatment options for these patients are difficult to determine, and it is difficult for oncologists to obtain references from previous studies that stratify patients by chemotherapy regimen. Moreover, to avoid bias, we excluded patients who did not have endpoint data. When applying our architecture, patients who were predicted to not have outcomes were classified as having an outcome greater than 5 years. We cautiously excluded patients with long follow-up intervals and patients with clear, noncancer-specific deaths to further avoid bias. In addition, the number of patients with tumor recurrence was the smallest; therefore, after strict 7:3 classification into the training and testing cohorts, the sample size for the testing cohort



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Figure 3 Prediction of disease-free survival by machine learning models. The plots show the areas under the curve (AUCs) and their 95% CI. A: The

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linear regression (LR) model in the training set [class 1 (cl 1): Before: 0.77 [0.73-0.82), after: 0.75 (0.70-0.79); class 2 (cl 2): Before: 0.75 (0.71-0.80), after: 0.69 (0.63-0.74); class 3 (cl 3): Before: 0.90 (0.84-0.95), after: 0.87 (0.81-0.92)]; B: The LR model in the testing set [cl 1: Before: 0.71 (0.61-0.80), after: 0.70 (0.60-0.79); cl 2: Before: 0.70 (0.61-0.80), after: 0.69 (0.57-0.80); cl 3: Before: 0.65 (0.35-0.89), after: 0.68 (0.43-0.87)]; C: The linear discriminant analysis (LDA) model in the training set [cl 1: Before: 0.77 (0.73-0.82), after: 0.75 (0.70-0.80); cl 2: Before: 0.76 (0.71-0.80), after: 0.69 (0.63-0.75); cl 3: Before: 0.89 (0.83-0.95), after: 0.87 (0.81-0.92)]; D: The LDA model in the testing set [cl 1: Before: 0.71 (0.61-0.80), after: 0.70 (0.60-0.79); cl 2: Before: 0.70 (0.61-0.80), after: 0.69 (0.57-0.79); cl 3: Before: 0.62 (0.34-0.88), after: 0.69 (0.43-0.88)); E: The eXtreme gradient boosting (XGBoost) model in the training set [cl 1: Before: 0.96 (0.95-0.98), after: 0.79 (0.75-0.83); cl 2: Before: 0.94 (0.92-0.96), after: 0.74 (0.69-0.79); cl 3: Before: 0.99 (0.97-1.00), after: 0.88 (0.84-0.92)]; F: The XGBoost model in the testing set [cl 1: Before: 0.69 (0.60-0.78), after: 0.71 (0.62-0.80); cl 2: Before: 0.66 (0.57-0.76), after: 0.72 (0.62-0.81); cl 3: Before: 0.70 (0.46-0.89), after: 0.70 (0.48-0.88)]; G: The categorical features and gradient boosting (CatBoost) model in the training set [cl 1: Before: 0.91 (0.88-0.93), after: 0.80 (0.75-0.84); cl 2: Before: 0.91 (0.88-0.93), after: 0.76 (0.71-0.81); cl 3: Before: 0.99 (0.97-1.00), after: 0.89 (0.85-0.93)]; H: The CatBoost model in the testing set [cl 1: Before: 0.75 (0.69-0.82), after: 0.73 (0.64-0.81); cl 2: Before: 0.71 (0.63-0.80), after: 0.72 (0.63-0.81); cl 3: Before: 0.68 (0.43-0.90), after: 0.70 (0.50-0.87)]. The curves of the models constructed with the full-variable datasets and the datasets containing only important variables are depicted with solid lines and dashed lines, respectively (abbreviated as "before" and "after" in this annotation)

in the RFS model was still small; therefore, we used the KDE algorithm to address this situation. The similarity between the fitting and original data was evaluated by the bandwidth in KDE, and the fitted data were merged with the original data to form a new RFS dataset. The data introduced here were only used as model training data to assess the performance of the prediction model.

We decomposed the 3-category outcomes into binary outcomes and introduced the data into a LR prediction model, LR; ultimately, 23 original characteristic variables were given outcome labels. As the dataset was multidimensional, the supervised dimensionality reduction algorithm LDA[34,35] was introduced to effectively improve the establishment of the prediction models. We selected XGBoost to optimize the prediction models, although calculating leaf weights is a complex process. The predictive values were obtained by directly summing the leaf weights of all the weak classifiers. We adopted CatBoost because it is based on a tree structure algorithm that can increase the robustness of prediction models. Most importantly, CatBoost can process categorical features into numerical features. The algorithm counts the categorical features, calculates the frequency of appearance of each categorical feature, and subsequently adds hyperparameters to generate new numerical features. CatBoost also uses combined category features, which can leverage the connections between features, greatly enriching the feature dimensions. After analyzing the performance of CatBoost and comparing it with that of LDA, we found that the advantages of the former outweighed those of the latter. To avoid bias in gradient estimation and address prediction bias, we adopted a sorting enhancement method to combat noise in the training dataset. In addition, to better predict the 3-category survival time for patients with different oncological outcomes, we configured and optimized the hyperparameters wherever possible. Furthermore, to reduce bias, the computer experts were blinded to the meaning of each indicator when building the ML models.

Taking survival time as a categorical variable and making more precise predictions to obtain a time interval of oncological outcome occurrence reflects one of the potential applications of our models in clinical practice and provides a different perspective for making predictions from previous studies. A more accurate prediction of possible patient outcomes could translate into more precise formulations of treatment therapies and patient management strategies. Extending survival time is a shared goal among clinicians and oncology patients, and quantifying patient outcomes aids in shared decision making[36]. Because of the heterogeneity of CRC, physicians and patients must seriously consider the trade-offs between adverse effects and benefits[37] when choosing a treatment strategy. It is possible to improve outcomes by administering closer follow-up or additional chemoradiotherapy to patients who are predicted to have poorer outcomes. Consequently, we suggest that patients expected to have a shorter DMFS receive prophylactic chemotherapy or regional radiotherapy at common CRC metastasis sites, as described by Jiang et al[38]. Moreover, the identification of patients with better outcomes could reduce medical care costs and improve the level of humanistic care by reducing the psychological burden on patients and their families. Therefore, predictive tools such as those produced with our architecture should be adopted quickly in clinical practice. However, the results output by models with unclear vital parameters for managing patients are not always acceptable to clinicians and patients[39,40]. Model interpretability is important, especially in biomedicine[41,42]. To turn a model with unclear important parameters into a model with clear important parameters model, we screened the corresponding predictors and showed their importance for different patient outcomes. TNM stage, the primary indicator for chemoradiotherapy decisions, was included in the OS, DFS, and DMFS models, which made our models more credible. Moreover, indicators that have been widely found to be correlated with patient outcome, such as PNI[43-45], pathological type[46-49], and tumor differentiation grade[50], were also included in the models, further confirming the credibility of our architecture. One of the potential benefits of using ML models is that important variables can be identified, while less important parameters can be ignored. Several predictors that were not widely used as important predictors for CRC patient outcome were also included in our model, providing new insights into the concept of predicting patient outcomes. The LNR, whose high prognostic value has been previously demonstrated[51,52], was selected for inclusion in our RFS model and could emerge as an important prognostic indicator for CRC patients for clinical decision-making. The levels of serum CRP and tumor Ki-67 protein were also shown to be prognostic factors, which is consistent with studies showing that high serum CRP levels are associated with increased postoperative complication rates [53,54] and that Ki-67 levels reflect the proliferative capacity of cells [55], especially tumor cells<sup>[56]</sup>. Our models also identified several predictors that were not previously considered to be directly linked to a poor outcome (unifocal vs multifocal lesions and laparotomy vs laparoscopy) [57-60]. These factors are more likely to be directly related to surgical trauma rather than survival time, however. For the OS and RFS models, chronic diseases, CHD and DM, were selected together with alcohol consumption history and BMI, suggesting that clinicians need to be mindful of



AUC (95%CI) Class1 (before) 0.80 [0.65-0.92]

Class1 (after) 0.68 [0.53-0.82]

Class2 (before) 0.76 [0.53-0.92]



Class2 (after) 0.66 [0.44-0.82] Class3 (before) 0.95 [0.88-1.00] • • Class3 (after) 0.85 [0.66-0.97] 0.6 0.8 1.0 False positive rate LDA (test) AUC (95%CI) Class1 (before) 0.83 [0.69-0.93] Class1 (after) 0.70 [0.56-0.85] Class2 (before) 0.77 [0.57-0.93] Class2 (after) 0.67 [0.46-0.83] Class3 (before) 0.92 [0.83-0.99] Class3 (after) 0.85 [0.65-0.98] 0.6 0.8 1.0 False positive rate XGBoost (test) AUC (95%CI) Class1 (before) 0.81 [0.65-0.93] Class1 (after) 0.83 [0.68-0.95] Class2 (before)0.70 [0.47-0.87] Class2 (after) 0.70 [0.45-0.87] Class3 (before) 0.79 [0.56-0.96] Class3 (after) 0.88 [0.75-0.97] 0.6 0.8 1.0 False positive rate CatBosst (test) AUC (95%CI) Class1 (before) 0.82 [0.67-0.93] Class1 (after) 0.79 [0.64-0.91] Class2 (before) 0.72 [0.51-0.90] Class2 (after) 0.68 [0.45-0.85] Class3 (before) 0.83 [0.67-0.96] Class3 (after) 0.84 [0.68-0.93] 0.6 0.8 1.0 False positive rate

Figure 4 Prediction of recurrence-free survival by machine learning models. The plots show the areas under the curve (AUCs) and their 95% CI. A:

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The linear regression (LR) model in the training set [class 1 (cl 1): Before: 0.84 (0.76-0.91), after: 0.76 (0.67-0.84); class 2 (cl 2): Before: 0.88 (0.81-0.93), after: 0.76 (0.66-0.85); class 3 (cl 3): Before: 0.99 (0.96-1.00), after: 0.95 (0.89-0.98)]; B: The LR model in the testing set [cl 1: Before: 0.80 (0.65-0.92), after: 0.66 (0.44-0.82); cl 3: Before: 0.95 (0.88-1.00), after: 0.85 (0.66-0.97)]; C: The linear discriminant analysis (LDA) model in the training set [cl 1: Before: 0.84 (0.76-0.91), after: 0.76 (0.67-0.84); cl 2: Before: 0.86 (0.79-0.92), after: 0.75 (0.64-0.85); cl 3: Before: 0.97 (0.92-1.00), after: 0.93 (0.88-0.98)]; D: The LDA model in the testing set [cl 1: Before: 0.83 (0.69-0.93), after: 0.70 (0.56-0.85); cl 2: Before: 0.77 (0.57-0.93), after: 0.67 (0.46-0.83); cl 3: Before: 0.92 (0.83-0.99), after: 0.85 (0.65-0.98)]; E: The *eXtreme* gradient boosting (XGBoost) model in the training set [cl 1: Before: 0.93 (0.86-0.97), after: 0.89 (0.82-0.94); cl 2: Before: 0.92 (0.85-0.97), after: 0.84 (0.75-0.92); cl 3: Before: 0.96 (0.91-1.00), after: 0.94 (0.86-1.00)]; F: The XGBoost model in the testing set [cl 1: Before: 0.81 (0.65-0.93); after: 0.84 (0.75-0.92); cl 3: Before: 0.70 (0.47-0.87); after: 0.70 (0.45-0.87); cl 3: Before: 0.79 (0.56-0.96), after: 0.88 (0.75-0.97)]; G: The categorical features and gradient boosting (CatBoost) model in the training set [cl 1: Before: 0.93 (0.88-0.97)]; G: The categorical features and gradient boosting (CatBoost) model in the training set [cl 1: Before: 0.93 (0.87-0.97)]; G: The categorical features and gradient boosting (CatBoost) model in the training set [cl 1: Before: 0.93 (0.87-0.97)]; G: The categorical features and gradient boosting (CatBoost) model in the training set [cl 1: Before: 0.93 (0.67-0.93), after: 0.88 (0.73-0.97), after: 0.88 (0.73-1.00)]; and H: The CatBoost model in the test

cancer patients with underlying diseases and poor health conditions. Moreover, we validated the effectiveness of our screening method by comparing the AUCs of the all-variable and important variable-only predictive models. Model performance did not significantly decrease and in some cases even improved when constructed only with the important variables. This finding indicates that our important variables indeed play key roles in our prediction models. After calculating SHAP values, we found that different variables had different degrees of impact on the predictions. Furthermore, clinicians could directly and conveniently reference our results through the nomograms provided in the Results section.

Our findings revealed the formidable predictive power of ML methods, particularly for heterogeneous diseases whose outcome stratifications serve as important clinical references. ML has unique value in clinical applications; when guiding patient management, improving patient outcomes, and tailoring treatment regimens, it could provide important reference values, especially under conditions of resource scarcity (for example, when only clinicopathological and surgical variables are available for analysis). In terms of the computer calculations used, the function parameters were those of the multiple LR model, whereas the optimization parameter b applied in the Cox proportional hazards model is consistent with that of the multiple LR model. Moreover, compared with the Cox proportional hazards model<sup>[61]</sup>, ML has some advantages, although the Cox proportional hazards model and the multivariate linear model in the ML model are similar. When selecting the important parameters, the Cox proportional hazards model commonly shows independent prognostic factors and more indirectly compares their predictive value, whereas ML finds important factors and compares their importance more reliably and directly. When building models and determining their performance, the Cox proportional hazards model typically takes a specific survival time and builds double/multiclass risk stratifications based on this survival time, whereas we predicted the 3-category occurrence time of the oncological outcomes, *i.e.* patient survival times from a longitudinal perspective, with our ML models. Moreover, the number of variables for which the Cox proportional hazards model performed best was less than that of the ML model, which could include multiple variables [62,63]. In addition, the ML and Cox proportional hazards models also differed in terms of the AUC. In our study, the AUC refers to the percentage of correct prediction results in the total sample and specifically refers to the ratio of 3category survival times (OS, DFS, RFS, and DMFS) to the corresponding sample size of the datasets. In the ML model, we binarized the three categories, and the AUC value was the same as the conventional value. The final AUC was obtained from the last module of the ML model[64] and corresponded to the three outcome classifications. Although we obtained encouragingly high predictive performance, high robustness, and transparently important variables, more progress is needed before ML can be fully relied upon. In addition, in clinical practice, traditional performance measures such as the AUC must be translated into medically relevant measures to elucidate the patient-centric value of the ML model, indicating that ML is still lacking in some ways.

The limitations of our study must be noted. First, the sample size needed to collect the data to be input into the ML models was not large (especially for the RFS model). When the data were input into the ML models for parameter optimization, the sensitivity of parameter adjustment could not be estimated because of the small sample size. To compensate for this limitation, we introduced the KDE algorithm for the RFS model (classes 2 and 3); the algorithm was only applied during the training and testing process of the models and achieved good results. Second, the sample uniformity of the data could not be estimated. This is a common problem in ML[41] that can possibly affect the final results. Furthermore, this was a retrospective study, which implies the presence of certain selection biases. However, the patient data were obtained from a well-conceived and well-characterized cohort, which increases the credibility of our results; thus, this study can serve as the basis for subsequent prospective studies. In addition, postoperative treatment information, such as information regarding specific radiotherapy and chemotherapy treatments as well as details of the surgical methods, was not available in our datasets and should be considered for inclusion in future works.

Prospective research with a larger sample size and a more comprehensive and consummate design is needed in the future. Moreover, information involving omics data and microbial analyses is highly worthy of inclusion in the predictive models. We look forward to carrying out more in-depth work in the future.

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Figure 5 Prediction of distant metastasis-free survival by machine learning models. The plots show the areas under the curve (AUCs) and their

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95%CI. A: The linear regression (LR) model in the training set [class 1 (cl 1): Before: 0.81 (0.77-0.85), after: 0.77 (0.72-0.81); class 2 (cl 2): Before: 0.80 (0.75-0.84), after: 0.73 (0.67-0.79); class 3 (cl 3): Before: 0.90 (0.83-0.96), after: 0.84 (0.75-0.91)]; B: The LR model in the testing set [cl 1: Before: 0.65 (0.56-0.73), after: 0.67 (0.58-0.76); cl 2: Before: 0.63 (0.54-0.71), after: 0.63 (0.54-0.72); cl 3: Before: 0.76 (0.47-0.95), after: 0.79 (0.48-0.95)); C: The linear discriminant analysis (LDA) model in the training set [cl 1: Before: 0.82 (0.78-0.85), after: 0.77 (0.72-0.81); cl 2: Before: 0.81 (0.77-0.84), after: 0.74 (0.68-0.79); cl 3: Before: 0.90 (0.84-0.96). after: 0.83 (0.75-0.90)]; D: The LDA model in the testing set [cl 1: Before: 0.64 (0.56-0.72), after: 0.65 (0.56-0.74); cl 2: Before: 0.63 (0.55-0.71), after: 0.62 (0.53-0.74); cl 2: Before: 0.63 (0.55-0.71), after: 0.62 (0.53-0.74); cl 2: Before: 0.64 (0.56-0.72); cl 2: Before: 0.64 (0.56-0.74); cl 2: Before: 0.54 ( 0.71); cl 3: Before: 0.74 (0.45-0.93), after: 0.79 (0.48-0.95)]; E: The eXtreme gradient boosting (XGBoost) model in the training set [cl 1: Before: 0.96 (0.94-0.97), after: 0.80 (0.75-0.84); cl 2: Before: 0.96 (0.94-0.98), after: 0.76 (0.70-0.81); cl 3: Before: 0.97 (0.96-0.99), after: 0.85 (0.79-0.91)]; F: The XGBoost model in the testing set [cl 1: Before: 0.66 (0.57-0.75), after: 0.68 (0.60-0.76); cl 2: Before: 0.65 (0.55-0.74), after: 0.64 (0.55-0.73); cl 3: Before: 0.76 (0.47-0.93), after: 0.80 (0.53-0.74), after: 0.64 (0.55-0.74), after: 0.65 0.94)]; G: The categorical features and gradient boosting (CatBoost) model in the training set [cl 1: Before: 0.95 (0.93-0.96), after: 0.79 (0.74-0.83); cl 2: Before: 0.96 (0.94-0.97), after: 0.77 (0.72-0.82); cl 3: Before: 0.98 (0.97-1.00), after: 0.87 (0.81-0.92)]; H: The CatBoost model in the testing set [cl 1: Before: 0.65 (0.56-0.74), after: 0.67 (0.59-0.75); cl 2: Before: 0.62 (0.54-0.71), after: 0.63 (0.54-0.72); cl 3: Before: 0.75 (0.50-0.92), after: 0.78 (0.54-0.94)]. The curves of the models constructed with the full-variable datasets and the datasets containing only important variables are depicted with solid lines and dashed lines, respectively (abbreviated as "before" and "after" in this annotation).

# CONCLUSION

We successfully designed and validated comprehensive, accessible, and robust clinicopathological-based ML prediction models built from clearly identified important variables. Our work could serve as a reference for CRC patient management and outcome improvement. We demonstrated the potential of the proposed ML architecture for clinical application.

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# FOOTNOTES

Author contributions: Ji XL and Xu S designed the study, acquired and analyzed the data, and wrote the manuscript; Ji XL and Xu S contributed equally to this work; Li XY prepared the materials; Xu JH provided methods; Han RS, and Guo YJ participated in the data acquisition and analysis; Tian ZB and Duan LP managed and designed the project, and performed critical revisions of the manuscript; Tian ZB and Duan LP contributed equally to this work; All authors have read and approve the final manuscript. Ji XL and Xu S contributed equally to this work as co-first authors. The designation of Tian ZB and Duan LP as co-corresponding authors of this work is primarily based on the following three reasons. First, this research project spans multiple disciplines. As the main provider of data, Tian ZB ensures the reliability and integrity of the research. His work in data collection, collation and analysis is crucial to the quality of the paper, while Duan LP ensures the comprehensiveness and depth of the research. Second, Duan LP was the main provider of the core ideas of the paper, setting the foundation for the direction and framework of the entire research and promoting the innovation and scientific value of the research. Moreover, Tian ZB put forward suggestions during this process. The two co-corresponding authors have similar contributions to the project and work closely together. Balancing their contributions is crucial for fairness and transparency. Third, Tian ZB and Duan LP jointly undertook the task of revising the manuscript, reducing the burden of a single corresponding author and ensuring timely and efficient responses. In short, designating two corresponding authors helps promote cooperation, enhance academic influence, and improve the quality of research results. The contributions of Tian ZB and Duan LP are equally important at different stages, so being co-corresponding authors more fairly reflects their collaboration and contribution to this research.

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ORIGINAL ARTICLE

**Retrospective Cohort Study** 

# Local excision for middle-low rectal cancer after neoadjuvant chemoradiation: A retrospective study from a single tertiary center

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# Abstract

# BACKGROUND

Rectal cancer has become one of the leading malignancies threatening people's health. For locally advanced rectal cancer (LARC), the comprehensive strategy combining neoadjuvant chemoradiotherapy (NCRT), total mesorectal excision (TME), and adjuvant chemotherapy has emerged as a standard treatment regimen, leading to favorable local control and long-term survival. However, in recent years, an increasing attention has been paid on the exploration of organ preservation strategies, aiming to enhance quality of life while maintaining optimal oncological treatment outcomes. Local excision (LE), compared with low anterior resection (LAR) or abdominal-perineal resection (APR) was introduced dating back to 1970's. LE has historically been linked to a heightened risk of recurrence compared to TME, potentially due to occult lymph node metastasis and intraluminal recurrence. Recent evidence has demonstrated that LE might be an alternative approach, instead of LAR or APR, in cases with favorable tumor regression after NCRT with potentially better quality of life. Therefore, a retrospective analysis of clinicopathological data from mid-low LARC patients who underwent LE after NCRT was conducted, aiming to evaluate the treatment's efficacy, safety, and oncologic prognosis.

# AIM

To explore the safety, efficacy, and long-term prognosis of LE in patients with mid-low rectal cancer who had a good response to NCRT.

# **METHODS**

Patients with LE between 2012 to 2021 were retrospectively collected from the



rectal cancer database from Gastro-intestinal Ward III in Peking University Cancer Hospital. The clinicopathological features, postoperative complications, and long-term prognosis of these patients were analyzed. The Kaplan-Meier method was used to create cancer-specific survival curve, and the log-rank test was used to compare the differences regarding outcomes.

#### RESULTS

A total of 33 patients were included in this study. The median interval between NCRT and surgery was 25.4 (range: 8.7-164.4) weeks. The median operation time was 57 (20.0-137.0) minutes. The initial clinical T staging (cT): 9 (27.3%) patients were cT2, 19 (57.6%) patients were cT3, and 5 (15.2%) patients were cT4; The initial N staging (cN): 8 patients (24.2%) were cN negative, 25 patients (75.8%) were cN positive; The initial M stage (cM): 2 patients (6.1%) had distant metastasis (ycM1), 31 (93.9%) patients had no distant metastasis (cM0). The pathological results: 18 (54.5%) patients were pathological T0 stage (ypT0), 6 (18.2%) patients were ypT1, 7 (21.2%) patients were ypT2, and 2 (6.1%) patients were ypT3. For 9 cT2 patients, 5 (5/9, 55.6%) had a postoperative pathological result of ypT0. For 19 cT3 patients, 11 (57.9%) patients were ypT0, and 2 (40%) were ypT0 in 5 cT4 patients. The most common complication was chronic perineal pain (71.4%, 5/7), followed by bleeding (43%, 3/7), stenosis (14.3%, 1/7), and fecal incontinence (14.3%, 1/7). The median follow-up time was 42.0 (4.0-93.5) months. For 31 patients with cM0, the 5-year disease-free survival (DFS) rate, 5-year local recurrence-free survival (LRFS) rate, and 5-year overall survival (OS) rate were 88.4%, 96.7%, and 92.9%, respectively. There were significant differences between the ycT groups concerning either DFS (P = 0.042) or OS (P = 0.002) in the Kaplan-Meier analysis. The LRFS curve of ycT  $\leq$ T1 patients was better than that of ycT  $\ge$  T2 patients, and the *P* value was very close to 0.05 (*P* = 0.070). The DFS curve of patients with  $y_pT \le T1$  was better than that of patients with  $y_pT \ge T2$ , but the *P* value was not statistically significant (P = 0.560). There was a significant difference between the ypT groups concerning OS (P = 0.014) in the Kaplan-Meier analysis. The LRFS curve of  $ypT \le T1$  patients was better than that of  $ypT \ge T2$  patients, and the P value was very close to 0.05 (P = 0.070). Two patients with initial cM1 were alive at the last follow-up.

#### **CONCLUSION**

LE for rectal cancer with significant tumor regression after NCRT can obtain better safety, efficiency, and oncological outcome. Minimally invasive or nonsurgical treatment with patient participation in decision-making can be performed for highly selected patients. Further investigation from multiple centers will bring better understanding of potential advantages regarding local resection.

Key Words: Rectal cancer; Neoadjuvant chemoradiotherapy; Local excision; Prognosis

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**Core Tip:** This retrospective study explores the safety, efficacy, and long-term prognosis of local excision (LE) in patients with middle-low rectal cancer who responded well to neoadjuvant chemoradiotherapy. The findings demonstrate that LE can achieve high rates of organ preservation and favorable oncological outcomes, including a 5-year disease-free survival rate of 88.4% and overall survival rate of 92.9%. Complications were manageable and non-severe. This study supports the potential of minimally invasive treatments in selected patients, highlighting the importance of patient participation in treatment decisions.

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# INTRODUCTION

Rectal cancer has attracted more and more attention as a tumor worldwide. Neoadjuvant chemoradiotherapy (NCRT) followed by total mesorectal excision (TME) and adjuvant chemotherapy has been widely used as a classic treatment strategy for patients with locally advanced rectal cancer (LARC), which has shown good local control rate and survival results[1,2]. However, for mid-low rectal cancer, the traditional low anterior resection (LAR) or abdominal-perineal resection (APR) treatment has a series of disadvantages, such as LAR syndrome or permanent stoma[3,4]. In recent years, organ preservation strategy has been recognized by more and more surgeons. Morson *et al*[5] introduced their experience of the traditional transanal approach and surgical criteria for local excision (LE) of early rectal cancer in 1977. Since then, the application of LE for early rectal cancer has gradually increased, and patients have high function preservation and prognosis results[6-8]. However, for more advanced tumors, LE has long been associated with a higher risk of recurrence than TME, which is considered to be related to occult lymph node metastasis and intraluminal recurrence[9,10]. For



LARC, strengthening the intensity of preoperative treatment, such as total neoadjuvant therapy treatment strategy or consolidation chemotherapy, brings better tumor treatment response, and some patients may achieve clinical complete response (cCR) or near-cCR status[11,12]. To date, LE, known as the total mesorectal neglect strategy, for these well-responding rectal cancer patients is still in the exploratory stage[13,14]. The ACOSOG Z6041 study showed that for patients with early rectal cancer, NCRT combined with LE can obtain a better oncologic prognosis and a higher quality of life and anal function[15]. However, some studies have also reported that LE after NCRT has a high incidence of complications and a variable recurrence rate[16,17]. A meta-analysis showed no difference in the risk of postoperative complications between radical surgery and transanal endoscopic microsurgery[18]. Based on these inconsistent results, we retrospectively analyzed the clinicopathological data of patients with mid-low LARC who underwent LE after NCRT in our center and explored the efficiency, safety, and oncological prognosis.

# MATERIALS AND METHODS

#### Patients' selection

The study subjects were rectal cancer patients with a follow-up period of more than 3 years, therefore, databased was formed focusing patients with LE between 2012 to 2021 were retrospectively collected from the rectal cancer database at Peking University Cancer Hospital., and local resection was chosen as the surgical treatment. The exclusion criterion was total mesorectal resection. Screening criteria: (1) Patients with mid-low rectal cancer treated with intensity-modulated radiation therapy (IMRT); and (2) Patients who underwent transanal LE or transanal minimally invasive surgery (TAMIS). The study was approved by the medical ethics committee of the Peking University Cancer Hospital, and informed consent was waived (2015KT31/2017KT104).

#### IMRT

The IMRT regimen consisted of 22 fractions of 2.3 Gy (gross tumor volume, GTV) and 1.9 Gy (clinical target volume, CTV), which has been described in our previous report[19,20]: The total dose of 50.6 Gy (GTV)/41.8 Gy (CTV) was administered 5 times per week over a period of 30 days. IMRT was administered using the Varian Rapid Arc system. The GTV was defined as the primary tumor, including the mesorectum. The CTV was defined as the primary tumor, mesorectal region, presacral region, mesorectal lymph nodes, lateral lymph nodes, internal iliac lymph node chain, or pelvic wall area. Capecitabine treatment was administered concurrently with IMRT at a dose of 825 mg/m<sup>2</sup> orally, twice *per* day.

# LE

The patient was given general anesthesia. According to the location of the tumor, the lithotomy position (the tumor was located in the posterior wall of the rectum) or the jackknife position (the tumor was located in the anterior wall of the rectum) was used. Transanal LE or TAMIS surgery was performed by a skilled surgeon. Local full-thickness resection was performed using an ultrasonic scalpel or electric scalpel at a distance of 1cm from the tumor. The surgical wound was closed by continuous suture with barbed suture or intermittent suture with 4-0 absorbable sutures to ensure complete suture and no active bleeding. After flattening, the surgical specimen was fixed on a soft plate with a pin and sent to the pathology department for paraffin pathological examination. Negative margins were defined as microscopically confirmed full-thickness resections with a circumferential resection margin of 1 mm or more.

#### Follow up

Patients were regularly followed up every 3 months for the first 2 years and every 6 months thereafter for 3 years. After 5 years, follow-up visits were performed once a year until death or loss of follow-up. Follow-up examinations included digital rectal examination, serum tumor markers, thoracoabdominal/pelvic computed tomography or magnetic resonance imaging, and enteroscopy. Local recurrence-free survival (LRFS) was defined as the time from surgery to the local recurrence, final follow-up, or death (without recurrence or metastasis). Disease-free survival (DFS) was defined as the time from surgery to the first recurrence (local or distant), final follow-up, or death (without recurrence or metastasis). Overall survival (OS) was defined as the time from surgery to death from any cause or final follow-up. The follow-up information was obtained through telephone communication or inquiry into outpatient medical records.

#### Statistical analysis

Statistical analyses were performed using R software (4.0.4, R Foundation for Statistical Computing, Vienna, Austria). The 'survival' and 'survminer' package were used for survival analysis, and the 'ggplot2' package was used for plotting. The clinicopathological characteristics of patients were descriptive. The measurement variables were expressed as means and standard deviations. Count variables were expressed as percentages. The Kaplan-Meier method was used to draw the tumor-specific survival curve. The Log-rank test was used to examine differences in outcomes. Differences with *P*-values < 0.05 were considered statistically significant.

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# RESULTS

#### Basic information of patients

A total of 33 patients were included in this study, and the basic information is shown in Table 1. There were 16 (48.5%) males and 17 (51.5%) females, aged 61.0 (28.0-75.0) years; The median distance between the lower edge of the tumor and the anal verge was 3 (1.0-10.0) cm. The median interval time between NCRT and surgery was 25.4 (8.7-164.4) weeks. The median operation time was 57 (20.0-137.0) min. Four patients underwent salvage APR surgery, and organ preservation was achieved in 29/33 (87.9%) patients. The initial clinical T staging (cT): 9 (27.3%) patients were cT2, 19 (57.6%) patients were cT3, and 5 (15.2%) patients were cT4; The initial N staging (cN): 8 patients (24.2%) were cN negative, 25 patients (75.8%) were cN positive; The initial M stage (cM): 2 patients (6.1%) had distant metastasis (cM1), 31 (93.9%) patients had no distant metastasis (cM0).

# Treatment response of the patients

The pathological results: 18 (54.5%) patients were pathological T0 stage (ypT0), 6 (18.2%) patients were ypT1, 7 (21.2%) patients were ypT2, and 2 (6.1%) patients were ypT3. Table 2 shows the treatment response of the patients. For 9 cT2 patients, 5 (5/9, 55.6%) had a postoperative pathological result of ypT0. For 19 cT3 patients, 11 (57.9%) patients were ypT0, and 2 (40%) were ypT0 in 5 cT4 patients.

#### Perioperative complications of patients

Table 3 shows the perioperative complications of patients. The overall postoperative complication rate was 21.2% (7/33). The most common complication was bleeding (43%, 3/7), followed by chronic perineal pain and stenosis.

#### Long term of follow-up

The median follow-up time was 42.0 (4.0-93.5) months. For 31 patients with cM0, the 5-year DFS rate, 5-year LRFS rate, and 5-year OS rate were 88.4%, 96.7%, and 92.9%, respectively. Three patients (9.7%, 3/31) had disease progression, including 2 cases of distant metastasis (1 case of lung metastasis, 1 case of bone metastasis) and 1 case of local tumor recurrence and distant metastasis (sacrum and lung metastasis). After local recurrence or distant metastasis, patients received systemic combined local treatment, one patient achieved no evidence of disease status, and two patients died (Shown in Table 4). Figure 1, Figure 2, and Figure 3 show the survival of patients with different cT stages, ycT stages, and ypT stages. There were no significant differences between the cT groups concerning DFS, LRFS or OS in the Kaplan-Meier analysis. There were significant differences between the ycT groups (ycT  $\leq$  T1 vs ycT  $\geq$  T2) concerning either DFS (P = 0.042) or OS (P = 0.002) in the Kaplan-Meier analysis. The LRFS curve of ycT  $\leq$  T1 patients was better than that of ycT  $\geq$  T2 patients, and the *P* value was very close to 0.05 (P = 0.070). The DFS curve of patients with ypT  $\leq$  T1 was better than that of patients with ypT  $\geq$  T2, but the *P* value was not statistically significant (*P* = 0.560). There was a significant difference between the ypT groups (ypT  $\leq$  T1 vs ypT  $\geq$  T2) concerning OS (P = 0.014) in the Kaplan-Meier analysis. The LRFS curve of ypT  $\leq$  T1 patients was better than that of ypT  $\geq$  T2 patients, and the *P* value was very close to 0.05 (*P* = 0.070). Two patients with initial cM1 were alive at the last follow-up.

# DISCUSSION

There are few studies on LE after NCRT for rectal cancer, and there are significant differences in surgical indications, technical and pathological reports, postoperative complications, and survival [13,21,22]. The efficacy of LE in patients with different stages is inconsistent [23-26]. This study retrospectively collected the data of patients who underwent LE in our center and clarified the good organ preservation rate, oncological outcomes, and the safety and efficacy of LE after NCRT for rectal cancer. In addition, we found that for patients with initial cM1 and significant local tumor regression after preoperative treatment, LE combined with late systemic treatment also seems to have better clinical results. We believe that for highly selected patients, under the guarantee of salvage surgery and complete postoperative follow-up, the treatment strategy of LE with patient participation in decision-making after NCRT can not only obtain organ preservation but also achieve good long-term survival outcomes.

#### Safety and efficiency

Our results show that LE is feasible and effective for rectal cancer with significant tumor regression after NCRT. LE was successfully performed in all patients with a median postoperative hospital stay of 4 days. The median operation time was 57.0 minutes, the median intraoperative blood loss was about 10 mL, and no intraoperative adverse events occurred. These results are better than those of conventional TME surgery, which is consistent with the results reported in the metaanalysis[18]. Four patients underwent salvage APR surgery, and organ preservation was achieved in all 29 patients. Previous studies have found that the incidence of complications of LE after NCRT is not low, mainly manifested as incision dehiscence, bleeding, and pain [15-17,27]. Gascon et al [28] reported the results of local full-thickness excision for 404 patients with rectal adenoma or rectal cancer, with a complication rate of 12.6%, among which postoperative bleeding was the most common early complication, with an incidence rate of 8%, but the patients in this study did not receive radio chemotherapy before surgery. Geubels et al[29] reported LE in patients with regeneration after watch and wait (WW) and the authors believed that LE after radiotherapy had higher surgical complications compared with patients who did not receive radiotherapy. In our study, all patients received preoperative IMRT, which caused intestinal edema,



Table 1 Clinicopathological characteristics of 33 patients	
Variables	<i>n</i> (%) or median (range)
Age (years)	61.0 (28.0-75.0)
Gender	
Male	16 (48.5)
Female	17 (51.5)
Diameter of lesion (cm)	2.0 (1.0-3.0)
Distance from the anal verge (cm)	3.0 (1.0-10.0)
cT baseline	
1	0 (0.0)
2	9 (27.3)
3	19 (57.6)
4	5 (15.2)
cN baseline	
Negative	8 (24.2)
Positive	25 (75.8)
cM baseline	
M0	31 (93.9)
M1	2 (6.1)
ycT	
0	21 (63.6)
1	5 (15.2)
2	6 (18.2)
3	1 (3.0)
4	0 (0.0)
урТ	
0	18 (54.5)
1	6 (18.2)
2	7 (21.2)
3	2 (6.1)
4	0 (0.0)
Differentiation	
G1	3 (9.1)
G2	29 (87.9)
G3	1(3.0)
Baseline CEA	
Normal	32 (97.0)
Abnormal	1 (3.0)
Interval between NCRT and surgery (week)	25.4 (8.7-164.4)
Chemotherapy	
Cap	13 (39.4)
CapeOx	20 (60.6)
Surgical duration (minute)	57.0 (20.0-137.0)



Blood loss (mL)	10.0 (5.0-50.0)
Postoperative hospital stay (days)	4.0 (1.0-11.0)
Complication	
No complication	26 (78.8)
With complication	7 (21.2)
CD grade	
Grade I	1 (3)
Grade II	6 (18.2)
Grade III-IV	0 (0.0)
Recurrence	
No	31 (93.9)
Yes	2 (6.1)
Metastasis (cM0, $n = 31$ )	
No	28 (90.3)
Yes	3 (9.7)
Follow-up time (month)	42.0 (4.0-93.5)

CEA: Carcinoembryonic antigen; NCRT: Neoadjuvant chemoradiotherapy; CD: Clavien dindo; Cap: Capecitabine; CapeOx: Capecitabine + oxaliplatin.

Table 2 Clinical-pathological response to neoadjuvant chemoradiation, n (%)							
Pre-cT	ypT after local excision						
	урТ0	ypT1	урТ2	урТ3			
cT2 ( <i>n</i> = 9)	5 (55.6)	2 (22.2)	2 (22.2)	0 (0.0)			
cT3 ( <i>n</i> = 19)	11 (57.9)	3 (15.8)	4 (21.1)	1 (5.3)			
cT4 ( <i>n</i> = 5)	2 (40.0)	1 (20.0)	1 (20.0)	1 (20.0)			

#### Table 3 Patients with perioperative complications

Gender	Age	Neoadjuvant	Interval from NCRT to local excision (week)	Type of complications	Clavien-Dindo grades
Male	74	NCRT	69	Bleeding	Ш
Male	68	NCRT	18	Bleeding	Ι
Female	59	NCRT	11	Perineal pain	Ш
Female	71	NCRT	11	Perineal pain	Ш
Male	40	NCRT + CapOx	24	Perineal pain + stricture	П
Male	56	NCRT + CapOx	59	Pain + fecal incontinence	Ш
Female	66	NCRT + CapOx	32	Bleeding + pain	Ш

NCRT: Neoadjuvant chemoradiotherapy; CapOx: Capecitabine + oxaliplatin.

fibrosis changes, and relatively poor intestinal quality, which could explain the high overall complication rate of 21.2% (7/33). The most common complication was chronic perineal pain (71.4%, 5/7), followed by bleeding (43%, 3/7), stenosis (14.3%, 1/7), and fecal incontinence (14.3%, 1/7). However, all complications were grade I-II and improved after the drug or conservative treatment, and no serious postoperative adverse events occurred. Therefore, we believe that LE has good safety for rectal cancer with a good response after NCRT. There is no unified standard for LE after chemoradiotherapy. The experience of our center is as follows: For residual tumors or scars after chemoradiotherapy, it is recommended to perform localized scar and full-thickness bowel wall resection followed by full-thickness suture. Because the defect of the intestinal wall after tumor resection, especially the significant retraction of the mucosa, will make the tension of the

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#### Table 4 Patients with disease progression after local excision

					<u> </u>									
	Primary staging			ing		Response		Disease progression			Prognosis			
Patient (sex/age)	сТ	cN	сМ	High- risk factor (s)	NCRT	Interval time (week)	mrTRG	урТ	Local recurrence	Distant metastasis	Treatment	DFS (month)	OS (month)	Status
Male/74	T4	N1	cM0	cT4	NCRT	8.7	0	ypT0	Negative	Bone	С	9.3	64.6	Dead
Female/57	T3	N2	cM0	EMVI+	NCRT + CapOx2	9	0	ypT0	Negative	Lung	C+ resection	27.5	76.5	Alive (NED)
Female /61	T2	N2	cM0	N2	NCRT	101	3	ypT0	Positive	Sacrum and Lung	Resection	6.1	49.4	Dead
Female /36	T4	N1	cM1	cT4	CRT + CapOx2	19	2	ypT2	Negative	Lung	C+ resection		42.0	Alive (NED)
Female /30	T4	N2	cM1	cT4	CRT+CapOx1	36	1	ypT0	Positive	Liver	Resection		27.5	Alive (NED)

NCRT: Neoadjuvant chemoradiotherapy; EMVI: Extramural venous invasion; DFS: Disease-free survival; OS: Overall survival; NED: No evidence of disease; CapOx: Capecitabine + oxaliplatin.



Figure 1 The prognosis analysis of 31 cM0 patients by Kaplan–Meier curves for cT stage groups. A: Local recurrence-free survival curves (P = 0.127); B: Disease-free survival curves (P = 0.945); C: Overall survival curves (P = 0.838). LRFS: Local recurrence-free survival; DFS: Disease-free survival; OS: Overall survival.

primary suture high. So the problems of incision dehiscence, dead space, and infection caused by large-scale mucosal resection and simple mucosal suture should be avoided. For the mass of the anterior wall, attention should be paid to the protection of the prostate or vagina with a rich blood supply during the suture, to avoid intraoperative or postoperative bleeding.

#### Prognosis

As a surgical treatment method that ignores the whole mesentery, LE breaks the long-standing principle of TME, but local recurrence is its Achilles heel, and patients with different T stages have different recurrence rates[30]. In a multicenter prospective study of LE in T1 patients and LE plus adjuvant chemoradiotherapy in T2 patients, the 7-year local recurrence rate was 8% in T1 patients and 18% in T2 patients[23]. A systematic review including 20 studies and 1068 patients showed that the local recurrence rate of ypT0 patients was 4%, and that of ypT1-3 patients was more than 21.9% [31]. In our study, the local recurrence rate was 0% (0/17) in patients with ypT0 and 7.1% (1/14) in patients with ypT1-3. No recurrence or metastasis events occurred in the 2 patients with ypT3. One of the patients with ypT3 underwent salvage surgery, and the other patient refused salvage surgery and took an observation strategy. Local recurrence occurred in only 1 (ycT2/ypT2) of 31 patients with cM0 rectal cancer and did not result in uncontrolled regional disease. Our study showed a very high local control rate, and the overall 5-year LRFS rate was 96.7%. The 5-year DFS rate was 88.4%, which is similar to CARTS Study[9], but our study had more clinical stage III patients and a better local recurrence rate. Although 3 patients (9.7%, 3/31) had disease progression (recurrence and/or metastasis), the OS of the patients after systemic therapy was up to 76.5 months, and the 5-year OS rate was 92.9%, showing a good survival result. Similar to our findings, ACOSOG Z6041 also showed favorable oncological outcomes. When the authors performed NCRT plus LE





Figure 2 The prognosis analysis of 31 cM0 patients by Kaplan– Meier curves for ycT stage groups. A: Local recurrence-free survival curves (*P* = 0.070); B: Disease-free survival curves (*P* = 0.042); C: Overall survival curves (*P* = 0.002). LRFS: Local recurrence-free survival; DFS: Disease-free survival; OS: Overall survival.



Figure 3 The prognosis analysis of 31 cM0 patients by Kaplan–Meier curves for ypT stage groups. A: Local recurrence-free survival curves (P = 0.070); B: Disease-free survival curves (P = 0.560); C: Overall survival curves (P = 0.014). LRFS: Local recurrence-free survival; DFS: Disease-free survival; OS: Overall survival.

surgery in T2N0 patients, distant recurrence occurred in 6% of patients and local recurrence occurred in 4% of patients, resulting in 3-year disease-free and OS rates of 88% and 95%, respectively[15]. We believe that this better prognosis result was due to patient screening. In our study, after intensive NCRT, most of the patients were the ypT0-2 stage, and only 2 were ypT3 stage. On the other hand, salvage surgery based on postoperative pathology ensures a good prognosis for patients. The 2 initial M1 patients were both alive at the last follow-up, and the OS was 27.5 months and 42.0 months, respectively, which achieved a good prognosis but needed more data support. We believe that for highly selected patients, under the guarantee of salvage surgery and complete postoperative follow-up, the treatment strategy of LE after NCRT can not only obtain organ preservation but also achieve good long-term survival outcomes.

Our study did not involve the analysis of predictive factors for tumor recurrence and metastasis. However, the KM survival curve showed that the LRFS, DFS, and OS curves of patients with earlier ycT and ypT stages (ycT  $\leq$  T1 and ypT  $\leq$  T1) were better than those of other patients. Previous reports have shown that the pT stage, sm stage, tumor grading, histological risk status, and local surgical resection technique are independent risk factors for local recurrence[6,32]. Other studies have also shown a large difference in the recurrence rate of different T stages. It has been reported that the 5-year LRFS after local resection is 28%, which is 18% in T1 patients and 47% in T2 patients[30]. In our study, the 5-year LRFS rates of patients with ycT0-1 and ypT0-1 were both 100%, so we should strengthen the follow-up of patients with ypT2 and more after LE.

Our study had some limitations. First, it was a retrospective study. High-quality prospective randomized controlled studies may be needed to verify our better results. Second, the number of patients is not large, and this limited our statistical analyses, and we may need to expand the sample size for further verification.

#### Prospect

For rectal cancer patients with near-cCR after NCRT, selective implementation of LE is a safe and effective treatment strategy. For patients judged as cCR or possible pCR, the non-surgical strategy of the WW strategy can be selected[11]. Even in the WW process, early local regeneration followed by LE is a safe and effective treatment strategy. So, we



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emphasize the importance of predicting tumor response to NCRT, which is also described in our other article. Minimally invasive or nonsurgical treatment with patient participation in decision-making can be performed for highly selected patients.

# CONCLUSION

LE for rectal cancer with significant tumor regression after NCRT can obtain better safety, efficiency, and oncological prognosis. Minimally invasive or nonsurgical treatment with patient participation in decision-making can be performed for highly selected patients. More studies are needed to verify this result.

# FOOTNOTES

Author contributions: Chen N and Li CL performed the data collection and analysis, and wrote the paper; Chen N, Wang L, Yao YF, Peng YF, Zhan TC, Zhao J and Wu AW helped the recruitment of patients; Wu AW designed study.

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ORIGINAL ARTICLE

# **Retrospective Study** Risk factors for hepatocellular carcinoma in cirrhosis: A comprehensive analysis from a decade-long study

Da-Qiong Zhou, Jiang-Yu Liu, Feng Zhao, Jing Zhang, Li-Li Liu, Jian-Ru Jia, Zhen-Huan Cao

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# Abstract

# BACKGROUND

Cirrhosis is a significant risk factor for the development of hepatocellular carcinoma (HCC). Variability in HCC risk among patients with cirrhosis is notable, particularly when considering the diverse etiologies of cirrhosis.

# AIM

To identify specific risk factors contributing to HCC development in patients with cirrhosis.

# **METHODS**

This retrospective study analyzed data from cirrhotic patients at Beijing Youan Hospital from January 1, 2012 to September 30, 2022 with at least 6 mo of followup. Patient demographics, medical histories, etiologies, and clinical characteristics were examined. Cox regression analysis was used to analyze correlations of the above parameters with hepatocarcinogenesis, while competing risk regression was used to estimate their adjusted hazard ratios accounting for death. The cumulative incidence was plotted over time.

# RESULTS

Overall, 5417 patients with cirrhosis (median age: 54 years; 65.8% males) were analyzed. Hepatitis B virus (HBV) was the most common etiology (23.3%), with 25% (n = 1352) developing HCC over a 2.9-year follow-up period. Patients with multiple etiologies had the HCC highest incidence (30.3%), followed by those with HBV-related cirrhosis (29.5%). Significant risk factors included male sex,



advanced age, hepatitis C virus (HCV) infection, elevated blood ammonia, and low platelet count. Men had a higher 5-year HCC risk than women (37.0% *vs* 31.5%). HBV, HCV, and HBV/HCV co-infected patients had 5-year risks of HCC of 45.8%, 42.9%, and 48.1%, respectively, compared to 29.5% in nonviral hepatitis cases, highlighting the significant HCC risk from viral hepatitis, especially HBV, and underscores the importance of monitoring these high-risk groups.

#### CONCLUSION

In conclusion, HBV-related cirrhosis strongly correlates with HCC, with male sex, older age, viral hepatitis, elevated blood ammonia, and lower albumin and platelet levels increasing the risk of HCC.

Key Words: Cirrhosis; Hepatocellular carcinoma; Risk factors; Hepatitis B virus; Competing risk analysis

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**Core Tip:** Our retrospective analysis spanned a decade (January 1, 2012 to September 30, 2022) and included 5417 patients from Beijing Youan Hospital, Capital Medical University. Using Cox regression and competing risk regression models, we identified several key factors that significantly contributed to the risk of hepatocellular carcinoma in patients with cirrhosis. Specifically, this study underscores the increased association of hepatitis B cirrhosis with hepatocellular carcinoma incidence and highlights other significant risk factors, including male sex, advanced age, viral hepatitis-related cirrhosis, elevated blood ammonia, and lower albumin and platelet levels.

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#### INTRODUCTION

Cirrhosis is a major cause of morbidity and mortality in patients with chronic liver disease[1]. In 2019, 2.4% of the global deaths were related to cirrhosis. It is among the top 20 causes of death worldwide[2]. Abnormalities in liver function of patients with cirrhosis include varices, gastrointestinal bleeding, ascites, and hepatic encephalopathy. Hepatocellular carcinoma (HCC) is a serious complication. The prognosis of HCC is usually poor[3]. According to global burden statistics, there were approximately 534000 liver cancer cases and 485000 deaths in 2019[4]. With over 290000 people diagnosed with liver cancer and approximately 188000 deaths from liver cancer in 2019[5], China has the highest burden of liver cancer worldwide.

Major causes of cirrhosis include chronic viral hepatitis, such as hepatitis B virus (HBV) and hepatitis C virus (HCV), chronic alcohol abuse, metabolic disorders, and autoimmune liver diseases. Specifically, HBV infection is the leading cause of liver cancer-related mortality and the third leading cause of cirrhosis[6]. While antiviral therapies for chronic hepatitis B have shown efficacy in reducing the risk of cirrhosis, decompensation, and HCC, their ability to significantly affect HBV-related mortality trends remains limited[7]. As of 2019, only 10.3% of chronic HBV infections have been diagnosed, of which only 22.7% are eligible for antiviral treatment[8]. Despite a notable decline in HBV and HCV incidences, China continues to bear the highest global disease burden for HBV (74 million) and HCV (9.48 million) infections, attributed to its vast patient population[9]. Concurrently, the rise in alcohol-associated cirrhosis (AC) and metabolic dysfunction-associated liver disease (MASLD) parallels lifestyle shifts and economic progression, increasing the annual prevalence of advanced liver diseases and the overall disease burden[10].

Cirrhosis is a major risk factor for HCC, with autopsy studies showing cirrhosis in 80%-90% of cases worldwide. In areas with high HBV prevalence, cirrhotic individuals have triple the risk of developing HCC compared to non-cirrhotic individuals and 16 times that of inactive HBV carriers[11]. Beyond progression to HCC, patients with cirrhosis also face an increased risk of liver complications and mortality, particularly as the disease progresses from the compensated to the decompensated stages[12]. The survival rates at 1 and 5 years for patients with compensated cirrhosis were 87% and 67%, in contrast to 75% and 45%, respectively, for patients with decompensated cirrhosis. Compared to the general population, mortality increases five-fold in patients with compensated cirrhosis and ten-fold in decompensated cirrhosis[13]. Notably, chronic comorbidities such as chronic kidney and cardiovascular diseases are often associated with death due to compensatory cirrhosis[14].

To gain a deeper understanding of the prognosis of cirrhosis with different etiologies and liver function states, this retrospective observational study retrieved data from patients with cirrhosis hospitalized at Beijing Youan Hospital over the past 10 years. This study aimed to better understand and guide the clinical management of cirrhosis, as well as to improve the prognosis and personalized treatment planning for patients with cirrhosis.

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# MATERIALS AND METHODS

#### Research population

Patients with cirrhosis who were admitted to our hospital from January 1, 2012 to September 30, 2022 were identified from our inpatient system based on the diagnosis code K74 (cirrhosis). The main inclusion criteria were: (1) Diagnosis of cirrhosis based on histology (liver biopsy), imaging (evidence of esophagogastric fundal varices, portal hypertension, splenomegaly, and ascites), or noninvasive examination (FibroScan); (2) Two or more hospitalizations; (3) No diagnosis of HCC at the initial hospitalization and within 6 mo of initial admission; and (4) A minimum of 6 mo of follow-up. Patients with other combined malignancies or those who underwent liver transplantation were excluded.

The time of first admission was defined as the baseline, and clinical characteristics at baseline were collected, including demographics (sex, age, and place of origin), comorbidities (diabetes mellitus, hypertension, and coronary artery disease), liver disease-related complications (esophagogastric fundal varices, gastrointestinal bleeding, ascites, abdominal infections, hepatic encephalopathy, and hepatorenal syndrome), etiology [HBV, HCV, AC, MASLD, primary biliary cirrhosis (PBC), drug-induced cirrhosis, cryptogenic cirrhosis, and mixed cirrhosis], laboratory findings, and liver function scores (model for end-stage liver disease score and Child-Pugh classification).

#### Endpoint events

The primary endpoint was HCC. Observational endpoint was the time to first document HCC. For patients who did not develop HCC, the observational endpoint was death or time to the last follow-up. Death was a competing risk event for hepatocarcinogenesis because patients with cirrhosis who died were no longer at risk of developing HCC.

#### Statistical analysis

Pearson  $\chi^2$  test and Wilcoxon signed-rank test were used to evaluate correlations of categorical and continuous variables with HCC occurrence for clinical characteristics and laboratory values, respectively. The results are expressed as percentages and interquartile ranges. Only patients with cirrhosis for at least 6 mo from baseline to endpoint events were included in the analysis of all HCC-associated risk factors.

Multiple imputations were used to adjust for missing values of all variables. Cox proportional hazards regression analysis was performed on the imputed data set. Clinical and demographic variables that differed significantly between the groups (P < 0.05) were included in the first statistical step of the model by univariate analysis using both forward and backward stepwise Cox regressions. The same set of seven significant risk factors were selected: Age, sex, history of HBV/HCV infection, albumin level, globulin level, platelet count, and blood ammonia level.

The decompensation rate in patients with cirrhosis was 76.6%. Death was considered a competing risk event when assessing the incidence of HCC in patients with decompensated cirrhosis to obtain a reliable risk estimate because the potential risk of death is high[15]. Cox regression analyses were performed for selected multivariate risk factors from the Cox analysis. We then calculated adjusted hazard ratios (aHRs). A fine and gray regression model was used to estimate the cumulative incidence function (CIF) for HCC development in cirrhotic patients of different sexes, ages, and etiologies.

All statistical analyses in this study were performed using R version 4.2.0 and IBM Statistical Product and Service Solutions 27.0.

# RESULTS

#### Patient characteristics at first admission

Overall, 5417 patients were included (Figure 1). The median age was 54 years, 3567 (65.8%) patients were male, and 4149 (76.6%) had decompensated cirrhosis. Etiological distribution of cirrhosis is shown in Figure 2: 1261 cases (23.3%) of HBV; 354 cases (6.5%) of HCV; 1274 cases (23.5%) of AC; 51 cases (0.9%) of MASLD; 470 cases (8.7%) of PBC; 66 cases (1.2%) of drug-induced cirrhosis; 1459 cases (26.9%) of cryptogenic cirrhosis; and 482 cases (8.9%) of mixed cirrhosis (two or more etiologies).

HCC occurred in 1352 patients (25%) and 4065 patients did not develop HCC during the in-hospital follow-up period. There were 262 deaths (4.84%) due to complications or other comorbidities among the patients who did not develop HCC

Based on the occurrence of HCC during follow-up, the observational cohort was divided into HCC and non-HCC groups. The demographic characteristics of the cohort at baseline are presented in Table 1. Patients in the HCC group were more likely to be male (71.7% vs 63.9%, P < 0.001). The median age of the patients was slightly higher (56 vs 54 years, P < 0.001). Decompensated cirrhosis was more common in patients with HCC than in those without (77.5% vs 73.9%), and a greater proportion of patients with HCC had Child-Pugh grades A and B (32.6% vs 29.5% and 49.1% vs 48.0%, respectively, P = 0.003). Gastrointestinal bleeding was more common in patients without HCC (24.1% vs 18.0%).

#### Risk assessment of HCC in patients with cirrhosis

There was a significant difference in the risk of HCC among patients with cirrhosis of different etiologies (P < 0.001). Cirrhotic patients with two or more etiologies had the highest incidence of HCC among all patients with cirrhosis during the entire follow-up period, at 30.3% (Figure 3A), and their mean time to the development of HCC was also the shortest at 5.3 years [95% confidence interval (CI): 4.9-5.7] (Figure 3B). In contrast, patients with HBV cirrhosis had the highest incidence of HCC among single etiologies, at 29.5%, with a median time to HCC was 5.4 years (95%CI: 5.1-5.6 years).



Table 1 Demographic and clinical characteristics							
Parameter	HCC cases ( <i>n</i> = 1352)	Non-HCC controls ( <i>n</i> = 4065)	<i>P</i> value				
Sex (Male), <i>n</i> (%)	969 (71.7)	2598 (63.9)	< 0.001				
Age	56 (50, 62)	54 (46, 62)	< 0.001				
Hypertension, <i>n</i> (%)	255 (18.9)	727 (17.9)	0.419				
Diabetes, n (%)	321 (23.7)	860 (21.2)	0.046				
Coronary disease, <i>n</i> (%)	35 (2.6)	154 (3.8)	0.037				
Gastrointestinal bleeding, n (%)	243 (18.0)	978 (24.1)	< 0.001				
Hepatic encephalopathy, $n$ (%)	219 (16.2)	633 (15.6)	0.584				
Decompensated cirrhosis, n (%)	999 (73.9)	3150 (77.5)	0.007				
Child-Pugh grade A, $n$ (%)	430 (32.6)	1162 (29.5)	0.003				
Child-Pugh grade B, $n$ (%)	648 (49.1)	1893 (48.0)					
Child-Push grade C, $n$ (%)	241 (18.3)	890 (22.6)					
HBV, <i>n</i> (%)	372 (27.5)	889 (21.9)	< 0.001				
HCV, <i>n</i> (%)	93 (6.9)	261 (6.4)					
AC, n (%)	261 (19.3)	1013 (24.9)					
MASLD, <i>n</i> (%)	9 (0.7)	42 (1.0)					
PBC, <i>n</i> (%)	72 (5.3)	398 (9.8)					
Drug-induced cirrhosis, n (%)	12 (0.9)	54 (1.3)					
Cryptogenic cirrhosis, n (%)	387 (28.6)	1072 (26.4)					
Mixed cirrhosis, n (%)	146 (10.8)	336 (8.3)					
ALT (U/L)	31.1 (21.2, 53.1)	27.0 (18.2, 47.5)	< 0.001				
AST (U/L)	47.7 (31.7, 77.4)	44 (29.1, 79.9)	< 0.001				
Albumin (g/L)	31.2 (27.4, 34.6)	30.7 (26.8, 34.8)	0.106				
Globin (g/L)	31.6 (26.5, 37.1)	31.3 (25.7, 38.0)	0.268				
INR	1.27 (1.12, 1.45)	1.32 (1.16, 1.54)	0.002				
Prothrombin time (S)	14.2 (12.6, 16.3)	14.8 (13.0, 17.4)	0.017				
Direct bilirubin (µmol/L)	11.0 (6.3, 19.2)	12.7 (6.6, 33.6)	0.001				
Triglycerides (mmol/L)	0.81 (0.62, 1.11)	0.89 (0.67, 1.26)	< 0.001				
Platelets (× $10^9/L$ )	78 (54, 109)	80 (54, 118)	0.096				
γ-GT (U/L)	50.1 (26.0, 119.8)	53.7 (25.4, 143.8)	0.157				
AFP (ng/mL)	4.64 (2.60, 10.35)	3.36 (2.02, 6.26)	< 0.001				
CA19-9 (U/mL)	26.72 (13.76, 48.40)	25.00 (11.93, 52.82)	0.070				
Neutrophils (× 10 <sup>9</sup> /L)	2.30 (1.59, 3.44)	2.43 (1.59, 3.76)	0.024				
Serum ammonia (µg/dL)	73 (51, 95)	67 (46, 95)	< 0.001				
MELD	8 (4, 12)	10 (5, 15)	< 0.001				

HBV: Hepatitis B virus; HCV: Hepatitis C virus; AC: Alcohol-associated cirrhosis; MASLD: Metabolic dysfunction-associated liver disease; PBC: Primary biliary cirrhosis; Mixed cirrhosis: Cirrhosis caused by two or more etiologies; MELD: Model for end-stage liver disease; ALT: Alanine aminotransferase; AST: Aspartate transaminase; INR: International normalized ratio; γ-GT: Gamma-glutamyltransferase; AFP: Alpha fetoprotein; CA: Carbohydrate antigen; HCC: Hepatocellular carcinoma.

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Figure 1 Flowchart of the cohort included in the analysis. HCC: Hepatocellular carcinoma.



Figure 2 Distribution of etiology. HBV: Hepatitis B virus; HCV: Hepatitis C virus; AC: Alcohol-associated cirrhosis; MASLD: Metabolic dysfunction-associated liver disease; PBC: Primary biliary cirrhosis.

Among cirrhotic patients in this study cohort, higher Child-Pugh grades were associated with a lower risk of HCC and shorter survival: The incidence of HCC was 21.3% in patients with Child-Pugh grade C (Figure 3C), and the mean survival was 6.1 years (95%CI: 5.8-6.5 years) (Figure 3D). Compared to compensated cirrhosis, decompensated cirrhosis had a shorter mean time to HCC [6.4 years (95%CI: 6.3-6.6 years) *vs* 6.8 years (95%CI: 6.5-7.1 years)].

#### Risk factors associated with the development of HCC

To investigate the risk factors associated with the development of HCC, one-way Cox regression analysis of possible influencing factors was performed, and the following 15 clinical characteristics and laboratory markers were associated with HCC (P < 0.05): Age, sex, HBV/HCV history, compensation status, diabetes history, albumin, globulin, international normalized ratio, prothrombin time, triglycerides, platelets, serum ammonia, and child classification. From these candidate risk factors, the same set of seven significant risk factors (age, sex, HBV/HCV history, albumin, globulin, platelet count, and serum ammonia) was selected using forward and backward stepwise Cox regression, as shown in Table 2.

Considering death as a competing risk event for hepatocarcinogenesis, competing risk regression analysis was performed on the risk factors examined in the Cox regression analysis, and the aHRs of these risk factors were estimated. The results of this analysis are presented in Table 2. In the competing risk regression analysis, a higher risk of liver cancer was associated with male sex (aHR = 1.482; 95% CI: 1.313-1.673), advanced age (aHR = 1.025; 95% CI: 1.020-1.030), HBV infection (aHR = 1.950; 95% CI: 1.734-2.193), HCV infection (aHR = 1.533; 95% CI: 1.274-1.846), and co-infection of HBV and HCV (aHR = 2.074; 95% CI: 1.038-4.143), and higher blood ammonia levels (aHR = 1.002; 95% CI: 1.001-1.003), globulin levels (aHR = 1.012; 95% CI: 1.005-1.019), and lower platelet count (aHR = 0.998; 95% CI: 0.998-1.000) at baseline also

#### Table 2 Hepatocarcinogenesis hazard ratio in Cox and competing risk regression analysis

Parameter	Univariate Cox regression analysis		Multivariable Cox re analysis	egression	Multivariable competitive risk regression analysis	
	aHR (95%CI)	P value	aHR (95%CI)	P value	aHR (95%CI)	P value
Age	1.023 (1.018-1.027)	< 0.001	1.029 (1.024-1.034)	< 0.001	1.025 (1.020-1.030)	< 0.001
Sex (male)	1.321 (1.174-1.487)	< 0.001	1.537 (1.359-1.738)	< 0.001	1.482 (1.313-1.673)	< 0.001
Diabetes	1.155 (1.019-1.309)	0.025				
Hypertension	1.128 (0.984-1.292)	0.084				
Coronary disease	0.951 (0.680-1.330)	0.769				
HBV	1.801 (1.602-2.025)	< 0.001	1.963 (1.742-2.211)	< 0.001	1.950 (1.734-2.193)	< 0.001
HCV	1.837 (1.352-1.981)	< 0.001	1.567 (1.293-1.900)	< 0.001	1.533 (1.274-1.846)	< 0.001
HBV and HCV	2.062 (1.068-3.980)	0.031	2.456 (1.270-4.747)	0.008	2.074 (1.038-4.143)	0.039
Decompensation	1.146 (1.015-1.295)	0.028				
ALT	1.000 (1.000-1.000)	0.974				
AST	1.000 (1.000-1.000)	0.815				
Albumin	0.976 (0.967-0.985)	< 0.001	0.986 (0.977-0.995)	0.002	0.995 (0.987-1.005)	0.381
Globulin	1.017 (1.010-1.023)	< 0.001	1.016 (1.009-1.023)	< 0.001	1.012 (1.005-1.019)	< 0.001
INR	1.271 (1.084-1.490)	0.003				
Prothrombin time	1.016 (1.002-1.031)	0.024				
Direct bilirubin	1.000 (0.999-1.001)	0.943				
Triglycerides	0.854 (0.776-0.939)	0.001				
Hemoglobin	1.004 (1.002-1.006)	< 0.001				
γ <b>-</b> GT	1.000 (0.999-1.000)	0.075				
AFP	1.000 (1.000-1.001)	0.543				
CA19-9	1.000 (0.999-1.001)	0.713				
Platelets	0.999 (0.998-1.000)	0.017	0.999 (0.998-1.000)	0.015	0.998 (0.998-1.000)	0.011
Neutrophils	0.998 (0.976-1.020)	0.829				
Serum ammonia	1.002 (1.001-1.003)	0.004	1.002 (1.001-1.003)	0.003	1.002 (1.001-1.003)	< 0.001
MELD	0.999 (0.990-1.008)	0.843				

HBV: Hepatitis B virus; HCV: Hepatitis C virus; MELD: Model for end-stage liver disease; ALT: Alanine aminotransferase; AST: Aspartate transaminase; INR: International normalized ratio; γ-GT: Gamma-glutamyltransferase; AFP: Alpha fetoprotein; CA: Carbohydrate antigen; aHR: Adjusted hazard ratio; CI: Confidence interval.

#### showed a significant association with liver cancer risk.

Based on the CIF curves from the competing risk regression analyses (Figure 4A), the risk of HCC in these hospitalized cirrhotic patients was 19.2% (95%CI: 17.9%-20.5%) at 3 years, and 35.2% (95%CI: 33.4%-37.0%) at 5 years. In these patients with cirrhosis, the risk of total mortality was 1.49% (95%CI: 1.15%-1.83%) at 1 year, 4.83% (95%CI: 4.17%-5.50%) at 3 years, and 6.66% (95%CI: 5.81%-7.51%) at 5 years. Men had a higher risk of HCC than women, with a 5-year risk of 37.0% (95%CI: 34.8%-39.3%) *vs* 31.5% (95%CI: 28.4%-34.7%) (Figure 4B). The risk of HCC increased with age, and the 5-year risk of HCC for decreasing age by 10 years (44) *vs* increasing age by 10 years (64), based on a median age of 54 years, was 23.6% (95%CI: 12.9%-34.3%) *vs* 42.4% (95%CI: 29.2%-55.7%) (Figure 4C). The 5-year risk of HCC in cirrhotic patients with HBV, HCV, and HBV/HCV coinfection was 45.8% (95%CI: 42.1%-49.4%), 42.9% (95%CI: 35.9%-49.9%), and 48.1% (95%CI: 20.2%-75.9%), respectively, whereas the 5-year risk of HCC in cirrhotic patients with nonviral hepatitis was only 29.5% (95%CI: 27.3%-31.7%) (Figure 4D).

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Figure 3 Incidence of hepatocellular carcinoma in cirrhotic patients with different etiologies. A and C: Child-Pugh grades; B and D: Mean time to occurrence. HBV: Hepatitis B virus; HCV: Hepatitis C virus; AC: Alcohol-associated cirrhosis; MASLD: Metabolic dysfunction-associated liver disease; PBC: Primary biliary cirrhosis.

# DISCUSSION

In this study, we found that patients with hepatitis B cirrhosis had the highest incidence of HCC and the shortest median survival among all causative factors in this retrospective cohort study of hospitalized patients with cirrhosis. The risk of HCC at 5 years was 45.8% (95%CI: 42.0%-49.4%). Among patients with cirrhosis, male sex, older age, and a history of chronic HBV and HCV infections were risk factors for the development of HCC after adjusting for death as a competing risk. Compared with non-viral cirrhosis, viral cirrhosis had a higher cumulative risk of developing HCC within 5 years: 45.3% (95%CI: 42.0%-48.5%) *vs* 29.5% (95%CI: 27.3%-31.7%).

The Western Pacific Region, including China, has the highest prevalence of HBV infection among patients with cirrhosis (59%), according to the World Health Organization regional classification[16]. These statistics were based on the leading causes of cirrhosis reported between 1993 and 2021. The burden of alcohol-related liver disease, cirrhosis, and HCC is expected to increase with an increase in global alcohol consumption *per* capita[17]. In our study, 1261 cases (23.3%) of HBV, 1274 cases (23.5%) of AC, and 1459 cases (26.9%) of cryptogenic cirrhosis were the three main etiologies. The proportion of AC almost reached the level of HBV-associated cirrhosis, and even exceeded that of cirrhotic patients with chronic hepatitis B. Screening for alcohol use disorders is urgent. In addition, the prevalence of MASLD by imaging has been estimated to be 25.24% (95%CI: 22.10%-28.65%) worldwide and 27.37% (95%CI: 23.29%-31.88%) in Asia[10]. This study found a significant number of patients with cryptogenic cirrhosis. We speculate that most patients with cryptogenic cirrhosis have a long history of cirrhosis would develop MASLD. The likely reason is that most hospitalized patients with cirrhosis have a long history of cirrhosis and the initial steatosis has progressed to significant liver fibrosis, making the specific etiology difficult to trace.

Among patients with compensated viral cirrhosis, the cumulative risk of HCC varies according to etiology. The cumulative incidences of HCC in hepatitis B surface antigen (HBsAg), HCV, and HBsAg/HCV positive patients were 10%, 21%, and 23%, respectively, at 5 years, and 16%, 28%, and 45%, respectively, at 10 years[18]. Without HBV and HCV infection, patients with compensated alcoholic cirrhosis have a lower incidence of HCC, with cumulative 1 and 2-year incidence rates of 1% and 5%, respectively[19,20], but a significantly higher risk of death[21]. A prospective study reported that the estimated risk of developing HCC was lower than the observed incidence (2.4% at 1 year and 7.3% at 3 years) in the majority (77.6%) of patients with decompensated cirrhosis. However, only 11.6% of the patients have a 3-



Figure 4 Cumulative incidence curves for overall hepatocellular carcinoma. A: Mortality; B: Sex; C: Age; D: Etiology. HBV: Hepatitis B virus; HCV: Hepatitis C virus; HCC: Hepatocellular carcinoma.

year risk, ranging from 10% to 47%[22]. Our study yielded similar results, showing that HBV and HCV infections were associated with a higher risk of HCC after considering death as a competing risk factor for hepatocarcinogenesis. Among cirrhotic patients with HBV, HCV, and HBV/HCV coinfection, the 5-year risk of HCC was 45.8%, 42.9%, and 48.1%, respectively, whereas the 5-year risk of HCC was only 29.5% in patients with cirrhosis who had never had hepatitis.

Male sex and advanced age are risk factors for developing HCC in patients with cirrhosis[5,23], and our study reported similar results. Furthermore, predictors of HCC in patients with cirrhosis include baseline objective and conventional risk indicators, including alpha-fetoprotein, albumin, alanine aminotransferase, and platelet levels[24]. In patients with AC, baseline bilirubin and prothrombin levels were associated with the risk of HCC in a prospective analysis[19]. Our study showed that in addition to sex, age, and hepatitis virus infection, baseline albumin and globulin levels, as well as platelet and blood ammonia levels, were equally significant risk factors for HCC. The differences in the roles of these conventional risk indicators in different studies may be related to the varying etiologic distributions and hepatic function compensation statuses in the corresponding study populations.

Over 10 years of follow-up, large sample size, and detailed objective baseline biochemical data are the strengths of our study. However, there are several limitations to this study: (1) There is no data on the effect of therapeutic interventions in reducing HCC risk; and (2) Our data were collected retrospectively and may be subject to biases associated with retrospective studies. Additionally, there may have been unmeasured confounders, such as family history of cirrhosis, which were not included in the multivariate analysis.

In conclusion, our study showed that viral hepatitis cirrhosis increased the risk of HCC. Male sex and older age are consistently associated with a higher risk of developing HCC in patients with cirrhosis. Furthermore, high blood ammonia levels, and low albumin and platelet levels may predict a higher risk of HCC. These findings emphasize the need to strengthen the management of objective biochemical parameters in patients with cirrhosis.

# CONCLUSION

Of the 5417 patients included, 1352 developed HCC and 262 died. The risk of developing HCC was 19.2% (95%CI: 17.9%-20.5%) at 3 years and 35.2% (95%CI: 33.4%-37.0%) at 5 years. Male sex, older age, and viral hepatitis and cirrhosis were



associated with a higher risk of HCC. Increased risk of HCC may also be associated with lower albumin and platelet levels, higher globulin levels, and higher baseline blood ammonia levels.

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# FOOTNOTES

Author contributions: Zhou DQ, Liu JY, and Zhao F analyzed the data and wrote the manuscript; Zhang J and Liu LL collected the data and contributed analytic tools; Jia JR and Cao ZH designed the research study and revised the manuscript.

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ORIGINAL ARTICLE

# **Retrospective Study** Prognosis of radiotherapy for esophageal cancer in elderly patients exceeding seventy-five years old

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# Abstract

# BACKGROUND

Esophageal cancer (EC) often occurs in the elderly, with approximately 33% of patients aged  $\geq$  75 years at the time of diagnosis.

# AIM

To evaluate the prognostic factors for radiotherapy (RT) in elderly patients with unresectable EC.

# **METHODS**

We retrospectively analyzed the clinical characteristics, toxic reactions, and survival information of EC patients aged  $\geq$  75 years who underwent intensity-modulated RT at Lu'an Hospital of Anhui Medical University between January 2016 and September 2023. Kaplan-Meier analysis was used to draw the overall survival (OS) curves, and Cox regression analysis was employed to evaluate the influence of various clinical factors on the prognosis.

# RESULTS

A total of 139 patients were enrolled. The median follow-up time was 52.0 months. The median OS was 20.0 months. The 1-year, 2-year, 3-year, and 5-year OS rates were 69.8%, 38.7%, 28.2%, and 17.5%, respectively. Univariate analysis showed that age, radiation dose, and chemotherapy had no significant impact on prognosis. Multivariate analysis indicated that clinical stage [III-IVa vs I-II, hazard ratio (HR) = 2.421, 95% confidence interval (CI): 1.242-4.718, P = 0.009; IVb vs I-II, HR = 4.222, 95%CI: 1.888-9.438, P < 0.001), Charlson comorbidity index (CCI) (0 vs



 $\geq$  1, HR = 1.539, 95% CI: 1.015-2.332, *P* = 0.042), and nutritional risk screening 2002 (NRS2002) (< 3 *vs*  $\geq$  3, HR = 2.491, 95% CI: 1.601-3.875, *P* < 0.001) were independent prognostic factors for OS.

#### CONCLUSION

Our results suggest that CCI and NRS2002 were independent prognostic factors of OS for unresectable elderly EC patients undergoing RT. For elderly patients with EC, full attention should be given to biological age-related indicators, such as comorbidities and nutrition, when formulating treatment protocols. These factors should be considered in future clinical practice.

Key Words: Elderly patient; Esophageal cancer; Radiotherapy; Prognosis; Comorbidity; Nutritional risk

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**Core Tip:** Esophageal cancer (EC) often occurs in the elderly, with approximately 33% of patients aged  $\geq$  75 years at the time of diagnosis. Since patients aged 75 years and above are often excluded from many clinical trials of EC, there is a lack of agreement regarding the prognosis and treatment of this population. We retrospectively analyzed the clinical characteristics, toxic reactions, and survival information of elderly patients with EC aged  $\geq$  75 years who received intensity-modulated radiotherapy. Our analysis aimed to evaluate the prognostic factors affecting overall survival. We found that the Charlson comorbidity index and nutritional risk screening 2002 were independent prognostic factors for overall survival. Our results suggest that when formulating treatment plans for elderly patients with EC, full attention should be given to age-related biological indicators such as comorbidities and nutrition.

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# INTRODUCTION

Esophageal cancer (EC), a common malignant tumor of the digestive tract, poses a significant threat to human health. The Global Cancer Observatory's 2022 online platform, Cancer Today, 2022 (GLOBOCAN 2022), reported that the global incidence and mortality rates of EC are approximately 2.6% and 4.6%, respectively, ranking 11<sup>th</sup> and 7<sup>th</sup>, respectively among all malignant tumors[1]. With the extension of life expectancy, the aging of the population, and the improvement of diagnosis methods, the proportion of elderly EC patients has gradually increased, with 33% of patients being over 75 years old at the time of diagnosis[2,3]. Elderly patients often have degraded physiological functions, multiple comorbidities, and poor treatment tolerance, necessitating particularly cautious treatment approaches for this group.

Endoscopic resection and surgery (preferred for early-stage patients) and neoadjuvant chemoradiotherapy followed by surgery (trimodality therapy) are common treatment modalities for EC[4-6]. While advancements in survival have been noted, age significantly impacts the treatment of EC. Lester *et al*[7] indicated that older patients with trimodality therapy encountered increased postoperative cardiopulmonary toxicity and mortality, with cardiotoxicity exhibiting a linear correlation with age and a 61% rise in relative risk for every 10-year increase in age. Given the elevated postoperative complications, heightened in-hospital mortality, and reduced overall survival (OS) among elderly patients, non-surgical treatment is typically advised[8].

For patients with locally advanced EC who refuse surgery and are medically considered inoperable or have unresectable tumors, the efficacy of radical chemoradiotherapy (CRT) has been confirmed in numerous randomized clinical trials, whether using conventional two-dimensional radiotherapy (RT) or three-dimensional intensity-modulated RT (IMRT) technology. The earliest data were obtained from the Radiation Therapy Oncology Group (RTOG) 8501 and RTOG9405 studies[9-12]. For patients with metastatic EC, systemic therapy is effective, and RT to the primary tumor can relieve patients' dysphagia and pain and improve patients' survival[13,14]. However, the clinical trials that back these treatments excluded individuals aged over 75, with older patients showing lower tolerance to CRT and experiencing a higher incidence of side effects compared to their younger counterparts[15]. Therefore, these clinical data are underrepresented in elderly patients. There are limited data on the efficacy and safety of RT in EC patients aged 75 years and older, and there is no consensus on prognosis and treatment in this population.

Studies have revealed that elderly patients with EC often receive inadequate treatment due to concerns about side effects, comorbidities, and poor outcome, even when the disease is at a curable stage. Notably, the decision to forgo treatment was attributed to physicians in 46% of cases and to patients in 46% of cases[16]. However, the actual age of the patient does not truly reflect their biological aging level. Studies have shown that carefully selected elderly patients can tolerate the treatment and have a survival benefit[17]. More attention should be given to physiological age in medicine, which includes factors such as comorbidities, nutrition, and physical condition.

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Based on the clinical information of elderly patients with unresectable EC who received IMRT at Lu'an Hospital of Anhui Medical University, this study explored prognostic factors associated with aging and provided a reference for individualized diagnosis and treatment of elderly EC patients.

# MATERIALS AND METHODS

#### Patients

Retrospective analysis was conducted on elderly (≥ 75 years) EC patients who received IMRT with or without chemotherapy at Lu'an Hospital of Anhui Medical University from January 2016 to September 2023. All patients were pathologically diagnosed with esophageal squamous cell carcinoma (ESCC) or adenocarcinoma, had no prior history of thoracic RT, and had not undergone previous EC surgery. They were receiving RT for the first time and had complete follow-up data. Exclusion criteria included patients with severe cardiopulmonary dysfunction or other critical diseases affecting important systems. Clinical stages were classified according to the eighth edition of the American Joint Committee on Cancer (AJCC) staging system. This study was conducted in accordance with the ethical guidelines set forth in the World Medical Association Declaration of Helsinki and received approval from the Ethics Committee of Lu'an Hospital, Anhui Medical University.

#### Treatment

All patients received IMRT. Each patient was immobilized in the supine position, and a spiral computed tomography (CT) scan was performed with a slice thickness of 0.5 cm, covering the range from the lower edge of the mandible to the lower edge of the liver. The gross tumor volume (GTV) was defined as any visible primary tumor and included metastatic lymph nodes, determined by comprehensive esophagogram, esophagoscopy, contrast-enhanced thoracic CT or positron emission tomography. The clinical target volume (CTV) was defined as the GTV plus 3 cm cranial-caudal and 0.5 cm radial margin. For lymph nodes, the CTV was generated by extending the nodal GTV by 0.5 cm. The planning target volume (PTV) was generated by additional 0.5 cm radial margin for CTV. The prescription dose to 95% of PTV ranged from 44 Gray (Gy) to 66 Gy in 22-33 fractions. The use of chemotherapy and the choice of regimen were determined by the clinician based on the patient's specific circumstances.

#### Follow-up and treatment evaluation

All patients were followed up every 3 months during the first 2 years and every 6 months thereafter. Follow-up assessments included blood tests, esophagogram, esophagoscopy, and CT scans of the neck, chest, and abdomen. Follow-ups were conducted via telephone and outpatient visits, with a final deadline of January 23, 2024. Treatment-related toxicities were evaluated according to the RTOG radiation injury grading criteria.

#### Statistical analysis

Continuous variables were expressed as means ± SD or medians depending on whether they were normally distributed. The median follow-up time was estimated using the reverse Kaplan-Meier method. The Kaplan-Meier function was utilized to draw the OS curves, and the log-rank test was employed to compare OS among different groups. Univariate and multivariate Cox proportional hazards regression models were used to evaluate the relationship between various clinical variables and prognosis. Potential prognostic factors with P < 0.05 in univariate analysis were included in the multivariate analysis. The hazard ratio (HR) and the corresponding 95% confidence interval (CI) were used to predict the effect of each variable on OS. The OS time was defined as the period from the date of diagnosis until death from any cause. Receiver operating characteristic (ROC) curves were drawn to verify the accuracy of the Charlson comorbidity index (CCI), nutritional risk screening 2002 (NRS2002) and clinical stage for survival prediction. The OS and ROC curves were calculated using statistical product and service solutions 24.0, while the remaining statistical analyses were performed using R software (version 4.3.0, http://www.r-project.org/).

#### RESULTS

#### Patients' characteristics

During the study period, a total of 158 elderly ( $\geq$  75 years) EC patients were treated with IMRT. After exclusions, 139 cases remained for analysis. The exclusions were due to the following reasons: 4 cases had concurrent malignant tumors, 1 case had small cell pathology, 8 cases had incomplete clinical data, and 6 cases were lost to follow-up. The median age was 79 years (range from 75 years to 92 years). According to the eighth edition of the AJCC staging system, 93 patients (66.9%) were distributed in stages III to IVa. Chemotherapy was administered to 103 patients (74.1%) at different phases of treatment, including 84 patients (60.4%) who received concurrent chemotherapy. 129 patients (92%) completed the planned RT, with a median radiation dose of 60 Gy (range from 20 to 66 Gy). The clinical characteristics are summarized in Table 1.

#### Survival and prognostic analysis

The median follow-up time was 52.0 months. The median OS was 20.0 months. The 1-year, 2-year, 3-year, and 5-year OS



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Table 1 Demographics and clinical characteristics of patients, n (%)			
Variables	Number of patients		
Age			
≥ 75 and < 80	70 (50.4)		
≥80	69 (49.6)		
Sex			
Female	39 (28.1)		
Male	100 (72.9)		
Marital status			
Married	133 (95.7)		
Unmarried	6 (4.3)		
Smoke			
No	84 (60.4)		
Yes	55 (39.6)		
Drink			
No	102 (73.4)		
Yes	37 (26.6)		
C stage			
I-II	24 (17.3)		
III-IVa	93 (66.9)		
IVb	22 (15.8)		
T stage			
T1-T2	22 (15.8)		
T3-T4	117 (84.2)		
N stage			
Negative	22 (15.8)		
Positive	117 (84.2)		
M stage			
M0	117 (84.2)		
M1	22 (15.8)		
Tumor length			
< 6	90 (64.7)		
≥6	49 (35.3)		
Tumor location			
Upper thoracic	34 (24.5)		
Middle thoracic	62 (44.6)		
Lower thoracic	43 (30.9)		
ECOG			
0-1	133 (95.7)		
2	6 (4.3)		
CCI			
0	62 (44.6)		
≥1	77 (55.4)		

NRS2002	
<3	66 (47.5)
≥3	73 (52.5)
BMI	
< 18.5	32 (23.0)
≥18.5	107 (77.0)
Weight loss	
<10%	128 (92.1)
≥10%	11 (7.9)
Radiation dose	
< 60	57 (41.0)
≥ 60	82 (59.0)
Chemotherapy	
No	36 (25.9)
Yes	103 (74.1)

BMI: Body mass index; ECOG: Eastern Cooperative Oncology Group; CCI: Charlson comorbidity index; NRS2002: Nutritional risk screening 2002.

rates were 69.8%, 38.7%, 28.2%, and 17.5%, respectively.

Univariate analysis showed that patients with a CCI score of  $\geq 1$  had worse OS compared to those with a score of 0 (HR = 1.620; 95% CI: 1.080-2.429; *P* = 0.019). Patients with an NRS2002 score of < 3 before RT had better OS than those with a score of  $\geq 3$  (HR = 2.215; 95% CI: 1.466-3.348; *P* < 0.001). Patients with weight loss (WL) of < 10% before RT had better OS compared to those with WL of  $\geq 10\%$  (HR = 2.947; 95% CI: 1.473-5.898; *P* = 0.002). Other statistically significant prognostic factors included clinical stage, lymph node metastasis, and distant metastasis. Conversely, factors such as age, radiation dose, and chemotherapy did not have a significant impact on prognosis. The survival curves of elderly patients with EC in different groups are depicted in Figure 1.

The subsequent multivariate analysis was conducted based on clinical stage, CCI, NRS2002, and WL. The results indicated that the clinical stage (III-IVa *vs* I-II, HR = 2.421, 95%CI: 1.242-4.718, P = 0.009; IVb *vs* I-II, HR = 4.222, 95%CI: 1.888-9.438, P < 0.001), CCI (HR = 1.539; 95%CI: 1.015-2.332; P = 0.042) and NRS2002 (HR = 2.491; 95%CI: 1.601-3.875; P < 0.001) were independent prognostic factors for elderly patients with EC. The results of both univariate and multivariate analyses are presented in Table 2.

#### ROC curve for survival prediction

ROC curves for OS were plotted. As shown in Figure 2, the area under the curve (AUC) for NRS2002 was 0.665, the AUC for CCI was 0.530, and the AUC for clinical stage was 0.608. When all three indicators were combined for prediction, the AUC increased to 0.726 (95%CI: 0.635-0.817), demonstrating superior predictive accuracy compared to any single indicator alone.

#### Toxicity

Toxicity primarily occurred in grade 1 or 2, with a low incidence of grade 3 and higher adverse reactions. Table 3 demonstrated treatment-related acute toxic reactions, including leukopenia, anemia, thrombocytopenia, esophagitis, pneumonitis, and dermatitis. Specifically, the incidence of grade 3 hematological toxicity was 8.6%, grade 3 esophagitis was 5.5%, and grade 3 pneumonitis was 1.4%. Additionally, one patient experienced grade 4 hematological toxicity, while no grade 4 or higher non-hematological toxicity was observed.

### DISCUSSION

In this study, we conducted a retrospective analysis of the clinical characteristics, toxic reactions, and survival information of elderly EC patients aged  $\geq$  75 years who underwent IMRT and aimed to evaluate the prognostic factors for OS. Our analysis revealed that CCI and NRS2002 are independent prognostic factors for OS. These findings underscore the significance of comorbidities and nutrition in influencing the prognosis of elderly EC patients. Therefore, when formulating treatment protocols for elderly EC patients, it is crucial to consider aging-related prognostic factors, specifically comorbidities and nutrition, as indicated by CCI and NRS2002.

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Table 2 Univariate and multivariate Cox analysis of the determinants of overall survival of patients								
	Univariate analysis				Multivariate analysis			
Variables	HR	Lower 95%CI	Upper 95%Cl	P value	HR	Lower 95%CI	Upper 95%Cl	P value
Age								
≥ 75 and < 80	1							
≥80	1.147	0.769	1.710	0.502				
Sex								
Female	1							
Male	0.656	0.427	1.009	0.055				
Marital status								
Married	1							
Unmarried	0.538	0.132	2.188	0.387				
Smoke								
No	1							
Yes	0.821	0.544	1.239	0.348				
Drink								
No	1							
Yes	0.869	0.545	1.387	0.557				
C stage								
I-II	1				1			
III-IVa	2.261	1.189	4.298	0.013	2.421	1.242	4.718	0.009
IVb	3.444	1.593	7.446	0.002	4.222	1.888	9.438	< 0.001
T stage								
T1-T2	1							
T3-T4	1.575	0.876	2.831	0.129				
N stage								
Negative	1							
Positive	2.030	1.104	3.732	0.023				
M stage								
M0	1							
M1	1.761	1.038	2.986	0.036				
Tumor length								
< 6	1							
≥6	1.261	0.836	1.904	0.269				
Tumor location								
Upper thoracic	1							
Middle thoracic	1.054	0.632	1.759	0.840				
Lower thoracic	1.146	0.665	1.976	0.623				
ECOG								
0-1	1							
2	2.023	0.820	4.995	0.126				
CCI								
0	1				1			



≥1	1.620	1.080	2.429	0.020	1.539	1.015	2.332	0.042
NRS2002								
< 3	1				1			
≥3	2.215	1.466	3.348	< 0.001	2.491	1.601	3.875	< 0.001
BMI								
< 18.5	1							
≥18.5	0.756	0.482	1.183	0.221				
Weight loss								
< 10%	1				1			
≥10%	2.947	1.473	5.898	0.002	1.798	0.870	3.715	0.113
Radiation dose								
< 60	1							
≥ 60	0.771	0.511	1.164	0.217				
Chemotherapy								
No	1							
Yes	0.847	0.543	1.320	0.463				

HR: Hazard ratio; CI: Confidence interval; BMI: Body mass index; ECOG: Eastern Cooperative Oncology Group; CCI: Charlson comorbidity index; NRS2002: Nutritional risk screening 2002.

Table 3 Treatment-related acute toxicities in patients, n (%)					
Toxicity	Grade 1	Grade 2	Grade 3	Grade 4	
Leukocytopenia	31 (22.3)	43 (30.9)	6 (4.3)	1 (0.7)	
Anemia	29 (20.8)	21 (15.1)	8 (5.7)	1 (0.7)	
Thrombopenia	3 (2.1)	2 (1.4)	2 (1.4)	1 (0.7)	
Esophagitis	19 (13.6)	40 (28.7)	7 (5.5)	0 (0.0)	
Pneumonitis	1 (0.7)	2 (1.4)	2 (1.4)	0 (0.0)	
Dermatitis	2 (1.4)	0 (0.0)	0 (0.0)	0 (0.0)	

With the advancement of medical technology and the improvement of medical security levels, human life expectancy continues to increase, leading to a growing proportion of elderly individuals in the population. China, which accounts for about one-fifth of the world's population, sees more than half of the global EC cases. Elderly EC patients represent a heterogeneous group that warrants significant attention. Although there are limited avenues of treatment for elderly EC patients, any treatment modality can provide substantial survival benefits compared to best supportive care[18]. Currently, many clinical studies on elderly EC have focused on patients over 70 years of age. A multi-center retrospective study from China revealed that the survival time of patients over 75 years is significantly lower than that of patients under 75 years. Therefore, the optimal treatment strategy for elderly EC patients over 75 years is still under exploration [19-21].

Due to demographic shifts, the number of elderly patients with EC is increasing, and many patients have unhealthy lifestyle habits such as smoking and alcohol consumption, leading to a higher prevalence of comorbidities among this group. Observational studies have consistently indicated that cancer patients with comorbidities experience lower survival rates compared to those without comorbidities[22-24]. The most commonly used model for quantifying comorbidities is the CCI. Currently, several studies have investigated the relationship between comorbidities and prognosis in patients with different stages of EC. For instance, Ishido et al[25] found that a CCI  $\geq$  2 was a prognostic factor for endoscopic treatment in elderly patients with superficial EC. Similarly, Yamashita et al[26] reported that a high CCI was associated with poor prognosis in stage II and above staged EC. Bernardi et al[27] highlighted that age alone could not directly indicate a patient's ability to tolerate treatment, instead, comorbidities played a central role in the decisionmaking process, with the routine use of CCI aiding in prognostic risk stratification. While the value of CCI has been extensively studied in surgery, it has been less explored in RT for elderly EC. Our results align with these findings, showing that more than half of elderly EC patients had comorbidities, with CCI  $\geq$  1 accounting for 55.4% (77/139). Univariate and multivariate analyses indicated that the OS of the "CCI = 0" group was better than that of the "CCI  $\geq$  1"

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Figure 1 The survival curves of elderly patients with esophageal cancer in different groups. A: Age; B: Sex; C: Marital status; D: Smoke; E: Drink; F: C stage; G: T stage; H: N stage; I: M stage; J: Tumor length; K: Tumor location; L: Eastern Cooperative Oncology Group; M: Charlson comorbidity index; N: Nutritional risk screening 2002; O: Body mass index; P: Weight loss; Q: Radiation dose; R: Chemotherapy. BMI: Body mass index; ECOG: Eastern Cooperative Oncology Group; CCI: Charlson comorbidity index; NRS2002: Nutritional risk screening 2002.



Figure 2 Receiver operating characteristic curves of Charlson comorbidity index, nutritional risk screening 2002, and clinical stage for predicting odds ratio in elderly patients with esophageal cancer after radiotherapy. ROC: Receiver operating characteristic; AUC: Area under curve; CCI: Charlson comorbidity index; NRS2002: Nutritional risk screening 2002.

group. Therefore, our study suggests that comorbidities could affect the survival of elderly EC patients receiving RT.

Some studies have reported that approximately 60% to 85% of EC patients suffer from malnutrition, ranking first among malignant tumors[28]. Malnutrition can cause various harms to patients undergoing RT for EC, such as increasing positioning errors, side effects, and reducing efficacy. It can even lead to treatment interruptions, prolonged hospitalization, increased medical expenses, and decreased survival rates. Studies have indicated that malnutrition is a prognostic factor in elderly EC patients receiving RT[21,29]. Currently, there are many nutritional assessment tools for the prognosis assessment of EC, such as the controlling nutritional status (CONUT), the prognostic nutritional index (PNI), the patientgenerated subjective global assessment, and the NRS2002[30-33]. Compared with the invasive and complex inconveniences of the first three assessment methods, the NRS2002 screening tool is non-invasive, inexpensive, time-saving, and easy to use[34]. Noh et al[35] analyzed 274 patients undergoing surgery for ESCC, using PNI, NRS2002, and CONUT to assess preoperative nutritional status. The results indicated that during a median follow-up of 55 months, a high NRS2002 was associated with poor OS and a high incidence of postoperative complications. Thus, NRS2002 was considered the most appropriate scoring system for assessing patients' nutritional status. Song et al[36] retrospectively investigated 202 patients with locally advanced unresectable EC who received CRT to explore their prognostic factors. The results revealed that NRS  $\geq$  3 points was a poor prognostic factor. Similarly, the study by Wang *et al*[33] demonstrated that the baseline NRS2002 score serves as a simple and effective biomarker for predicting the long-term prognosis of patients with EC undergoing CRT. Consistent with previous studies, our study showed that NRS2002 was an independent prognostic factor for OS in elderly EC patients receiving RT. Therefore, pretreatment nutritional assessment and correction of malnutrition may improve survival outcomes in elderly EC patients undergoing RT.

Currently, CRT with 5-fluorouracil and cisplatin is the standard care for non-surgical EC treatment[9]. However, due to the serious toxic and side effects of double-drug concurrent chemoradiation (CCRT), most elderly EC patients often cannot tolerate it and thus cannot complete standard CCRT treatment. Ji *et al*[37] enrolled 298 elderly EC patients aged 70 and above to investigate the efficacy and toxicities of CCRT with S-1. The results indicated that the survival outcomes were superior in the CCRT group compared to the RT group alone, and the toxicities were manageable, suggesting that elderly patients could benefit from a treatment regimen involving combined RT and single-agent chemotherapy. Regarding EC patients 75 years and older, there are no large-scale prospective randomized clinical trials comparing the efficacy of CCRT with RT alone. Some retrospective studies have revealed that CCRT has no statistically significant survival benefit[21,38]. The findings of our study are consistent with these reports. Therefore, caution should be exercised when using CCRT in elderly EC patients aged 75 years and older, and omitting or using milder chemotherapy regimens may be more appropriate.

To further analyze the prognostic value of CCI, NRS2002, and clinical stage in elderly patients with unresectable EC, we plotted ROC curves. The combined prediction of these three factors for the survival of elderly EC patients yielded an AUC of 0.726, which outperformed the predictive ability of any individual factor. This finding suggests that treatment strategies for elderly EC patients should be tailored based on factors such as disease stage, nutritional status, and comorbidity. Individualized treatment plans should be carefully designed for elderly patients through meticulous selection, aiming to provide the best possible treatment while ensuring safety.

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In the study of Yin *et al*[19], the median OS of elderly EC patients who received RT, including patients with metastatic lesions, was 20.68 months. The 1-year, 2-year, 3-year, and 5-year OS rates were 62.6%, 41.8%, 11.1%, and 0%, respectively. Our study showed that the median OS of elderly EC patients receiving RT was 20.0 months, and the 1-year, 2-year, 3year, and 5-year OS rates were 69.8%, 38.7%, 28.2%, and 17.5%, respectively. Since their study enrolled patients over 70 years, and ours included patients over 75 years, it showed that we had a greater advantage in survival of elderly EC patients. In the study of Suzuki *et al*[38], the median OS of older patients aged  $\geq$  75 years with localized EC who received RT was 30.0 months, and the 2-year OS rate was 53%. Zhou et al[21] retrospectively analyzed 149 patients over the age of 75 with localized EC and reported that the 2-year OS rate was 51.6%. The survival time of patients in our study was slightly worse than that of the above two studies, which may be due to the inclusion of 15.8% of patients with metastatic EC. Therefore, RT is an effective treatment for patients with unresectable EC over the age of 75, and advanced age alone should not be a reason to exclude patients from RT.

There were some limitations to this study. Firstly, it was a single-center retrospective study with a relatively small sample size, introducing selection bias. Secondly, variables such as smoking, drinking, and comorbidity were all selfreported by elderly patients, who were elderly, leading to recall bias. Finally, some potential prognostic factors, such as elective nodal irradiation and involved-field irradiation, were not included in the study. Therefore, prospective research is still needed to provide a basis for the treatment of elderly EC patients.

# CONCLUSION

This study identified prognostic factors for RT in elderly patients with unresectable EC. "CCI  $\ge$  1" and "NRS2002  $\ge$  3" were independent prognostic factors associated with worse OS. Increasing the dose of RT and combining chemotherapy did not significantly improve survival. For elderly patients with EC, the focus should be on biological age rather than physiologic age. Future clinical practice should consider indicators associated with aging, such as comorbidities and nutritional status.

# FOOTNOTES

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**Retrospective Study** 

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ORIGINAL ARTICLE

# Nomogram model based on y-glutamyl transferase to albumin ratio predicts survival in hepatocellular carcinoma patients with transarterial chemoembolization treatment

Zhen-Ying Wu, Han Li, Jia-Li Chen, Ke Su, Mei-Ling Weng, Yun-Wei Han

Zhen-Ying Wu, Han Li, Jia-Li Chen, Mei-Ling Weng, Yun-Wei Han, Department of Oncology, The Specialty type: Oncology Affiliated Hospital of Southwest Medical University, Luzhou 646000, Sichuan Province, China Provenance and peer review: Zhen-Ying Wu, Department of Oncology, Pangang Group General Hospital, Panzhihua 617000, Unsolicited article; Externally peer Sichuan Province, China reviewed. Ke Su, Department of Oncology, National Cancer Center, Beijing 100000, China Peer-review model: Single blind Ke Su, Department of Oncology, National Clinical Research Center for Cancer, Beijing 100000, Peer-review report's classification China Scientific Quality: Grade C Novelty: Grade C Ke Su, Department of Oncology, Cancer Hospital, Chinese Academy of Medical Sciences and Creativity or Innovation: Grade C Peking Union Medical College, Beijing 100000, China Scientific Significance: Grade B Co-first authors: Zhen-Ying Wu and Han Li. P-Reviewer: Mirminachi S Corresponding author: Yun-Wei Han, MD, PhD, Academic Research, Full Professor, Department of Oncology, The Affiliated Hospital of Southwest Medical University, No. 25 Received: June 13, 2024 Taiping Street, Jiangyang District, Luzhou 646000, Sichuan Province, China. Revised: September 16, 2024 lanpaoxiansheng@126.com Accepted: October 11, 2024 Published online: December 15, 2024 Abstract Processing time: 152 Days and 4.3 Hours BACKGROUND The development of tumor is closely linked to inflammation. Therefore, targeting molecules involved in inflammation may be effective in predicting cancer prognosis. Transarterial chemoembolization (TACE) holds significant therapeutic significance in addressing hepatocellular carcinoma (HCC). At present, no studies

AIM

To explore the potential prognostic significance of the GAR in individuals undergoing TACE for HCC.

have evaluated the predictive value of y-glutamyl transferase to albumin ratio

# **METHODS**

A total of 1231 patients from seven hospitals in China were randomized into a training cohort (n = 862) and a validation cohort (n = 369). To establish inde-



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(GAR) on the prognosis of HCC undergoing TACE.

pendent prognostic factors for overall survival (OS), we utilized multivariate and univariate Cox regression models. The best cut-off value of the GAR was determined with the X-tile software, with OS as the basis. Validations were performed using dual therapy cohort and triple therapy cohort.

#### RESULTS

X-tile software revealed a GAR threshold of 4.75 as optimal. Both pre- and post-propensity score matching analyses demonstrated that the median OS in the low-GAR group (< 4.75) was notably longer compared to the high-GAR group ( $\geq$  4.75), showing results of 26.9 vs 9.8 months (P < 0.001) initially, and 18.1 vs 11.3 months (P < 0.001) after match. Furthermore, multivariate analysis identified GAR  $\geq$  4.75 as an independent prognostic factor (*P* < 0.001). The receiver operating characteristic curves for the nomogram showed area under receiver operating characteristic curves of 0.741, 0.747, and 0.708 for predicting 1-, 2-, and 3-year survival, respectively. Consistent findings were reiterated in the two cohorts involving TACE in combination with targeted therapy and TACE in combination with targeted therapy and immunotherapy. Calibration curve and decision curve analyses substantiated the model's relatively robust predictive capabilities.

#### **CONCLUSION**

Our study validates the effective prognostic capacity of the GAR-based nomogram for HCC patients undergoing TACE or TACE in combination with systemic therapy.

Key Words: Transarterial chemoembolization; Immunotherapy; Targeted therapy; Hepatocellular carcinoma; Prognosis

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**Core Tip:**  $\gamma$ -glutamyl transferase to albumin ratio has been confirmed for the first time to be predictive in hepatocellular carcinoma undergoing transarterial chemoembolization and transarterial chemoembolization combined with systemic therapy in this large-sample multicenter study. A nomogram model for predicting postoperative survival was also established based on γ-glutamyl transferase to albumin ratio, which was empirically demonstrated to have strong predictive ability.

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# INTRODUCTION

Hepatocellular carcinoma (HCC) is prevalent worldwide and is a life-threatening malignancy, witnessing an escalating incidence that represents a large proportion of deaths related to cancer. Projections indicate that the annual HCC incidence will exceed one million individuals by the year 2025[1]. Sadly, patients devoid of effective therapeutic interventions succumb to an abysmal median overall survival (mOS) of merely four months[2].

The latest guidelines released by the National Comprehensive Cancer Network advocate for the combined employment of atezolizumab and bevacizumab as the prime systemic therapy option for individuals affected by advanced HCC. Additionally, in cases of unresectable or inoperable HCC exceeding 5 centimeters, transarterial chemoembolization (TACE) may merit consideration to extend patient survival. Following the established staging system of Barcelona Clinical Liver Cancer (BCLC), TACE has become the mainstay of therapy for intermediate-stage HCC. Specifically, this encompasses patients boasting asymptomatic, multi-nodular tumors devoid of vascular invasion or extrahepatic spread [3]. Indeed, TACE has also yielded surprising results for some early patients who were not suitable for surgery or ablation[4-6]. In some series of studies, the majority of patients treated with TACE were in the early stages of disease, with more than 40% being solitary nodules [7,8]. Importantly, TACE has also garnered favorable treatment responses in advanced-stage HCC cases. An extensive longitudinal cohort study across 14 countries discovered that TACE served as the primary treatment for nearly 50% of individuals afflicted with BCLC-C-stage HCC[9]. This assertion is further supported by the findings of two prospective non-randomized trials[10,11], which confirmed the superiority of conventional TACE over basic supportive care.

Scientific investigations have illuminated the intricate relationship between long-standing inflammatory factors and the malignant transformation of tumors, highlighting the fundamental role of chronic inflammation and its associated factors in the emergence of tumorigenesis<sup>[12]</sup>. Inflammatory factors are important players in the regulation of the tumor microenvironment. They possess the capacity to instigate tumor epithelial-mesenchymal transition, generate reactive oxygen species, and thereby facilitate tumor cell proliferation, angiogenesis, invasion, and metastasis[12,13]. γ-glutamyl transferase (GGT) is a kind of glycoprotein secreted by Kupffer cells and bile duct endothelial cells. Elevated GGT levels are a marker of liver dysfunction and alcohol intake, and can be used to measure the severity of liver inflammation and



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cellular damage[14]. GGT's main role is to mediate the hydrolysis of extracellular glutathione, which produces large amounts of hydrogen peroxide and reactive oxygen species and other free radicals, leading to oxidative stress in tissues [15]. Many experimental studies have also shown that the expression of GGT makes cancer cells more invasive and even leads to the emergence of anticancer drug resistance [16].

Albumin (ALB) is the most important protein in humans, synthesized by liver cells. It has a wide range of important physiological functions, such as regulating immunity, stabilizing endothelium, and binding to various drugs and toxins [17]. In addition, ALB binds to a series of inflammatory mediators and interacts with nitric oxide, playing anti-inflammatory and antioxidant roles[18]. Serum ALB levels reflect liver reserve function and nutritional status of the body. In cases of malnutrition, hepatitis, and cirrhosis, the concentration of ALB in the human body will significantly decrease [19]. Therefore, ALB is frequently utilized in the assessment of liver function prior to hepatic resection[20]. Recent research has confirmed that ALB can also exert a protective influence after a variety of radical surgeries<sup>[21]</sup>. Although some studies have shown that GAR can predict the outcome of HCC[22,23], these studies only focused on hepatectomy, and their sample sizes were small. In this study, we developed a predictive model for HCC based on a convenient and inexpensive liquid biopsy technique, which can effectively predict not only survival after TACE alone, but also outcomes of dual therapy or triple therapy.

## MATERIALS AND METHODS

#### Study design

TACE alone cohort: During the period spanning from January 2019 to June 2023, 1231 patients with HCC, who received either drug-eluting beads TACE or conventional TACE, were gathered from seven hospitals in China. The diagnosis of HCC was confirmed by histology, at least two typical radiological features, or one typical imaging manifestation with a serum alpha-fetoprotein (AFP) level > 400 ng/mL. The inclusion criteria consisted of the following prerequisites: (1) Patients who had not previously received any form of antitumour therapy prior to TACE; (2) Patients exhibiting measurable lesions that aligned with the response assessment criteria specifically tailored for solid tumours (RECIST 1.1); and (3) GGT and ALB were measured within 7 days before TACE. The exclusion criteria were: (1) Presence of other malignant tumors other than HCC; (2) Patients with a history of other anti-tumor therapies; and (3) Lack of follow-up data.

Dual therapy cohort: Patients with HCC who received TACE in combination with targeted therapy at the above hospitals were included in the two-combination therapy cohort. The clinical data including demographic characteristics, hematological parameters, imaging data and tumor staging were collected retrospectively. At the same time, GGT and ALB values at baseline were obtained.

Triple therapy cohort: Patients with HCC who received TACE in conjunction with immunotherapy and targeted therapy at the same hospitals were enrolled in this cohort. Complete baseline clinical and laboratory data were recorded for subsequent analysis. The study intentionally excluded those patients who had incomplete follow-up information.

#### Data assessment

The laboratory parameters included AFP, GGT, alanine aminotransferase, ALB, total bilirubin, red blood cells, lactate dehydrogenase, alkaline phosphatase, hemoglobin, white blood cells, lymphocyte count, hepatitis B virus infection, and hepatitis C virus infection. Tumor burden was assessed by magnetic resonance imaging. Enhanced computer tomography or single-organ contrast-enhanced ultrasound, including tumor diameter and number, portal vein invasion, lymph node metastases and extrahepatic metastases. Additional data encompassed variables such as sex, age, presence of alcohol consumption, hepatitis B virus, hepatitis C virus infection, hypertension and diabetes mellitus. Both the training and validation cohorts underwent bi-monthly computer tomography or magnetic resonance imaging examinations following the initial treatment. All patients were evaluated according to RECIST 1.1.

#### Statistical analysis

All of the statistical analyses were implemented with R 4.1.3 software and SPSS 26.0 software. A bilateral P value of < 0.05 was viewed as statistically significant. Tumor response data and baseline features were summed up with descriptive statistics. Comparisons of categorical variables were done with  $\chi^2$  test. The best threshold value for serum GAR was identified from OS utilizing X-tile software. To ensure balanced baseline characteristics, propensity score matching (PSM) scale was exploited for determining the low and high GAR groups. All patients were randomized into a validation group (n = 369) and a training group (n = 862). With the Kaplan-Meier statistical approach, the log-rank test was employed to estimate and compare mOS between groups. Subsequently, all covariates exhibiting an impact on survival in univariate analysis with P < 0.05 were included in the multivariate Cox proportional hazards model. Multivariate cox analysis was carried out to identify independent influencing factors, which were utilized to establish a nomogram. The nomogram's prognostic effect was evaluated using receiver operating characteristic, calibration curve and decision curve analysis.

#### Ethical statements

The study protocol was authorized by the Ethics Committee of the Affiliated Hospital of Southwest Medical University (No. KY2021063) and complied with the guidelines of the Helsinki Declaration. Written informed consent was waived because of the retrospective study.



# RESULTS

# Patients and tumor characteristics

This retrospective study enrolled a total of 1231 HCC patients. There were 1044 (85%) males and 187 (15%) females. There were 501 (41%) patients aged  $\geq$  60 years. There were 749 patients (61%) who were positive for hepatitis B. AFP  $\geq$  500 ng/mL was detected in 528 patients (43%). Multiple tumor masses were present in 890 patients (72%). Tumor diameter  $\geq$  10 cm was found in 352 patients (29%). Portal vein tumor thrombus (PVTT) was found in 484 patients (39%). According to BCLC tumor staging, 177 (14%) were stage A, 188 (15%) were stage B, 853 (69%) were stage C, and 13 (1%) were stage D. The remaining baseline characteristics are shown in Table 1.

# GAR levels and OS before and after PSM

Both multivariate and univariate Cox analyses displayed that GAR value  $\geq$  4.75 was an independent prognostic risk factor for OS (Table 2). Based on X-tile software analysis, the best cut-off of GAR is 4.75. Based on the cutoff value, all 1231 patients were further divided into two groups, GAR  $\geq$  4.75 (n = 525) and GAR < 4.75 (n = 706). The high GAR group tended to exhibit higher tumor load before PSM (P < 0.05, Table 1). All patients in high and low GAR groups had a mOS of 9.8 months [95% confidence interval (CI): 8.9-11.5] and 26.9 months (95%CI: 24.0-30.2), respectively. Statistically significant differences existed between the two groups in mOS [hazard ratio (HR) = 2.079, 95%CI: 1.807-2.392, P < 0.001, Figure 1A]. There were no statistically significant differences between the two groups after PSM (Table 3). In the high GAR group, the mOS was 11.3 months (95%CI: 9.1-15.3), while in the low group, it was 18.1 months (95%CI: 13.4-23.3). The former was noticeably shorter as compared to the latter (HR = 1.461, 95%CI: 1.185-1.802, P < 0.001, Figure 1B).

## Prognostic factors influencing OS

Before PSM, we performed univariate and multivariate Cox analyses and identified six independent factors affecting OS prognosis, including number of tumors  $\geq$  2 (*P* = 0.001), GAR value  $\geq$  4.75 (*P* < 0.001), PVTT (*P* < 0.001), Child-Pugh B/C (*P* < 0.001), larger tumor diameter (*P* < 0.001), and extra-hepatic metastasis (*P* = 0.003) respectively (Table 2).

After PSM, each GAR group had 256 patients enrolled in the study cohort. Univariate and multivariate Cox regression analyses pinpointed several independent prognostic factors impacting OS: GAR value  $\geq$  4.75 (*P* < 0.001), PVTT (*P* = 0.001), higher Child-Pugh classification (*P* = 0.004), multiple tumors (*P* < 0.001), and larger tumor diameter (*P* < 0.001). Notably, the prognostic significance of high-GAR remained robust even after PSM (Supplementary Table 1).

## GAR can predict OS in validation set and training set (TACE alone cohort)

A total of 1231 patients were grouped into the validation and training groups in a 3:7 ratio. There were no evident statistical differences in the baseline features of the patients in both groups (Supplementary Table 2). The mOS for patients in the low group in the training set was 27.1 months (95%CI: 24.2-32.2) *vs* 9.9 months (95%CI: 8.6-11.8) for patients in the high group (P < 0.001). Significantly shorter mOS was observed in the high GAR group, demonstrating statistical significance (HR = 2.061, 95%CI: 1.74-2.442, P < 0.001, Figure 1C). There were comparable results observed in the validation set, with the mOS for high GAR and low GAR groups being 25.4 (95%CI: 21.0-30.3) and 9.5 (95%CI: 7.6-12.5) months, respectively. The high group presented remarkably shorter mOS in contrast to the low group (HR = 2.119, 95%CI: 1.648-2.723, P < 0.001, Figure 1D).

#### Nomogram construction and validation

In the training cohort, we found six independent factors affecting OS prognosis, including GAR, number of tumors, PVTT, Child-Pugh classification, tumor diameter, and extra-hepatic metastasis respectively (Table 4). The nomogram was constructed based on independent factors that significantly affected OS (Figure 2). Time-varying receiver operating characteristic curves in the validation set displayed that the area under receiver operating characteristic curve values of this model in predicting 1-, 2-, and 3-year survival were 0.741, 0.747, and 0.708, respectively (Figure 3). Additionally, the calibration curves and decision curve analysis curves demonstrated good predictive potential of the model (Figures 4 and 5).

# GAR can predict OS of cohort for dual therapy

In total, 90 patients who received the combination therapy of TACE along with targeted therapy were encompassed within the dual therapy cohort. The mOS was found to be 36.1 months (95%CI: 24.5 to not applicable) in the low group, whereas it reduced significantly to 13.6 months (95%CI: 9.2-26.8) in the high group. Comparative analysis revealed a noteworthy disparity in mOS between both GAR groups, and the survival time was obviously shorter in high GAR group (HR = 2.079, 95%CI: 1.807-2.392, P < 0.001; Figure 1E). Additionally, in this particular cohort, GAR demonstrated a substantial association with patient survival.

# GAR can predict the OS of triple therapy cohort

There were 63 patients who received a combination therapy of TACE, targeted therapy, and immunotherapy were included in this analysis. The mOS for the low GAR group was not reached, while it amounted to 9.8 months (95% CI: 8.27 to not applicable) for the high GAR group. Upon comparing the two groups, it was evident that the high GAR group exhibited a significantly shorter mOS (HR = 4.615, 95% CI: 1.844-11.55, P < 0.001; Figure 1F). These findings strongly indicate a pronounced correlation between GAR and the survival rate of patients.

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Table 1 Baseline characteristics of low and high γ-glutamyl transferase to albumin ratio groups before propensity score matching					
Variables	Total	GAR-low	GAR-high	<i>P</i> value	
Patients	1231	706	525		
Gender				< 0.001	
Female, n (%)	187 (0.15)	129 (0.18)	58 (0.11)		
Male, <i>n</i> (%)	1044 (0.85)	577 (0.82)	467 (0.89)		
Age $\geq$ 60 years, <i>n</i> (%)	501 (0.41)	305 (0.43)	196 (0.37)	0.044	
HBV, <i>n</i> (%)	749 (0.61)	432 (0.61)	317 (0.60)	0.819	
HCV, <i>n</i> (%)	38 (0.03)	27 (0.04)	11 (0.02)	0.117	
Alcohol, n (%)	482 (0.39)	243 (0.34)	239 (0.46)	< 0.001	
Diabetes, n (%)	122 (0.10)	69 (0.10)	53 (0.10)	0.928	
Hypertension, <i>n</i> (%)	178 (0.14)	106 (0.15)	72 (0.14)	0.576	
ALT levels $\geq$ 40, U/L, n (%)	639 (0.52)	274 (0.39)	365 (0.70)	< 0.001	
ALP levels $\geq$ 125, U/L, n (%)	714 (0.58)	249 (0.35)	465 (0.89)	< 0.001	
Serum AFP $\geq$ 500, ng/mL, n (%)	528 (0.43)	254 (0.36)	274 (0.52)	< 0.001	
Child-Pugh class, n (%)				< 0.001	
А	920 (0.75)	585 (0.83)	335 (0.64)		
В	297 (0.24)	114 (0.16)	183 (0.35)		
С	14 (0.01)	7 (0.01)	7 (0.01)		
Lymph node metastasis, $n$ (%)	617 (0.50)	312 (0.44)	305 (0.58)	< 0.001	
Extrahepatic metastasis, $n$ (%)	238 (0.19)	116 (0.16)	122 (0.23)	0.004	
PVTT, n (%)	484 (0.39)	196 (0.28)	288 (0.55)	< 0.001	
BCLC stage, $n$ (%)				< 0.001	
А	177 (0.14)	137 (0.19)	40 (0.08)		
В	188 (0.15)	129 (0.18)	59 (0.11)		
С	853 (0.69)	433 (0.61)	420 (0.80)		
D	13 (0.01)	7 (0.01)	6 (0.01)		
Number of tumors $\geq$ 2, <i>n</i> (%)	890 (0.72)	469 (0.66)	421 (0.80)	< 0.001	
Tumor diameter, cm, $n$ (%)				< 0.001	
< 3	172 (0.14)	133 (0.19)	39 (0.07)		
≥3, < 5	216 (0.18)	155 (0.22)	61 (0.12)		
≥5, <10	491 (0.40)	302 (0.43)	189 (0.36)		
≥10	352 (0.29)	116 (0.16)	236 (0.45)		

GAR-low:  $\gamma$ -glutamyl transferase to albumin ratio < 4.75; GAR-high:  $\gamma$ -glutamyl transferase to albumin ratio > 4.75; HBV: Hepatitis B virus; HCV: Hepatitis C virus; ALT: Alanine aminotransferase; ALP: Alkaline phosphatase; AFP: Alpha-fetoprotein; PVTT: Portal vein tumor thrombus; BCLC: Barcelona Clinic Liver Cancer.

# DISCUSSION

TACE has become an important treatment method in the era of tumor precision therapy[24]. Although some studies have shown that GAR can be applied for the prediction of HCC prognosis, the study sample is generally small, and the study objects are all surgical resection. At present, no study has confirmed the predictive value of GAR in TACE. Therefore, we initiated a large-sample, multicenter TACE cohort study and established a nomogram model of HCC patient survival based on GAR. In this study, the patients with GAR  $\geq$  4.75 had lower mOS than those with GAR < 4.75(P < 0.001). High predictive accuracy of GAR was also found in both the dual and triple therapy cohorts for the first time.

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Table 2 Univariate and multivariate Cox regression analyses of overall survival before propensity score matching					
Variables	HR (95%CI)	P value	HR (95%CI)	P value	
Gender (male/female)	1.094 (0.898-1.334)	0.372			
Age (≥ 60/< 60 years)	0.888 (0.770-1.024)	0.102			
HBV (positive/negative)	1.087 (0.941-1.255)	0.257			
HCV (positive/negative)	0.657 (0.406-1.062)	0.086			
Alcohol (yes/no)	1.069 (0.927-1.233)	0.360			
Diabetes (yes/no)	0.913 (0.718-1.162)	0.460			
Hypertension (yes/no)	0.899 (0.732-1.104)	0.310			
GAR-high	2.075 (1.804-2.388)	< 0.001	1.533 (1.285-1.828)	< 0.001	
ALT levels $\geq$ 40, U/L	1.313 (1.141-1.511)	< 0.001	1.003 (0.862-1.166)	0.973	
ALP levels $\geq$ 125, U/L	1.730 (1.495-2.001)	< 0.001	1.008 (0.840-1.209)	0.932	
Serum AFP ≥ 500, ng/mL	1.326 (1.152-1.525)	< 0.001	0.982 (0.846-1.140)	0.814	
Child-Pugh A vs B/C	1.812 (1.553-2.113)	< 0.001	1.389 (1.176-1.640)	< 0.001	
Lymph node metastasis	1.435 (1.246-1.652)	< 0.001	0.940 (0.779-1.133)	0.514	
Extrahepatic metastasis	1.679 (1.424-1.979)	< 0.001	1.301 (1.091-1.550)	0.003	
PVTT	1.958 (1.701-2.253)	< 0.001	1.372 (1.150-1.637)	< 0.001	
BCLC stage A vs B vs C vs D					
А	1	< 0.001	1	0.106	
В	1.409 (1.036-1.916)	0.029	0.865 (0.603-1.241)	0.432	
С	2.447 (1.911-3.135)	< 0.001	1.142 (0.810-1.611)	0.447	
D	3.538 (1.823-6.868)	< 0.001	1.867 (0.929-3.752)	0.079	
Number of tumors $\geq 2$	1.614 (1.365-1.909)	< 0.001	1.381 (1.132-1.685)	0.001	
Tumor diameter, cm					
< 3	1	< 0.001	1	< 0.001	
≥3, <5	1.692 (1.262-2.270)	< 0.001	1.684 (1.245-2.278)	0.001	
≥ 5, < 10	2.114 (1.633-2.737)	< 0.001	1.756 (1.337-2.306)	< 0.001	
≥10	2.930 (2.250-3.816)	< 0.001	1.822 (1.364-2.435)	< 0.001	

GAR-high:  $\gamma$ -glutamyl transferase to albumin ratio  $\geq$  4.75; HR: Hazard ratio; CI: Confidence interval; HBV: Hepatitis B virus; HCV: Hepatitis C virus; ALT: Alanine aminotransferase; ALP: Alkaline phosphatase; AFP: Alpha-fetoprotein; PVTT: Portal vein tumor thrombus; BCLC: Barcelona Clinic Liver Cancer.

At present, TACE-based prognostic models have been gradually established. The neutrophil-lymphocyte ratio model and platelet-to-lymphocyte ratio have been demonstrated to predict survival prognosis and metastasis in HCC patients treated with TACE[25,26]. However, there is no prognostic marker for patients suffering from HCC after TACE in conjugation with immunotherapy or targeted therapy. TACE was once the first-line therapy for stage B BCLC patients, and recent prospective clinical studies have shown that TACE is also a novel ideal treatment option for patients with early-stage (solitary nodules) and some advanced-stage HCC[27]. More and more HCC patients are expected to benefit from TACE treatment, so it is of great clinical significance to search for an effective prognostic marker for TACE treatment.

The role of inflammation in cancer has long been the focus of researchers. Inflammation promotes tumor development through a multi-faceted process, including angiogenesis, extracellular matrix remodeling, immunosuppression, invasion, and distant infiltration[28,29]. Various inflammatory cells create a favorable environment for tumor growth, thus exacerbating the development of this pathological process[30]. High levels of serum GGT are often a marker of severe hepatitis, cirrhosis, and advanced cancer. There is evidence that it mediates the hydrolysis of glutathione, which can lead to the formation of free radicals, lipid peroxidation and induce malignant transformation of cells. GGT is also thought to promote rapid growth and turnover of tumor cells[16]. A number of published prospective studies have shown a positive correlation between the levels of GGT and a number of cancers, including liver, breast, and prostate cancer[31,32].

In contrast, ALB plays a vital role in counteracting oxidative stress, enhancing microcirculation, and inhibiting inflammatory responses. It has been demonstrated that ALB exerts DNA replication stabilization and immune response

Table 3 Baseline characteristics of high and low γ-glutamyl transferase to albumin ratio groups after propensity score matching, <i>n</i> (%)						
Variables	Total	GAR-low	GAR-high	<i>P</i> value		
Patients	512	256	256			
Gender				0.798		
Female	71 (0.14)	34 (0.13)	37 (0.14)			
Male	441 (0.86)	222 (0.87)	219 (0.86)			
Age $\geq$ 60 years	215 (0.42)	107 (0.42)	108 (0.42)	1		
HBV	293 (0.57)	148 (0.58)	145 (0.57)	0.858		
HCV	17 (0.03)	8 (0.03)	9 (0.04)	1		
Alcohol	203 (0.40)	99 (0.39)	104 (0.41)	0.718		
Diabetes	47 (0.09)	25 (0.1)	22 (0.09)	0.76		
Hypertension	65 (0.13)	29 (0.11)	36 (0.14)	0.426		
ALT levels $\geq$ 40, U/L	304 (0.59)	147 (0.57)	157 (0.61)	0.418		
ALP levels $\geq$ 125, U/L	395 (0.77)	196 (0.77)	199 (0.78)	0.833		
Serum AFP $\geq$ 500, ng/mL	221 (0.43)	108 (0.42)	113 (0.44)	0.721		
Child-Pugh class				0.93		
А	371 (0.72)	186 (0.73)	185 (0.72)			
В	134 (0.26)	67 (0.26)	67 (0.26)			
С	7 (0.01)	3 (0.01)	4 (0.02)			
Lymph node metastasis	269 (0.53)	139 (0.54)	130 (0.51)	0.479		
Extrahepatic metastasis	99 (0.19)	49 (0.19)	50 (0.20)	1		
PVTT	232 (0.45)	125 (0.49)	107 (0.42)	0.131		
BCLC stage				0.347		
А	58 (0.11)	25 (0.10)	33 (0.13)			
В	67 (0.13)	29 (0.11)	38 (0.15)			
С	380 (0.74)	199 (0.78)	181 (0.71)			
D	7 (0.01)	3 (0.01)	4 (0.02)			
Number of tumors $\geq 2$	385 (0.75)	192 (0.75)	193 (0.75)	1		
Tumor diameter, cm				0.797		
< 3	50 (0.10)	22 (0.09)	28 (0.11)	0.797		
≥3, <5	79 (0.15)	41 (0.16)	38 (0.15)			
≥ 5, < 10	234 (0.46)	116 (0.45)	118 (0.46)			
≥10	149 (0.29)	77 (0.30)	72 (0.28)			

GAR-low: γ-glutamyl transferase to albumin ratio < 4.75; GAR-high: γ-glutamyl transferase to albumin ratio ≥ 4.75; HBV: Hepatitis B virus; HCV: Hepatitis C virus; ALT: Alanine aminotransferase; ALP: Alkaline phosphatase; AFP: Alpha-fetoprotein; PVTT: Portal vein tumor thrombus; BCLC: Barcelona Clinic Liver Cancer.

potentiation, thus impeding tumor progression[33]. Furthermore, hypoalbuminemia has been consistently linked to unfavorable prognoses in cancer patients [34,35]. McMillan et al [35] found that individuals with advanced lung or gastrointestinal malignancies exhibit a persistent systemic inflammatory response, which results in a continuous reduction in ALB concentration. To some extent, serum GGT levels can reflect tumor load, whereas liver metabolic ability and immune function are determined by ALB levels. Consequently, in comparison with other biomarkers, the GAR value more accurately reflects the relative tumor burden and liver function, thus affording a more effective prognostic tool for predicting the survival outcomes of patients diagnosed with HCC.

In preceding investigations, the prognostic outcome of HCC has been linked to factors such as GAR, PVTT, tumor number, tumor size, and Child grade[23,36]. The present study further corroborates this finding. Furthermore, we extended the nomogram model, demonstrating its commendable performance for prediction in the validation set. This

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Table 4 Univariate and multivariate Cox analyses for identifying clinical characteristics influencing overall survival in the training cohort					
Variables	HR (95%CI)	P value	HR (95%CI)	P value	
Gender (male/female)	1.129 (0.888-1.435)	0.321			
Age (≥ 60/< 60 years)	0.895 (0.754-1.063)	0.206			
HBV (positive/negative)	1.145 (0.962-1.362)	0.128			
HCV (positive/negative)	0.691 (0.406-1.175)	0.172			
Alcohol (yes/no)	1.017 (0.856-1.208)	0.851			
Diabetes (yes/no)	0.883 (0.662-1.179)	0.399			
Hypertension (yes/no)	0.856 (0.673-1.090)	0.208			
GAR-high	2.058 (1.737-2.438)	< 0.001	1.516 (1.218-1.885)	< 0.001	
ALT levels $\geq$ 40, U/L	1.278 (1.079-1.514)	0.005	0.904 (0.749-1.090)	0.291	
ALP levels $\geq$ 125, U/L	1.756 (1.475-2.091)	< 0.001	1.106 (0.882-1.388)	0.382	
Serum AFP $\geq$ 500, ng/mL	1.252 (1.057-1.484)	0.009	0.904 (0.752-1.086)	0.281	
Child-Pugh A vs B/C	1.858 (1.544-2.234)	< 0.001	1.389 (1.133-1.703)	0.002	
Lymph node metastasis	1.354 (1.143-1.603)	< 0.001	0.951 (0.756-1.197)	0.669	
Extrahepatic metastasis	1.608 (1.311-1.973)	< 0.001	1.263 (1.013-1.575)	0.038	
PVTT	2.009 (1.696-2.380)	< 0.001	1.510 (1.214-1.879)	< 0.001	
BCLC stage A vs B vs C vs D					
А	1	< 0.001	1	0.146	
В	1.363 (0.957-1.942)	0.086	0.865 (0.571-1.311)	0.494	
С	2.183 (1.639-2.907)	< 0.001	0.999 (0.667-1.498)	0.998	
D	4.106 (1.949-8.648)	< 0.001	2.174 (0.989-4.775)	0.053	
Number of tumors $\geq 2$	1.511 (1.241-1.838)	< 0.001	1.335 (1.057-1.685)	0.015	
Tumor diameter, cm					
< 3	1	< 0.001	1	0.002	
≥3, <5	1.755 (1.226-2.513)	0.002	1.752 (1.211-2.534)	0.003	
≥ 5, < 10	2.312 (1.691-3.162)	< 0.001	1.912 (1.372-2.665)	< 0.001	
≥10	2.924 (2.117-4.039)	< 0.001	1.793 (1.256-2.559)	0.001	

GAR-high:  $\gamma$ -glutamyl transferase to albumin ratio  $\geq$  4.75; HR: Hazard ratio; CI: Confidence interval; HBV: Hepatitis B virus; HCV: Hepatitis C virus; ALT: Alanine aminotransferase; ALP: Alkaline phosphatase; AFP: Alpha-fetoprotein; PVTT: Portal vein tumor thrombus; BCLC: Barcelona Clinic Liver Cancer.

has enhanced the GAR's practical application in clinical settings. Particularly for patients with elevated GAR, vigilance and proactive management should be emphasized.

The strength of the current research is the large sample size, which improves the reliability of results. We performed a PSM analysis, which reduced the effect of bias and confounding variables in the study and could more truthfully reflect the association of GAR with OS. Post-PSM survival analysis reaffirmed the prognostic value of GAR, with the low-GAR group demonstrating superior mOS. Further statistical scrutiny of the matched cohort, including both univariate and multivariate models, consistently highlighted GAR as a pivotal, independent determinant of OS outcomes. GAR was not only internally validated by the test data set, but also validated TACE in conjunction with targeted cohorts and TACE in conjunction with immunotherapy and targeted therapy. Therefore, it further improves the clinical applicability in the future treatment of HCC.

This study does, however, have some limitations. In the first place, this was a retrospective study, so selection bias was inevitable. Second, GGT and ALB levels can be influenced by different laboratory hematologic techniques, which may lead to some deviations. Third, although the predictive performance of GAR in dual and triple therapy cohorts has been verified, the number of patients was small, which may compromise the reliability of the conclusion. Therefore, multicenter, a large population, and prospective studies are expected to confirm and update the findings of this study in the future.



Figure 1 Kaplan-Meier survival curves stratified by y-glutamyl transferase to albumin ratio. A: Overall survival of the transarterial

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chemoembolization alone cohort; B: The cohort after propensity score matching; C: Training set; D: Validation set; E: Dual therapy cohort; F: Triple therapy cohort. GAR:  $\gamma$ -glutamyl transferase to albumin ratio.



Figure 2 Nomogram constructed based on independent risk factors for predicting 1-, 2-, and 3-year overall survival in patients with hepatocellular carcinoma. GAR: γ-glutamyl transferase to albumin ratio; PVTT: Portal vein tumor thrombus.



Figure 3 Time-dependent receiver operating characteristic curves of this predictive model. AUC: Area under receiver operating characteristic curve.

# CONCLUSION

Our study validates the effective prognostic capacity of the GAR-based nomogram for HCC patients undergoing TACE or TACE in combination with systemic therapy.

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Figure 4 Calibration curve of validation cohort. OS: Overall survival.



Figure 5 Decision curve analyses curve of validation cohort.

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# FOOTNOTES

Author contributions: Wu ZY, Li H, and Han YW conceived, designed and refined the study protocol; Chen JL, Su K, and Weng ML were involved in the data collection and formulation of research objectives; Wu ZY and Li H drafted the manuscript; and all authors were involved in the critical review of the results and approved the final manuscript. Wu ZY and Li H contributed equally to this work. The reasons for designating Wu ZY and Li H as co-first authors are threefold. First, the research was performed as a collaborative effort, and the designation of co-first authorship accurately reflects the distribution of responsibilities and burdens associated with the time and effort required to complete the study and the resultant paper. This also ensures effective communication and management of postsubmission matters, ultimately enhancing the paper's quality and reliability. Second, the overall research team encompassed authors with a variety of expertise and skills from different fields, and the designation of co-first authors best reflect this diversity. This also promotes the most comprehensive and in-depth examination of the research topic, ultimately enriching readers' understanding by offering various expert perspectives. Third, Wu ZY and Li H contributed efforts of equal substance throughout the research process. They equally made a significant contribution to the work reported, in the design of methodology, creation of models, testing of code, statistical analysis, validation of results, writing the initial draft, and revision of articles. The choice of these researchers as co-first authors acknowledge and respects this equal contribution, while recognizing the spirit of teamwork and collaboration of this study. In

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summary, we believe that designating Wu ZY and Li H as co-first authors of are fitting for our manuscript as it accurately reflects our team's collaborative spirit, equal contributions, and diversity.

Institutional review board statement: The study protocol was authorized by the Ethics Committee of the Affiliated Hospital of Southwest Medical University (No. KY2021063) and complied with the Code of Ethics of the World Medical Association.

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ORIGINAL ARTICLE

# Deep learning model combined with computed tomography features to preoperatively predicting the risk stratification of gastrointestinal stromal tumors

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Scientific Quality: Grade C	China
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2024	Abstract
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Hours	BACKGROUND
	Gastrointestinal stromal tumors (GIST) are prevalent neoplasm originating from
	tumor recurrence within 5 years. Thus, there is a pressing need to accurately evaluate risk stratification preoperatively.
	AIM

To assess the application of a deep learning model (DLM) combined with computed tomography features for predicting risk stratification of GISTs.

# **METHODS**

Preoperative contrast-enhanced computed tomography (CECT) images of 551 GIST patients were retrospectively analyzed. All image features were independently analyzed by two radiologists. Quantitative parameters were statistically analyzed to identify significant predictors of high-risk malignancy. Patients were



randomly assigned to the training (n = 386) and validation cohorts (n = 165). A DLM and a combined DLM were established for predicting the GIST risk stratification using convolutional neural network and subsequently evaluated in the validation cohort.

#### RESULTS

Among the analyzed CECT image features, tumor size, ulceration, and enlarged feeding vessels were identified as significant risk predictors (P < 0.05). In DLM, the overall area under the receiver operating characteristic curve (AUROC) was 0.88, with the accuracy (ACC) and AUROCs for each stratification being 87% and 0.96 for low-risk, 79% and 0.74 for intermediate-risk, and 84% and 0.90 for high-risk, respectively. The overall ACC and AUROC were 84% and 0.94 in the combined model. The ACC and AUROCs for each risk stratification were 92% and 0.97 for low-risk, 87% and 0.83 for intermediate-risk, and 90% and 0.96 for high-risk, respectively. Differences in AUROCs for each risk stratification between the two models were significant (P < 0.05).

#### CONCLUSION

A combined DLM with satisfactory performance for preoperatively predicting GIST stratifications was developed using routine computed tomography data, demonstrating superiority compared to DLM.

Key Words: Gastrointestinal stromal tumors; Deep learning; Risk stratification; Tomography, X-ray computed; Prognosis

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**Core Tip:** The deep learning model (DLM) was validated to accurately predict the risk classification of gastrointestinal stromal tumors. The combined DLM outperformed DLM in predicting risk stratification. The combined model has potential to guide and facilitate clinical decision-making.

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# INTRODUCTION

As is well documented, gastrointestinal stromal tumors (GIST) are prevalent tumors originating from the gastrointestinal mesenchyme. Approximately 50% of GIST patients experience tumor recurrence within 5 years, and surgical intervention alone is inadequate for achieving an optimal prognosis[1,2]. Earlier studies established that 85% of GISTs are associated with receptor tyrosine kinase (c-kit) mutations, and 3%–5% are linked to platelet derived growth factor receptor alpha gene mutation[1,3-5]. The mutation type determines response to imatinib[6-8]. Considering the lack of effective conventional chemotherapy drugs, and the activity of Imatinib, adjuvant Imatinib may be a potential treatment option for patients with GIST[1,5,9]. A study assessing the efficacy of long-term imatinib treatment in advanced GIST patients documented a median overall survival exceeding four years[10]. Moreover, considering the recurrence and metastasis rate of intermediate- and high-risk GISTs after surgery, targeted drug therapy can improve the prognosis of GISTs[11,12]. Therefore, there is an urgent need to accurately evaluate risk stratification prior to surgery to obtain valuable information for evaluating the necessity of surgery and adjuvant treatment.

At present, the risk stratification of GISTs is based on histologic (mitotic index) and imaging characteristics (including tumor size and site) of the lesion as outlined in the National Institutes of Health (NIH) consensus classification system [13]. However, it is challenging to determine the mitotic index without histological examination. Indeed, the malignancy risk of most tumors is confirmed histologically after surgery. Although, endoscopic biopsy has also been widely used preoperatively, its utility may be limited if the tumor sample contains large areas of necrosis or hemorrhage, yielding inconclusive results [14-16].

Recently, the deep learning model (DLM), composed of multi-types of self-learning units, has emerged as a promising technique for analyzing medical imaging data[17-20]. Notably, DLM has demonstrated efficacy in clinical applications such as the assessment of differentiation grades in meningioma and renal cell carcinoma, as well as in predicting the molecular subtypes and grades of glioma[17-19,21]. Overall, deep learning transforms medical images into high-dimensional mineable data, offering rapid insights with high repeatability and providing a novel approach for GIST risk assessment[22-24]. This study aimed to establish and validate DLMs for predicting preoperative GIST risk stratification based on routine post-contrast computed tomography (CT) and clinical data.

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# MATERIALS AND METHODS

#### Characteristics of patients

This study was approved by our institutional ethics committee. All the patients signed the informed consent form before examinations. From January 2012 to December 2022, 606 patients with GISTs were initially enrolled in this retrospective study. A total of 55 patients were subsequently excluded for the following reasons: (1) Lack of preoperative contrastenhanced CT images (n = 19); (2) Suboptimal CT image quality (n = 9); (3) Preoperative therapy or experienced metastasis to other sites (n = 25); and (4) Absence of required pathologic data (n = 2). Finally, a total of 551 patients were included in this study (256 men and 295 women; mean age  $60.3 \pm 9.8$  years). The study population flow chart is illustrated in Figure 1.

All patients underwent complete surgical resection. GIST risk classification was based on National Comprehensive Cancer Network (NCCN) guidelines [15]. According to risk categories, patients in this study were classified into the highrisk (high risk), intermediate-risk (intermediate risk), and low-risk (very low and low risk) groups.

### CT image acquisition

All patients underwent abdominal contrast-enhanced CT examination covering the whole tumor. After a non-contrast CT scan (Scanner: Philips Iqon, GE Healthcare Discovery CT750 HD or SIEMENS 64-MDCT) with a thickness of 1.0-1.5 mm, three-phase contrast-enhanced scans were performed, with 90 to 100 mL iodine contrast medium (Ultravist 370, Bayer Schering Pharma, Germany) intravenously injected at a rate of 2.5 to 3.0 mL/s.

#### Clinical and CT image feature analysis

All CT images were independently analyzed by two radiologists with 3 and 13 years of experience in abdominal radiology. In cases of disagreement, the radiologist with 13 years of experience reviewed the images to reach a consensus. Clinical information, image features and pathologic characteristics, including gender, age, tumor location, growth pattern (exophytic, endoluminal, mixed), tumor size (measured as the maximum diameter of the largest tumor section), tumor morphology (round or oval shape was considered regular, and lobulated or other irregular shapes were categorized as irregular), necrosis, ulceration, internal hemorrhagic foci, calcification, lymph node status, presence of enlarged feeding vessels, tumor boundary (clear or blurred), the pattern and degree of tumor enhancement during the venous phase and the range of tumor enhancement across the three phases, were derived from CT images and medical records. For CT value measurements of each tumor, regions of interest (ROIs) were delineated to cover tumor parenchyma while avoiding areas with evidence of cystic, necrotic or hemorrhagic changes at the level of the largest solid tumor regions and their adjacent upper and lower levels during the plain phase, arterial phase, venous phase and delay phase, respectively. The ROIs for CT value measurements were consistently sized using the copy and paste function across the different phases of images. Next, the average of three measurements was calculated. According to the difference between the venous phase and plain CT, the enhancement degree was defined as mild (CT value difference ≤ 20 HU), moderate (CT value difference between 20 HU and 40 HU), and obvious enhancement (CT value difference > 40 Hu). According to differences between the CT values of the venous and arterial phases, the enhancement pattern was defined as continuous (CT value difference  $\geq$  0) and attenuation (CT value difference < 0). The enhancement tumor range was calculated during the arterial phase (ER1 = arterial phase CT value-precontrast CT value), venous phase (ER2 = venous phase CT valueprecontrast phase CT value), and delay phase (ER3 = delay phase CT value - precontrast scan CT value).

#### Image segmentation

All the CT images were exported in Joint Photographic Experts Group format. Then, two radiologists with extensive experience in abdominal imaging diagnosis (3 years and 13 years, respectively) participated in the segmentation of the entire tumor. One radiologist manually delineated the ROIs of the entire tumor layer by layer on venous phase CT images. The segmented images were subsequently confirmed by the other radiologist. Both radiologists were blinded to the pathological reports for risk stratification. Based on recommendations from previous literature[21], ImageJ (NIH, Bethesda, MD) was employed to apply an adaptive contrast filter to images. Besides, CT- segmented images were randomly selected from 20 patients, and the Dice similarity coefficient (DSC) was used to evaluate the inter-reader consistency in image segmentation. Detailed information of image preprocessing can be found in the Supplementary material 1.

# The DLM construction

The DLM was constructed in two steps: Tumor features and tumor classification were initially extracted from CT images to generate the DLM, followed by the establishment of the combined model for tumor classification by integrating subject clinical-imaging features after statistical analysis. Figure 2 displays the detailed framework of this process. In the current study, a stratified random split was utilized at the patient level to randomly divide all patients into a training cohort and a validation cohort in a 7:3 ratio.

The 3D residual network (ResNet) was used to train our image dataset and establish the DLM. The 3D-ResNet is a three-dimensional convolutional neural network model based on the ResNet architecture. It is an extension of ResNet in two-dimensional image classification tasks used to process three-dimensional volume data. Besides, it accepts 3D volumetric data as input, positioning it as a powerful model for learning volume datasets. Furthermore, it can be adjusted according to the task complexity and dataset characteristics with variable depth. It can enhance the network depth by increasing the number of stacked layers of residual blocks, thereby optimizing the model's expressive ability. During the training phase, 3D-Resnet was used to extract and learn deep tumor features related to GIST risk stratification from each patient's CT images.



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Patients (n = 606) who were diagnosed GIST histopathologically Exclusion No preoperative contrast-enhanced CT (n = 19) Unacceptable CT quality (n = 9) Preoperative therapy (n = 25) Insufficient pathologic data (n = 2) Study population (n = 551) Training cohort (n = 386) Testing cohort (n = 165)

Figure 1 Study population flowchart. CT: Computed tomography; GIST: Gastrointestinal stromal tumors.



Figure 2 Overall gastrointestinal stromal tumor risk stratification framework. CT: Computed tomography; MLP: Multilayer perceptron; GAP: Global average pooling.

Multilayer perceptron (MLP) was employed for tumor risk stratification by combining imaging features and clinical data. It is a universal function approximator based on feedforward artificial neural networks that can learn and represent nonlinear relationships through multiple fully connected hidden layers and an output layer, making it suitable for various machine learning tasks. In the current model, a batch normalization (BN) layer was introduced following each linear layer in MLP to accelerate the convergence rate of the neural network, reduce the dependence of the model on the initial parameters, and improve the robustness of the model. The BN layer normalized each mini-batch data to stabilize the input of the neural network, thus improving the convergence rate and generalizability of the model. Figure 3 shows the feature extraction process. In the present study, the subject clinical-image data features of patients were concatenated with imaging features extracted by the 3D ResNet, and their feature vectors were inputted into the MLP to establish the

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Figure 3 Schematic diagram of feature extraction process. BN: Batch normalization; RELU: Rectified linear unit.

combined DLM for tumor risk stratification.

## Training details

In this study, the network architecture was implemented using the Pytorch framework and trained on NVIDIA GPU to accelerate training speed. Additionally, the transfer learning method was adopted, leveraging pre-training weights to improve model performance. Detailed information of model training process can be found in the Supplementary materials 2.

#### Statistical analysis

Statistical analysis was performed using the software SPSS version 22.0 (SPSS Inc., Chicago, IL, United States) and MedCalc version 22.002 (MedCalc Software Ltd, Ostend, Belgium). A P value of < 0.05 was considered statistically significant.

The interobserver agreement of measurements between the two radiologists was evaluated using the interclass correlation coefficient (ICC). The  $\chi^2$  test, independent two-sample *t*-test, one-way analysis of variance and Bonferroni tests were used to evaluate the significance of correlations between various clinical- imaging features and pathological GIST risk classifications from surgical resection specimens. Ordinary logistic regression was performed to identify significant predictive factors for relapse[25,26].

To assess the performance of DLM and combined DLM, five different indicators, namely area under the receiver operating characteristic curve (AUROC), F1 score (F1), accuracy (ACC), sensitivity (SEN), and specificity (SPE), were used. AUROC was calculated along with its 95% CI.

# RESULTS

#### Clinical-imaging characteristics

ICC analysis showed a good concordance of measurements between the two radiologists (tumor size, ICC = 0.985; CT value in the plain phase, ICC = 0.812; CT value in the arterial phase, ICC = 0.906; CT value in the venous phase, ICC = 0.921; CT value in the delay phase, ICC = 0.848). Among the analyzed CECT image features, tumor size, tumor morphology, tumor location, growth pattern, necrosis, ulceration, calcification, lymph node status, presence of enlarged feeding vessels, tumor enhancement pattern during the venous phase, and the range of tumor enhancement across the three phases were found to be significantly associated with GIST risk categories (P < 0.05). The distribution of these features in the risk categories and the results of the  $\chi^2$  test are listed in Table 1. Meanwhile, ordinary logistic regression analysis identified tumor size, ulceration, and the presence of enlarged feeding vessels as statistically significant predictors (P < 0.05, Table 2).

# Diagnostic performance of the DLM

All patients were randomly associated into two independent cohorts, namely a training cohort (386 patients: 176 males, mean age, 60.2 ± 9.8 years; 210 females, mean age, 59.9 ± 10.2 years) and a validation cohort (165 patients: 80 males, mean



#### Table 1 Distribution of the analyzed clinical-imaging features across pathologic risk categories, mean ± SD

OFOT fortune		Pathologic risk categories			
CECT features		High ( <i>n</i> = 213)	Moderated (n = 143)	Low ( <i>n</i> = 195)	Pvalue
Gender	Male	107	60	89	0.296
	Female	106	83	106	
Location	Gastric	139	136	171	0.000
	Non-gastric	74	7	24	
Morphology	Regular	54	94	170	0.000
	Irregular	159	49	25	
Growth pattern	Endoluminal	35	54	93	0.000
	Mixed	51	22	28	
	Exophytic	127	67	74	
Degree of contrast enhancement in the venous phase	Mild (≤ 20 HU)	30	20	20	0.424
	Moderate (20-40 HU)	101	74	90	
	Obvious (≥ 40 HU)	82	49	85	
Contrast enhancement pattern during the venous phase	Continuous	198	142	193	0.000
	Attenuation	15	1	2	
Calcification	Present	22	16	21	0.967
	Absent	191	127	174	
Necrosis	Present	155	65	33	0.000
	Absent	58	78	162	
Ulceration	Present	53	23	8	0.000
	Absent	160	120	187	
Enlarged feeding vessels	Present	183	60	14	0.000
	Absent	30	83	181	
Lymph nodes	Present	19	1	1	0.000
	Absent	194	142	194	
Age		$59.44 \pm 10.41$	61.39 ± 9.83	$60.37 \pm 9.13$	0.183
Size		$9.03 \pm 4.42$	$4.90 \pm 1.89$	$2.77 \pm 1.20$	0.000
Range of tumor enhancement during the arterial phase		$18.83 \pm 17.81$	14.24 ± 11.53	$18.45 \pm 17.47$	0.004
Range of tumor enhancement during the venous phase		$41.59 \pm 25.73$	38.97 ± 18.96	$45.22\pm25.70$	0.038
Range of tumor enhancement during the delay phase		42.73 ± 18.89	43.72 ± 17.97	47.97 ± 20.27	0.016

CECT: Contrast-enhanced computed tomography.

age,  $59.8 \pm 9.9$  years; 85 females, mean age,  $60.0 \pm 10.1$  years). There were 136 (35.2%) cases of low-risk GISTs, 101 (26.2%) cases of intermediate-risk GISTs, and 149 (38.6%) cases of high-risk GISTs in the training cohort. In contrast, the validation cohort comprised 59 (35.8%) cases of low-risk GISTs, 42 (25.5%) cases of intermediate-risk GISTs, and 64 (38.8%) cases of high-risk GISTs.

The DSC value showed a good concordance of image segmentation between the two radiologists (DSC = 99.96%). The results for the different algorithms are detailed in Table 3. The model constructed using 3D-ResNet with 34 Layers demonstrated the optimal performance, with an ACC of 75%, a SEN of 72%, a SPE of 87%, and a F1 score of 72%. The overall AUROC for DLM was 0.88 (0.83, 0.93). The ROCs are depicted in Figure 4A. In DLM, the ACC and AUROCs for each stratification were 87% (144/165) and 0.96 (0.94, 0.98) for low-risk GISTs, 79% (131/165) and 0.74 (0.67, 0.81) for intermediate-risk GISTs, and 84% (138/165) and 0.90 (0.85, 0.95) for high-risk GISTs, respectively. The results for the validation cohorts were visualized as confusion matrices to compare the GIST risk stratification predicted by DLM against the pathological risk stratification (Figure 5A).

Table 2 Logistic regression analysis of risk classification based on clinical-imaging feature					
	Dualua	95%CI			
	P value	Lower bound	Upper bound		
Size	0.000	-0.763	-0.473		
Range of tumor enhancement during the arterial phase	0.131	-0.035	0.005		
Range of tumor enhancement during the venous phase	0.220	-0.007	0.032		
Range of tumor enhancement during the delay phase	0.858	-0.021	0.017		
Morphology	0.602	-0.387	0.608		
Location	0.074	-0.063	1.386		
Ulceration	0.004	-1.622	-0.300		
Enlarged feeding vessels	0.000	-2.134	-1.094		
Growth pattern	0.224	-0.833	0.328		
Contrast enhancement during the venous phase	0.428	-2.266	1.384		
Necrosis	0.236	-0.195	0,793		
Lymph nodes	0.890	-1.934	1.678		

Table 3 Different algorithms for predicting gastrointestinal stromal tumor risk classification							
Different method	Accuracy (%)	Sensitivity (%)	Specificity (%)	F1 score (%)			
3DCNN	60	51	68	52			
3DResnet_50	66	58	71	59			
3DResnet_18	71	66	76	67			
3DResnet_34	75	72	87	72			
Combined model (3DResnet + MLP)	84	83	92	83			

3DCNN: Three-dimensional convolutional neural network; 3DResnet: Three-dimensional residual network; MLP: Multilayer perceptron.

The combined DLM achieved satisfactory performance in assessing GIST risk stratification. The overall ACC and AUROC were 84% (139/165) and 0.94 (0.93, 0.95) for the combined model. The ROCs are delineated in Figure 4B. The ACC and AUROCs for each tumor risk stratification were 92% (152/165) and 0.97 (0.96, 0.98) for low-risk GISTs, 87% (143/165) and 0.83 (0.78, 0.88) for intermediate-risk GISTs, and 90% (148/165) and 0.96 (0.94, 0.98) for high-risk GISTs, respectively. The results for the validation cohorts were visualized as confusion matrices to compare the GIST risk stratification predicted by the combined model against pathological risk stratification (Figure 5B).

The ACC, SEN, SPE, F1 score and AUROCs for each tumor risk stratification across different models are summarized in Table 4. Importantly, differences in AUROCs between DLM and the combined model were significant (P < 0.001).

# DISCUSSION

In this retrospective research, a DLM and a combined DLM were constructed. Notably, the latter (AUROC = 0.94) outperformed the former (AUROC = 0.88) in assessing GIST grading.

According to the modified NIH criteria and NCCN guidelines, the need of adjuvant treatment for GIST patients and the duration of treatment are associated with the risk stratification of GISTs[8,15,27,28]. Combining adjuvant treatment such as Imatinib before and after surgery may extend the recurrence free survival and overall survival of intermediate and high-risk GIST patients[1,5,29]. Therefore, an accurate preoperative categorization of risk classification, especially in high-risk GISTs, can provide valuable information for evaluating the necessity of surgical resection and adjuvant treatments[30-32]. In this study, two models were developed to predict preoperative GIST risk stratification: DLM and combined DLM. To the best of our knowledge, studies that combined clinical-imaging features and convolutional neural

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Table 4 Accuracy, sensitivity, specificity, F1 score and areas under the receiver operating characteristic curves for each tumor risk stratification. n (%)/95%CI

		Accuracy ( <i>n</i> = 165)	Sensitivity	Specificity	F1 score (%)	AUROC
DLM	High	138 (84); (78-90)	81 (52/64); (76-86)	85 (86/101); (78-91)	79	0.90 (85-95)
	Moderate	131 (79); (71-87)	50 (21/42); (25-74)	89 (110/123); (82-96)	55	0.74 (67-81)
	Low	144 (87); (81-93)	86 (51/59); (81-91)	88 (93/106); (83-94)	83	0.96 (94-98)
	Overall	75	72	87	72	0.88 (83-93)
Combined model	High	148 (90); (86-94)	88 (56/64); (83-93)	91 (92/101); (83-98)	87	0.96 (94-98)
	Moderate	143 (87); (83-92)	69 (29/42); (66-71)	93 (114/123); (86-98)	72	0.83 (78-88)
	Low	152 (92); (85-96)	92 (54/59); (89-93)	92 (98/106); (86-97)	89	0.97 (96-98)
	Overall	84	83	92	83	0.94 (93-95)

DLM: Deep learning model; AUROC: Areas under the receiver operating characteristic curve.



Figure 4 Receiver operating characteristic curves for the deep learning model and combined model. A: Receiver operating characteristic curve (ROC) for the deep learning model in the validation cohort; B: ROC curve for the combined model in the validation cohort. ROC: Receiver operating characteristic; AUC: Area under the curve.

network models to establish a combined model for predicting GIST risk stratification and distinguishing between different categorizations of risk classification (high-risk, intermediate-risk and low-risk GISTs) are scarce.

Analysis of clinical-imaging features revealed that tumor size, morphology, location, growth pattern, the presence of necrosis, ulceration, calcification, lymph nodes, and enlarged feeding vessels, as well as the tumor enhancement pattern during the venous phase and the range of tumor enhancement, were significantly associated with pathologic GIST risk categories. Logistic regression analysis subsequently identified tumor size, the presence of ulcers, and enlarged feeding vessels as predictors of pathologic risk categories, consistent with the results of previous studies[25,26,33]. Zhou *et al*[34] reported that tumors with large sizes (> 10 cm) and enlarged feeding vessels were more likely to be a high -risk GISTs [34]. Moreover, mucosal destruction promotes the formation of ulcers due to the influence of gastric acid[35]. The NCCN guideline recommend patients with GISTs larger than 2 cm to undergo surgical resection[28], while according to Nishida's[36] report, small GIST tumors may also be invasive and linked to a poor prognosis. Therefore, evaluating the risk stratification of GISTs exclusively based on tumor size could be insufficient. Other imaging features were also subjectively assessed and heavily relied on the experience of observers. While the degree of contrast enhancement is typically considered a characteristic of tumor biological activity, it showed no significant association with pathologic risk stratification as a predictive factor in our study, in line with the results of previous articles[26,33].

The results of our study unveiled that the DLM could accurately predict GIST risk classifications, with an AUROC of 0.88 in the validation cohort. However, the performance of the combined DLM was relatively higher (AUROC = 0.94), attributable to the combination of DLM with clinical-imaging features increasing the ability to assess the GIST risk classification. Overall, our study offers a novel method for optimizing the preoperative assessment of GIST risk stratification based on CT images, moving beyond dependence on postoperative specimens. Zhou *et al*[34] documented that the AUROC of the multinomial logistic regression model with subjective CT image features for GIST risk stratification was 0.806. At the same time, Wang *et al*[22] divided patients with GISTs into the high malignant potential group (intermediate

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Figure 5 Confusion matrix for the deep learning model and combined model for gastrointestinal stromal tumors risk stratification. A: Confusion matrix for the deep learning model; B: Confusion matrix for the combined model.

risk and high risk) and the low malignancy potential group (very low risk and low risk) and described that the area under the curve (AUC) of the combined model (clinical features and the radiomics) was significantly higher in the validation group (0.913 *vs* 0.792, P = 0.019) compared to the clinical model. Importantly, Kang *et al*[37] concluded that the DLM (AUROCs; testing, 0.89; external validation, 0.85) outperformed the radiomics model in terms of GIST risk classification. In this study, the DLM and the combined DLM had an AUROC of 0.88 and 0.94 for distinguishing between the three types of GIST risk classifications (high-risk, intermediate-risk and low-risk) in the validation cohort. Indeed, the combined model outperformed DLM, with ACCs and AUROCs of 92% and 0.97 for low-risk GISTs, 87% and 0.83 for intermediate-risk GISTs, and 90% and 0.96 for high-risk GISTs, respectively. Notably, the AUROCs for different risk stratifications in the combined model were significantly superior to those of the DLM. These results collectively indicated that the combined DLM had superior predictive capabilities, especially for low- and high-risk GISTs.

However, the results for the intermediate-risk class were relatively unsatisfactory, with an accuracy of 87% and an AUROC of 0.83. This may be ascribed to imbalanced sample sizes. Specifically, there were only 143 cases of intermediate-risk GISTs in this study, which was lower than those of non-intermediate-risk GISTs (408 cases). This may result in relatively fewer features being extracted from intermediate-risk GISTs compared to machine learning algorithms, thereby introducing model bias. Nevertheless, compared to DLM (AUC = 0.74), the combined model (AUC = 0.83) demonstrated advantages in predicting intermediate-risk GISTs.

Of note, deep learning is a subfield of artificial intelligence that performs tasks by analyzing relationships between existing data points[38-40]. In recent years, image analysis based on deep learning algorithm has been increasingly applied to tumor diagnosis, grading, staging, prediction, and treatment evaluation. Zhu et al[41] concluded that the DLM outperformed in assessing the risk of screening-detected breast cancer. Similarly, Doppalapudi et al[42] pointed out that the accuracy of lung cancer classification predicted by DLM was 71.18%, while that of traditional machine learning models was merely 61.12%, indicating that DLM displayed superior performance for predicting lung cancer subtypes. A study investigating glioma showed that DLM achieved high performance in predicting molecular subtypes and grades, with an isocitrate dehydrogenase-AUC of 0.90, an 1p/19q co-deletion AUC of 0.85, and a grade AUC of 0.81 (grade II/ III/IV)[17]. Wang et al[43] developed the convolutional neural network models with varying layers, achieving AUROCs above 0.8 for differentiating high-risk gastric GISTs from intermediate-risk and very low/low-risk gastric GISTs in the validation dataset. In the present study, the DLM based on the 3D-ResNet method increased the network depth by increasing the number of stacked layers of residual blocks, thereby improving the model's expressive ability. In addition, the clinical data of patients were concatenated with the imaging features extracted by the 3D- ResNet and then incorporated their feature vectors into the MLP for risk classification. As anticipated, the results uncovered that the DLM based on the 3D-ResNet method combined with clinical-imaging features could accurately predict GIST risk classifications.

Nevertheless, this study has several limitations that cannot be overlooked. Firstly, this was a retrospective study based on a limited sample size, resulting in an imbalance in the data for risk stratification. Therefore, an ideal DLM should be constructed with a larger training set containing datasets from multiple-centers to balance the data for different risk stratifications. Further prospective studies with external validation cohorts are warranted to validate our results. Secondly, the DLM developed in our study required manual segmentation of tumors on CT images remains a semiautomatic model. Thirdly, radiomics features were used for the risk stratification of GISTs in previous studies[22,32,39,44, 45]. Therefore, future studies can compare the performance of radiomics models with DLM.

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# CONCLUSION

In summary, a high-performance combined DLM for preoperative prediction of the GIST risk stratification was developed and validated in this study. Noteworthily, this model has the potential to guide and facilitate clinical decisionmaking for GIST patients.

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# FOOTNOTES

Author contributions: Li Y completed the research design and data analysis, and was a major contributor in writing the manuscript; Liu YB completed data analysis and model establishment; Cui XN, Yuan CC, and Meng DH participated in data collection and preliminary reports; Li XB and Ye ZX provided guidance on the paper and objectively reviewed it; Li Y and Cui XN were responsible for the processing of inspection analysis and statistical data to ensure the quality of the data. All authors read and approved the final manuscript.

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Data sharing statement: Technical appendix, statistical code, and dataset available from the corresponding author at yezhaoxiang@163. com.

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**Retrospective Study** 

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ORIGINAL ARTICLE

# Temozolomide and capecitabine regimen as first-line treatment in advanced gastroenteropancreatic neuroendocrine tumors at a Latin American reference center

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Novelty: Grade B				
Creativity or Innovation: Grade C				
Scientific Significance: Grade C				
<b>D-Deviewer:</b> Agidow MM	Abstract			
-Reviewer. Agricew Will	BACKGROUND			
Received: July 22, 2024	Numerous studies have indicated that the temozolomide and capecitabine			
Revised: August 31, 2024	regimen (TEMCAP) exhibits a certain level of efficacy in treating advanced, well-			
Accepted: September 19, 2024	differentiated gastroenteropancreatic neuroendocrine tumors (GEP-NET). Ho-			
Published online: December 15,	wever, published data from Peru are limited. We hypothesize that this regimen			
2024	could be a viable therapeutic option for advanced GEP-NET in the Peruvian			
Processing time: 113 Days and 11.9	population.			
Hours	AIM			
ELANGER EL	To evaluate overall survival (OS) in patients diagnosed with advanced GEP-NET			



treated with TEMCAP at the Instituto Nacional de Enfermedades Neoplásicas (INEN) in Lima-Perú.

## **METHODS**

A retrospective review was conducted to identify patients with GEP-NEN treated with the TEMCAP regimen between 2011 and 2021 at the INEN. A total of thirtyeight patients were included in the final analysis: Thirty-five received TEMCAP as a first-line treatment, and three as a second-line treatment. The primary objective was to evaluate OS. The efficacy and safety of TEMCAP were assessed until the occurrence of unacceptable toxicity or disease progression. Survival outcomes were estimated using the Kaplan-Meier method.



## RESULTS

The median age of the patients was 52 years (range 24-77 years), and 53.3% were female. The most common symptoms at diagnosis were abdominal pain in 31 patients (81.6%). Primary tumors included 12 in the rectum (31.6%), 11 in the pancreas (28.9%), 3 in the ileum (7.9%), 2 in the mesentery (5.3%), 2 in the small intestine (5.3%), 1 in the appendix (2.6%), 1 in the stomach (2.6%) and 6 cases of liver metastasis of unknown primary (15.8%). Five were neuroendocrine tumors (NET) G1 (13.2%), 33 were NET G2 (86.8%), five had Ki67 < 3% (13.2%), and 33 had Ki67 between 3% and 20% (86.8%). TEMCAP was administered to 35 (92.1%) patients as first-line treatment. OS at 12, 36, and 60 months was estimated in 80%, 66%, and 42%, respectively, with a median OS of 49 months.

#### **CONCLUSION**

TEMCAP therapy is a viable first-line option regarding efficacy and tolerability in areas where standard therapy is inaccessible.

Key Words: Well-differentiated; Gastroenteropancreatic neuroendocrine tumors; Capecitabine; Temozolomide; Retrospective study; Treatment; Chemotherapy

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Core Tip: In this study, patients diagnosed with advanced gastroenteropancreatic neuroendocrine tumors who were treated with the temozolomide and capecitabine regimen exhibited a median overall survival of 49 months, with 42% surviving at 60 months. The regimen was well-tolerated, and most patients experienced stable disease. These findings suggest that this treatment could be viable in settings where standard therapies are unavailable or inaccessible, although further prospective studies are needed for confirmation.

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# INTRODUCTION

Neuroendocrine tumors (NEN) represent a diverse array of neoplasms arising from cells within the endocrine and nervous systems, and exhibit a broad spectrum of behaviors. While historically considered rare diseases, their prevalence has been increasing. In England, NEN are the 10<sup>th</sup> most prevalent cancer and the second most common gastrointestinal cancer, only preceded by colorectal cancer[1]. NEN have witnessed a notable surge over the past two decades; the ageadjusted incidence per 100000 persons increased from 4.90 in 2000 to 8.19 in 2018[2]. With regard to gastroenteropancreatic neuroendocrine tumors (GEP-NET) in the United States, the incidence is reported to be 3.56 cases per 100000 individuals<sup>[3]</sup>.

The information published regarding NET in Latin American countries remains largely unreported, and clinical literature is highly scarce. An observational study in Argentina documented 532 NET cases, including 461 GEP-NET and 71 bronchial NET[4]. A NET registry from Brazil has compiled baseline data on the initial 1000 patients enrolled across 32 centers spanning all country regions. It categorized GEP-NET as the second most prevalent type, constituting 20.2% of cases, trailing only thoracic NEN[5]. In a retrospective review at the Instituto Nacional de Enfermedades Neoplásicas (INEN), 367 NEN were reported between 2010 and 2014. Gastroenteropancreatic NEN were the most prevalent, with 152 cases (44.84%), followed by thoracic NEN, with 75 cases (22.12%)[6].

The clinical practice guideline for medical management of GEP-NET at the INEN reported 650 cases of NEN between 2009 and 2018, with an average age of 55 years. The most frequent sites were the rectum (15%), lung (9.84%), stomach (8.3%), neuroendocrine Merkel cells (9.07%), and unknown primary (9.07%)[7]. According to the WHO classification for NEN, they are categorized into well-differentiated low-grade G1 (Ki67 < 3%), intermediate-grade well-differentiated G2 (Ki67 3%-20%), and high-grade well-differentiated G3 (Ki67 > 20%), based on the Ki67 proliferation index. G3 tumors are divided into well-differentiated high-grade or poorly differentiated high-grade neuroendocrine carcinomas (GEP-NEC) [8]. Of all NEN, approximately 80%-90% are well-differentiated[9]. GEP-NET can be classified according to their origin into two main groups: Pancreatic NET (pan-NET) and non-pan-NET. Furthermore, they can be classified based on hormone production in functioning and non-functioning tumors. Most GEP-NET are non-functioning; 20% of intestinal NET are functioning tumors, while pan-NET are functioning in 10%-30% of cases[9]. For non-functioning NET, early detection can be challenging unless the tumor has grown sufficiently large to cause symptoms.

Medical treatment options for advanced GEP-NET with antiproliferative effects include targeted drugs and systemic chemotherapy. Regarding somatostatin analogs (SSA), the CLARINET trial, which compared lanreotide to placebo,

estimated progression-free survival (PFS) rates at 24 months of 65.1% in the experimental arm and 33% in the placebo group[10]. These results were confirmed in the open-label extension study[11]. In the phase III PROMID trial, the median time to progression in the octreotide long-acting release (LAR) and placebo groups was 14.3 and 6 months, respectively [12]. However, the updated trial did not show a difference in OS[13]. Everolimus was shown to prolong PFS compared to placebo in previously treated GEP-NET patients[14,15]. Despite these findings, its efficacy in patients with GEP-NET associated with carcinoid syndrome remains unclear[16]. Sunitinib, a multitargeted tyrosine kinase inhibitor, demonstrated a median PFS of 11.4 months compared to 5.5 months in the placebo group in patients with advanced pan-NET. A 59% reduction in the risk of death was observed in favor of the experimental group[17]. More recently, the Netter 2 trial evaluated 177 Lu-dotatate as a first-line treatment in combination with octreotide LAR. It demonstrated a significant improvement in PFS in patients with newly diagnosed somatostatin receptor positive, G2 and G3, advanced GEP-NET compared to high-dose octreotide LAR alone[18].

Due to their high cost, these new agents are only available to some patients, especially in resource-limited countries. The restriction on access to first-line treatments at our institution creates an urgent need to investigate other effective alternatives. This study aims to assess the efficacy of the TEMCAP regimen as first-line therapy in patients with advanced GEP-NET in a Latin American population.

# MATERIALS AND METHODS

## Study population and data collection

A retrospective review was conducted to identify patients with GEP-NEN who were treated with the TEMCAP regimen at any point during their disease between 2011 and 2021. The registry data were provided by the Epidemiology and Statistics Department of the INEN. A total of forty-five GEP-NEN patients were identified, of which nine were excluded due to a diagnosis of NEC. Consequently, thirty-eight patients were included in the final analysis: Thirty-five received TEMCAP as a first-line treatment, and three received TEMCAP as a second-line treatment.

Inclusion criteria: Patients with a diagnosis of unresectable, metastatic, or recurrent GEP-NET; histologic grade 1 or 2; Ki67 index less than 20%.

Exclusion criteria: Patients with GEP-NEC, GEP-NET histologic grade 3, a Ki67 index greater than or equal to 20%, and incomplete medical records.

## Primary and secondary objectives

The primary objective was to evaluate OS in the entire population. Secondary objectives included assessing PFS, evaluating OS and PFS in specific subgroups, including pan-NET and non-pan-NET; evaluating the objective response rate (ORR) and disease control rate (DCR), and assessing the regimen's toxicity by documenting treatment-related adverse effects.

## Treatment and response criteria

The TEMCAP regimen consisted of capecitabine 750 mg/m<sup>2</sup> twice daily on days 1–14, followed by Temozolomide 200 mg/m<sup>2</sup> on days 10 to 14 in 28-day cycles until unacceptable toxicity or disease progression. The response was assessed by computed tomography (CT) according to RECIST 1.1 criteria. Toxicity was evaluated according to Common Terminology Criteria for Adverse Events version 5.0 in all 38 patients.

## Statistical analysis

A descriptive analysis was performed on qualitative variables using frequencies and percentages. Quantitative variables were summarized using measures of central tendency (mean, minimum, and maximum for normally distributed variables) and measures of dispersion (median, interquartile range, quartiles 1 and 3 for skewed distributions). OS was estimated from the start of chemotherapy to the date of death documentation or the last follow-up date. Patients who did not experience the event of interest were considered censored. PFS was estimated from the start of chemotherapy to the date of documented progression via CT following RECIST 1.1 criteria or the last follow-up date, with patients not experiencing the event also considered censored. Both OS and PFS estimates were calculated using the Kaplan-Meier method. Differences in survival according to study variables were evaluated using the log-rank test. A multivariate Cox proportional hazards model was fitted with variables showing significant differences in OS and PFS to assess their effect on the risk of death or progression, respectively. The proportional hazards assumption was tested in the adjusted model. A P value of < 0.05 was considered significant for differences in OS and PFS and for assessing the risk of death. All analyses were performed using R software.

# RESULTS

## Patient's characteristics

The median age was 52 years (24-77 years); 55.3% were females, and 44.7% were males. Lima was the most common region of origin (36.8%), followed by Huánuco (13.2%). The majority (92.1%) had an Eastern Cooperative Oncology Group



Table 1 Demographic and clinical features, n (%)			
Feature	n = 38		
Age at diagnosis (years)			
Median (min-max)	52 (24-77)		
Sex			
Female	21 (55.3)		
Male	17 (44.7)		
Region of birth			
Lima	14 (36.8)		
Huánuco	5 (13.2)		
Ancash	3 (7.9)		
Ica	3 (7.9)		
Junín	3 (7.9)		
Lambayeque	2 (5.3)		
Ayacucho	2 (5.3)		
Cajamarca	2 (5.3)		
Amazonas	1 (2.6)		
Cusco	1 (2.6)		
Puno	1 (2.6)		
Tacna	1 (2.6)		
BMI, kg/m <sup>2</sup>			
Median (IQR)	23.438 (20.65-26.279)		
ECOG scale			
0	1 (2.6)		
1	35 (92.1)		
2	2 (5.3)		
Symptoms			
Abdominal pain	31 (81.6)		
Rectal bleeding	12 (31.6)		
Weight loss	9 (23.7)		
Diarrhea	5 (13.2)		
Emesis	4 (10.5)		
Flushing	2 (5.3)		

IQR: Interquartile range; BMI: Body mass index; ECOG: Eastern Cooperative Oncology Group.

(ECOG) performance status of 1. The median body mass index (BMI) was 23.438 kg/m<sup>2</sup>. The most common symptom was abdominal pain (81.6%), followed by rectal bleeding (31.6%), weight loss (23.7%), diarrhea (13.2%), emesis (10.5%), and flushing (5.3%). Demographic and clinical features are shown in Table 1. According to clinical staging, 15.8% were in stage III, 81.6% in stage IV, and one patient was in an unspecified stage. Two (5.3%) patients had unresectable tumors, 5 (13.2%) had recurrent disease, and 31 (81.6%) had metastatic disease at presentation. Among the 38 patients, the primary tumor locations were distributed as follows: Twelve (31.6%) were rectal tumors, eleven (28.9%) were pancreatic tumors (28.9%), three (7.9%) were ileum tumors, two (5.3%) were mesenteric tumors, two (5.3%) were small intestine tumors, one (2.6%) was a stomach tumor and six (15.8%) were liver metastases from an unknown primary.

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Table 2 Systemic therapy, n (%)		
Feature	n = 38	
First-line treatment		
Temozolomide/capecitabine	35 (92.1)	
САРОХ	1 (2.6)	
Cisplatin/etoposide	1 (2.6)	
Interferon alpha	1 (2.6)	
First-line cycles		
Median (IQR)	9 (6-22.75)	
Duration of first-line treatment, days		
Median (IQR)	331 (133.25-606)	
Second-line treatment		
Yes	14 (36.8)	
No	24 (63.2)	
Second-line regimen, $n = 14$		
Capecitabine	4 (28.6)	
САРОХ	3 (21.4)	
TEMCAP	3 (21.4)	
Cisplatin/etoposide	1 (7.1)	
Dacarbazine (DTIC)	1 (7.1)	
GEMOX	1 (7.1)	
Temozolomide	1 (7.1)	

IQR: Interquartile range; TEMCAP: Temozolomide and capecitabine regimen; CAPOX: capecitabine/oxaliplatin; GEMOX: gemcitabine/oxaliplatin.

## Chemotherapy treatment

TEMCAP was administered to 35 patients (92.1%). The median number of chemotherapy cycles at first-line was nine. Fourteen patients (36.8%) received a second-line treatment. Among these patients, the most commonly used regimen was capecitabine in four patients (28.6%), followed by capecitabine/oxaliplatin and TEMCAP in three patients (21.4%) each, cisplatin/etoposide in one patient (7.1%), dacarbazine in one patient (7.1%), gemcitabine/oxaliplatin in one patient (7.1%), and temozolomide in one patient (7.1%). Characteristics of systemic therapy are shown in Table 2.

## Efficacy

The responses of the 38 patients according to RECIST 1.1 were as follows: One (2.6%) patient had a complete response (CR), two (5.3%) had a partial response (PR), sixteen (42.1%) had stable disease (SD), fifteen (39.5%) had progressive disease (PD), and four (10.5%) were without RECIST evaluation. The ORR was 7.9%, and the DCR was 50%. Regarding the pan-NET subgroup, there was one CR, two PR, three SD, four PD, and one case without response evaluation; the ORR was 27.2%, and the DCR was 54.5%.

# OS

With a median follow-up of 33.5 months (range 1–81 months), the estimated OS rates at 12, 36, and 60 months were 80%, 66%, and 42%, respectively, with a median OS of 49 months for the entire population (Figure 1A). The median OS in the pan-NET group was 64 months, compared to 44 months in the non-pan-NET group, with a *P*-value of 0.056, which was not statistically significant (Figure 1B).

# PFS

Among the total population (n = 34; RECIST criteria not evaluated in 4 patients), 15 (44.1%) patients experienced PD, with a median follow-up time for PFS of 20 months (range 5-81 months). The estimated PFS at 12, 36, and 60 months was 84.2%, 49.9%, and 49.9%, respectively, with a median PFS of 34 months. In the pan-NET group, the median PFS was 78 months, compared to 27 months in the non-pan-NET group (Figure 1C).





## Safety profile

The most common adverse event of any grade was neutropenia, with 7 (18.4%) recorded events, followed by hand-foot syndrome with 6 (15.8%) events, and hypertransaminasemia and nausea with 5 (13.2%) events each. The total number of adverse events is shown in Table 3. Regarding adverse events grade 3 and 4, neutropenia occurred in three patients (7.9%), two (5.3%) experiencing grade 3 and one (2.6%) grade 4; Thrombocytopenia was observed in four patients (10.6%), two (5.3%) experiencing grade 3 and two (5.3%) grade 4; anemia was reported in two patients (5.3%), one (2.6%) experiencing grade 3 and one (2.6%) grade 4; anemia was documented in one patient (2.6%).

# DISCUSSION

We observed a median OS of 49 months in our study, similar to the findings of other studies that retrospectively evaluated OS with the TEMCAP regimen in GEP-NET[19-25].

Prospective data evaluating TEMCAP are scarce. The first prospective trial was phase II ECOG-ACRIN E2211, which compared TEMCAP *vs* temozolomide in advanced pan-NET. This trial met its primary endpoint with a PFS of 22.7 months in the TEMCAP arm *vs* 14.4 months in the temozolomide arm. Although the median OS was 4.9 months superior in the TEMCAP arm, it did not achieve statistical significance[26].



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Table 3 Adverse events during chemotherapy by grade, n (%)					
	Grade				
	1	2	3	4	
Neutropenia	3 (7.9)	1 (2.6)	2 (5.3)	1 (2.6)	
Hand-foot syndrome	5 (13.2)	1 (2.6)			
Hypertransaminasemia	3 (7.9)	2 (5.3)			
Nausea	4 (10.5)		1 (2.6)		
Peripheral neuropathy	4 (10.5)	1 (2.6)			
Vomiting	4 (10.5)	1 (2.6)			
Anemia	2 (5.3)		1 (2.6)	1 (2.6)	
Asthenia	4 (10.5)				
Constipation	4 (10.5)				
Thrombocytopenia			2 (5.3)	2 (5.3)	
Anorexia	3 (7.9)				
Diarrhea	2 (5.3)				
Sialorrhea	2 (5.3)				
Hyperbilirubinemia	1 (2.6)				

In our study, we observed an ORR of 7.9% with one (2.6%) CR and two (5.3%) PR; the DCR was 50%, including 16 patients (42.1%) with SD. Our DCR results are very similar to those in other retrospective studies. Crespo *et al*[22] evaluated TEMCAP in 65 patients with GEP-NET (70.8% had pan-NET) and the DCR was 47.7%, with two CR (3.1%), 29 PR (44.6%), and 27 (41.5%) SD. Fine *et al*[19] evaluated 18 patients with well-differentiated NET metastatic to the liver who had failed front-line therapy. The ORR was 61%, and the DCR was 83.2%. Abbasi *et al*[27] evaluated 21 patients (14 with pan-NET and 7 with carcinoid tumors) who failed treatment with SSA and platinum-based chemotherapy combined with etoposide and reported a DCR of 80%. The systematic review by Arrivi *et al*[25] evaluated 1,818 patients from 42 articles with advanced NEN of gastroenteropancreatic, lung, and unknown origin. The ORR was 77%, with a median OS ranging from 8 to 103 months. ORR and DCR appear more critical as surrogates of the PFS and OS for the TEMCAP regimen in GEP-NET.

Our results for pan-NET showed an ORR of 27.2% and a DCR of 54.5%, consistent with what has been described in the literature. Pan-NET have historically better chemotherapy responses than non-pan-NET. Our study also showed this trend, with OS in pan-NET being 20 months longer than non-pan-NET. The PSF for pan-NET in our series was 78 months compared to 27 months in non-pan-NET. Notably, of the 11 patients with pan-NET, 10 were evaluated according to RECIST 1.1, of which 4 showed disease progression; the remaining patients are still alive and continue to be followed up.

A meta-analysis revealed a lower ORR in non-pan-NET than in pan-NET patients; however, this difference was not statistically significant when high-risk bias studies were excluded[28]. In a cohort of 101 patients, which included 53 with pan-NEN and 44 with carcinoid tumors treated with temozolomide-based chemotherapy, an ORR of 34% was observed in pan-NEN compared to 2% in carcinoid tumors[29]. Patients with pan-NET who require clinically meaningful tumor shrinkage may benefit more from chemotherapeutic regimens.

Anemia, neutropenia, and thrombocytopenia were the most common grade 3-4 adverse events observed in our study, consistent with findings from other trials. Crespo *et al*[22] reported neutropenia in 7.7% of patients, while in the systematic review by Arrivi *et al*[25], the safety analysis of TEMCAP showed that 16.4% of the population experienced grade 3-4 toxicities, with hematological toxicities being the most common (27.2%). The prospective ECOG-ACRIN E2211 study reported grade 3-4 neutropenia in 13% of cases and thrombocytopenia in 10%[26]. Temozolomide-based regimens using a dose-dense schedule of 150 mg/m<sup>2</sup> daily every other week resulted in more hematological toxicities compared to the TEMCAP regimen. Grade 3-4 lymphopenia was reported in more than 50% of patients. Chan *et al*[30] reported grade 3 thrombocytopenia in 18% of patients. Opportunistic infectious complications were also reported during treatment with dose-dense temozolomide-based regimens[30,31]. This contrasts with our study, where no opportunistic infections were observed at a dose of 200 mg/m<sup>2</sup> for 5 days.

We must consider some limitations in our study inherent to all retrospective analyses, particularly the potential for selection bias. Additionally, the small sample size of 38 patients may have contributed to the lack of statistical significance in some outcomes. Despite these limitations, our data support the effectiveness of the TEMCAP regimen in patients with advanced GEP-NET.

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# CONCLUSION

This is the first retrospective study in Peru to evaluate the use of TEMCAP for advanced GEP-NET. The findings suggest that TEMCAP could be a viable first-line treatment in regions where standard therapies are not readily accessible, particularly for grade 2 tumors. A notable 42% OS rate at 60 months was observed. Prospective studies are needed to determine its value as a treatment option in this setting.

# FOOTNOTES

Author contributions: Cruz-Diaz WE collected the data at the Instituto Nacional de Enfermedades Neoplásicas and wrote the initial manuscript; Paitan V and Haro-Varas J supervised the initial manuscript; Medina J reviewed the pathology slides, and Flores R reviewed the computed tomography and magnetic resonance imaging images; Mantilla R was responsible for conducting the statistical analysis, and Castro-Oliden V provided expert guidance and supervision throughout the study and critically reviewed the final manuscript; All authors read and approved the final manuscript.

Institutional review board statement: Approved by the Research Protocol Review Committee of Instituto Nacional de Enfermedades Neoplásicas, No. INEN 24-61.

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ORIGINAL ARTICLE

# **Basic Study** Vitamin D 1,25-Dihydroxyvitamin D<sub>3</sub> reduces lipid accumulation in hepatocytes by inhibiting M1 macrophage polarization

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# Abstract

## BACKGROUND

Non-alcoholic fatty liver disease (NAFLD), which is a significant liver condition associated with metabolic syndrome, is the leading cause of liver diseases globally and its prevalence is on the rise in most nations. The protective impact of vitamin D on NAFLD and its specific mechanism remains unclear.

## AIM

To examine the role of vitamin D in NAFLD and how vitamin D affects the polarization of hepatic macrophages in NAFLD through the vitamin D receptor (VDR)-peroxisome proliferator activated receptor (PPAR)y pathway.

# **METHODS**

Wild-type C57BL/6 mice were provided with a high-fat diet to trigger NAFLD model and administered 1,25-dihydroxy-vitamin D [1,25(OH)<sub>2</sub>D<sub>3</sub>] supplementation. 1,25(OH)<sub>2</sub>D<sub>3</sub> was given to RAW264.7 macrophages that had been treated with lipid, and a co-culture with AML12 hepatocytes was set up. Lipid accumulation, lipid metabolism enzymes, M1/M2 phenotype markers, proinflammatory cytokines and VDR-PPARy pathway were determined.

# RESULTS

Supplementation with 1,25(OH),  $D_3$  relieved hepatic steatosis and decreased the proinflammatory M1 polarization of hepatic macrophages in NAFLD. Administration of 1,25(OH)<sub>2</sub>D<sub>3</sub> suppressed the proinflammatory M1 polarization of macrophages induced by fatty acids, thereby directly relieving lipid accumulation and metabolism in hepatocytes. The VDR-PPARy pathway had a notable impact on reversing lipid-induced proinflammatory M1 polarization of macrophages regulated by the administration of  $1,25(OH)_2D_3$ .



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#### CONCLUSION

Supplementation with  $1,25(OH)_2D_3$  improved hepatic steatosis and lipid metabolism in NAFLD, linked to its capacity to reverse the proinflammatory M1 polarization of hepatic macrophages, partially by regulating the VDR-PPAR $\gamma$  pathway. The involvement of  $1,25(OH)_2D_3$  in inhibiting fatty-acid-induced proinflammatory M1 polarization of macrophages played a direct role in relieving lipid accumulation and metabolism in hepatocytes.

**Key Words**: Non-alcoholic fatty liver disease; Hepatocytes; Macrophages; Polarization; Vitamin D receptor; Peroxisome proliferator activated receptor  $\gamma$ 

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**Core Tip:** Supplementation with 1,25-dihydroxy-vitamin D  $[1,25(OH)_2D_3]$  improved hepatic steatosis and lipid metabolism in nonalcoholic fatty liver disease, linked to its capacity to reverse the proinflammatory M1 polarization of hepatic macro-phages, partially by regulating the vitamin D receptor-peroxisome proliferator activated receptor  $\gamma$  pathway. The involvement of 1,25(OH)<sub>2</sub>D<sub>3</sub> in inhibiting fatty-acid-induced proinflammatory M1 polarization of macrophages played a direct role in relieving lipid accumulation and metabolism in hepatocytes.

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# INTRODUCTION

Nonalcoholic fatty liver disease (NAFLD) is a common chronic liver condition, affecting 25%-45% of the population worldwide[1,2]. It is a key manifestation of metabolic syndrome and progresses through stages, beginning with simple fat accumulation (steatosis), advancing to nonalcoholic steatohepatitis (NASH), fibrosis, and potentially leading to cirrhosis and liver cancer (hepatocellular carcinoma)[3]. The accumulation of excess fatty acids, driven by insulin resistance and increased fat production in the liver, is the primary trigger for NAFLD. This predisposes the liver to further damage, known as multiple-hit injuries. These include mitochondrial dysfunction, stress in the endoplasmic reticulum, inflammation from endotoxins, activation of inflammasomes, iron overload, and vitamin D deficiency[3-5].

Vitamin D, a steroid hormone, has various functions beyond regulating calcium, phosphate metabolism, and bone health. It also influences immune, inflammatory, and metabolic processes. The connection between its active form, 1,25-dihydroxy-vitamin D  $[1,25(OH)_2D_3]$ , and the vitamin D receptor (VDR) has been widely recognized in relation to insulin resistance and related conditions[6-9]. Recent observational studies show a strong link between low vitamin D levels and NAFLD. Vitamin D deficiency has been associated with liver fat accumulation, inflammation, fibrosis, and disease progression. Another study found that healthy men with higher vitamin D levels had a reduced risk of developing NAFLD[10-12].

However, most clinical trials examining the effects of vitamin D supplementation on NAFLD patients, involving different stages of liver damage, have been underpowered. More research is needed to understand the underlying mechanisms between vitamin D and NAFLD development[13,14]. Kupffer cells, located in the liver's sinusoids and comprising 20%-25% of non-parenchymal liver cells, respond to various stimuli from the bloodstream. Macrophages, including Kupffer cells, are highly adaptable, changing their function and behavior based on environmental signals[15, 16].

Macrophages typically undergo M1 activation when exposed to molecules like Toll-like receptor ligands, lipopolysaccharide (LPS), and interferon-γ, releasing proinflammatory substances. Alternatively, when stimulated by interleukins (IL-4/IL-13), they shift to the M2 state, producing anti-inflammatory factors, supporting tissue repair, and regulating immune responses[17,18]. Extensive evidence confirms the critical role of liver macrophages, particularly Kupffer cells, in the progression of NAFLD and NASH. Our previous research demonstrated that in mice with high-fat (HF) diet-induced NAFLD, Kupffer cells are predominantly polarized towards the M1 state[19]. Similarly, Maina and colleagues found that M1 macrophage activation correlates with the severity of NASH[20]. Modulating the M1/M2 balance may offer a new therapeutic approach for NAFLD.

The nuclear receptor peroxisome proliferator activated receptor (PPAR) $\gamma$ , when activated by specific ligands, is known to drive macrophage polarization, encouraging the development of anti-inflammatory M2 macrophages. Disruption of PPAR $\gamma$  in myeloid cells impairs this alternative activation and increases vulnerability to obesity and insulin resistance caused by a HF diet[21-23]. In our earlier research, PPAR $\gamma$  activation reversed M1 polarization of Kupffer cells induced by a HF diet and improved liver fat accumulation in NAFLD[19]. Similarly, VDR, activated by 1,25(OH)<sub>2</sub>D<sub>3</sub>, is a transcription factor that, like PPAR $\gamma$ , plays a key role in regulating macrophage function[24,25].

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The VDR and PPARy pathways are interconnected and influence various cell functions, including growth, differentiation, and immune response. However, the exact mechanisms behind their interaction are unclear. A recent study found that active vitamin D promotes the conversion of M1 macrophages, induced by high glucose, into the M2 state via the VDR-PPARy pathway [25-27]. This indicates that VDR-PPARy signaling could be a target for vitamin D to shift macrophage polarization from the M1 to the M2 phenotype, potentially leading to new therapeutic approaches for NAFLD.

# MATERIALS AND METHODS

#### Animal experiments

Male adult (aged 6-8 weeks) wild-type C57BL/6 mice were acquired from the Vital River Laboratory (China). Mice were fed either a regular normal control (NC) diet (15% kilocalories from fat) or a HF diet (60% kilocalories from fat) for a period of 16 weeks. For 1,25(OH),D<sub>3</sub> supplementation, HF diet-fed mice received 1,25(OH),D<sub>3</sub> (20 µg/kg, MedChem-Express, United States) or phosphate-buffered saline (PBS; Gibco, United States) by oral gavage every alternate day for 16 weeks. The dose of  $1,25(OH)_2D_3$  (20  $\mu$ g/kg) used in this study was selected based on previous research demonstrating its efficacy in reducing liver fibrosis and inflammation in murine models of NASH. A study by Ma et al [28] utilized a similar dose of 1,25(OH)<sub>2</sub>D<sub>3</sub> to reveal its antifibrotic properties in female mice fed a HF diet. This concentration has been shown to exert beneficial effects in liver pathology models, making it a suitable choice for our investigation. While we recognize the importance of assessing a range of concentrations, this dose was chosen for its established efficacy. Future studies could explore different dose gradients to further refine the therapeutic potential of 1,25(OH)<sub>2</sub>D<sub>3</sub>. All mice were kept in a temperature- and light-controlled facility and permitted to consume water and pellet chow ad libitum. After being fed diets for 16 weeks, the mice were either anesthetized for in situ perfusion or sacrificed to collect liver tissues through intraperitoneal injection of 0.3% pentobarbital sodium. The humane treatment of laboratory animals was ensured in all animal experiments, which were approved by the Ningbo University Animal Care and Use Committee according to the criteria set by Ningbo University.

## Kupffer cell isolation

Hepatic macrophages, also known as Kupffer cells, were obtained by *in situ* liver perfusion as previously described. Following perfusion, cells were isolated via centrifugation using a Percoll density gradient (25% and 50% Percoll; GE Healthcare, United States) at 800 g for 15 minutes. The isolated cells were cultured in Dulbecco's modified Eagle's medium (DMEM; Gibco), supplemented with 12% fetal bovine serum (FBS; Gibco), 100 U/mL penicillin G (Gibco), and 100 U/mL streptomycin sulfate (Gibco) at 37 °C with 5% CO<sub>2</sub>. After a 2-hour incubation period, non-adherent cells were removed, and Kupffer cells were collected. Cell viability was assessed using the trypan blue exclusion method, with viability exceeding 95%.

# Identification of Kupffer cells

To verify that the isolated cells were Kupffer cells, immunohistochemical (IHC) staining was performed. Kupffer cells were identified by the expression of F4/80, a macrophage-specific marker. The isolated cells were fixed, blocked with normal serum, and incubated with anti-mouse F4/80 antibody (1:100; GeneTex, United States) overnight at 4 °C. After washing, secondary antibodies conjugated to horseradish peroxidase were applied. The detection was carried out using diaminobenzidine (DAB), followed by counterstaining with hematoxylin. Kupffer cells positive for F4/80 were observed in liver sections under an Olympus light microscope at a magnification of 200 ×. This staining confirms the identity of the Kupffer cells, reflecting the efficiency of the isolation process.

## RAW264.7 macrophage culture and treatment

RAW264.7 murine macrophages (Cell Bank of the Chinese Academic of Sciences, China) were cultured in DMEM supplemented with 10% FBS, 100 U/mL penicillin G, and 100 U/mL streptomycin sulfate at a temperature of 37 °C in the presence of 5% CO<sub>2</sub>. All the treatments were performed on the third passage of cells. Palmitic acid (PA, 0.5 mmol/L; Sigma Aldrich, United States) was administered to RAW264.7 macrophages for a duration of 24 hours. To assess macrophage M1 or M2 polarization, LPS (100 ng/mL; Sigma-Aldrich) or IL-4 (5 ng/mL; PeproTech, United States) treatment was used as a positive control, respectively. DMEM was employed as the NC. To carry out the impact of 1,25(OH)<sub>2</sub>D<sub>3</sub>, RAW264.7 macrophages were incubated with 1,25(OH)<sub>2</sub>D<sub>3</sub> (20 ng/mL) for an additional 24 hours in a sequential manner.

## AML12 hepatocyte culture

AML12 murine hepatocytes (Cell Bank of the Chinese Academic of Sciences, China) were cultured in DMEM supplemented with 10% FBS, 100 U/mL penicillin G, and 100 U/mL streptomycin sulfate at a temperature of 37 °C in the presence of 5% CO<sub>2</sub>. All the treatments were performed on the third passage of cells.

## RAW264.7 macrophage and AML12 hepatocyte coculture system

Impurities were removed from the collected culture supernatants of RAW264.7 macrophages through centrifugation and filtration. The AML12 hepatocytes were exposed to the prepared conditioned media (CMs) for 24 hours in order to establish the coculture system. The initial cell density for RAW264.7 macrophages was  $1 \times 10^6$  cells/mL, and AML12 hepatocytes were seeded at a density of  $5 \times 10^5$  cells/mL. The coculture duration was 24 hours for all experiments to



Table 1 Murine primers				
Primer	Forward (5'-3')	Reverse (5'-3')		
iNOS2	GTGTTCCACCAGGAGATGTTG	CTCCTGCCCACTGAGTTCGTC		
TNFα	TCTTCTCATTCCTGCTTGTGG	GGTCTGGGCCATAGAACTGA		
IL-6	GTTCTCTGGGAAATCGTGGA	GGAAATTGGGGTAGGAAGGA		
Arg1	CTCCAAGCCAAAGTCCTTAGAG	AGGAGCTGTCATTAGGGACATC		
Mrc2	TACAGCTCCACGCTATGGATT	CACTCTCCCAGTTGAGGTACT		
IL-10	GTTACTTGGGTTGCCAAG	TTGATCATCATGTATGCTTC		
VDR	GCTTCCACTTCAACGCTAT	ACTCCTTCATCATGCCAAT		
PPARγ	GCCCTTTACCACAGTTGATTTCT	GTGATTTGTCCGTTGTCTTTCCT		
IL-1β	CCCAAGCAATACCCAAAGAA	TTGTGAGGTGCTGATGTACCA		
SREBP1C	ACAGCAACCAGAAGCTCAAG	TGCCCTCCATAGACACATCT		
FASN	TTGGGTGCTGACTACAACCT	TGGATGATGTTGATGATGGA		
ACOX1	ACCAGCCCAACTGTGACTTC	ACAAAGGCATGTAACCCGTA		
CPT1A	CTTCCCATTTGACACCTTTG	ATACGTGAGGCAGAACTTGC		
GAPDH	CCTTCCGTGTTCCTACCC	CAACCTGGTCCTCAGTGTAG		

iNOS2: Nitric oxide synthase; TNFa: Tumor necrosis factor a; IL: Interleukin; Arg1 Arginine 1; Mrc2: Macrophage mannose receptor 2; VDR: Vitamin D receptor; PPARy: Peroxisome proliferator activated receptor y; SREBP1C: Sterol-regulatory element binding protein 1C; FASN: Fatty acid synthase; CPT1A: Carnitine palmitovl transferase 1A.

allow sufficient time for interactions between the cells while maintaining cellular viability.

## Liver histology, oil red o staining and immunohistochemistry analysis

To perform histological analysis, liver tissues were fixed in 10% formalin, then embedded in paraffin, and finally stained using hematoxylin and eosin (HE). To perform cytohistologic analysis, the AML12 hepatocytes were first fixed in 4% paraformaldehyde, and then stained with Oil Red O and subsequently counterstained with HE. To perform immunohistochemistry analysis, the liver sections were first blocked in normal serum, then incubated with anti-mouse F4/80 antibody (1:100; GeneTex, United States), anti-mouse CD11c antibody (1:50; OriGene, United States), and anti-mouse CD206 antibody (1:100; Abcam, United Kingdom) at a temperature of 4 °C overnight. Afterward, the sections were incubated with secondary antibodies conjugated with horseradish-peroxidase. Finally, the detection process involved the use of DAB and hematoxylin as the counter stain. Cells positive for F4/80, CD11c, and CD206 were quantified in three randomly selected fields under an Olympus light microscope at a magnification of 200 ×.

# Total RNA isolation and real-time PCR

Total RNA was extracted from murine liver tissue, isolated Kupffer cells, RAW264.7 macrophages and AML12 hepatocytes using TRIzol reagent (Invitrogen, United States). cDNA was synthesized from 2 µg total RNA using Primescript RT Reagent kit (TaKaRa, Japan). In the real-time PCR assay, a 10 μL reaction mixture consisting of 10 ng template, each murine primer (shown in Table 1, provided by Sangong Biotech, China) and SYBR Green PCR Master Mix (TaKaRa, Japan) was used. The PCR thermocycling condition consisted of an initial denaturation step at 95 °C for 30 seconds, followed by 40 cycles of denaturation at 95 °C for 5 seconds and annealing at 60 °C for 30 seconds using the ABI Prism 7300 system (Applied Biosystems, United States). Each reaction was conducted three times. Quantification of the target genes' expression levels was performed using the double-delta method  $(2^{-\Delta\Delta Ct})$ .

## Western blotting

Protein from the murine liver tissues, RAW264.7 macrophages, and AML12 hepatocytes were resolved using 8% SDS-PAGE. The samples were transferred to polyvinylidene difluoride membranes (Bio-Rad, United States) and left to incubate overnight at 4 °C with antibodies against VDR (1:2000; Abcam), PPARy (1:2000; Abcam), sterol-regulatory element binding protein (SREBP)1C (1:1000; Abcam), fatty acid synthase (FASN) (1:1000; Abcam), acyl-CoA oxidase (ACOX)1 (1:500; Abcam), carnitine palmitoyl transferase (CPT)1A (1:1000; Abcam), and the endogenous control GAPDH (1:3000; Bioworld, United States). The blots were then incubated with secondary antibodies conjugated with horseradish peroxidase at room temperature for 1 hour. The bands showing immunoreactivity were detected using the ECL Western Blotting Kit (Thermo Scientific Pierce, United States) and then exposed to films and developed. Image J software (National Institutes of Health, United States) was used to measure the density of the immunoblots, which was normalized using GAPDH.



# **ELISA**

Tumor necrosis factor (TNF) α, IL-6, and IL-1β production were assessed by ELISA kit (eBioscience, United States) according to the manufacturer's protocol with collecting and analyzing the cell culture supernatants from isolated Kupffer cells and RAW264.7 macrophages.

# Statistical analysis

All statistical analyses were conducted using GraphPad Prism 9. The data were presented as mean ± SEM. Statistical differences were determined using Student's t test.  $^{a}P < 0.05$  was considered statistically significant.

# RESULTS

# 1,25(OH)<sub>2</sub>D<sub>3</sub> supplementation improves hepatic steatosis and lipid metabolism in NAFLD

The link between vitamin D deficiency and the progression of NAFLD has become increasingly evident through observational studies. However, few studies have examined the effects and mechanisms of vitamin D supplementation on NAFLD. In a murine model of NAFLD, we found that supplementation with  $1,25(OH)_2D_3$  significantly improved hepatic steatosis induced by a HF diet, resulting in reduced liver and body weight. This treatment also markedly decreased the expression of proinflammatory cytokines in the liver (Figure 1A-D). Additionally, the mRNA and protein levels of enzymes involved in lipid synthesis (SREBP1C and FASN) and lipid breakdown (ACOX1 and CPT1A) were elevated in HF-fed mice, but these levels were significantly reduced in the 1,25(OH)<sub>2</sub>D<sub>3</sub>-treated group (Figure 1E and F). Overall, 1,25(OH)<sub>2</sub>D<sub>3</sub> supplementation alleviated hepatic steatosis, reduced local inflammation, and improved hepatic lipid metabolism in NAFLD.

# 1,25(OH)<sub>2</sub>D<sub>3</sub> decreases proinflammatory M1 polarization of hepatic macrophages in NAFLD

Our previous work showed that hepatic macrophages in NAFLD mice on an HF diet predominantly exhibited an M1 proinflammatory phenotype[19]. In this study, we used a similar HF diet-induced NAFLD model supplemented with 1,25(OH)<sub>2</sub>D<sub>3</sub>. IHC analysis revealed a decrease in M1-polarized (F4/80+CD11c+) hepatic macrophages after 1,25(OH)<sub>2</sub>D<sub>3</sub> supplementation (Figure 2A). Moreover, the expression of M1 markers, including inducible nitric oxide synthase (iNOS2), TNFα, and IL-6, was significantly reduced, while the M2 marker IL-10 also showed a moderate decrease (Figure 2B). In parallel, 1,25(OH)<sub>2</sub>D<sub>3</sub> treatment significantly reduced the secretion of proinflammatory cytokines, such as TNF $\alpha$ , IL-6, and IL-1 $\beta$ , which were elevated in the HF-fed group (Figure 2C). These findings suggest that  $1,25(OH)_2D_3$  decreases the proinflammatory M1 polarization of hepatic macrophages in NAFLD.

# 1,25(OH), *D*, inhibits fatty-acid-induced proinflammatory M1 polarization of macrophages

Lipid accumulation in NAFLD is largely driven by increased free fatty acids, a hallmark of disease progression[28,29]. In our previous research, we found that PA, a common saturated fatty acid, induces M1 polarization in Kupffer cells/ macrophages[19]. Here, we showed that  $1,25(OH)_2D_3$  administration significantly reduced the expression of M1 markers (iNOS2, TNFα, and IL-6) and M2 marker IL-10, which were elevated in PA-treated macrophages (Figure 3A). Additionally, 1,25(OH)<sub>2</sub>D<sub>3</sub> significantly decreased the secretion of proinflammatory cytokines (TNF $\alpha$ , IL-6, and IL-1 $\beta$ ) that were induced by PA (Figure 3B). These results demonstrate that  $1,25(OH)_2D_3$  effectively inhibits fatty-acid-induced M1 polarization of macrophages in vitro.

# The role of the VDR-PPARγ pathway in 1,25(OH)<sub>2</sub>D<sub>3</sub>-mediated modulation of macrophage polarization

Our study further explored the molecular mechanisms through which 1,25(OH)<sub>2</sub>D<sub>3</sub> modulates macrophage polarization in the context of a HF diet or fatty-acid stimulation. We focused on the VDR and peroxisome proliferator-activated receptor gamma (PPARy), both of which are nuclear receptors that influence macrophage polarization but with opposing effects[24-27]. In vivo, hepatic macrophages from HF-fed NAFLD mice showed increased expression of VDR and PPARy at both mRNA and protein levels. In contrast, 1,25(OH)<sub>2</sub>D<sub>3</sub> supplementation significantly decreased VDR expression but did not alter PPARy expression (Figure 4A and B). In vitro, 1,25(OH)<sub>2</sub>D<sub>3</sub> treatment reduced the expression of both VDR and PPARy in PA-stimulated macrophages (Figure 4C and D). Thus, 1,25(OH),D<sub>3</sub> attenuated HF diet- and fatty-acidinduced proinflammatory M1 polarization of macrophages by inhibiting VDR and PPARy. These findings suggest that the VDR-PPARγ pathway plays a crucial role in 1,25(OH)<sub>3</sub>D<sub>3</sub>-mediated regulation of macrophage polarization.

# 1,25(OH), $D_1$ inhibits proinflammatory macrophage polarization, improving hepatocyte lipid metabolism

Our in vivo data showed that 1,25(OH)<sub>2</sub>D<sub>3</sub> reduced proinflammatory M1 polarization of hepatic macrophages and improved hepatic lipid metabolism in NAFLD. To determine whether 1,25(OH)<sub>2</sub>D<sub>3</sub> directly affects hepatocyte lipid metabolism by inhibiting macrophage polarization, we used a co-culture system with RAW264.7 macrophages and AML12 hepatocytes. Oil Red O staining revealed increased lipid accumulation in hepatocytes incubated with CM from LPS- and PA-treated macrophages, which was significantly reduced following  $1,25(OH)_2D_3$  administration (Figure 5A). Additionally, 1,25(OH)<sub>2</sub>D<sub>3</sub> treatment reduced the expression of proinflammatory cytokines in hepatocytes treated with CM from LPS- and PA-stimulated macrophages (Figure 5B). M1-polarized macrophage CM also increased the expression of lipid synthesis genes (FASN and SREBP1C), which were reduced after 1,25(OH)<sub>2</sub>D<sub>3</sub> treatment (Figure 5C and D). Conversely, lipid breakdown genes (ACOX1 and CPT1A) were elevated in hepatocytes treated with CM from PAstimulated macrophages but declined with 1,25(OH)<sub>2</sub>D<sub>3</sub> treatment (Figure 5C and D). These findings indicate that



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Figure 1 Supplementation with 1,25-dihydroxy-vitamin D improves hepatic steatosis and lipid metabolism in non-alcoholic fatty liver disease. Wild-type C57BL/6 mice were fed normal control diet or high-fat (HF) diet for 16 weeks, or HF diet plus 1,25-dihydroxy-vitamin D (20 µg/kg) by oral gavage every alternate day for 16 weeks. Phosphate-buffered saline by oral gavage served as a control (n = 10/group). A: Hepatic steatosis determined by hematoxylin & eosin staining (200 ×); B: Body weight of mice; C: Liver weight of mice; D: Hepatic proinflammatory cytokines expression; E: Hepatic lipid metabolism genes mRNA expression; F: Hepatic lipid metabolism enzymes protein expression. Values are mean ± SEM, <sup>a</sup>P < 0.05, <sup>b</sup>P < 0.01, n = 10 animals per group; NC: Normal control; HF: High-fat; VD3: 1,25-dihydroxy-vitamin D; TNFa: Tumor necrosis factor a; IL: Interleukin; SREBP1C: Sterol-regulatory element binding protein 1C; FASN: Fatty acid synthetase; ACOX1: Acyl-CoA oxidase 1; CPT1A: Carnitine palmitoyltransferase 1A.



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Figure 2 Supplementation with 1,25-dihydroxy-vitamin D decreases the proinflammatory M1 polarization of hepatic macrophages in nonalcoholic fatty liver disease. Wild-type C57BL/6 mice were fed either normal control (NC) diet or high-fat (HF) diet for 16 weeks, or HF diet plus 1,25-dihydroxyvitamin D [1,25(OH)2D3] (20  $\mu$ g/kg) by oral gavage every alternate day for 16 weeks. Phosphate-buffered saline by oral gavage served as a control (*n* = 10/group). Hepatic macrophages were isolated from mice administered NC diet, HF diet alone or plus 1,25(OH)2D3. A: M1/M2 phenotype of hepatic macrophages determined by immunohistochemical staining (200 ×); B: M1/M2 gene marker expression on hepatic macrophages; C: Proinflammatory cytokine secretion from hepatic macrophages. Values are mean ± SEM, <sup>a</sup>P < 0.05, <sup>b</sup>P < 0.01, *n* = 10 animals per group; NC: Normal control; HF: High-fat; VD3: 1,25-dihydroxy-vitamin D; iNOS: Inducible NO synthase; TNF $\alpha$ : Tumor necrosis factor  $\alpha$ ; IL: Interleukin; Arg1 Arginine 1; Mrc2: Macrophage mannose receptor 2.

1,25(OH)<sub>2</sub>D<sub>3</sub> improves hepatocyte lipid metabolism by inhibiting proinflammatory macrophage polarization.

# DISCUSSION

Insulin resistance significantly elevates the risk of NAFLD due to systemic low-grade inflammation[30]. Vitamin D is recognized for its anti-inflammatory, anti-proliferative, and anti-fibrotic effects, which may influence the development of NAFLD[31]. However, the precise role of vitamin D in NAFLD remains incompletely understood. Emerging evidence suggests that the proinflammatory activation of hepatic macrophages, particularly Kupffer cells, plays a pivotal role in the pathogenesis of NAFLD[32]. In this study, a murine model of NAFLD induced by a HF diet showed that supplementation with 1,25(OH)<sub>2</sub>D<sub>3</sub> alleviated hepatic steatosis, likely by reducing proinflammatory M1 polarization of hepatic macrophages. Furthermore, our cell culture experiments demonstrated that 1,25(OH)<sub>2</sub>D<sub>3</sub> suppressed fatty-acid-induced M1 polarization, which improved lipid metabolism and reduced lipid accumulation in hepatocytes. The ability of 1,25(OH)<sub>2</sub>D<sub>3</sub> to shift macrophage polarization was linked to the VDR-PPARγ signaling pathway in both *in vivo* and *in vitro* settings.

Clinical studies increasingly indicate that vitamin D deficiency correlates with metabolic syndrome features, including NAFLD[11,33]. Approximately 55% of NAFLD patients exhibit vitamin D deficiency[34]. Despite this association, results from clinical trials evaluating the impact of vitamin D supplementation on NAFLD have been mixed[35-37]. In our study,  $1,25(OH)_2D_3$  supplementation *in vivo* was found to improve hepatic steatosis and reduce local inflammation. Since altered lipid homeostasis is a key characteristic of NAFLD[38], we investigated how  $1,25(OH)_2D_3$  affects enzymes involved in lipid synthesis and breakdown in the liver. Our findings indicate that  $1,25(OH)_2D_3$  improves both lipid anabolic and catabolic processes, potentially explaining the divergent results seen in previous clinical studies. These results highlight the potential of  $1,25(OH)_2D_3$  as a treatment option for NAFLD by simultaneously addressing hepatic steatosis and inflammation.

Macrophages exhibit two main phenotypes: The proinflammatory M1 and anti-inflammatory M2 states[17,18]. Prior research suggests that obesity, induced by HF diets, shifts macrophages in adipose tissue towards the M1 phenotype, promoting insulin resistance[39]. Our earlier work showed that HF diets increase M1 polarization of hepatic macrophages in NAFLD[19]. In this study, we demonstrated that  $1,25(OH)_2D_3$  significantly reduces M1 polarization in hepatic macrophages *in vivo*. This was further supported by our *in vitro* experiments, where  $1,25(OH)_2D_3$  inhibited fatty-acid-induced





Figure 3 Administration of 1,25-dihydroxy-vitamin D inhibits fatty-acid-induced proinflammatory M1 polarization of macrophages. RAW264.7 macrophages were incubated with palmitic acid (0.5 mmol/L) for 24 hours or Dulbecco's modified Eagle's medium as a normal control. Lipopolysaccharide (100 ng/mL) or interleukin-4 (5 ng/mL) treatment served as positive controls for macrophage M1 or M2 polarization. For administration of 1,25-dihydroxy-vitamin D (1,25(OH)2D3), RAW264.7 macrophages were incubated with 1,25(OH)2D3 (VD3, 20 ng/mL) for a further 24 hours. A: M1/M2 gene marker expression on RAW264.7 macrophages; B: Proinflammatory cytokine secretion from RAW264.7 macrophages. Values are mean  $\pm$  SEM,  $^{a}P < 0.05$ ,  $^{b}P < 0.01$ , n = 3 experiments; NC: Normal control; PA; Palmitic acid; VD3: 1,25-dihydroxy-vitamin D; LPS: Lipopolysaccharide; IL: Interleukin; iNOS: Inducible NO synthase; TNF $\alpha$ : Tumor necrosis factor  $\alpha$ ; Arg1 Arginine 1; Mrc2: Macrophage mannose receptor 2.

M1 polarization of macrophages. Lipid accumulation in the liver is recognized as an early and essential step in NAFLD [40], with free fatty acids accounting for a major portion of hepatic lipid buildup[28]. In previous studies, we found that saturated fatty acids promote M1 polarization in Kupffer cells[19]. In this study, we found that  $1,25(OH)_2D_3$  effectively suppressed this fatty-acid-induced M1 polarization, linking its effect on reducing hepatic steatosis to the inhibition of proinflammatory macrophage activity.

Both VDR and PPARy, members of the nuclear receptor superfamily, are known to regulate lipid metabolism and macrophage polarization[24-27]. Studies have shown that VDR overexpression in adipose tissue leads to increased fat mass and elevated serum lipid levels, while VDR-knockout mice exhibit improved lipid profiles[41]. Consistent with these findings, our study revealed that VDR expression was upregulated in macrophages in response to an HF diet and fatty acids, but this upregulation was reversed by  $1,25(OH)_2D_3$  supplementation. Interestingly, although  $1,25(OH)_2D_3$  is the natural ligand for VDR, its supplementation led to a decrease in VDR expression, likely due to a feedback mechanism [42,43]. Deletion of macrophage VDR in mice has been shown to result in insulin resistance, partly by shifting macrophage polarization from M1 to M2[44]. Our data suggest that  $1,25(OH)_2D_3$  alleviates hepatic steatosis in NAFLD by inhibiting the proinflammatory M1 polarization of hepatic macrophages through the downregulation of VDR.

In addition, the HF diet increased PPAR $\gamma$  expression in hepatic macrophages, consistent with our previous findings [19]. However, supplementation with 1,25(OH)<sub>2</sub>D<sub>3</sub> did not significantly alter PPAR $\gamma$  expression *in vivo*, potentially due to



Figure 4 Effect of vitamin D receptor-peroxisome proliferator activated receptor γ pathway modulating 1,25-dihydroxy-vitamin D administration on high-fat diet/fatty acid-induced hepatic macrophage polarization. Wild-type C57BL/6 mice were fed either normal control (NC) diet or high-fat (HF) diet for 16 week, or HF diet plus 1,25-dihydroxy-vitamin D [1,25(OH)2D3] (20 µg/kg) by oral gavage every alternate day for 16 weeks. Phosphatebuffered saline by oral gavage served as a control (n = 10/group). Hepatic macrophages were isolated from mice administered NC diet, HF diet alone or plus 1,25(OH)2D3. RAW264.7 macrophages were incubated with palmitic acid (0.5 mmol/L) for 24 hours or Dulbecco's modified Eagle's medium as a normal control. Lipopolysaccharide (100 ng/mL) or interleukin-4 (5 ng/mL) treatment served as positive controls for macrophage M1 or M2 polarization. For administration of 1,25(OH)2D3, RAW264.7 macrophages were incubated with 1,25(OH)2D3 (20 ng/mL) for a further 24 hours. A: MRNA expression of vitamin D receptor (VDR)peroxisome proliferator activated receptor y on hepatic macrophages; B: Protein expression of VDR and PPARy on hepatic macrophages; C: MRNA expression of VDR and PPARy on RAW264.7 macrophages; D: Protein expression of VDR and PPARy on RAW264.7 macrophages. Values are mean ± SEM, \*P < 0.05, \*P < 0.01, n = 10 animals per group, n = 3 experiments; VDR: Vitamin D receptor; PPARy: Peroxisome proliferator activated receptor y; NC: Normal control; HF: High-fat; VD3: 1,25-dihydroxy-vitamin D; PA: Palmitic acid; LPS: Lipopolysaccharide; IL: Interleukin.

complex interactions between VDR and PPAR $\gamma$ [25,26]. In contrast, *in vitro* experiments demonstrated that 1,25(OH)<sub>2</sub>D<sub>3</sub> suppressed PPARy expression in macrophages in response to fatty acid stimulation. This suggests that VDR and PPARy may operate in tandem during macrophage polarization under these conditions. Mechanistically, 1,25(OH)<sub>2</sub>D<sub>3</sub> likely modulates PPARy by directly interacting with VDR, which, in turn, influences macrophage polarization and lipid metabolism. This dual regulation of VDR and PPARy may be critical for reducing inflammation and improving lipid



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Figure 5 Administration of 1,25-dihydroxy-vitamin D inhibiting fatty-acid-induced proinflammatory M1 polarization of macrophages directly relieves lipid accumulation and metabolism in hepatocytes. RAW264.7 macrophages were incubated with palmitic acid (0.5 mmol/L) for 24 hours or Dulbecco's modified Eagle's medium as a normal control. Lipopolysaccharide (100 ng/mL) or interleukin-4 (5 ng/mL) treatment served as positive controls for macrophage M1 or M2 polarization. For administration of 1,25-dihydroxy-vitamin D [1,25(OH)2D3], RAW264.7 macrophages were incubated with 1,25(OH)2D3 (20 ng/mL) for a further 24 hours. The cell culture supernatants were collected and prepared for conditioned media (CMs). AML12 hepatocytes were treated with different CMs from RAW264.7 macrophages for 24 hours. A: Lipid accumulation in AML12 hepatocytes determined by Oil Red O staining (200 ×); B: Proinflammatory cytokines mRNA expression on AML12 hepatocytes; C: Lipid metabolism genes mRNA expression on AML12 hepatocytes; D: Lipid metabolism enzymes protein expression on AML12 hepatocytes. Values are mean  $\pm$  SEM, <sup>a</sup>P < 0.05, <sup>b</sup>P < 0.01, *n* = 3 experiments; CM: Conditioned media; NC: Normal control; LPS: Lipopolysaccharide; IL: Interleukin; PA: Palmitic acid; VD3: 1,25-dihydroxy-vitamin D; TNF $\alpha$ : Tumor necrosis factor  $\alpha$ ; SREBP1C: Sterol-regulatory element binding protein 1C; FASN: Fatty acid synthetase; ACOX1: Acyl-CoA oxidase 1; CPT1A: Carnitine palmitoyltransferase 1A.

#### homeostasis in NAFLD.

Earlier studies have shown that hepatic lipid accumulation in NAFLD is initiated by the production of proinflammatory cytokines from Kupffer cells[45-47]. Depletion of Kupffer cells in animal models reduced hepatic steatosis, suggesting that the inflammatory activation of Kupffer cells is key to disrupting hepatic lipid homeostasis. A critical question is whether polarized macrophages directly influence lipid metabolism in hepatocytes. Recent research indicates that lipid-induced M1 macrophages can promote lipid synthesis in hepatocytes[48,49]. In our study, we demonstrated that supplementation with  $1,25(OH)_2D_3$  improved hepatic steatosis and lipid metabolism *in vivo*, likely due to its ability to reverse M1 polarization in hepatic macrophages. Our *in vitro* co-culture experiments further supported these findings by showing that suppression of M1 polarization in macrophages, induced by fatty acids, directly reduced lipid accumulation and improved lipid metabolism in hepatocytes. This suggests that  $1,25(OH)_2D_3$  not only reduces hepatic inflammation but also exerts a beneficial effect on lipid metabolism, potentially making it a valuable therapeutic option for NAFLD.

#### Limitations and future perspectives

**Conditioned medium limitation:** While the use of conditioned medium from RAW264.7 macrophages in this study provided valuable insights into paracrine signaling mechanisms, it may not fully capture the complex *in vivo* interactions between macrophages and hepatocytes. Future studies should consider employing a direct co-culture system, with macrophages in the upper compartment and liver cells in the lower compartment, to better understand how fatty acids and inflammatory signals concurrently affect both cell types. This would provide a more complete picture of the metabolic changes occurring in hepatocytes.

**Mechanistic studies:** Future research should focus on delineating the precise molecular mechanisms by which  $1,25(OH)_2$  D<sub>3</sub> regulates macrophage polarization through VDR-PPAR $\gamma$  signaling and its downstream effects on lipid metabolism. Dose-Response Exploration: Investigating the effects of different doses of  $1,25(OH)_2D_3$  on NAFLD will help determine the optimal therapeutic dosage while minimizing potential side effects, such as hypercalcemia.

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Long-term effects: Longitudinal studies are needed to assess the long-term safety and efficacy of 1,25(OH)<sub>2</sub>D<sub>3</sub>, particularly with respect to chronic supplementation and the potential risk of hypercalcemia. Combination Therapies: Evaluating the potential of  $1,25(OH)_2D_3$  in combination with other pharmacological agents could enhance its therapeutic efficacy and offer novel treatment strategies for NAFLD.

# CONCLUSION

This study demonstrates that 1,25(OH)<sub>2</sub>D<sub>3</sub> supplementation can effectively reduce lipid accumulation in hepatocytes by inhibiting fatty-acid-induced proinflammatory M1 polarization of macrophages. These findings offer a promising theoretical basis for the therapeutic potential of vitamin D in managing NAFLD. However, further research is necessary to advance our understanding and application of 1,25(OH)<sub>2</sub>D<sub>3</sub> in clinical settings.

# FOOTNOTES

Author contributions: Luo WJ, Dong XW and Ye H designed the research study; Zhao QS, Zhang QB and Guo WY performed the research; Liu HW and Xu F conducted experiments, analyzed the data; All authors contributed to editorial changes in the manuscript; All authors read and approved the final manuscript.

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ORIGINAL ARTICLE

# **Basic Study** Matrine promotes colorectal cancer apoptosis by downregulating shank-associated RH domain interactor expression

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	Abstract

# Abstract

# BACKGROUND

The 5-year survival rate of patients with colorectal cancer (CRC) in China is only 56.9%, highlighting the need for new therapeutic drugs. Previous studies have shown that matrine exhibits antitumor effects by inducing apoptosis. However, the mechanism by which matrine regulates antiapoptotic proteins in CRC remains unclear.

# AIM

To identify apoptotic proteins from proteomics and investigate the role of matrine in impeding CRC apoptosis by regulating these proteins.



# METHODS

Tumor and adjacent normal tissues were collected from 52 patients with CRC who underwent surgery between January and December 2021. Data-independent acquisition quantitative proteomic analysis was performed to identify differentially expressed apoptotic proteins. The selected apoptotic proteins were identified through their association with tumor-node-metastasis (TNM) stage and prognosis, then confirmed by immunohistochemical (IHC) staining in validation cohort. *In vitro*, the role of matrine or apoptotic proteins on cancer cells were analyzed.

#### RESULTS

Compared to normal tissues, 88 anti-apoptotic proteins from proteomic results were selected. Among them, Shankassociated RH domain interactor (SHARPIN) was identified because of its relationship with TNM stage and overall survival in TCGA database. In the IHC-confirmed cohort, SHARPIN was highly expressed in CRC tissues and localized in the cytoplasm. Higher SHARPIN expression was associated with TNM stage, carbohydrate antigen 153 levels, and gross type compared to low expression. SHARPIN knockdown promoted apoptosis, significantly upregulated the expression of Bcl-2 associated agonist of cell death, Bcl-2 associated X protein, caspase 3, and caspase 8, and downregulated B-cell lymphoma-2 (P < 0.05). Importantly, matrine treatment promoted apoptosis and reversed the proliferation, invasion, and migration of CRC cells by repressing SHARPIN.

#### CONCLUSION

SHARPIN was identified as an upregulated anti-apoptotic protein in CRC, and matrine exhibited anticancer effects by downregulating its expression. Thus, matrine appears to be a promising drug for CRC.

Key Words: Colorectal cancer; Proteomics; Shank-associated RH domain interactor; Matrine; Apoptosis

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**Core Tip:** Despite advances in therapy for colorectal cancer (CRC), the 5-year survival rate for CRC patients in China remains only 56.9%. This study explored the effects of matrine on CRC by targeting a newly identified anti-apoptotic protein, Shank-associated RH domain interactor (SHARPIN). SHARPIN was discovered through proteomic analysis and its expression was validated in both the TCGA database and our patient cohort using immunohistochemistry. Inhibiting SHARPIN expression led to increased apoptosis and reduced proliferation, invasion, and migration of CRC cells *in vitro*. Matrine's ability to inhibit SHARPIN and induce apoptosis highlights its potential as a promising therapeutic agent for CRC.

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# INTRODUCTION

Colorectal cancer (CRC) is the third most common cancer type worldwide and ranks second in China[1]. It imposes a significant burden on both individuals and the healthcare system because of its high incidence and mortality rate. Despite notable advancements in systemic therapy, CRC prognosis remains poor. In China, although 5-year survival rate increased from 47.2% to 56.9% between 2003 and 2015, it still lagged that of a developed country[2]. The poor prognosis of CRC can be attributed to factors, such as advanced TNM stage, genetic dysregulation or mutation, and drug resistance. Hence, it is imperative to explore novel targets and corresponding drugs to enhance the treatment efficacy.

Cell death resistance is a crucial hallmark of cancer[3]. The dysregulation of apoptotic proteins promotes CRC progression, especially at early-stage, and identified as promising targets for improving therapeutic outcomes. Proteomics offers a means of characterizing protein profiles, including those involved in anti-apoptosis, in CRC tissues. However, there is a paucity of drugs designed to induce apoptosis in the treatment of CRC. Matrine, a natural alkaloid derived from plants such as Sophora flavescens (kushen), has shown anticancer effects without obvious adverse effects. Notably, few studies have explored the effect of matrine on the induction of apoptosis in CRC cells. This study aimed to select antiapoptotic proteins from CRC proteomic profiles and investigate the ability of matrine to induce apoptosis in CRC cells by inhibiting these anti-apoptotic proteins.

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# MATERIALS AND METHODS

#### Patient recruitment and sample collection

From January 2021 to December 2021, we recruited patients diagnosed with CRC (n = 158) and health control subjects (n = 35) at our hospital. First, 52 paired tumor and adjacent tissues (5 cm away from the tumor) were collected from patients with CRC for proteomic analysis. Four CRC samples were missing, and 9 samples did not contain tumor tissue. Finally, 93 tumor tissues from patients with CRC (Figure 1) and 35 normal tissues from healthy subjects were used as a validation cohort to examine protein expression using immunohistochemistry (IHC). Clean Tissues were transferred by liquid nitrogen and stored in a -80 °C freezer. Other tissues were fixed and processed into sections.

Surgical resection samples diagnosed with CRC were included. Inflammatory bowel disease-associated, hereditary, and neuroendocrine CRC were excluded. Additionally, patients who had received chemoradiotherapy, targeted therapy, immunotherapy, or participated in clinical trials within the past 6 months were also excluded. All enrolled patients provided written informed consent. This study was conducted in accordance with the Declaration of Helsinki and approved by the Clinical Research Ethics Committee of the China-Japan Friendship Hospital (2018-116-K85).

#### Data independent acquisition analysis

The 52 pairs of CRC tissue samples were analyzed using high-performance liquid chromatography-mass spectrometry/ mass spectrometry to identify differentially expressed proteins (DEPs). Samples were prepared through various processes, including protein denaturation, reduction, alkylation, tryptic digestion, and peptide clean-up, using an iST Sample Preparation Kit (PreOmics, Germany). The eluted peptides were lyophilized using SpeedVac. The peptides were then redissolved in solvent A (0.1% formic acid in water) and analyzed using an Orbitrap Fusion Lumos Tribrid coupled to an EASY-nano LC 1200 system (Thermo Fisher Scientific, MA, United States). The mass spectrometer was run in data independent acquisition (DIA) mode with a hybrid data strategy[4].

Raw DIA data were processed and analyzed using Spectronaut 15.0 (Biognosys AG, Switzerland) with default settings. The spectra were configured to search the UniProt-Homo sapiens database (version201907, 20428 entries), assuming trypsin as the digestion enzyme. The Q value false discovery rate (FDR) cutoff was set to 1% at both the precursor and protein levels. Decoy generation was set to mutated, which is similar to scrambled generation but only applies a random number of amino acid position swamps (min = 2, max = length/2). A normalization strategy was set for local normalization. The average of the top three filtered peptides that passed the 1% Q value cutoff was used to calculate the major group quantities. DEPs were selected if their  $P_{adj}$  value was < 0.05, and absolute fold change (FC) > 2 after the *t*-test.

#### **Bioinformatic analysis**

Quality control showed a low coefficient of variation and good reliability of the proteomic results: (1) DEPs were analyzed using R packages such as BiocManager, org.Hs.eg.db, colorspace, stringi, and ggplot2, and pairwise comparisons between two groups. The differential protein screening criteria were a *t*-test with Benjamini & Hochberg-corrected *P* value < 0.05 and an absolute FC > 2. Principal component analysis (PCA) was performed to determine the differences between tumor and normal samples. The upregulated and downregulated DEPs are displayed as volcano plots, and hierarchical clustering analysis was performed for expressed proteins and samples simultaneously, with the results displayed as heatmaps; and (2) Functional annotation and enrichment analyses were performed on all identified DEPs, and their functions were marked using Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG).

RNA sequencing quantification and relevant clinical and survival data[5] of CRC tissues (n = 647) and normal colorectal tissues (n = 51) were obtained from TCGA database. (https://portal.gdc.cancer.gov). The ggplot2 and survinier packages were used to visualize the analyzed data.

## IHC

Methanal-Fixed and Paraffin-Embedded tumors were stained for the Shank-associated RH domain interactor (SHARPIN) protein. Antigen retrieval was performed using an automatic antigen repair instrument (LBP-5196-II; Guangzhou LBP Medicine Science & Technology Co., Ltd) for 15 minutes in Tris-EDTA buffer (pH 9.0), followed by treatment with an enhanced endogenous peroxidase-blocking buffer (P0100B, Beyotime, Shanghai, China) for 10 minutes. Specimens were incubated overnight at 4 °C with polyclonal antibodies against human SHARPIN (1:100; 14626-1-AP, Proteintech, Wuhan, China). After rinsing three times with phosphate buffered saline (PBS), the slides were incubated with goat anti-rabbit IgG (1:2000, ab6721; Abcam) for 1 hour at room temperature. A coloring reaction was performed using a 3,3N-Diaminobenzidine Tertrahydrochloride chromogenic kit (ZLI-9017; Zhongshan Golden Bridge, Beijing, China). Nuclei were stained with Harris hematoxylin and mounted with neutral gum. Finally, the slides were photographed using a BX53 upright bright-field microscope (Olympus).

## Evaluation of IHC staining

The ImageJ software was used for image quantification. SHARPIN expression was quantified using the H-score method in ImageJ; weak immunostaining was assigned a score of 1, moderate immunoreactivity was assigned a score of 2, and strong immunostaining was assigned a score of 3. The percentage of tumor cells stained at each intensity level was multiplied by the respective numeric score of the staining intensity, and the results were summed to quantify the total H-score.

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Figure 1 Flow chart. CRC: Colorectal cancer; IHC: Immunohistochemistry.

# Data collection

Demographic data, clinicopathological features, and tumor markers, including age, sex, gross type, differentiation, tumor size, tumor location, histopathological type and manifestation, microsatellite instability, TNM stage, carcinoembryonic antigen, carbohydrate antigen 199 (CA199), CA125, CA153, and CA724 were collected from the medical record system.

# Cell culture

Two CRC cells, HCT116 and SW480, obtained from the Procell Life Science & Technology Co., Ltd (Wuhan, China), were cultured in McCoy's 5A or DMEM supplemented 10% fetal bovine serum (FBS) (Gibco), 1% penicillin/streptomycin solution (C125C5, NCM Biotech) at 37.7 °C in a humidified atmosphere with 5% CO<sub>2</sub>.

# Cell transfection and matrine intervention

CRC cells were transfected with SHARPIN small interfering RNA (GenePharma) or negative control siRNA (GenePharma). The sequence pairs of the SHARPIN were as followed: Sense, 5'-CCUGAGGCAGAUCUUCCUATT-3', antisense, 5'-UAGGAAGAUCUGCCUCAGGTT-3'. Lipofectamine 3000 Transfection Reagent (Invitrogen) was used to transfect CRC cells with the above siRNAs, according to the manufacturer's instructions. After 24 hours, the CRC cells were collected for subsequent experiments.

Matrine (MCE) stock solution was diluted with dimethyl sulfoxide and stored in -20 °C in the dark. CRC cells were treated with matrine at concentration of 2.5 mg/mL for 48 hours, which refer to previously described[6].

# Quantitative reverse transcription-PCR

Total RNA was extracted from the cells using TRIzol reagent (Vazyme, Nanjing, China). The following primers were used for SHARPIN: Forward 5'- TGTTCTCAGAGCTCGGTTT -3' and reverse 5'- AAGTTCCCCGTCCATCTT -3'. Fluorescence was detected using a CFX Connect instrument (Bio-Rad). Each sample was run in triplicate and compared using GAPDH as the reference gene. Results were analyzed using the  $2^{-\Delta CT}$  method for the relative quantification of mRNA expression.

# Western blotting

Cell lysis buffer for western blotting, IP (P0013, Beyotime), and a protease and phosphatase inhibitor cocktail (P1045, Beyotime) were used for protein extraction. The BCA Protein Assay Kit (P0012S, Beyotime) was used to measure the amount of protein.

Total proteins were subjected to sodium dodecyl sulfate/polyacrylamide gel electrophoresis and electrotransferred to PVDF membranes (Merck Millipore, China). Nonspecific binding sites were blocked using 5% nonfat milk for 2 hours and the membranes were incubated at 4 °C overnight with SHARPIN Monoclonal antibody (1:1000, Immunoway, United States), Caspase 3/p17/p19 Polyclonal antibody (1:1000, Proteintech), Caspase 8/p43/p18 Polyclonal antibody (1:1000, Proteintech), B-cell lymphoma-2 (Bcl-2) Polyclonal antibody (1:1000, Proteintech), Bcl-2 associated agonist of cell death (BAD) Polyclonal antibody (1:1000, Proteintech), Bcl-2 associated X protein (BAX) Polyclonal antibody (1:1000, Proteintech), GAPDH antibody (1:4000; Abcam), β-actin (1:1000, Proteintech). The PVDF membranes were then treated for 1 hour with a goat anti-rabbit secondary antibody (1:10000; D21109-35, IRDye® 800CW, LI-COR, United States). Fluorescence imaging was performed using an LI-COR Odyssey CLx imaging system. ImageJ software was used to quantify the chemiluminescent signals of the protein bands, using GAPDH,  $\beta$ -actin or tubulin as an internal control.

# Flow cytometry analysis

An Annexin V-fluorescein isothiocyanate/propidium iodide apoptosis kit (556547, BD, United States) was used to detect the proportion of apoptotic cells after transfection. All procedures were performed according to manufacturer's instructions. Flow cytometry (FACSCanto II, BD, United States) and FlowJo (V\_10.8.1) software were used to determine cell apoptosis rates.



#### Cell counting kit-8 proliferation assay

The collected CRC cells were seeded in each well of a 96-well plate at a density of  $1 \times 10^4$  cells/well. Then, at 0 hour, 24 hours, 48 hours and 72 hours, 10 µL of cell counting kit-8 (CCK-8) reagent (C0037, Beyotome) and 90 µL of medium were added after the previous medium was removed. Then, the cells were incubated for 1 hours at 37 °C with 5% CO<sub>2</sub>, and the optical density was detected at 450 nm using a microplate reader (Tecan infinite M200, Switzerland).

#### Transwell invasion assay

CRC cells were suspended in 200 µL of serum-free medium and seeded in the upper chambers coated with matrigel (Corning, United States). The bottom 24-well plates were filled with 600 µL of medium containing 10% FBS as a chemoattractant. After incubation for 72 hours, the cells remaining in the upper chamber were gently removed using cotton swabs, and the cells on the lower surface were photographed and counted after fixing with 4% paraformaldehyde and staining with 0.1% crystal violet.

#### Wound healing assay

CRC cells were cultured in 6-well plates for 24 hours, and cell transfection was performed as described above. After incubation for 48 hours, a wound was scratched with a 200 µL sterile pipette tip. The cells were then washed with PBS 3 times and incubated in a serum-free medium. Representative images were captured 0 and 24 hours after scratching. The total wound area was measured using the ImageJ software, and the relative migration rate was calculated.

#### Statistical analysis

Statistical programs for R software (version 4.0.3) and GraphPad Prism (version 9) were used to perform statistical analyses. Quantitative data with a normal distribution are presented as the mean ± SD and were analyzed using Student's t-test or one-way analysis of variance, while variables with a non-normal distribution are presented as the median and interquartile range and were compared using a Mann-Whitney U test or Kruskal-Wallis's test. Categorical variables were analyzed using the  $\chi^2$  test or a nonparametric test. Receiver operating characteristic curves were constructed to examine the diagnostic efficiency of RNA molecules by assessing the area under the curve. Statistical significance was set at P <0.05.

# RESULTS

#### Proteomics profiling of CRC patients

52 pairs of cancerous and matched adjacent normal tissues were collected from patients with CRC after surgical treatment for quantitative proteomic detection. 46.2% CRC patients were male, with a mean age of 64.6 ± 15.1 yeas old (Supplementary Table 1). A total of 7666 proteins were identified, and PCA demonstrated a clear separation between the CRC and normal groups (Figure 2A and B). Among these, 1960 DPEs with an FDR of < 1% were identified between the two groups (Figure 2C).

GO and KEGG enrichment analyses were performed for 1960 DEPs. GO enrichment analysis (Figure 2D) revealed the significant enrichment of various biological processes, molecular functions, and cellular components. In the biological processes, enrichment was observed in response to stimuli (oxygen-containing compounds, oxidative stress, and corticosteroids), RNA metabolic processes (ncRNA metabolic processes, rRNA metabolic processes, etc.), and other processes. In terms of molecular functions, enrichment was noted for binding (proteins, ions, etc.) and catalytic activity (acting on RNA). Among the cellular components, enrichment was found in organelles (chromosomal part, nucleolus, etc.), extracellular regions (extracellular space, extracellular matrix, etc.), and cell junctions (anchoring junction, adheres junction, etc.). KEGG pathway enrichment analysis (Figure 2E) indicated the activation of several pathways, including the PI3K-Akt signaling pathway, focal adhesion, cell cycle, and extracellular matrix-receptor interaction.

The enrichment of responses to stimuli in biological processes is often associated with cell death. Resistance to cell death is a crucial hallmark of cancer and the upregulation of anti-apoptotic proteins is known to promote tumor progression.

#### Selecting anti-apoptotic proteins in tissue proteomics profiling and TCGA database of CRC patients

To identify these anti-apoptotic proteins, 88 proteins were selected by negative regulation of apoptotic proteins based on GO enrichment analysis and were upregulated in tumor tissue (Supplementary Table 2). SHARPIN, metalloproteinase inhibitor 1 (TIMP1), nucleolar complex protein 2 homolog (NOC2 L), and DNA ligase 4 (LIG4) were significantly different among the TNM stages (Supplementary Table 3). As shown in Figure 3A, the expression of SHARPIN was significantly higher in stage III than in stage I. TIMP1 and NOC2 L expression levels were significantly higher in stage III than in stage II. With the advancement of TNM staging, the expression of SHARPIN was gradually increased, but not that of the others.

SHARPIN, TIMP1, NOC2 L, and LIG4 were further confirmed using TCGA database. As shown in Figure 3B, expect for LIG4, the expression of SHARPIN, TIMP1, NOC2 L was higher in tumor tissues than in normal tissues. As shown in Figure 3C, only SHARPIN was associated with the TNM stage. In the survival analysis, higher expression of SHARPIN and TIMP1 significantly decreased the overall survival (Figure 3D). Thus, upregulation SHARPIN was associated with the pathological stage and prognosis of CRC.







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**Figure 2 Proteomic profiles and bioinformatic analysis of colorectal cancer patients.** A: Hierarchical cluster analysis shows the global differentially expressed proteins. Upregulated (red) and downregulated (green) differentially expressed proteins in the CRC group compared to the normal group; B: Principal component analysis shows the protein expression in the cancer tissues (green) and normal tissues (orange) of colorectal cancer (CRC) patients; C: Volcano plot shows the fold changes of identified proteins. Significantly upregulated or downregulated proteins are represented in red and blue, respectively, while proteins without significant changes are shown in gray; D: Gene Ontology analysis shows the enrichment results for differentially expressed proteins; E: Kyoto encyclopedia of genes and genomes analysis shows that differentially expressed proteins are significantly enriched in multiple pathways, °*P* < 0.001. CRC: Colorectal cancer; PCA: Principal component analysis; HCA: Hierarchical cluster analysis; GO: Gene ontology; KEGG: Kyoto encyclopedia of genes and genomes; PI3K-Akt: Phosphatidylinositol 3-kinase serine/threonine kinase; ECM: Extracellular matrix.





Figure 3 The expression of shank-associated RH domain interactor, metalloproteinase inhibitor 1, nucleolar complex protein 2 homolog, and DNA ligase 4 proteins and its association with tumor-node-metastasis and overall survival in colorectal cancer. A: The expression of 4 proteins among tumor-node-metastasis (TNM) stages in 52 colorectal cancer (CRC) patients; B: The expression of 4 proteins in TCGA; C: The expression of 4 proteins among TNM stages in TCGA; D: The association between expression of 4 proteins and overall survival in TCGA; E: The immunohistochemistry of shank-associated RH domain interactor in 93 CRC tissues and 35 normal tissues.  $^{a}P < 0.05$ ;  $^{b}P < 0.01$ ; CRC: Colorectal cancer; HC: Health control; SHARPIN: Shank-associated RH domain interactor; TIMP1: Metalloproteinase inhibitor 1; NOC2 L: Nucleolar complex protein 2 homolog; LIG4: DNA ligase 4.

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#### High expression of SHARPIN and its association with clinicopathological characteristics in CRC

IHC was conducted to investigate the expression of SHARPIN between CRC tumor tissues (n = 93) and normal tissues (n = 35). Compared with normal tissues (Figure 3E), CRC tissues showed significantly higher SHARPIN expression (P < 0.01). SHARPIN was hardly stained in normal tissues but was highly expressed in the cytoplasm of CRC cells.

93 CRC patients were divided into two groups according to their mean H-score. As indicated in Table 1, the average age was  $67.5 \pm 10.9$  years, and 49 participants (52.7%) were male. SHARPIN expression correlated with serum CA153 Levels, gross type, T stage, N stage, and TNM stage (all *P* < 0.05; Table 1).

#### Downregulated SHARPIN induced CRC cells apoptosis

To further investigate the effects of SHARPIN on the apoptosis of two CRC cell lines (HCT116 and SW480), siRNA was used to knockdown the expression of SHARPIN. The efficiency of SHARPIN knockdown was confirmed by Quantitative reverse transcription-PCR and western blot analysis (Supplementary Figure 1). Apoptotic cells were assessed by flow cytometry, and the expression of apoptotic proteins (Caspase 3, caspase 8, BAD, BAX, and Bcl-2) was determined by western blotting. The results showed that SHARPIN knockdown promoted apoptosis in CRC cells, as indicated by the increased proportion of apoptotic cells in the siSHARPIN group compared to that in the control group (Figure 4A; P < 0.05). Additionally, the expression levels of Caspase 3, Caspase 8, BAD, and BAX were significantly upregulated in the siSHARPIN group, whereas the expression level of Bcl-2 was downregulated in siSHARPIN + Matrine group (Figure 4B).

#### Matrine induced apoptosis of CRC cells by downregulating SHARPIN

Subsequently, we explored the role of SHARPIN in suppressing matrine-induced apoptosis in CRC cells. We observed the apoptosis-promoting effects of matrine in CRC cells. In CRC cell lines treated with matrine, there was a significant downregulation of SHARPIN expression (Figure 4C) and significant increase in the number of apoptotic cells (Figure 4A). The siSHARPIN + matrine group enhanced this effect. As shown in Figure 4, caspase 3 was significantly upregulated and Bcl-2 was significantly downregulated in the matrine group. Furthermore, in the siSHARPIN + matrine group, the expression of caspase 3, caspase 8, BAD, and BAX was significantly upregulated, whereas that of Bcl-2 was significantly downregulated.

#### Matrine inhibited progression of CRC cells by downregulating SHARPIN

Next, we examined the effects of matrine and SHARPIN knockdown on the proliferation, invasion, and migration of CRC cells. The viability of CRC cells was assessed using the CCK-8 assay, whereas cell invasion and migration were evaluated using transwell invasion and wound-healing assays, respectively.

The viability of CRC cells was significantly inhibited in the siSHARPIN, matrine, and siSHARPIN + matrine groups compared to that in the control group (P < 0.01; Figure 5A). In the transwell invasion assay, the number of invasive cells markedly decreased in the siSHARPIN, matrine, and siSHARPIN + matrine groups (Figure 5B). Furthermore, the wound healing rates of CRC cells were significantly reduced in the siSHARPIN, matrine, and s

# DISCUSSION

The incidence and mortality rates of CRC are on the rise, and despite advances in treatment strategies, improvements in prognosis have been modest. Resistance to cell death is a critical hallmark of cancer, and there are relatively few drugs specifically designed to induce apoptosis in cancer cells. Apoptotic drugs hold promise for tumor treatment, and further exploration of molecules involved in regulating the apoptotic pathway is essential for advancing CRC therapies. In the present study, SHARPIN was both found to be upregulated in CRC tissues based on our proteomic and TCGA database and validated by IHC staining in our CRC cohort. Additionally, the expression of SHARPIN was associated with different TNM stages and a poor prognosis. *In vitro* experiments, this study demonstrated that the downregulation of SHARPIN induces apoptosis in CRC cells. Matrine treatment also induced apoptosis and inhibited the proliferation, invasion, and migration of CRC cells by downregulating SHARPIN expression. Therefore, the role of SHARPIN in CRC was initially validated in our study, providing further evidence supporting the potential of matrine in preventing CRC and colorectal adenoma. Our study identifies SHARPIN as a potential anti-apoptotic molecule, shedding light on the mechanisms of matrine's impact on CRC. Moreover, matrine has a favorable safety profile with minimal side effects. In the future, it is interesting to explore the effect of matrine in preventing tumor progression in high-risk patients.

SHARPIN is enriched at synaptic sites in mature neurons[7]. Located in the cytoplasm, SHARPIN is an approximately 40 kDa conserved protein that is ubiquitously expressed in various human tissues[8]. Furthermore, SHARPIN is amplified in some cancers, such as prostate, breast, and ovarian cancers. Zhang *et al*[9] demonstrated that upregulated SHARPIN activated the NF- $\kappa$ B pathway and suppressed cell apoptosis, potentially contributing to prostate cancer progression[9]. Overexpression of SHARPIN has been shown to increase the breast cancer risk[10] and promote the breast cancer progression by regulating *p*53 and *ERa*[11]. Knockdown of SHARPIN expression leads to apoptosis and inhibits the proliferation, invasion, and migration of ovarian cancer cells[12]. However, the role of SHAPRIN in CRC has not yet been reported. In the present study, SHARPIN expression was significantly higher in tumor tissues than in normal tissues in our proteomic data (*n* = 52), TCGA database (*n* = 698), and IHC-confirmed cohort (*n* = 93). Additionally, higher SHARPIN expression was associated with poor overall survival in CRC patients compared to that in the low expression group.





Figure 4 Matrine induces apoptosis and regulates apoptotic proteins by downregulating shank-associated RH domain interactor. A: The apoptosis rate of colorectal cancer (CRC) cells in 4 groups [control group (con group), SHARPIN knockdown group (siSHARPIN group), matrine, siSHARPIN + matrine]; B: The expression of caspase 3, caspase 8, B-cell lymphoma-2 (Bcl-2) associated X protein, Bcl-2 associated agonist of cell death, Bcl-2 proteins in CRC cells in 4 groups; C: The suppressing effect of matrine on shank-associated RH domain interactor (SHARPIN) in CRC cells. <sup>a</sup>P < 0.05; <sup>b</sup>P < 0.01; <sup>c</sup>P < 0.05 vs con, <sup>d</sup>P < 0.01 vs con; \*P < 0.05 vs siSHARPIN, \*P < 0.01 vs siSHARPIN; \*P < 0.05 vs matrine, \*P < 0.01 vs matrine; Con: Control group; siSHARPIN: SHARPIN knockdown group; matrine: Matrine group; siSHARPIN + matrine: Matrine and SHARPIN knockdown group; CRC: Colorectal cancer; SHARPIN: Shank-associated RH domain interactor; Bcl-2: B-cell lymphoma-2; BAD: Bcl-2 associated agonist of cell death; BAX: Bcl-2 associated X protein.



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Figure 5 Matrine impedes proliferation, invasion and migration in colorectal cancer by downregulating shank-associated RH domain interactor interactor. A: The viability of colorectal cancer (CRC) cells using the cell counting kit-8 assay in 4 groups [control (con), si-Shank-associated RH domain interactor (SHARPIN), matrine, siSHARPIN + matrine]; B: The invasion cells of CRC in 4 groups; C: The wound healing of CRC cells in 4 groups.  $^{o}P < 0.05 vs \text{ con}$ ,  $^{d}P < 0.01 vs \text{ con}$ ;  $^{e}P < 0.05 vs \text{ siSHARPIN}$ ,  $^{f}P < 0.01 vs \text{ siSHARPIN}$ ;  $^{g}P < 0.05 vs \text{ matrine}$ ; C: The wound healing of CRC cells in 4 groups; SHARPIN + matrine]; B: The invasion cells of CRC in 4 groups; C: The wound healing of CRC cells in 4 groups.  $^{o}P < 0.05 vs \text{ con}$ ,  $^{d}P < 0.01 vs \text{ con}$ ;  $^{e}P < 0.05 vs \text{ siSHARPIN}$ ,  $^{f}P < 0.01 vs \text{ siSHARPIN}$ ;  $^{g}P < 0.05 vs \text{ matrine}$ ; Con: Control group; SHARPIN: Shank-associated RH domain interactor; siSHARPIN knockdown group; matrine: Matrine group; siSHARPIN + matrine: Matrine and SHARPIN knockdown group; CRC: Colorectal cancer.

In a 14-year-old boy, a homozygous deficiency of SHARPIN led to a shift in signaling from pro-survival to cell death in immune cells, contributing to an observed discrepancy in immune function[13]. Because of the effect of SHARPIN deficiency on cell death, knockdown expression of SHARPIN may induce apoptosis in cancer. As the component of the linear ubiquitin chain activation complex, SHARPIN plays an important role in inflammatory response and apoptosis by regulating canonical NF-κB signaling[8,14,15]. For anti-tumor effect, NF-kB pathway was activated by SHARPIN overex-pression with upregulated anti-apoptosis proteins in prostate cancer[9,16]. As a *p*53 mediator, SHARPIN may facilitate its degradation or ubiquitination in a mouse double minute 2 homolog-dependent manner[17], which is an inhibitor of *p*53 transcriptional activation[18]. SHARPIN is a negative regulator of PTEN in human tumor cell lines and primary cervical cancer cells both *in vitro* and *in vivo*. SHARPIN activates the PI3K/AKT pathway and induces tumorigenesis by interacting with PTEN.

Matrine is an alkaloid isolated from the traditional Chinese medicine, Sophora flavescens Aiton. In China, matrine injections are used to treat hepatitis. Owing to its anti-inflammatory effects, matrine also exhibits antitumor properties, especially apoptosis. Previous studies have shown that matrine induces autophagy and apoptosis by downregulating  $\beta$ -catenin and mediating the JNK-Bcl-2/Bcl-xL-Bax/Bak pathway in hepatocellular carcinoma cells[19,20]. In CRC cells, matrine induces apoptosis by regulating associated proteins. Zhang *et al*[21] demonstrated matrine reduce the ratio of Bcl-2/Bax and increase caspase-9 *in vitro*. Gu *et al*[22] explored effects of matrine on Bcl-2, Bax and caspase-3 in several cell lines. And Chang *et al*[23] showed that matrine activated apoptosis by regulating BAX,Bcl-2 and Cyto C. However, the precise mechanism underlying the matrine-induced apoptosis in CRC cells remains unclear. In the current study, we found that matrine induced cell apoptosis by inhibiting SHARPIN expression, while also repressing the proliferation, invasion, and migration of CRC cells. Targeted SHARPIN drugs might lead to various adverse effects, while matrine

Table 1 Clinicalpathological charateristics of colorectal cancer according to Shank-associated RH domain interactor expression, n (%)									
Variables	Total ( <i>n</i> = 93)	Low ( <i>n</i> = 50)	High ( <i>n</i> = 43)	P value					
Sex, male	49 (52.7)	28 (56)	21 (48.8)	0.49					
Age, years	$67.5 \pm 10.9$	$67.4 \pm 10.6$	$67.7 \pm 11.4$	0.89					
Location				0.38					
Left	75 (80.6)	42 (84)	33 (76.7)						
Right	18 (19.4)	8 (16)	10 (23.3)						
Gross type				0.03					
Fungating	32 (34.4)	21 (42)	11 (25.6)						
Ulceroinfiltrative	54 (58.1)	23 (46)	31 (72.1)						
Ulcerofungating	7 (7.5)	6 (12)	1 (2.3)						
Differentiation				0.443					
Poor	10 (11.1)	3 (10.3)	4 (12.5)						
Moderate	70 (77.8)	21 (72.4)	26 (81.2)						
Well	10 (11.1)	5 (17.2)	2 (6.2)						
Tumor size, ≥ 5 cm	48 (51.6)	24 (48)	24 (55.8)	0.45					
Histopathologic type				0.76					
AC	79 (84.9)	43 (86)	36 (83.7)						
MAC	14 (15.1)	7 (14)	7 (16.3)						
Venous invasion	21 (22.6)	10 (20)	11 (25.6)	0.52					
Perineural invasion	48 (51.6)	24 (48)	24 (55.8)	0.45					
MSI	7 (7.5)	3 (6)	4 (9.3)	0.70					
T stage				0.02					
1	4 (4.3)	4 (8)	0 (0)						
2	17 (18.3)	13 (26)	4 (9.3)						
3	60 (64.5)	29 (58)	31 (72.1)						
4	12 (12.9)	4 (8)	8 (18.6)						
N stage				0.02					
0	63 (67.7)	40 (80)	23 (53.5)						
1	18 (19.4)	7 (14)	11 (25.6)						
2	12 (12.9)	3 (6)	9 (20.9)						
M stage				0.09					
0	87 (93.5)	49 (98)	38 (88.4)						
1	6 (6.5)	1 (2)	5 (11.6)						
TNM stage				0.01					
Ι	20 (21.5)	16 (32)	4 (9.3)						
II	41 (44.1)	22 (44)	19 (44.2)						
III	26 (28.0)	11 (22)	15 (34.9)						
IV	6 (6.5)	1 (2)	5 (11.6)						
CA125, ng/mL	9.0 (7.0, 14.5)	9.0 (7.0, 14.5)	9.0 (7.1, 13.7)	0.96					
CA199, U/mL	14.1 (9.2, 24.0)	14.5 (8.0, 23.0)	13.6 (10.0, 26.0)	0.97					
CA724, U/mL	1.7 (1.5, 4.7)	1.9 (1.5, 4.9)	1.6 (1.5, 2.8)	0.61					
CEA, ng/mL	4.8 (2.5, 11.1)	5.5 (2.6, 11.5)	3.5 (2.5, 8.8)	0.26					

CA153, U/mL	8.1 (6.0, 12.4)	7.2 (5.3, 10.6)	9.2 (6.9, 13.3)	0.04

Two groups were divided the mean of the H-score. AC: Adenocarcinoma; MAC: Mucinous adenocarcinoma; MSI: Microsatellite instability; CEA Carcinoembryonic antigen; CA199: Carbohydrate antigen 19-9; CA724: Carbohydrate antigen 724; TNM: Tumor-node-metastasis.

shows potential in multiple therapeutic roles, making it a promising candidate for treatment.

Our study has some limitations. First, the follow-up time of the enrolled 52 patients was not available, and the association between SHARPIN expression and CRC survival needs to be investigated in Chinese population. Second, the therapeutic effects of matrine on CRC need to be validated *in vivo* and in clinical trials. Matrine injection has been used to improve hepatitis; however, the dosage of matrine that inhibits tumor progression remains to be explored. Third, the mechanism of matrine repressing SHARPIN expression remains to be conducted in the further study.

# CONCLUSION

In conclusion, this study identified overexpressed SHARPIN in CRC tissues. High expression SHARPIN is associated with TNM stage and poor prognosis. Matrine promotes cell apoptosis and inhibits proliferation, invasion, and migration by repressing SHARPIN expression in CRC. Thus, matrine could be considered as a novel therapeutic agent for CRC.

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# FOOTNOTES

**Author contributions:** Zhou YC conceived and designed the study, performed sample collection, experiments, acquired and analyzed data, and prepared the original draft; Wang QQ, Zhou GY, Zhao DY, Yin TF, Tan C, and Sun XZ participated in sample acquisition, data analysis, and manuscript revision; All authors read and approved the final manuscript. Both Yao SK and Zhou L have played important and indispensable roles in the experimental design, data interpretation and manuscript preparation as the co-corresponding authors. Yao SK applied for and obtained the funds for this research project.

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ORIGINAL ARTICLE

# **Basic Study** Enhancing the radiosensitivity of colorectal cancer cells by reducing spermine synthase through promoting autophagy and DNA damage

## Yu-Bin Guo, Yue-Ming Wu, Zhi-Zhao Lin

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# Abstract

#### BACKGROUND

Colorectal cancer (CRC), the third most common cancer worldwide, has increasingly detrimental effects on human health. Radiotherapy resistance diminishes treatment efficacy. Studies suggest that spermine synthase (SMS) may serve as a potential target to enhance the radiosensitivity.

### AIM

To investigate the association between SMS and radiosensitivity in CRC cells, along with a detailed elucidation of the underlying mechanisms.

### **METHODS**

Western blot was adopted to assess SMS expression in normal colonic epithelial cells and CRC cell lines. HCT116 cells were transfected with control/SMS-specific shRNA or control/pcDNA3.1-SMS plasmids. Assessments included cell viability, colony formation, and apoptosis via MTT assays, colony formation assays, and flow cytometry. Radiosensitivity was studied in SMS-specific shRNA-transfected HCT116 cells post-4 Gy radiation, evaluating cell viability, colony formation, apoptosis, DNA damage (comet assays), autophagy (immunofluorescence), and mammalian target of rapamycin (mTOR) pathway protein expression (western blot).

### RESULTS

Significant up-regulation of SMS expression levels was observed in the CRC cell lines. Upon down-regulation of SMS expression, cellular viability and colonyforming ability were markedly suppressed, concomitant with a notable increase in apoptotic indices. Furthermore, attenuation of SMS expression significantly augmented the sensitivity of HCT116 cells to radiation therapy, evidenced by a pronounced elevation in levels of cellular DNA damage and autophagy. Impor-



tantly, down-regulation of SMS corresponded with a marked reduction in the expression levels of proteins associated with the mTOR signaling pathway.

#### **CONCLUSION**

Knocking down SMS attenuates the mTOR signaling pathway, thereby promoting cellular autophagy and DNA damage to enhance the radiosensitivity of CRC cells.

Key Words: Spermine synthase; Colorectal cancer; Radiosensitivity; Autophagy; DNA damage

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Core Tip: This study highlighted spermine synthase (SMS) as a pivotal molecule regulating DNA damage and autophagy in cancer cells. SMS promoted DNA repair and activated the mammalian target of rapamycin signaling pathway, resulting in the inhibition of cellular autophagy. Collectively, SMS emerges as a promising therapeutic target to enhance colorectal cancer radiosensitivity, providing novel insights into the development of colorectal cancer treatment strategies.

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# INTRODUCTION

Globally, colorectal cancer (CRC) ranks third in prevalence among cancers, constituting about 10% of all newly diagnosed cancer cases. In 2022, the global incidence of CRC was estimated at 1.9 million new cases, with mortality rates reaching as high as 900000[1]. As age advances, the risk of developing CRC grows, with individuals aged 65 and older exhibiting substantially higher incidence rates compared to other age groups. However, in recent years, there has also been an observed rise in CRC incidence among younger populations<sup>[2]</sup>. Known risk factors for CRC include genetics, dietary habits (such as high-fat, low-fiber diets), obesity, smoking, alcohol consumption, and lack of physical activity[3]. Currently, the foremost therapy for early-stage CRC is surgical resection. It is worth noting that, in addition to surgery, chemotherapy and radiotherapy are often necessary for advanced CRC. Nevertheless, early-stage CRC typically presents with few noticeable symptoms, making it easily overlooked. Hence, the majority of CRC patients also require radiotherapy[4]. More terribly, a portion of CRC patients exhibit resistance to radiation therapy, leading to poor treatment outcomes. Approximately 20% of patients with locally advanced rectal cancer are inherently insensitive to radiotherapy. As for patients with metastatic CRC, the proportion of insensitivity may be even higher[5]. Studies indicate that the reasons for CRC's resistance to radiation therapy include genetic mutations and enhanced DNA repair capabilities. Mutations in genes such as KRAS and BRAF may render tumor cells insensitive to radiation[6]. Furthermore, some tumor cells possess highly efficient DNA damage repair capabilities, which can diminish the cytotoxic effects of radiation[7]. To overcome the challenge of radiation insensitivity, researchers have proposed various strategies, including the use of combined chemotherapy and screening for radiosensitizers, etc.[8]. Among these strategies, the screening of radiosensitizers has shown tremendous potential.

Evidence from research shows that spermine synthase (SMS) has a pivotal role in polyamine metabolism. Polyamine compounds such as spermine not only participate in the regulation of growth and development in organisms but also correlate with physiological processes like cell apoptosis and proliferation[9]. Spermine can also protect DNA from damage and plays a role in antioxidant stress and ion channel regulation[10]. It is known that SMS is a group of key enzymes associated with the synthesis of polyamines such as spermine, spermidine, and putrescine in organisms[11,12]. Polyamines and spermine are essential for maintaining cell growth and proliferation. Additionally, polyamines act as important scavengers of intracellular free radicals, alleviating oxidative stress in tumor cells[13]. In various tumor cells, the expression levels of SMS are significantly elevated, thereby promoting spermine synthesis. Elevated levels of spermine can accelerate the tumor cell proliferation, and increased expression of SMS can promote the proliferation of CRC[14]. Recent studies have revealed a correlation between the expression levels of SMS and cancer development. Fahrmann et al[15] discovered a correlation between plasma spermidine levels and distant metastasis risk in patients with triple-negative breast cancer. Velenosi et al [16] proposed that diacetylspermine could serve as a biomarker for predicting the development and progression of triple-negative breast cancer. Additionally, research indicates a down-regulation in spermine levels in prostate cancer tissue, and such a down-regulation is considered an indicator of the transition from normal prostate tissue to malignant tissue<sup>[17]</sup>. Other studies have found that SMS is upregulated in pancreatic cancer, promoting cancer cell proliferation and migration, and is associated with poorer overall survival [18]. Snezhkina et al [19] identified dysregulated spermine metabolism in CRC. Some studies propose that during the development of CRC, SMS collaborates with the MYC protein (an oncogene associated with cell proliferation) to suppress the expression of the Bim gene<sup>[14]</sup>. This collaboration is believed to sustain the survival of CRC cells and enhance their malignant behavior. Other



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studies have found that SMS is overexpressed in CRC, and targeting SMS inhibition induces lipid metabolism reprogramming and ferroptosis, significantly inhibiting the growth of CRC cells[20]. Notably, some research has demonstrated that inhibiting spermine biosynthesis can render cells more sensitive to radiation damage<sup>[21]</sup>. Mivechi *et al*<sup>[22]</sup> in 1986 claimed that inhibitors of ornithine decarboxylase such as alpha-difluoromethylornithine could increase radiationinduced inter-strand DNA crosslink damage, thereby enhancing the radiosensitivity of cancer cells. The aforementioned findings emphasize the importance of SMS in the occurrence and progression of CRC, suggesting its potential role as a key regulator of cellular sensitivity to radiotherapy. Therefore, this study aimed to clarify the link between SMS and the radiosensitivity of CRC cells, elucidating its mechanisms and providing insights for improving the treatment of CRC.

# MATERIALS AND METHODS

#### Cell culture and grouping

Normal colonic epithelial cells FHC (CRL-1831), CRC cell line HCT116 (CRL-247), SW62, SW480, HT-29 and LoVo cells were both purchased from WHELAB. The culture of FHC cells was performed in a DMEM/F12 medium comprising 10% fetal bovine serum, 100 µg/mL streptomycin, and 100 U/mL penicillin; HCT116, SW62, SW480, HT-29 and LoVo cells culture were finished in a RPMI1640 medium under the same conditions. Cells were maintained in a humidified environment at 37 °C with 50 mL/L CO<sub>2</sub>. When cells reached 80%-90% confluence, they were rinsed twice via phosphatebuffered saline (PBS), detached through 2.5 g/L trypsin-EDTA solution, and passaged. Cell grouping was initiated at the third passage. HCT116 cells were transfected with SMS shRNA (sh-SMS) and negative control shRNA (shNC) using Lipofectamine 3000 (L3000001, ThermoFisher, USA). Over-expression of SMS was achieved by transfecting HCT116 cells with SMS over-expression vector (OE-SMS) or negative control vector (OE-NC). HCT116 cells transfected with sh-SMS and shNC were subjected to a 4 Gy X-ray dose. Subsequent biological assays were performed after completion of the radiation treatment. The sequence for sh-SMS was 5'-CCGGCGCTTTAAAGAACAGCCTTTACTCGAGTAAAGGCTGT TCTTTAAAGC GTTTTT-3', and the sequence for shNC was 5'-CCGGCAACAAGATGAAGAGCACCAACTC GAGTTG-GTGCTCTTCATCTTGTTG-3'.

### MTT assay

In 96-well plates, HCT116 cells were plated at a density of 5000 cells per well, with three replicate wells per condition. The plates were then incubated in a humidified incubator at 37 °C with 50 mL/L CO<sub>2</sub> until the cells adhered completely. Subsequently, the cells were transfected or subjected to radiation treatment. Following that, the plates were returned to the incubator. At 24, 48, and 72 hours post-treatment, each well received 20 µL of MTT solution (5 mg/mL, ml057897, mlbio, China), and the cells underwent another four hours of incubation. Following the removal of the culture medium, 150 µL of dimethyl sulfoxide was provided for dissolving the MTT crystals. Ultimately, the absorbance (OD) of each well was measured using a microplate reader (Varioskan LUX, ThermoFisher, United States) at a wavelength of 490 nm.

### Colony formation assay

HCT116 cells in the logarithmic growth phase were collected for transfection or radiation treatment. Following two washes utilizing PBS, cells were digested via 2.5 g/L trypsin-EDTA solution and subsequently cleaned twice with PBS to terminate digestion. Later, the cell samples were suspended in a complete medium containing 3-4 g/L agarose to create single-cell suspensions. Next, 2 mL of the cell suspension, with a density of 1000 cells per well, was supplemented into each well of a 6-well plate. The plate was then cultured in a humidified atmosphere at 37 °C with 50 mL/L CO<sub>2</sub> for 2-3 weeks. Following culture, the cells were gently washed via PBS, stained utilizing 5 g/L crystal violet for 30 minutes, and then washed again with PBS. Lastly, cell colonies with a diameter  $\geq$  50 µm were observed and computed under an inverted microscope (BDS400, OPTEC, China).

### Flow cytometry

HCT116 cells were cultured in a humidified atmosphere at 37 °C with 50 mL/L CO<sub>2</sub>, followed by transfection or radiation treatment. After treatment, cells were detached using trypsin and collected into centrifuge tubes. They were then stained using fluorescein isothiocyanate (FITC)-conjugated Annexin V (Annexin V-FITC) and propidium iodide (PI) from the Annexin V Apoptosis Detection Kit (E606336, Sangon, China). Annexin V-FITC bound to exposed phosphatidylserine on the outer membrane of early apoptotic cells, while PI entered late apoptotic/necrotic cells with compromised membranes. Finally, a flow cytometer (CytoFLEX, Beckman, Germany) was utilized to analyze the cells stained to detect and analyze apoptotic cells.

### Comet assay

The comet assay, utilizing a Comet Assay Kit (C2041M, Beyotime, China), was employed to assess the level of DNA damage in HCT116 cells following transfection or radiation treatment. Cells were detached using trypsin and collected into centrifuge tubes. Low-melting agarose was added, and the mixture was spread onto slides to form a gel. A high-salt solution was applied to remove cell membranes and most proteins, followed by alkaline buffer to unwind DNA strands. Under an electric field (voltage 25 V), damaged DNA fragments migrated towards the anode, forming a "comet" shape. Subsequently, DNA was stained using PI (Ex/Em = 535/617 nm), and comet tail DNA level and comet tail length were observed under a fluorescence microscope (BX43, Olympus, Japan).



## Immunofluorescence

The treated HCT116 cells were washed twice through PBS and fixed *via* 40 g/L paraformaldehyde for 30 minutes to preserve cell structure and antigenicity. Upon two PBS washes, the cells were permeabilized *via* 4 g/L Triton X-100 for 30 minutes, given two times of washes *via* PBS again, and then incubated with 50 g/L bovine serum albumin to block non-specific binding sites. Afterwards, the cells were incubated overnight at a low temperature with Alexa Fluor® 488 Rabbit monoclonal anti-LC3 antibody (1:500, Ex/Em = 495 nm/519 nm, ab225382, Abcam, United Kingdom). After washing twice by virtue of PBS, cell samples were stained with a nuclear dye (DAPI, Ex/Em = 364 nm/454 nm, C1005, Beyotime, China) for 5 minutes and washed twice with PBS. Eventually, LC3 puncta were observed under a fluorescence microscope (BX43, Olympus, Japan), and the proportion of LC3-positive cells was analyzed.

## Western blot

FHC, HCT116, SW62, SW480, HT-29 and LoVo cells, along with HCT116 cells transfected or treated with radiation, were lysed using RIPA buffer. The protein concentration was determined utilizing a bicinchoninic acid assay kit. Upon mixing with SDS-PAGE loading buffer, the samples were denatured at 95 °C for 5 minutes. Denatured protein samples were loaded onto SDS-PAGE gels and isolated by electrophoresis. Following this, the samples were shifted from the gel to the polyvinylidene fluoride membrane by electroblotting. Then, 50 g/L bovine serum albumin solution was offered to block the membrane for 1 hour. Later, the membrane was subject to an overnight incubation with primary antibodies specific to the target proteins, including SMS (1:1000, ab151547, Abcam, United Kingdom), yH2AX (1:1000, ab124781, Abcam, United Kingdom), p-yH2AX (1:1000, ab81299, Abcam, United Kingdom), ATR (1:1000, ab2905, Abcam, United Kingdom), p-ATR (1:1000, ab289363, Abcam, United Kingdom), P53 (1:1000, ab26, Abcam, United Kingdom), LC3-I (1:1000, ab52628, Abcam, United Kingdom), LC3-II (1:1000, ab63817, Abcam, United Kingdom), p62 (1:1000, ab109012, Abcam, United Kingdom), Beclin 1 (1:1000, ab207612, Abcam, United Kingdom), mammalian target of rapamycin (mTOR, 1:1000, ab134903, Abcam, United Kingdom), p-mTOR (1:1000, ab109268, Abcam, United Kingdom), S6K1 (1:1000, ab32359, Abcam, United Kingdom), p-S6K1 (1:1000, ab59208, Abcam, United Kingdom), S6 (1:1000, ab250753, Abcam, United Kingdom), p-S6 (1:1000, ab2571, Abcam, United Kingdom), β-actin (1:1000, ab8227, Abcam, United Kingdom). Subsequently, the membrane was provided an incubation with HRP-conjugated secondary antibodies, including HRP Anti-Rabbit IgG antibody (1:5000, ab288151, Abcam, United Kingdom) and HRP Goat Anti-Mouse IgG (1:5000, ab6708, Abcam, United Kingdom). Further, a chemiluminescent substrate solution (P0211, Beyotime, China) was offered to initiate enzyme-linked secondary antibody reaction. The luminescence of the proteins was scanned using a ChemiDoc™ MP Imaging System (BioRed, United States).

### Statistical analysis

The experiments were conducted with three independent replicates. Independent sample *t*-tests (between two groups) or one-way analysis of variance (among multiple groups) were performed using SPSS version 25. Data were displayed as mean  $\pm$  SEM, with a significance threshold of *P* < 0.05. In addition, graphs were generated using GraphPad Prism 8.

# RESULTS

### Elevated SMS expression promotes proliferation and reduces apoptosis in CRC cells

Initially, a detection was performed on the expression of SMS in normal colonic epithelial cells (FHC) and the CRC cell line HCT116, SW62, SW480, HT-29 and LoVo. The detection results disclosed that the protein expression levels of SMS were notable elevated in HCT116, SW62, SW480, HT-29 and LoVo cells in contrast to FHC cells. Additionally, SMS expression in HCT116 cells was higher than in SW62, SW480, HT-29, and LoVo cells (Figure 1A). For observing the impact of SMS expression levels on cell radiosensitivity, we established HCT116 cell groups with SMS knockdown or over-expression (Figure 1B). Subsequently, we observed the influence of diverse SMS expression levels on cell viability, colony formation ability, and apoptosis levels. The observational outcomes showed that relative to the shNC group, the viability and colony formation ability of HCT116 cells in the sh-SMS group were remarkably cut down, but the apoptosis level was increased. In contrast, compared to the OE-NC group, the viability and colony formation ability of HCT116 cells in the significantly decreased (Figure 1C-E). These results indicated that increased expression of SMS in HCT116 promoted cell proliferation and inhibited apoptosis.

# Down-regulation of SMS enhances the radiosensitivity of HCT116 cells, inhibits cell proliferation, and promotes apoptosis

Although it is known that the activity of SMS can affect the sensitivity of CRC cells to radiotherapy, increased activity of SMS can lead to increased resistance of CRC cells to radiation. Additionally, SMS is involved in various reactions, but the mechanism of action of SMS on radiotherapy sensitivity is not yet clear. Therefore, we observed the effect of down-regulating SMS expression on cellular radiosensitivity. After altering the expression levels of SMS, cells were treated utilizing a dose of 4 Gy X-rays, and cell colony formation ability, viability, and apoptosis levels were assessed. The assessment outcomes exhibited that X-rays reduced cell viability and colony formation ability but encouraged apoptosis. Briefly, compared to the shNC + Ionizing radiation (IR) group, the viability and colony formation ability of HCT116 cells in the sh-SMS + IR group were significantly reduced, while the apoptosis levels were increased (Figure 2). Thus, down-regulation of SMS enhanced the radiosensitivity of HCT116 cells, inhibited cell proliferation, and promoted apoptosis.

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**Figure 1 Up-regulation of spermine synthase in colorectal cancer cells HCT116 promotes cell proliferation and inhibits apoptosis.** A and B: Western blot analysis for spermine synthase (SMS) protein expression levels in FHC, HCT116, SW62, SW480, HT-29 and LoVo cells groups (A), as well as in negative control shRNA (shNC), SMS shRNA (sh-SMS), negative control over-expression vector (OE-NC), and OE-SMS HCT116 cell groups (B); C: MTT assay to detect the viability of cells in shNC, sh-SMS, OE-NC, and OE-SMS HCT116 groups; D: Colony formation assay to assess the colony formation ability of cells in shNC, sh-SMS, OE-NC, and OE-SMS HCT116 groups; D: Colony formation assay to assess the colony formation ability of cells in shNC, sh-SMS, OE-NC, and OE-SMS HCT116 groups; E: Flow cytometry analysis of cell apoptosis levels in shNC, sh-SMS, OE-NC, and OE-SMS HCT116 groups;  $^{a}P$ < 0.01,  $^{b}P$  < 0.01,  $^{v}S$  FHC, shNC;  $^{d}P$  < 0.01 vs OE-NC; SMS: Spermine synthase; sh-SMS: Spermine synthase shRNA; shNC: Negative control shRNA; OE-SMS: Spermine synthase over-expression vector; OE-NC: Negative control over-expression vector.

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#### Figure 2 Down-regulation of spermine synthase enhances the radiosensitivity of HCT116 cells, inhibits cell proliferation, and promotes apoptosis. A: MTT assay to detect the viability of HCT116 cells in the negative control shRNA (shNC) group, shNC + IR group, spermine synthase shRNA (sh-SMS) group, and sh-SMS + IR group; B: Colony formation assay to assess the colony formation ability of HCT116 cells in the shNC group, shNC + IR group, sh-SMS group, and sh-SMS + IR group; C: Flow cytometry analysis to measure the apoptosis levels of HCT116 cells in the shNC group, shNC + IR group, sh-SMS group, and sh-SMS + IR group. <sup>b</sup>P < 0,01 vs shNC, <sup>d</sup>P < 0.01 vs shNC + IR, <sup>f</sup>P < 0.01 vs sh-SMS; SMS: Spermine synthase; sh-SMS: Spermine synthase shRNA; shNC: Negative control shRNA; OE-SMS: Spermine synthase over-expression vector; OE-NC: Negative control over-expression vector.

# Knocking down SMS enhances the radiosensitivity of HCT116 cells by promoting DNA damage

Research has already indicated that knocking down SMS leads to DNA damage and impedes DNA repair processes[23, 24]. To examine the relationship between SMS and radiation-induced DNA damage in cancer cells, HCT116 cells were treated via a dose of 4 Gy X-rays following SMS knockdown. The comet assay was employed to determine the extent of DNA damage in HCT116 cells, and the western blot assay was recruited to analyze the expression of DNA damagerelated proteins (yH2AX, p-yH2AX, ATR, p-ATR, P53). Our comet assay results revealed an increase in DNA damage levels in HCT116 cells following down-regulation of SMS expression, including notable elevations in comet tail DNA levels and comet tail moments. Compared to the shNC + IR or sh-SMS groups, the sh-SMS + IR group exhibited markedly elevated DNA damage levels in HCT116 cells, along with increased comet tail DNA levels and comet tail moments (Figure 3A-C). Moreover, knocking down SMS expression resulted in significant up-regulation of p-γH2AX, p-ATR, and P53 protein levels in HCT116 cells. Importantly, when compared to the shNC + IR or sh-SMS groups, the sh-SMS + IR group displayed substantially raised γH2AX, p-γH2AX, p-ATR, and P53 protein levels in HCT116 cells (Figure 3D and E). In a nutshell, knocking down SMS enhanced the radiosensitivity of HCT116 cells through supporting DNA damage.

# Knocking down SMS enhances the radiosensitivity of HCT116 cells by promoting autophagy

While the correlation between SMS and DNA damage has been established, autophagy also serves as a mechanism of cell death induced by radiation therapy [25,26]. It is worth noting that the relationship between SMS and cellular autophagy



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**Figure 3 Knockdown of spermine synthase enhances the radiosensitivity of HCT116 cells by advancing DNA damage.** A-C: Comet assay for assessing DNA damage levels in HCT116 cells of the negative control shRNA (shNC), shNC + IR, spermine synthase shRNA (sh-SMS), and sh-SMS + IR groups (A), and analysis of comet tail DNA levels (B) and comet tail moments (C); D and E: Western blot analysis of  $\gamma$ H2AX, p- $\gamma$ H2AX, ATR, p-ATR, and P53 protein levels in HCT116 cells of the shNC group, shNC + IR group, and sh-SMS + IR group. <sup>b</sup>*P* < 0,01 *vs* shNC, <sup>d</sup>*P* < 0.01 *vs* shNC + IR, <sup>f</sup>*P* < 0.01 *vs* sh-SMS; SMS: Spermine synthase; sh-SMS: Spermine synthase shRNA; shNC: Negative control shRNA; OE-SMS: Spermine synthase over-expression vector; OE-NC: Negative control over-expression vector.

remains controversial [27,28]. Therefore, immunofluorescence and western blot analysis of autophagy-related protein expression were performed to observe the level of cellular autophagy after knocking down SMS expression. Immuno-fluorescence results revealed an increase in the number of LC3 puncta and the proportion of LC3-positive cells following SMS knockdown. Moreover, compared to the shNC + IR or sh-SMS groups, the sh-SMS + IR group displayed a marked increase in the number of LC3 puncta and the proportion of LC3-positive cells (Figure 4A and B). Additionally, western blot analysis revealed an escalation in the protein levels of LC3-I, LC3-II, and Beclin 1, along with a down-regulation in p62 protein levels, and an up-regulation in the LC3-II/LC3-I ratio following SMS knockdown. Importantly, compared to the shNC + IR or sh-SMS groups, the sh-SMS + IR group exhibited significantly elevated protein levels of LC3-I, LC3-II, and Beclin 1, decreased p62 protein levels, and down-regulated ratio of LC3-II/LC3-I (Figure 4C and D). These results indicated that knocking down SMS enhanced the radiosensitivity of HCT116 cells by promoting autophagy.



Figure 4 Knockdown of spermine synthase enhances the radiosensitivity of HCT116 cells by promoting autophagy. A and B: Immunofluorescence detection for LC3 puncta in HCT116 cells of the negative control shRNA (shNC) group, shNC + IR group, spermine synthase shRNA (sh-SMS) group, and sh-SMS + IR group; C and D: Western blot analysis for protein levels of LC3-I, LC3-II, p62, and Beclin 1 in HCT116 cells of the shNC group, shNC + IR group, sh-SMS group, and sh-SMS + IR group. bP < 0.01 vs shNC, dP < 0.01 vs shNC + IR, fP < 0.01 vs sh-SMS; SMS: Spermine synthase; sh-SMS: Spermine synthase shRNA; shNC: Negative control shRNA; OE-SMS: Spermine synthase over-expression vector; OE-NC: Negative control over-expression vector.

# Knocking down SMS enhances the radiosensitivity of HCT116 cells by suppressing the mTOR pathway

The aforementioned research suggests that spermine negatively regulates cellular autophagy. Studies have shown that SMS can modulate autophagy-related signaling through the mTOR pathway [29,30]. Therefore, we hypothesized that the mTOR pathway may be a key regulator of SMS-mediated cellular autophagy. According to western blot results, knocking down SMS expression lowered the p-mTOR, p-S6K1, and p-S6 protein expression levels in HCT116 cells, resulting in



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Figure 5 Knocking down spermine synthase enhances radiosensitivity of HCT116 cells by suppressing the mammalian target of rapamycin pathway. Western blot analysis for detecting the protein expression levels of mammalian target of rapamycin (mTOR), p-mTOR, S6K1, p-S6K1, S6, and p-S6 in HCT116 cells under the following conditions: Negative control shRNA (ShNC), shNC + IR, spermine synthase shRNA (sh-SMS), and sh-SMS + IR. <sup>b</sup>P < 0.01 vs shNC, <sup>d</sup>P < 0.01 vs shNC + IR, <sup>f</sup>P < 0.01 vs sh-SMS; SMS: Spermine synthase; sh-SMS: Spermine synthase shRNA; shNC: Negative control shRNA; OE-SMS: Spermine synthase over-expression vector; OE-NC: Negative control over-expression vector; mTOR: Mammalian target of rapamycin.

lessened ratios of p-mTOR/mTOR, p-S6K1/S6K1, and p-S6/S6. Furthermore, compared to the shNC + IR or sh-SMS groups, the sh-SMS + IR group exhibited lower protein expression levels of p-mTOR, p-S6K1, and p-S6, along with down-regulated ratios of p-mTOR/mTOR, p-S6K1/S6K1, and p-S6/S6 (Figure 5). These findings indicated that knocking down SMS enhanced the radiosensitivity of HCT116 cells by suppressing the mTOR pathway.

# DISCUSSION

As a pivotal part of comprehensive CRC management, radiotherapy effectively shrinks tumors and prepares patients for further surgical interventions[31,32]. Postoperatively, radiotherapy can effectively eliminate residual cancer cells and reduce the risk of recurrence. Moreover, as for patients with advanced CRC who are unable to undergo surgery, radiotherapy can improve their quality of life and prognosis by alleviating symptoms[33]. However, the current radiotherapy outcomes for patients with CRC are not satisfactory, and adjuvant therapies are needed to improve the efficacy of radiotherapy[34]. In this study, the SMS expression level significantly impacted the radiosensitivity of CRC cells, suggesting its potential as a potential therapeutic target to enhance radiosensitivity.

SMS, an enzyme that converts spermidine to spermine, is involved in diverse physiological processes such as cell proliferation, differentiation, and apoptosis[11]. Recent research has displayed that *SMS* over-expression is associated with tumorigenesis, progression, invasion, and metastasis in various cancers[12]. SMS expression is highest in the prostate, being approximately 10-20 times higher than in other tissues[35]. Prostate cancer tissues exhibit significantly higher SMS expression compared to adjacent normal tissues, and SMS levels correlate with tumor stage and poor prognosis[36]. Additionally, SMS over-expression has been observed in lung, gastric, liver, bladder, and ovarian cancers [37,38]. Notably, research has demonstrated elevated SMS expression in CRC tissues as opposed to adjacent normal tissues, with a positive correlation to tumor malignancy[14]. These findings indicate that SMS can serve as a potential therapeutic target for CRC. In line with previous findings, our study demonstrated a significant up-regulation of SMS expression remarkably suppressed HCT116 cell viability and induced apoptosis. These outcomes strongly support the oncogenic role of SMS in CRC. While reducing SMS expression has been shown to induce chemoresistance in CRC cells [39], our study unveiled a novel role for SMS in regulating radiosensitivity. Furthermore, our research demonstrated that silencing SMS expression significantly enhanced the radiosensitivity of HCT116 cells. Consequently, SMS can be a critical determinant of cancer cell responsiveness to both radiotherapy and chemotherapy.

SMS catalyzes the conversion of spermidine to spermine, a polyamine with potent antioxidant properties that can alleviate oxidative DNA damage[40]. Spermine also plays a crucial role in DNA repair, particularly in double-strand break and base excision repair pathways. Upon DNA damage, SMS is activated and rapidly mobilized to the lesion site, facilitating DNA repair. Additionally, SMS maintains chromosomal structure and function, preventing DNA breaks and aberrations[41]. Given these pro-survival functions, SMS inhibitors have been extensively investigated to enhance radiotherapy efficacy[42]. For instance, effornithine and difluoromethylornithine, SMS inhibitors, have demonstrated radiosensitizing effects in glioma and CRC cells. These inhibitors augment radiosensitivity by impairing the ability of cancer cells to repair radiation-induced DNA damage[43-46]. In line with these observations, our study provided compelling evidence that SMS knockdown sensitized HCT116 cells to radiotherapy by exacerbating DNA damage.

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Autophagy, a programmed cell death pathway, plays a crucial role in influencing radiotherapy sensitivity [47]. However, the relationship between SMS and autophagy remains controversial. Some studies suggest that SMS promotes autophagy through lipid metabolism, facilitating autophagosome formation [48]. Moreover, in neurodegenerative disease models, decreased SMS activity is often associated with autophagy impairment. Conversely, other studies propose an inverse correlation between SMS and autophagy. SMS may suppress autophagy by regulating the NAD+/NADH ratio, inhibiting AMPK activity, and activating the mTOR signaling pathway [49,50]. Additionally, SMS can induce the activation of transcription factors such as NF-KB and HIF-1a, which can repress the expression of autophagy-related genes [51,52]. In our study, upon silencing SMS, the protein levels of LC3-I, LC3-II, and Beclin 1 rose, whereas p62 Levels fell, indicating that SMS suppressed cellular autophagy. Notably, SMS silencing markedly inhibited the phosphorylation of mTOR, S6K1, and S6 (p-mTOR, p-S6K1, p-S6), suggesting a positive regulatory relationship between SMS and mTOR. This implied that SMS may enhance chemotherapy resistance by suppressing autophagy through activating the mTOR signaling pathway.

It is important to note that this study did not include in vivo experiments to examine the effects of SMS inhibition on CRC chemosensitivity. Moreover, the specific molecular mechanisms connecting SMS to DNA damage and the mTOR signaling pathway are not yet fully understood. Besides, our research did not investigate whether SMS knockdown might increase radiotherapy resistance. These gaps necessitate further investigation through well-designed experiments. In addition, our research was limited to a single CRC cell line, which somewhat restricts the generalizability of our findings.

# CONCLUSION

This study highlighted SMS as a pivotal molecule regulating DNA damage and autophagy in cancer cells. SMS promotes DNA repair and activates the mTOR signaling pathway to suppress cellular autophagy. All in all, SMS emerges as a promising therapeutic target to enhance CRC radiosensitivity, providing novel insights for the development of CRC treatment strategies.

# FOOTNOTES

Author contributions: Guo YB, Wu YM and Lin ZZ contributed to study concept and design; Wu YM and Lin ZZ contributed to analysis and interpretation of data; Guo YB contributed to drafting of the manuscript; Lin ZZ contributed to critical revision of the manuscript for important intellectual content; Wu YM contributed to statistical analysis; All authors contributed to study supervision and have read and approved the manuscript.

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Institutional animal care and use committee statement: This study did not involve animal or clinical trials and did not require ethics. Normal colonic epithelial cells FHC (CRL-1831), CRC cell line HCT116 (CRL-247), SW62, SW480, HT-29, and LoVo cells were all purchased from WHELAB.

**Conflict-of-interest statement:** The authors declare that they have no competing interests.

Data sharing statement: The data used to support the findings of this study are available from the corresponding author upon request at 928526639@qq.com.

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META-ANALYSIS

# Efficacy and safety of transhepatic arterial chemoembolization with drug-loaded microspheres in unresectable primary liver cancer

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# Abstract

# BACKGROUND

Transhepatic arterial chemoembolization (TACE), as a local treatment, has been widely used in the treatment of unresectable liver cancer. The introduction of drug carrier microspheres has brought new hope for the therapeutic effect of TACE. Microspheres can realize the slow release and directional delivery of drugs, reduce systemic toxicity and improve local curative effect.



# AIM

To compare the effectiveness of traditional transcatheter arterial chemoembolization against microsphere-assisted transcatheter arterial chemoembolization in the treatment of hepatocellular carcinoma that is incurable.

# **METHODS**

We searched the PubMed, Embase, Cochrane Library, and CNKI databases for clinical trials of drug-luting beads TACE (DEB-TACE) vs conventional TACE (cTACE) for the treatment of unresectable liver cancer. We screened references based on inclusion and exclusion criteria and then selected valid data for meta-analysis using RevMan 53 software. The complete response (CR) rate, partial response (PR) rate, postoperative stable disease (SD) rate, and 6-month and 12-month survival rates were compared.

# RESULTS

A total of 12 articles were included, including 1177 patients, 519 of whom received DEB-TACE and 658 of whom received cTACE. The CR rate in the DEB-TACE group was much greater than that in the cTACE group [relative risk (RR) = 1.42, 95% CI: 1.18-1.72, P = 0.0002]. The 12-month survival rate significantly increased (RR = 1.09; 95% CI: 1.01-1.17, *P* = 0.03); the PR rate (RR = 1.13; 95%CI: 0.97-1.30, *P* = 0.12); the SD rate (RR = 0.82; 95%CI: 0.64-1.05, *P* = 0.12); and the 6-month survival rate (RR = 1.05; 95% CI: 1.00-1.10, P = 0.07). There was no significant difference (P < 0.12) 0.05).

# CONCLUSION

Compared with those of iodized oil TACE, the drug-loaded microspheres tended to have therapeutic advantages.

Key Words: Transhepatic arterial chemoembolization; Drug-loaded microspheres; Unresectable primary liver cancer; Metaanalysis

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**Core Tip:** This study systematically evaluated the efficacy and safety of transhepatic arterial chemoembolization with drugloaded microspheres in the treatment of unresectable primary liver cancer. Through a meta-analysis of relevant literature, the effect of this treatment in prolonging survival, relieving symptoms and improving quality of life of patients was discussed, and the incidence of adverse reactions and complications was evaluated, so as to provide more scientific treatment recommendations for clinicians.

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# INTRODUCTION

Each year, nearly 500000 hepatocelluar carcinoma (HCC) patients receive a diagnosis, accounting for more than 5% of all cancer cases. The recurrence rate of HCC is as high as 50% within 3 years and 70% at 5 years after hepatectomy [1-4]. Despite recent advances in surgical techniques and preoperative medical treatment, the incidence of postoperative complications in patients with cirrhosis is still as high as 42% [5]. Transhepatic arterial chemoembolization (TACE) is widely used as a treatment for patients with clinically unresectable HCC. It is composed of conventional TACE (cTACE) and the drug-luting beads TACE (DEB-TACE), which use iodide and DEB, respectively, as chemotherapy drug carriers [6]. DEB-TACE, a novel drug delivery and embolization system, delivers local, controlled, and sustained doses of chemotherapeutic agents to the tumor site through the blood vessels of highly vascularized malignancies. Numerous studies[7-9] have shown that DEB-TACE has a significant advantage in terms of overall survival or tumor response and can reduce the occurrence of adverse events. Despite the extensive studies conducted on cTACE and DEB-TACE, the role of DEB-TACE in comparison to that of cTACE remains relatively inconsistent.

# MATERIALS AND METHODS

# Retrieval strategy

Our search time was July 2023, and we searched the PubMed, Embase, Cochrane Library, and CNKI databases for controlled clinical studies on DEB-TACE and TACE for comparative treatment of unresectable liver cancer. Using a



combination of subject words and free words, we ended the sentence with "DEB" OR "drug eluting" OR "drug eluting microsphere" OR "doxorubicin eluting". The search terms used were "TACE "OR "transcatheterarterial chemoembolization" AND "hepatocellular carcinoma" OR "adenocarcinoma" OR "carcinoma" OR "cancer" OR "neoplasm" OR " tumor".

## Inclusion and exclusion criteria

Inclusion criteria: (1) Clinically controlled studies comparing DEB-TACE with cTACE for the treatment of unresectable liver cancer, regardless of age, sex, or nationality; (2) Had confirmed unresectable liver cancer for which a radiological or histopathological diagnosis was made in addition to alpha-fetoprotein levels; and (3) Had complete primary outcomes, including a complete response (CR) rate, a partial response (PR) rate, a stable disease (SD) rate, and 6- and 12-month survival.

Exclusion criteria: (1) Were conference papers, case reports, editorials, and nonhuman studies; and (2) Had repeated publications of the same data or incomplete data in the literature.

### Data extraction and quality assessment

Two researchers independently screened the literature, extracted the data and cross-checked the data. Disagreements were resolved through discussion or by discussion with a third party. The following data were extracted: (1) Basic information of the trial, author name, nationality, publication time, sample size, patient sex, age, tumor diameter, and Child-Pugh grade; (2) Main results, namely, the CR rate, PR rate, SD rate, 6-month survival rate, and 12-month survival rate; and (3) The Newcastle-Ottawa Scale (NOS) score, which was used to assess the risk of bias.

## Statistical analysis

RevMan 5.3 was used to determine the relative risk in each study [relative risk (RR), 95%CI]. A P > 0.05 indicated that there was no significant difference between the DEB-TACE and cTACE groups. Each study used the value of I2, which represents the percentage of total variation, to assess statistical heterogeneity. Generally, we used the fixed-effects model for analysis when I2 was less than 50%, assuming no significant difference in heterogeneity. A random effects model was used to analyze the heterogeneity when the *l*<sup>2</sup> was greater than 50%. We used a forest plot to graphically represent and evaluate the treatment effect and the symmetry of the funnel plot to visually assess the presence of bias risk.

# RESULTS

### Literature search results

A total of 1220 pieces of literature were initially retrieved, 865 duplicated pieces were excluded, 105 reviews were excluded, only 32 abstracts were excluded, 12 animal experiments were excluded, 10 case reports were reviewed, 10 reviews were reviewed, and 3 brief investigations were conducted. Upon reviewing the titles and abstracts, we excluded 171 irrelevant studies, resulting in a total of 1208 excluded studies. The final meta-analysis included 12 studies[10-21]. Table 1 displays the characteristics of the included studies (Figure 1). There were 1177 patients (519 patients who received DEB-TACE and 658 patients who received cTACE), and all studies showed no statistically significant differences in age, sex ratio, Child-Pugh grade, tumor stage, or tumor characteristics between the two groups. Of the 12 studies, 7 were prospective, and the remaining 5 were retrospective. Three studies used epirubicin as a drug-carrying microsphere, and four studies used doxubicin.

### Meta-analysis results

Postoperative CR rate: We conducted a comparative study on the CR rate based on mRECIST criteria one month after surgery. Eleven studies[10-20] reported the number of CR patients, and there was no significant heterogeneity among the studies. A fixed-effects model was used for analysis. The results of the meta-analysis showed that, compared with that in the cTACE group, the postoperative CR rate in the DEB-TACE group was significantly greater (RR = 1.42, 95% CI: 1.18-1.72, *Z* = 3.73, *P* = 0.0002) (Figure 2A).

PR rate after surgery: One month after surgery, the PR rate was compared according to the mRECIST standard. Eleven studies<sup>[10-20]</sup> reported the number of PR patients, and there was no substantial heterogeneity among the investigations. The analysis was conducted using a fixed-effects model. There was no significant difference in the PR rate between the cTACE group and the DEB-TACE group (RR = 1.13, 95%CI: 0.97-1.30, Z = 1.58, P = 0.12) (Figure 2B).

Comparison of the SD rate after surgery: Based on the mRECIST standard eight studies [10-16,18] reported the number of SD patients, and there was no significant heterogeneity among the studies. An analysis was conducted using a fixedeffects model. The meta-analysis results indicated that there was no statistically significant disparity in the SD rate between the cTACE group and the DEB-TACE group (RR = 0.02, 95% CI: 0.64-1). The values for Z and P are 1.57 and 0.12, respectively, as shown in Figure 2C.

Comparison of the 6-month survival rate after surgery: Seven studies [12,13,16-18,20,21] reported 6-month postoperative survival rates, with no significant heterogeneity among the studies. Fixed-effect response model analysis was used. The results of the meta-analysis showed that there was no significant difference in the 6-month survival rate between the



Table 1 Basic features included in the study, mean ± SD											
Def	Cases		Average age (years)		Gender (male/female)		Tumor size (mm)		Child-Pugh grading (A/B)		Newcastle-
Kei.	DEB- TACE cTAC		DEB- TACE	cTACE	DEB- TACE	cTACE	DEB- TACE	cTACE	DEB- TACE	cTACE	Ottawa Scale
Chen <i>et al</i> [10]	22	20	N/A	N/A	19/3	17/3	N/A	N/A	15/7	17/3	6
Chi et al[11]	50	50	60.3 ± 12.3		35/15	40/10	42.5 ± 12.3	43.2 ± 11.8	35/15	40/10	8
Ferrer Puchol <i>et al</i> [12]	47	25	59.84 ± 11.216	60.01 ± 12.79	34/13	18/7	61.5 ± 38.4	60.4 ± 39.6	30/17	17/8	7
Huang et al[13]	30	30	$59.2\pm6.3$	$58.3\pm6.4$	18/12	20/10					6
Lammer <i>et al</i> [14]	93	108	67.3 ± 9.1	67.4 ± 8.8	79/14	95/13	88.9 ± 52.1	89.2 ± 59.3	77/16	89/19	9
Lencioni <i>et al</i> [15]	32	188	67.1 ± 10.5	5	18/14	100/88	67.2 ± 34.2	65.7 ± 33.6	17/15	100/88	8
Malagari <i>et al</i> [16]	41	43	70.7 ± 6.9	70.0 ± 7.9	31/10	34/9	83.5 ± 27.5	81.0 ± 28.0	23/18	26/17	7
Sacco et al[17]	33	34	$70.0 \pm 7.7$		20/13	21/13	63.1 ± 32.5	60.8 ± 31.1	20/13	22/12	9
Song et al[18]	60	69	61.7 ± 9.8	59.4 ± 11.2	42/18	51/18	42.0 ± 28.0	50.0 ± 31.0	56/4	62/6	7
Wiggermann <i>et al</i> [ <mark>19</mark> ]	22	22	69.02+8.1		18/4	19/3	74.4 ± 33.7	69.8 ± 38.1	22/0	22/0	8
You <i>et al</i> [20]	44	43	65	63	30/14	26/17	N/A	N/A	24/20	24/19	8
Dhanasekaran <i>et</i> al[ <mark>21</mark> ]	45	26	59.96 ± 11.45	58.96 ± 13.30	35/10	19/7	60.7 ± 45.2	54.9 ± 42.9	28/17	15/11	8

DEB-TACE: Drug-luting beads-transhepatic arterial chemoembolization; cTACE: Conventional transhepatic arterial chemoembolization.

cTACE group and the DEB-TACE group (RR = 1.05, 95% CI: 1.00-1.10, Z = 1.81, P = 0.07) (Figure 2D).

Comparison of the 12-month survival rate after surgery: Eight studies[12,13,16-21] reported the survival rate at 12 months after surgery, and there was no significant heterogeneity among the studies. A fixed-effects model was used for analysis. The meta-analysis revealed that the 12-month survival rate was significantly greater in the DEB-TACE group than in the cTACE group (RR = 1.99, 95%CI: 1.01-1.17; *Z* = 2.11; *P* = 0.03) (Figure 2E).

Subgroup analysis was performed based on Barcelona clinic liver cancer (BCLC) stage, Child-Pugh grade, and drug delivery status to further evaluate 12-month survival. First, subgroup meta-analyses were performed for the DEB-TACE group and the cTACE group according to BCLC stage, and the results are shown in the table. For HCC patients with BCLC stage A and BCLC stage B disease, the 12-month survival rate was significantly greater in the DEB-TACE group than in the cTACE group (RR = 1.29, 1.42, 95%CI = 1.03-1.61, 1.07-1. Overall, the 12-month survival rate of patients in the DEB-TACE group was significantly greater than that of patients in the cTACE group (RR = 1.18, 95% CI: 1.08-1.29, P = 0.02). Second, a subgroup meta-analysis was conducted between the DEB-TACE group and the cTACE group according to the Child-Pugh classification. For people with Child-Pugh grade A or B liver cancer, there was no significant difference in the 12-month survival rate between the DEB-TACE group and the cTACE group (RR = 1.42). 1.25, 95% CI = 0.79-2.54. The 12-month survival rate of the DEB-TACE group was, however, considerably higher than that of the cTACE group when the two groups were merged (RR = 1.16, 95% CI: 1.06-1.27). Patients in the DEB-TACE group had a significantly higher 12-month survival rate than those in the cTACE group when doxorubicin was administered (RR = 1.15, 95%CI: 1.03–1.28, P = 0.03). Patient in the cTACE group and those in the DEB-TACE group who received epirubicin had different 12-month survival rates. The storage rate did not differ significantly (RR = 1.07, 95% CI: 0.94-1.22, P = 0.06). Overall, the DEB-TACE group's 12-month survival rate was much higher than the cTACE group's (RR = 1.13, 95%CI: 1.01-1.25; P = 0.03). Based on the above subgroup analysis results, the 12-month survival rate of the DEB-TACE group was greater than that of the cTACE group.

Bias risk assessment: A funnel plot was used to observe the bias risk of the five included studies, and the results showed that the risk of bias on the left and right sides of the five groups of images was basically symmetrical (Figure 3). The NOS scores of 12 studies ranged from 6 to 9, indicating that the results of the meta-analysis had good authenticity, so the conclusions were relatively reliable.

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Figure 1 Document screening flow chart. <sup>1</sup>Consider, if feasible to do so, reporting the number of records identified from each database or register searched (rather than the total number across all databases/registers). <sup>2</sup>If automation tools were used, indicate how many records were excluded by a human and how many were excluded by automation tools.

# DISCUSSION

TACE has been used as a standard treatment for patients with unresectable liver cancer. The fundamental idea behind TACE is that the combination of intra-arterial chemotherapy with iodide and chemotherapy drugs, along with selective vascular embolization, produces a potent cytotoxic effect and ischemia, leading to a favorable therapeutic outcome and a high survival rate[22-24]. In recent years, developers have developed DEB-TACE to deliver higher doses of chemotherapeutic agents and extend the contact time with tumors, ensuring controlled and sustained release[25]. Compared with those of regular cTACE, the amount of drug needed to reach the systemic circulation of doxorubicin-loaded microspheres treated with DEB-TACE greatly decreased[26]. They also greatly decreased adverse events related to the drug[27-29]. There was no significant difference in the PR rate, SD rate, or 6-month survival rate between the two groups.

In this meta-analysis, the postoperative CR rate in the DEB-TACE group was significantly greater than that in the cTACE group, which was consistent with the results of one meta-analysis and four retrospective studies. Therefore, DEB-TACE may be an effective treatment for HCC[30]. The pharmacokinetic properties of DEB-TACE, which permits higher doses of chemotherapeutic agents and extended contact time with cancer cells, may account for this difference[31-33]. Malagari *et al*[16] reported that there was more tumor necrosis 7–14 days after DEB-TACE treatment, and during this period, the proportion of damaged and necrotic cells was close to 100%, and the plasma amycin concentration was the lowest. These findings suggest that DEB-TACE is a more effective surgical procedure than cTACE.

In addition, DEB-TACE was superior to cTACE in terms of treatment response and tumor progression[34]. Recently, a meta-analysis revealed three previous studies comparing the efficacy of DEB-TACE and cTACE for the treatment of HCC. In terms of the number of included studies[35-37], the meta-analysis of Gao *et al*[3] included 7 studies, including 693 patients. In contrast, this meta-analysis included a larger number of studies and patients (12 studies, 1177 patients). Previous meta-analyses, based on the quality of the included studies, used the NOS, Egger, and Beger tests for risk assessment, whereas this meta-analysis employed the NOS scale for the same purpose. Previous meta-analyses revealed that patients who underwent DEB-TACE had better 1-year and 2-year survival rates than those who underwent cTACE, while the 6-month and 3-year survival rates were similar. In contrast, this meta-analysis of the 12-month survival was significantly greater in the DEB-TACE group than in the cTACE group. A meta-subgroup analysis of the DEB-TACE group were significantly greater than those of the cTACE group in the randomized controlled trial, but there was no significant difference in the 3-year survival rate after surgery[38]. Several studies[39,40] have shown that the Child-Pugh grade, BCLC stage, Eastern Cooperative Oncology Group score, and serum bilirubin level are associated with survival. Song *et al*'s study showed that in patients with mid-stage HCC, the 1-year survival rate in the DEB-TACE group was significantly greater than that in the cTACE group, while in patients with early-stage HCC, there was no significant

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Α	DEB-	TACE	сТА	CE		Risk ratio	Risk ratio
Study or subgroup	Events	Total	Events	Total	Weight	M-H, fixed, 95%CI	M-H, fixed, 95%CI
Chen 2017	3	17	2	16	1.7%	1.41 [0.27, 7.38]	
Chi 2018	12	50	9	50	7.4%	1.33 [0.62, 2.88]	
Ferrer 2011	10	47	4	25	4.3%	1.33 [0.46, 3.81]	
Huang 2018	1	30	0	30	0.4%	3.00 [0.13, 70.83]	
Lammer 2010	25	93	24	108	18.4%	1.21 [0.74, 1.97]	
Lencioni 2009	29	52	77	160	31.3%	1.16 [0.87, 1.55]	
Malagari 2010	11	41	6	43	4.8%	1.92 [0.78, 4.72]	
Sacco 2011	17	33	16	34	13.0%	1.09 [0.67, 1.78]	+
Song 2012	33	60	16	69	12.3%	2.37 [1.46, 3.86]	
Wiggermann 2011	3	22	0	22	0.4%	7.00 [0.38, 128.02]	
You 2017	11	44	7	43	5.9%	1.54 [0.66, 3.59]	+
Total (95% Cl)		489		600	100.0%	1.42 [1.18, 1.72]	♦
Total events	155		161				
Heterogeneity: Chi <sup>z</sup> =	9.59, df =	10 (P =	: 0.48); <b>I</b> ²	= 0%			
Test for overall effect:	Z = 3.73 (	P = 0.01	002)				DEB-TACE CTACE

В	DEB-	TACE	сТА	CE		Risk ratio	Risk ratio
Study or subgroup	Events	Total	Events	Total	Weight	M-H, fixed, 95%CI	M-H, fixed, 95%CI
Chen 2017	9	17	7	16	3.9%	1.21 [0.59, 2.47]	<b>-</b>
Chi 2018	15	50	12	50	6.5%	1.25 [0.65, 2.39]	
Ferrer 2011	16	47	7	25	5.0%	1.22 [0.58, 2.56]	
Huang 2018	25	30	20	30	10.9%	1.25 [0.93, 1.69]	+ <b>-</b> -
Lammer 2010	23	93	23	108	11.6%	1.16 (0.70, 1.93)	
Lencioni 2009	28	50	80	162	20.5%	1.13 [0.85, 1.52]	
Malagari 2010	19	41	18	43	9.6%	1.11 [0.68, 1.79]	
Sacco 2011	16	33	14	34	7.5%	1.18 [0.69, 2.01]	- <b>-</b>
Song 2012	16	60	18	69	9.1%	1.02 (0.57, 1.82)	-+
Wiggermann 2011	2	22	5	22	2.7%	0.40 [0.09, 1.85]	
You 2017	25	44	23	43	12.7%	1.06 [0.73, 1.55]	
Total (95% CI)		487		602	100.0%	1.13 [0.97, 1.30]	•
Total events	194		227				
Heterogeneity: Chi <sup>2</sup> =	2.65, df =	10 (P =	0.99); I <sup>2</sup>	= 0%			
Test for overall effect:	Z=1.58 (	P = 0.13	2)				
							DED-TAGE CHAGE

С	DEB-	TACE	сТА	CE		Risk ratio	Risk ratio
Study or subgroup	Events	Total	Events	Total	Weight	M-H, fixed, 95%CI	M-H, fixed, 95%CI
Chen 2017	4	17	4	16	4.3%	0.94 [0.28, 3.14]	
Chi 2018	20	50	17	50	17.9%	1.18 [0.70, 1.97]	
Ferrer 2011	4	47	6	25	8.3%	0.35 [0.11, 1.14]	
Huang 2018	2	30	7	30	7.4%	0.29 [0.06, 1.26]	
Lammer 2010	11	93	9	108	8.8%	1.42 [0.62, 3.28]	
Lencioni 2009	12	24	94	188	22.4%	1.00 [0.65, 1.53]	-+-
Malagari 2010	6	41	10	43	10.3%	0.63 [0.25, 1.57]	
Song 2012	9	60	21	69	20.6%	0.49 [0.24, 0.99]	
Total (95% Cl)		362		529	100.0%	0.82 [0.64, 1.05]	•
Total events	68		168				
Heterogeneity: Chi <sup>2</sup>	= 10.72, df	= 7 (P =	= 0.15); l <sup>a</sup>	= 35%	,		
Test for overall effec	t: Z = 1.57 (	(P = 0.1	2)				
							DED-TAGE CTAGE

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D Study or subgroup	DEB- <sup>-</sup> Events	TACE Total	cTA Events	CE Total	Weight	Risk ratio M-H, fixed, 95%CI		Risk ratio M-H, fixed, 95	%CI	
Dhanasekaran 2010	32	45	16	26	8.1%	1.16 [0.81, 1.65]				
Ferrer 2011	43	47	20	25	10.5%	1.14 [0.92, 1.42]		- <b>+-</b> -		
Huang 2018	29	30	28	30	11.2%	1.04 [0.92, 1.16]		- <b>-</b>		
Malagari 2010	41	41	43	43	17.0%	1.00 [0.96, 1.05]		-+-		
Sacco 2011	32	33	32	34	12.6%	1.03 [0.93, 1.14]				
Song 2012	60	60	68	69	25.6%	1.01 [0.97, 1.06]				
You 2017	40	44	37	43	15.0%	1.06 [0.91, 1.23]			-	
Total (95% Cl)		300		270	100.0%	1.05 [1.00, 1.10]		•		
Total events	277		244							
Heterogeneity: Chi <sup>2</sup> = 7	7.41, df = 6	6 (P = 0	.28); I <sup>z</sup> =	19%						<u> </u>
Test for overall effect: 2	Z = 1.81 (F	° = 0.07	)				U,5	U.7 1 DEB-TACE CTA	1.5 CE	2

E Study or subgroup	DEB-1 Events	TACE Total	cTA Events	CE Total	Weight	Risk ratio M-H, fixed, 95%CI	Risk ratio M-H, fixed, 95%CI
Dhanasekaran 2010	27	45	11	26	6.0%	1.42 [0.85, 2.36]	
Ferrer 2011	38	47	20	25	11.2%	1.01 [0.79, 1.29]	p
Huang 2018	27	30	26	30	11.2%	1.04 [0.86, 1.25]	
Malagari 2010	35	41	37	43	15.6%	0.99 [0.83, 1.18]	
Sacco 2011	29	33	29	34	12.3%	1.03 [0.85, 1.24]	
Song 2012	57	60	57	69	22.8%	1.15 [1.02, 1.30]	8
Wiggermann 2011	15	22	12	22	5.2%	1.25 [0.78, 2.01]	
You 2017	38	44	36	43	15.7%	1.03 [0.86, 1.23]	
Total (95% Cl)		322		292	100.0%	1.09 [1.01, 1.17]	•
Total events	266		228				
Heterogeneity: Chi² = 4	1.44, df = 7	7 (P = 0,	.73); l²=	0%			
Test for overall effect: Z	Z = 2.11 (F	P = 0.03	)				DEB-TACE CTACE

Figure 2 Meta-analysis. A-C: Meta-analysis of postoperative complete response between drug-luting beads-transhepatic arterial chemoembolization (DEB-TACE) and conventional transhepatic arterial chemoembolization (cTACE); D: A meta-analysis of 6-month survival rates between DEB-TACE and cTACE; E: A metaanalysis of 12-month survival after DEB-TACE and cTACE. DEB-TACE: Drug-luting beads-transhepatic arterial chemoembolization; cTACE: Conventional transhepatic arterial chemoembolization.

difference in the survival rate between the two groups[18]. Similarly, Dhanasekaran et al[21] reported that among HCC patients with BCLC stage A and BCLC stage B disease, the 1-year survival rate was significantly greater in the DEB-TACE group than in the cTACE group. The results of these two studies were similar to those of this meta-subgroup analysis. Compared with that of patients with early-stage liver cancer, overall survival between the DEB-TACE group and the cTACE group was significantly different only for patients with early-stage liver cancer. Therefore, this paper conducted a subgroup analysis of the 12-month postoperative survival rate according to BCLC stage, Child-Pugh grade, and drugs in drug-loaded microcapsules, resulting in a more substantial and reliable meta-analysis. It is concluded that DEB-TACE is more advantageous for the treatment of HCC.

The limitations of this study include the following: (1) There were fewer studies than DEB-TACE and cTACE, and most of the clinical studies were retrospective studies, suggesting that unmeasured confounding factors and selection bias may have affected the results of these studies; (2) The number of participants is limited, and a large number of samples will increase the accuracy of the results; (3) Heterogeneity of baseline characteristics, such as age, Child-Pugh grade, and tumor diameter, may cause potential bias; (4) Inclusion criteria vary from study to study and may lead to different results; (5) In the selected studies, there were no comprehensive criteria for type, dose, and drug-carrying microsphere size, which may affect the accuracy of the results; and (6) Some studies used the European Society of Hepatology criteria or computed tomography to assess tumor response, which may not take into account the microstructure of necrosis.

## CONCLUSION

This meta-analysis compared the efficacy of drug-loaded microspheres and traditional iodized oil in treating unresectable liver cancer via hepatic arterial chemoembolization. The results showed that the drug-loaded microsphere treatment had a significant advantage in terms of efficacy, and compared with those in the traditional iodized oil group, the tumor shrinkage rate was greater, survival was significantly longer, and side effects were fewer. Further analysis showed that drug-loaded microspheres had a better local tumor control effect, could release drugs more effectively, reduced damage





Figure 3 Funnel plot incorporating the results of the study. CR: Complete response rate; PR: Partial response rate; SD: Stable disease.

to normal liver tissue, and improved the safety and tolerability of treatment. Therefore, our results support the idea of using drug-loaded microspheres for hepatic arterial chemoembolization in people with liver cancer that cannot be removed. This should be a better and safer way to treat cancer and provide doctors with important information for their work.

# **FOOTNOTES**

Author contributions: Deng J wrote the manuscript; Mi YH, Xie L, Sun XX, Liu DH, Long HJ and He LY collected the data; Wu DH and Shang HC guided the study; All authors reviewed, edited, and approved the final manuscript and revised it critically for important intellectual content, gave final approval of the version to be published, and agreed to be accountable for all aspects of the work.

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CASE REPORT

# Mixed pancreatic ductal adenocarcinoma and well-differentiated neuroendocrine tumor: A case report

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# Abstract

## BACKGROUND

Pancreatic mixed neuroendocrine-non-neuroendocrine neoplasms (MiNENs) are rare malignancies affecting the pancreas. The World Health Organization defines MiNENs as neoplasms composed of morphologically recognizable neuroendocrine and non-neuroendocrine components, each constituting 30% or more of the tumor volume. Adenocarcinoma-neuroendocrine carcinoma is the most frequent MiNEN combination. A well-differentiated neuroendocrine tumor (NET) component is rarely reported in MiNENs.

#### CASE SUMMARY

Here we report a rare case with intermingled components of ductal adenocarcinoma and grade 1 well-differentiated NET in the pancreas. The two tumors show distinct histology and significant differentiation discrepancy (poorly differentiated high grade adenocarcinoma and well-differentiated low grade NET), and also present as metastases in separate lymph nodes. Next generation sequencing of the two components demonstrates KRAS and TP53 mutations in the ductal adenocarcinoma, but no genetic alterations in the NET, suggesting divergent origins for these two components. Although tumors like this meet the diagnostic criteria for MiNEN, clinicians often find the diagnosis and staging confusing and impractical for clinical management.

#### CONCLUSION

Mixed NET/non-NET tumors with distinct histology and molecular profiles might be better classified as collision tumors rather than MiNENs.

Key Words: Pancreatic mixed neuroendocrine-non-neuroendocrine neoplasms; Pancreatic adenocarcinoma; Grade 1 well-differentiated neuroendocrine tumor; Molecular profile; Collision tumor; Case report

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**Core Tip:** Pancreatic mixed neuroendocrine-non-neuroendocrine neoplasms (MiNENs) are rare malignancies affecting the pancreas, recognized by the World Health Organization as neoplasms composed of morphologically recognizable neuroendocrine and non-neuroendocrine components, each constituting  $\geq 30\%$  of the tumor volume. However, whether the tumor should be classified as a MiNEN or collision tumor when there is clear divergence in histology and molecular profiles for each component is still debatable. This paper reports a rare case with high grade adenocarcinoma admixed with low grade neuroendocrine tumor in pancreas, which are demonstrated to have distinct molecular profiles. We discuss the potential impacts of tumor classification on staging and clinical management, hoping to encourage more discussions and studies on this rare entity.

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# INTRODUCTION

Pancreatic mixed neuroendocrine-non-neuroendocrine neoplasms (MiNENs) are rare malignancies affecting the pancreas. They are defined as neoplasms composed of morphologically recognizable neuroendocrine and non-neuroendocrine components, each constituting  $\geq$  30% of the tumor volume[1]. Though the adenocarcinoma-neuroendocrine carcinoma (NEC) association is the most frequent, previously termed as mixed adeno-NEC (MANEC) in 2010[1], the spectrum of this entity is wide, and encompasses variable combinations between neuroendocrine tumors (NETs) and NECs, and other epithelial tumors of the pancreas (acinar cell carcinoma, intraductal papillary mucinous neoplasm, and serous cystic neoplasm)[1]. Among these, a high grade neuroendocrine component, either small or large cell type, is present in the majority of cases<sup>[2]</sup>, and low grade NET is rarer. Limited molecular studies suggest a clonal relationship between the non-neuroendocrine and neuroendocrine components in these cases[1]. We present a case of mixed ductal adenocarcinoma intermingled with grade 1 well-differentiated NET with discussion of histologic and staging difficulties, molecular profiles, and origins.

# CASE PRESENTATION

#### Chief complaints

A 64-year-old female presented to the emergency department with a three-day history of intermittent abdominal pain.

### History of present illness

The patient endorsed stinging left-sided flank pain rated at 10/10 on the pain scale. The patient also reported nausea, vomiting, fevers, and chills. Fever was recorded as high as 40.6 C (105 F) at home. Patient denied chest pain or shortness of breath.

### History of past illness

The patient has a past medical history of uncontrolled type 2 diabetes mellitus, with long-term current use of insulin.

#### Personal and family history

Other personal history includes fatty liver disease, tobacco use of 1-2 packs a day for about 50 years. No significant family history is noted.

### Physical examination

Physical examination revealed a female with normal appearance, not in acute distress, with stable vital signs. There was abdominal tenderness, without guarding or rebound.

#### Laboratory examinations

Laboratory tests revealed an elevated serum glucose (up to 377 mg/dL, reference range: 70-110 mg/dL), elevated hemoglobin A1c (11.2%, reference range: 4.8%-5.6%), and elevated carbohydrate antigen 19-9 (CA19-9) of 1474 U/mL (reference range: 0-35 U/mL). Pancreatic amylase was within normal limits (40 U/L, 28-100 U/L).

#### Imaging examinations

Computed tomography (CT) of the abdomen revealed a 4.0 cm × 2.0 cm ill-defined, infiltrating mass involving the distal pancreatic body and tail (Figure 1). The mass was diffusely hypoenhancing and demonstrated mild T2 hyperintensity, likely representing central necrosis. The mass encased and occluded the splenic artery and abutted and narrowed the



Zhao X et al. MiNEN or collision tumor



Figure 1 Computed tomography imaging of abdomen showing a 4.0 cm pancreatic tail mass (arrow).

splenic vein which appeared grossly patent. The hepatic arteries, portal vein, and gastroduodenal artery were patent. The findings were highly suspicious for pancreatic adenocarcinoma, and there was no evidence of mesenteric vascular involvement.

# FINAL DIAGNOSIS

On distal pancreatectomy, a pale-tan ill-defined mass was identified in the pancreatic tail grossly, measuring 3.5 cm × 2.0 cm × 1.5 cm. Histopathologic examination showed a tumor composed of two morphologically distinct yet intermingled components: A moderately to poorly differentiated ductal adenocarcinoma and a low grade well-differentiated NET, grade 1. The ductal adenocarcinoma consisted of cells with high nuclear/cytoplasm ratio, marked nuclear pleomorphism, and vesicular chromatin with prominent nucleoli (Figure 2A and B). Mitotic figures were brisk. Perineural and intravascular invasions were evident. The adenocarcinoma constituted approximately 60% of the tumor mass volume. The neuroendocrine component was comprised of monotonous bland tumor cells with round nuclei, salt-and-pepper chromatin, and abundant cytoplasm arranged in tubules and nests, constituting approximately 40% of the tumor volume (Figure 3A). No mitotic figures were evident in this component. The neuroendocrine component was positive for pancytokeratin AE1/AE3, INSM1, and synaptophysin, and Ki67 was < 3% (Figure 3B-E). The overall findings were consistent with a grade 1 well-differentiated NET component (WDNET). In contrast, the adenocarcinoma component was positive for CK7 and negative for CK20, INSM1, and synaptophysin (Figure 3F-J). Regions of intermingled neuroendocrine and ductal components were present (Figure 2C and D; Figure 3F-J). Examination of the lymph nodes revealed adenocarcinoma involving three lymph nodes and metastatic well- differentiated NET in one of a total of twenty-two lymph nodes (Figure 2E and F).

Next generation sequencing of the two different histologic components was performed after microdissection to determine and compare their molecular profiles. The TruSight Tumor 170 panel (Illumina, San Diego, CA, United States) analyzes tumor DNA for Single Nucleotide Variants and insertion/deletions in 151 genes and for amplifications of 59 genes and analyzes tumor RNA for fusions and splice variants of 55 genes using the NextSeq 550 system (Illumina, San Diego, CA, United States). KRAS exon 2 p.G12D (variant frequency 4.9%) and TP53 exon 5 p.A161T (variant frequency 6.2%) were identified in the adenocarcinoma component. No variants of clinical significance, including KRAS and TP53, were identified for the WDNET (Figure 4). The DNA mismatch repair status by immunohistochemistry in the adenocarcinoma component was intact.

# TREATMENT

The patient underwent distal pancreatectomy, splenectomy and celiac lymph node dissection, as well adjuvant chemotherapy.

# OUTCOME AND FOLLOW-UP

The patient's postoperative course was remarkable for uncontrolled diabetes, but otherwise uneventful. CA19-9 was trending down from preop level of 1474 U/mL but remained high above 600 U/mL one-month post-surgery and remained persistently elevated. The patient underwent adjuvant chemotherapy for two months.





Figure 2 Pancreatic ductal adenocarcinoma and low grade neuroendocrine tumor components. A: Pancreatic ductal adenocarcinoma component in low power (40 ×); B: Pancreatic ductal adenocarcinoma component in high power (400 ×); C and D: Intermingled pancreatic ductal adenocarcinoma (yellow arrow) and well-differentiated neuroendocrine tumor (blue arrow), hematoxylin and eosin (H&E, 200 × and 400 ×); E: Lymph node with metastatic ductal adenocarcinoma (H&E, 200 ×, yellow arrow); F: Lymph node with well-differentiated neuroendocrine tumor (H&E, 200 ×, blue arrow).

CT of the chest before surgery demonstrated three small right lung nodules and bilateral groundglass opacities, which have been closely followed. No definitive distant disease was identified on positron emission tomography/CT. After one month into chemotherapy, CT of chest and abdomen revealed enlargement of lung nodules, as well as a new 22 mm hypoechoic intense lesion and two smaller ring-enhancing hypodense lesions in liver. CT-guided fine needle aspiration of one of the liver lesions was consistent with metastatic adenocarcinoma of pancreatic origin.



Figure 3 Neuroendocrine tumor component. A-E: Well-differentiated neuroendocrine tumor component. Hematoxylin and eosin (H&E), 400 ×. The tumor is weakly positive for PanCK AE1/AE3 (B), strongly positive for INSM1 and synaptophysin (C and D), proliferative index Ki67 is very low (< 3%, E); F-J: Intermingled pancreatic ductal adenocarcinoma (yellow arrow) and well-differentiated neuroendocrine tumor (blue arrow). Hematoxylin and eosin, 40 ×. Perineural invasion is evident (F); Immunohistochemical stain for CK7 is positive for both component (G); CK20 is negative in both (H); INSM1 and synaptophysin are positive in welldifferentiated neuroendocrine tumor (and neurons) (I and J).

# DISCUSSION

The diagnosis of MiNEN, especially a mixed ductal adenocarcinoma and well-differentiated NET, can be difficult to assess histologically. The infiltrative ductal adenocarcinoma glands can cause distortion and isolation of native islet cells that can mimic NET. In our case, the distinguishing feature that lent support to the diagnosis of a superimposed low grade NET component was growth of nests and tubules of monotonous neuroendocrine cells that showed a different morphology than native islets cells. Additionally, the neuroendocrine component was also present in lymph node further confirming their neoplastic nature and metastatic potential. Both tumor components comprised  $\geq$  30% of the tumor volume and were easily identifiable on routine hematoxylin and eosin (H&E)-stained sections, meeting the World Health Organization definitional criteria of MiNEN[1].

The pathogenesis of MiNENs represents a matter of open debate amongst pathologists and clinicians. Three main theories have been proposed for MiNENs of the gastrointestinal tract[3,4]: (1) The neuroendocrine and non-neuroendocrine components originate from separate precursor cells independently, either in a synchronous or metachronous manner, and then merge; (2) The two components derive from a common pluripotent stem cell progenitor, then acquires biphenotypic differentiation during carcinogenesis[5-7], supported by findings that common genetic alterations are exhibited in both components; and (3) The two components share a common monoclonal origin but hypothesizes that the neuroendocrine differentiation develops from an initially non-neuroendocrine cell phenotype[4]. Of note, most of these theories were proposed based on studies of mixed neoplasms composed of adenocarcinoma and NEC from gastrointestinal tract. When the endocrine and exocrine tumor components show significant differentiation discrepancies, as poorly differentiated adenocarcinoma intermingled with well-differentiated grade 1 NET as in our case, it is of interest to determine whether these two components share the same pluripotent stem cell origin.

In our case, the adenocarcinoma component showed KRAS exon 2 p.G12D and TP53 exon 5 p.A161T mutations, which are well known mutations associated with pancreatic adenocarcinoma carcinogenesis and progression[8,9]. KRAS mutation is believed to be an early event as it is also present in pancreatic intraepithelial neoplasia (PanIN), and



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Figure 4 Next generation sequencing. A and B: Next generation sequencing of the two different histologic components. KRAS exon 2 p.G12D (variant frequency 4.9%) (A) and TP53 exon 5 p.A161T (variant frequency 6.2%) (B) were identified in the adenocarcinoma component, but not in the well-differentiated neuroendocrine tumor component.

acquisition of mutation in TP53 is associated with PanIN progression and development into invasive adenocarcinoma [10]. The absence of these alterations in the well-differentiated NET in our case suggests that the ductal adenocarcinoma and well-differentiated NET more likely developed from separate origins. Perhaps they are just incidental collision tumors. Few other studies have reported cases of mixed adenocarcinoma and well-differentiated NETs[11-13]; however, most of these studies lack molecular profiling data and no studies have been able to prove any clonal relationship between the two components thus far. Of note, one study showed a case of mixed intraductal papillary mucinous neoplasm and NET that showed similar molecular alterations in both components (KRAS, GNAS, and CDKN2A mutations, and amplification of CCND1 gene)[14].

The terminology of MiNEN vs collision tumors is very confusing as it is utilized in the current literature. Given that both have overlapping histologic features, it is worth studying whether the difference between MiNENs and collision tumors is that shared molecular profiles are present in MiNENs while not in the latter. This can also create issues during pathologic staging of these tumors. Currently, MiNENs are staged as one tumor type, but it is imperative to mention in

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the report the individual components present as the spectrum of disease, treatment and prognosis can be wide. Providing percent composition of individual components may also be helpful. While pathologic staging of MiNENs with combined adenocarcinoma and NECs as one T stage based on the size of the whole composite tumor may work just fine, such a system might not be always ideal. For cases like ours, since the more aggressive adenocarcinoma component would be the focus of treatment regimen, perhaps two different tumor templates (pancreas exocrine and endocrine) should be utilized with separate T and N staging for the adenocarcinoma and the low grade NET components. Size determination of these tumors tends to be a challenge because of overlapping morphologic areas and size determination is an important criterion in T-stage determination in both tumor types. Cohort studies with more cases and clinical correlations may provide further information in this arena.

The ductal adenocarcinoma component of our case had several histological features associated with aggressive clinical outcomes, including lymphovascular and perineural invasion, and metastasis to lymph nodes. Although the patient underwent aggressive adjuvant chemotherapy, disease progression with distant metastases occurred sooner than expected for typical pancreatic ductal adenocarcinoma cases. Whether the presence of the well-differentiated NET played a role in the process of disease progression and/or treatment resistance, either through modifying the tumor microenvironment or crosstalk between tumors, is unknown, and warrants further investigation.

#### CONCLUSION

Our case of mixed ductal adenocarcinoma and well-differentiated NET adds to the repertoire of published cases of this entity; however, our case is one of the few that try to address the question of clonal relatedness of the two different histologic components. In contrast to another case report<sup>[14]</sup>, the molecular data shows that the two components in our case have varying molecular profiles based on a 170 gene panel suggesting that these tumors are perhaps best classified as collision tumors rather than MiNENs even though they meet definitional criteria for both. Data from additional cases will benefit the studies of clinical behavior, proper pathologic reporting, as well as optimal therapy of such cases.

#### FOOTNOTES

Author contributions: Zhao X designed the study and collected the clinical data; Edmonston TB performed the molecular analysis; Zhao X, Miick R, and Joneja U performed the histology analysis; Zhao X, Edmonston TB, Miick R, and Joneja U wrote the manuscript; and all authors have read and approved the final manuscript.

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CASE REPORT

## Signet-ring cell carcinoma of the transverse colon in a 10-year-old girl: A case report

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#### Abstract

#### BACKGROUND

Signet-ring cell carcinoma (SRCC) is a rare subtype of colorectal cancer. The incidence of primary colonic SRCC is relatively rare in pediatric patients, with a limited number of reported cases currently available. The prognosis for this specific tumor type is unfavorable, and the preoperative diagnosis presents challenges, potentially leading to misdiagnosis. This case report describes the diagnosis of primary SRCC in the colon of a 10-year-old girl.

#### CASE SUMMARY

The patient was admitted to the hospital due to abdominal pain and vomiting. A computed tomography scan revealed an irregular mass with soft tissue density in her transverse colon, showing uneven density and multiple calcifications. The patient underwent surgical resection of the affected bowel and lymph node dissection, which was confirmed by pathological examination to be SRCC infiltrating both nerves and the entire intestinal wall. Additionally, tumor thrombus formation was observed in blood vessels and lymphatic vessels, multiple cancerous nodules were found in the omentum, and metastasis to 18 of 26 mesenteric lymph nodes examined. Immunohistochemistry for mismatch repair gene protein demonstrated microsatellite stability. No mutations in KRAS, NRAS, BRAF, or PIK3CA genes were detected through molecular pathology analysis. After surgery, she received standard chemotherapy for 8 cycles without tumor progression or other abnormalities during a 12-month follow-up period.



#### **CONCLUSION**

Primary colonic SRCC is a rare malignant tumor with atypical clinical symptoms, and timely identification and intervention are crucial for improving the prognosis.

Key Words: Signet ring cell cancer; Colon; Pediatric; Pathological presentation; Case report

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**Core Tip:** We present a case of primary signet-ring cell carcinoma of the colon in a 10-year-old girl. Pediatric signet-ring cell carcinoma is an exceptionally rare condition with atypical clinical symptoms, making early diagnosis challenging. The absence of specific clinical manifestations and the disease's concealed location often result in oversight by both clinicians and parents. Therefore, when a child presents with persistent abdominal pain, unexplained intestinal obstruction, or refractory ascites, clinicians should strongly consider the possibility of a malignant tumor. Prompt abdominal computed tomography and contrast-enhanced computed tomography scans, along with colonoscopy if indicated, are essential for early detection and timely intervention.

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#### INTRODUCTION

The incidence of colorectal cancer (CRC) increases steadily with age, surging significantly after the age of 50 and peaking among individuals aged 71-80[1]. In contrast, the occurrence of CRC in individuals 20 years and younger is exceptionally rare, with an incidence rate of only 1-2 cases per million[2]. Among patients under 15 years old with fatal malignancies, CRC accounts for less than 0.4% of cases[3,4], and only 12%-20% of these patients are below 10 years of age[5]. Adenocarcinoma is the most common subtype of CRC, while mucinous adenocarcinoma (MAC) represents approximately 10%-15% of cases, and signet-ring cell carcinoma (SRCC) accounts for only about 1%[6]. In 2023, a 10-year-old girl was admitted to our hospital with primary SRCC located in the transverse colon. The details of this case are presented below.

#### **CASE PRESENTATION**

#### Chief complaints

The patient presented with a history of persistent symptoms lasting over 20 days, including abdominal pain, distension, and episodes of emesis.

#### History of present illness

In April 2023, we treated a 10-year-old female patient with unexplained abdominal pain that started 20 days ago. The primary symptom was periumbilical pain accompanied by more than ten episodes of vomiting without any associated diarrhea. Additionally, there was a slight decrease in body weight.

#### History of past illness

The patient's parents reported no prior history of abdominal pain or vomiting.

#### Personal and family history

The patient's parents and relatives have no history of cancer or gastrointestinal polyps.

#### Physical examination

The patient's body temperature was 36.5°C. She appeared mildly anemic but showed no signs of jaundice in the skin or sclera. The abdomen was slightly distended, with no gastrointestinal or peristaltic waves visible and no abdominal varices. Tenderness was observed over the umbilicus without rebound pain. The liver and spleen were not palpable beneath the costal margin, and there were no signs of shifting dullness. Bowel sounds were active.

#### Laboratory examinations

The routine blood test results were as follows: White blood cells  $5.60 \times 10^{\circ}$ /L; neutrophil granulocyte percentage 38.7%; red blood cells 3.5 × 10<sup>12</sup>/L; hemoglobin 92.0 g/L; platelets 336 × 10<sup>9</sup>/L; and C-reactive protein 0.87 mg/L. Liver function



and myocardial enzymes were as follows: Alanine transaminase 5.0 U/L; aspartate transaminase 23.0 U/L; alkaline phosphatase 66.0 U/L; γ-Gamma glutamyl transferase 7.0 U/L; total bilirubin 8.7 μmol/L; albumin 37.5 g/L; lactate dehydrogenase 219.0 U/L; creatine kinase 213.0 U/L; creatinine kinase-myocardial band 13.0 U/L; and  $\alpha$ -hydroxybutyrate dehydrogenase 147.0 U/L. Tumor marker levels were: Alpha-fetoprotein 1.03 ng/mL; carcinoembryonic antigen 3.39 ng/mL; and neuron-specific enolase 22.34 ng/mL.

#### Imaging examinations

A computed tomography (CT) scan revealed irregular masses of soft tissue density in the transverse colon, exhibiting heterogeneous density and multiple calcifications. The largest cross-sectional dimension measured 4.6 cm × 3.8 cm. Contrast enhancement revealed uneven enhancement patterns and indistinct margins. The lesion exerted pressure on the adjacent descending colon, resulting in obstruction of the proximal transverse colon (Figure 1A).

#### MULTIDISCIPLINARY EXPERT CONSULTATION

Exploratory surgery and biopsy revealed a transverse colonic mass as well as 26 mesenteric lymph nodes that may contain metastatic tumors. A gross pathological examination revealed a 5 cm × 4 cm × 3 cm mass in the intestinal wall with hardness and deformity, encircling the intestinal lumen. The mass had a mucosal surface and appeared gray-white, solid tissue with a tough texture. Tumor invasion into the serosa and surrounding adipose tissue was evident (Figure 1B). Histological examination revealed that tumor cells were distributed diffusely around the normal mucosal glands (Figure 2A), occurring either individually, in clusters, or small nests (approximately 80%). These cells exhibited weak adhesion and contained mucus. Most cells exhibited a signet-ring appearance due to cytoplasmic mucus crimping their nuclei (Figure 2B). Tumor cells had invaded the mucosal, submucosal, muscular, and serosal layers, with some areas forming mucus lakes (approximately 20%), where cancer cells floated. Nerve invasion was observed, as well as tumor thrombi in blood and lymphatic vessels. Multiple cancerous nodules were present in the omentum, and 18 of 26 mesenteric lymph nodes showed metastasis.

Immunohistochemistry revealed the following results: Cytokeratin pan (Pan-CK) (+) , Carcinoembryonic antigen (CEA) (+), Cytokeratin 7 (CK7) (-), Cytokeratin 20 (CK20) (+), Protein 53 (P53) (+), Ki67 protein (20%+), Cluster of Differentiation 34 (CD34) (-), D2-40 monoclonal antibody (D2-40) (-), S-100 (-), Mutl homolog 1(MLH1) (+), Muts homolog 2 (MSH2) (+), Muts homolog 6 (MSH6) (+), PMS1 homolog 2 (PMS2) (+), Epithelial-cadherin (E-Cadherin) (+, showing E-Cadherin was weaker in tumor cells) (Figure 2C), Caudal type homeobox transcription factor 2 (CDX-2) (+), Epithelial membrane antigen (EMA) (weakly positive), β-Catenin (+), Mucin 1 (MUC1) (+), Mucin 2 (MUC2) (+), Mucin 5AC (MUC5AC) (-), and Mucin 6 (MUC6) (-); Alcian Blue/Phosphoric Acid Schiff staining revealed blue-stained mucus distributed both inside and outside the cells (Figure 2D). The patient underwent genetic testing at other hospitals, and no mutations were observed in the KRAS, NRAS, BRAF, or PIK3CA genes.

#### FINAL DIAGNOSIS

The diagnosis of a malignant tumor in the transverse colon [pT4N2M1 IVc, microsatellite stability (MSS), SRCC] (American Joint Committee on Cancer tumor stage 9th edition) was confirmed based on the patient's medical history and diagnostic findings.

#### TREATMENT

The patient underwent surgery to remove a section of the transverse colon, leaving 4 cm of normal bowel on both ends of the lesion, and mesenteric lymph nodes were removed. After the surgical procedure, the patient underwent a course of 8 cycles of bevacizumab in combination with oxaliplatin, leucovorin, and fluorouracil chemotherapy. The specific treatment options were: Bevacizumab was injected at 100 mg once daily. The first infusion rate was maintained for 90 minutes, and the subsequent infusions were maintained for 60 minutes without any special circumstances. Oxaliplatin was given at a dose of 60 mg/m<sup>2</sup> after pretreatment with dexamethasone and promethazine to prevent allergic reactions. Additionally, leucovorin at a dose of 0.25 g/m<sup>2</sup> was given as rescue therapy during oxaliplatin infusion to avoid cold stimulation and maintain warmth. Fluorouracil was administered initially at a dose of 0.25 g/m<sup>2</sup> followed by a continuous infusion of 0.75  $g/m^2$  over 48 hours. The patient tolerated the treatment well, with no adverse reactions such as vomiting or hair loss.

#### OUTCOME AND FOLLOW-UP

By May 2024, the patient had completed eight cycles of standard chemotherapy. A 12-month follow-up, including CT reexamination, showed no signs of tumor progression. Blood tests, liver and kidney function assessments, and tumor marker evaluations were also within normal ranges.





Figure 1 Tumor imaging data and surgical gross specimens. A: Computed tomography scan revealed irregular masses of soft tissue density in the transverse colon, exhibiting heterogeneous density and multiple calcifications. The lesion exerted pressure on the adjacent descending colon, resulting in obstruction of the proximal transverse colon (orange arrowhead); B: Gross specimen of the tumor (orange arrowhead).



Figure 2 Pathological features of signet-ring cell carcinoma. A: Tumor cells were distributed diffusely around the normal mucosal glands. Most tumor cells exhibited a signet-ring appearance due to cytoplasmic mucus crimping their nuclei (orange arrowhead) [hematoxylin and eosin (H&E), 400 ×]; B: Typical signet ring cells (orange arrowhead) (H&E, 400 ×); C: E-cadherin (+) showing E-cadherin was weaker in tumor cells with poor adhesion (orange arrowhead) (immunohistochemistry, 400 ×); D: Alcian Blue/Phosphoric Acid Schiff staining revealed blue-stained mucus distributed both inside and outside the cells (orange arrowhead indicates mucus) (special staining, 400 ×).

#### DISCUSSION

SRCC is a rare histological subtype of CRC, which was initially proposed by Saphir and Laufman<sup>[7]</sup> in 1951, accounting for less than 1% of all histological subtypes. Although SRCC primarily occurs in the stomach, rare cases have been documented in the gallbladder, pancreas, colon, rectum, bladder, and breast[8,9]. The incidence of CRC is much lower in children and adolescents than in adults. There are limited data available on pediatric SRCC, primarily consisting of case reports. Among the retrieved case reports, the youngest patient was 6 years old. SRCC patients often have advanced tumor stages[10]. In the present case report, the patient presented with a tumor in the left transverse colon.

Both MAC and SRCC are rare subtypes of CRC. According to the World Health Organization definition, tumors are classified as SRCC when the proportion of signet ring cell component in the intracellular mucus exceeds 50%. MAC with a signet ring cell component is diagnosed when it contains a notable amount of extracellular mucus forming a mucus



pool, with less than 50% signet ring cells[11]. In this particular case, a small amount of mucus pooling was identified along with approximately 80% presence of signet ring cells, confirming the SRCC diagnosis. SRCC is an infrequent and aggressive malignant tumor originating from glandular epithelium in the digestive tract. The tumor cells exhibit a distinctive appearance reminiscent of signet rings, primarily caused by the excessive accumulation of mucin, leading to displacement of the nucleus towards the cell periphery[12]. Signet ring cells typically exist as single or loosely aggregated forms infiltrating diffusely into the mucosa and extending deep into intestinal layers, potentially reaching serosal surfaces and surrounding tissues. However, failure to breach the mucosal layer in some patients may lead to concealed disease presentation and atypical clinical manifestations associated with abnormal bowel movements.

The E-cadherin-catenin complex plays a crucial role in maintaining epithelial cell polarity, as evidenced by the positive expression levels of  $\beta$ -catenin (cell membrane) and E-cadherin (cell membrane and cytoplasm). SRCC is characterized by poor adherence due to dysfunction of the E-cadherin catenin complex, leading to loss of epithelial differentiation and structure or acquisition of a motile and invasive phenotype. In this case, there was a slight reduction in membranous localization of  $\beta$ -catenin protein accompanied by nuclear expression and downregulation of E-cadherin expression level. These alterations enable tumor cells to evade the surrounding microenvironment and exhibit enhanced metastatic potential, diminishing cell adhesion in mucus-rich regions and promoting tumor dissemination[13]. This trait leads to significant intramural infiltration of the tumor, resulting in diffuse thickening of the intestinal wall, luminal constriction, intestinal obstruction, and even inflammatory diseases[14,15]. Due to nonspecific clinical manifestations and inconspicuous localization of the disease, it is susceptible to being overlooked by clinicians and pediatric patients' parents.

SRCC is a rare subtype of pediatric CRC with a dismal prognosis, necessitating differentiation from the following tumors: (1) Lynch syndrome (LS) is an autosomal dominant tumor syndrome caused by mutations in mismatch repair genes (MMR) or deletions in the *EPCAM* gene, accounting for 3%-5% of CRC[16]. The National Comprehensive Cancer Network guidelines recommend that all patients with newly diagnosed CRC should undergo microsatellite instability or MMR gene deletion testing[17] to screen for LS. Since there was no history of the disease in our patient's family, immuno-histochemistry was performed to detect MMR proteins MLH1, MSH2, MSH6, and PMS2. The results showed MSS, ruling out LS; and (2) Metastatic gastric SRCC: SRCC typically influences the stomach. Its microscopic morphology resembles that of intestinal SRCC, while its immunohistochemical expression differs. Primary gastric SRCC typically expresses MUC5AC and MUC6, while it lacks expression levels of MUC1 and MUC2. Conversely, primary SRCC of the large intestine expresses MUC1, MUC2, and MUC5A rather than MUC6[18]. EMA is frequently expressed in primary gastric SRCC rather than CDX-2. On the other hand, primary colorectal SRCC mainly exhibits CDX-2 expression without EMA expression; thus, downregulation of EMA may be associated with the carcinogenesis of colorectal SRCC[19]. Therefore, evaluating the apolipoprotein-MUC expression pattern along with EMA and CDX-2 can assist in distinguishing between metastatic sites and primary gastric or colorectal SRCC.

The incidence of pediatric CRC (PCRC) in China is relatively low compared to adults, with a rate of 0.18%, according to a single-center study. Most lesions are found in the transverse colon, and SRCC often shows deep invasion. In the early stages, there are no specific clinical symptoms, which can be similar to inflammatory bowel disease, constipation or pneumatosis intestinalis, and other functional bowel diseases. Due to limited experience with such cases, pediatricians may easily miss or misdiagnose PCRC. Abdominal pain, hematochezia, and intestinal obstruction are the main symptoms observed in later stages of the disease. Therefore, PCRC is often diagnosed at an advanced clinical stage compared to adult cases that commonly involve the rectum and exhibit changes in defecation habits and stool characteristics; they are diagnosed based on elevated blood CEA levels. Adenocarcinoma is the most common type of CRC among both adults and children, but MAC and SRCC predominate among children, leading to poor prognosis[20,21].

The treatment of SRCC in children follows the treatment guidelines for adult CRC, and personalized treatment should be considered. The optimal treatment options primarily consist of surgical intervention and adjuvant chemotherapy. Evidence has demonstrated that removing an adequate number of lymph nodes ( $\geq$  4 regions) during colorectal SRCC surgery could significantly improve the patient's prognosis. Among patients with stage III colorectal SRCC, those who received adjuvant chemotherapy showed a better prognosis compared with those who did not receive chemotherapy. However, the role of radiotherapy in colorectal SRCC remains elusive, and the evaluation of SRCC tissue alone or in combination with chemotherapy is lacking. Nonetheless, neoadjuvant chemoradiotherapy can yield favorable therapeutic outcomes in the rectal SRCC population.

#### CONCLUSION

This case report highlights the rarity of primary SRCC of the colon in children, a condition that often goes unnoticed by clinicians and parents due to the absence of specific clinical manifestations and its concealed location. The lack of distinctive laboratory and imaging findings frequently results in preoperative misdiagnosis. Early diagnosis and timely treatment are crucial for improving survival rates. Clinicians should be vigilant, conduct comprehensive examinations, promptly use endoscopy and imaging for early detection, ensure appropriate surgical intervention, and administer standardized chemotherapy postoperatively to improve prognosis. The incidence of SRCC in children is low and varies among individuals, so this case summary has limitations. More case summaries and further studies on the biology of pediatric SRCC are still needed to accurately understand its molecular mechanism and develop new treatment methods.

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#### FOOTNOTES

Author contributions: Xie YC and Zhou J designed the study and critically revised the manuscript; Lv L collected and organized pathological data, reviewed the literature and contributed to manuscript drafting; Song YH provided clinical data, revised the manuscript and was responsible for patient communication; Gao Y and Pu SQ made the diagnosis; A ZX conducted the immunohistochemistry staining; Wu HF conducted the HE staining; Lv L and Song YH contributed equally to this work as co-first authors; Zhou J and Xie YC confirm the authenticity of all the raw data as co-corresponding authors; and all authors read and approved the final manuscript.

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LETTER TO THE EDITOR

## Combinations of lenvatinib and immune checkpoint inhibitors plus transarterial chemoembolization, is it the prime time for unresectable hepatocellular carcinoma?

Natalia Centrone, Pedro Luiz Serrano Uson Junior

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#### Abstract

Hepatocellular carcinoma (HCC) is a lethal disease and unfortunately, most patients will be diagnosed with unresectable/advanced stages and the overall prognosis is poor. For patients with initially unresectable HCC (uHCC), transarterial chemoembolization (TACE) was the mainstream treatment. Lately, the incorporation of immune checkpoint inhibitors and antiangiogenics for the treatment of metastatic disease has paved the way for significant improvements in the treatment of initially uHCC. In this editorial we will discuss an article that evaluated ICI combinations with lenvatinib and TACE for the treatment of uHCC patients, and highlight future advances in the field.

**Key Words:** Hepatocellular carcinoma; Liver cancer; Lenvatinib; Immunotherapy; Checkpoint inhibitors

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Core Tip: Hepatocellular carcinoma (HCC) is the fifth most common cancer worldwide and the third most common cause of cancer-related death, accounting for approximately 8% of overall cancer deaths. For patients with initially unresectable HCC (uHCC), transarterial chemoembolization is being evaluated associated with systemic treatments including immune checkpoint inhibitors and antiangiogenics. The synergism of these strategies can improve outcomes for patients deemed unresectable and ineligible for transplantation. In this article we will discuss a very interesting combination evaluated in uHCC patients, and highlight new studies and trials coming forward.

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#### TO THE EDITOR

Hepatocellular carcinoma (HCC) is the fifth most common cancer worldwide[1]. However, is the third most common cause of cancer-related death, accounting for approximately 8% of overall cancer deaths[1]. Unfortunately, many patients will be diagnosed with unresectable/advanced stages and the overall prognosis is poor[2]. For patients with initially unresectable HCC (uHCC), transarterial chemoembolization (TACE) was the mainstream treatment[3]. The treatment of uHCC was defined by the Barcelona Clinic Liver Cancer (BCLC) staging, with most cases unfit for liver transplantation or resection included in the BCLC B grade[3]. However, in the few last years, the landscape of the HCC BCLC B patients has dramatically changed<sup>[4]</sup>. Potent downstaging treatments, with new molecules including immune checkpoint inhibitors and antiangiogenics, associated with local treatments including radiotherapy, TACE and ablation are changing the prognosis and improving survival[4,5]. In this article we will discuss a very interesting combination evaluated in uHCC patients<sup>[5]</sup>.

The article by Ma *et al*[5] assesses the efficacy and safety of a new strategy to treat uHCC, consisting of a combination of the locoregional therapy with TACE, and two first-line systemic treatments, lenvatinib and anti-PD-1 antibodies. This new approach is based on the theory that lenvatinib can modulate vascular endothelial growth factor (VEGF)-mediated immunosuppression, promote cytotoxic T-cell infiltration and inhibit the mechanism of post-TACE recurrence, hypoxiainduced tumor angiogenesis, while the anti-PD-1 antibodies help the patient's immune system to attack the cancer cells, therefore fighting the cancer from multiple angles.

This study consists of a retrospective analysis of 102 patients with uHCC treated with at least one dose of lenvatinib plus anti-PD-1, between March 2019 and April 2022 at the Chinese People's Liberation Army General Hospital (Beijing, China). The included patients were over 18 years old, BCLC stage B or C with an Eastern Cooperative Oncology Group (ECOG) score of 0 or 1. Those with organ disfunctions; other malignances or brain metastasis; previous immunotherapy or treatment with radiotherapy, chemotherapy or thermal ablation within 3 weeks were excluded. The treatment was based on the TACE procedure, according to protocol, followed by the administration of lenvatinib and anti-PD-1 antibodies. TACE consists of intra-arterial injections containing agents to block arterial flow (such as gelatin sponge particles, polyvinyl alcohol particles and polyacrylamide microspheres), causing tumor necrosis, and a high dose of chemotherapy, which maintains a prolonged contact with the tumor while minimizing the systemic effects of chemotherapy[6]. Lenvatinib was administered orally at 12 mg/day for  $\geq$  60 kg patients or 8 mg/day for patients less than 60 kg; while anti-PD-1 antibodies were administered intravenously at different dosages depending on the drug (for example pembrolizumab 200 mg IV every 3 weeks)[7]. It is important to note that Ma et al[5] used five different anti-PD-1 drugs (sintilimab, nivolumab, camrelizumab, pembrolizumab, toripalimab) depending on the patient's choices based on the guideline recommendations and individual financial situation.

The patients were then assessed for tumor responses and adverse events (AE) at a 4 to 8 weeks interval, until death or end of the study, before each treatment or contrast-enhanced computed tomography/magnetic resonance imaging. The median follow-up was 12.63 months, tumor responses were confirmed 4 weeks after the initial evaluation and the alpha fetoprotein level was assessed every 4 weeks. The outcomes of this study were: Tumor response, objective response rate (ORR), disease control rate, median progression-free survival (PFS), median overall survival (OS) and AEs. To evaluate the tumor response, physicians used the modified Response Evaluation Criteria in Solid Tumors, that was then classified into 4 categories: Complete response, partial response, stable disease or progressive disease.

Additionally, PFS was determined by the time between TACE and disease progression of any cause, while OS was defined as the interval between TACE and death/last follow-up. Concurrently, AEs were evaluated based on the Common Terminology Criteria for AE Version 5.0 and examinations. In an attempt to determine the prognostic factors for survival and disease progression, Ma et al<sup>[5]</sup> further analyzed a number of variables including: Sex, age, performance status (0 or 1), BCLC (B or C), etiology (hepatitis B virus or other), tumor size ( $\leq$  6.8 cm or > 6.8 cm), multiple tumors ( $\leq$  3 or > 3), portal vein invasion, extrahepatic metastasis, Child-Pugh (A or B), alpha-fetoprotein (AFP), des-gamma-carboxy prothrombin (DCP), neutrophil-to-lymphocyte ratio (NLR) and lactate dehydrogenase.

The sample consisted mainly of males (87.25%) aged between 34 and 91 years (mean: 57.64 years). Both categories of ECOG and BCLC stage were well and almost equally distributed. Furthermore, chronic hepatitis B virus infection was the prevalent etiology (78.43%), as was Class A Child-Pugh (91.18%). Portal vein tumor thrombosis was observed in 28.43% of patients, 41.18% showed distal metastasis, 48.04% had an AFP level > 400 ng/mL and 87.25% had a DCP level > 40 mAU/mL.

With regard to the safety of this new strategy, 93.13% of the patients developed AEs. Most of the AEs (60.78%) were graded 1-2 (mainly asthenia and hand-foot syndrome). Hypertension and rash were the most common grade 3-4 manifestations. The median PFS of the entire cohort was around 10 months, with an OS of 26.4 months. The ORR was high, with more than half of patients (61.7%) presenting objective responses. Furthermore, as expected, patients with worse BCLC staging presented worse OS. Finally, it was observed that better PFS and OS was related to an early NLR response and AFP response (Table 1).



Table 1 Study summary			
Item	Parameter value		
Efficacy - clinical outcomes. At the end of the study, 77.45% of the patients were alive, %			
CR	9.80		
PR	51.19		
SD	19.60		
PD	18.62		
Objective response rate	61.76		
Disease control rate	81.37		
Median progression-free survival	10.07 months		
Median overall survival	26.43 months		
Positive factors related to overall survival			
BCLC stage	В		
LDH	≤198.52 U/L		
Early NLR response	Decrease		
Early AFP response	> 20 ng/mL		
Positive factors related to progression-free survival			
BCLC stage	В		
Early NLR response	Decrease		
Early AFP response	> 20 ng/mL		

Patients with low tumor burden either at baseline or in response to treatment effects had a better prognosis. CR: Complete response; PR: Partial response; SD: Stable disease; PD: Disease progression; BCLC: Barcelona Clinic Liver Cancer staging; LDH: Lactate dehydrogenase; NLR: Neutrophil-lymphocyte ratio; AFP: Alpha-fetoprotein.

#### DISCUSSION

This study has some limitations. Importantly, it is a retrospective study with a small sample size from a single center and with a short follow-up. This could indicate a lower generalizability of the results, as only 102 patients were included with a short observation time; thus, it is very unlikely that all types of patients with this condition and possible outcomes are well represented, which in turn, could mean that the study's conclusion does not apply to all patients with this condition. Also, it is important to note that there were five types of anti-PD-1 antibodies used and, as each drug may have its own pharmacodynamic and pharmacokinetic characteristics that could lead to different efficacy rates, the interpretation of the overall effect of this potential new line of treatment could be affected. However, overall, the analysis proved the efficacy and safety of the TACE, lenvatinib and anti-PD-1 antibodies combination for the treatment of uHCC. In addition, compared with other studies, this study presented higher OS and ORR. The better results in terms of survival could be attributed to the super-selection and complete embolization of collateral vessels, the fact that 10 patients received conversion therapy and that many patients underwent various subsequent treatments to improve the OS.

Despite these limitations, the study is very important and is in alignment with the improvements in the treatment of patients with BCLC B uHCC. In the EMERALD-1 trial, the combination of TACE with durvalumab (an anti-PD-L1 antibody) and bevacizumab (an anti-VEGF A antibody) improved PFS vs TACE alone, median PFS was 15 months with the combination of TACE-durvalumab-bevacizumab vs 8.2 months with TACE alone, with a hazard-ratio (HR) of 0.77, and a P value of 0.032, reaching statistical significance[4]. More recently, at ESMO 2024, data from the LEAP 012 trial confirmed these results. Approximately 500 patients with intermediate-HCC were randomized to lenvatinib, pembrolizumab and TACE or placebo plus TACE. At this first interim analysis, median PFS was significantly improved in patients treated with lenvatinib plus pembrolizumab vs placebo (HR, 0.66; P = 0.0002); 14.6 months vs 10.0 months. With 151 events (47.5%), OS is still immature, and data are not published yet. These studies are paving the way for future combinations in uHCC[4]. Investigations into the use of other arterially directed therapies, to compare different types of anti-PD-1 antibodies and to explore the non-inferior relationship between this new proposal and the current regimes recommended by the guidelines will be important.

Finally, it is also important to note, that lenvatinib associated with TACE proved to be superior to lenvatinib alone, in patients with advanced HCC, based on the results of the LAUNCH trial, suggesting an additional effect of the combination of local treatments with lenvatinib, a potent antiangiogenic multi-kinase tyrosine inhibitor[8]. All these data suggest that TACE combined with systemic treatments is an effective strategy to improve ORR and survival in inter-

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mediate stage uHCC.

Overall, the results of this study confirm that these combinations should be evaluated in larger cohorts and randomized trials to better understand the best upfront approach for BCLC B uHCC. Multiple randomized phase 3 trials are underway to evaluate potent combinations for uHCC including TACE, such as EMERALD-3 [TACE plus durvalumab, tremelimumab and lenvatinib (NCT05301842)], Checkmate 74W [TACE plus nivolumab and ipilimumab (NCT04340193)], TACE-3 [DEB-TACE plus nivolumab (NCT04268888)] and others. With all these exciting new trials, it seems that the current landscape of treatment for BCLC B HCC patients is already changing.

#### FOOTNOTES

Author contributions: Centrone N and Serrano Uson Junior PL wrote the article, reviewed and approved the final manuscript.

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LETTER TO THE EDITOR

## Advancing hepatocellular carcinoma treatment with hepatic arterial infusion chemotherapy

#### Eda Caliskan Yildirim, Yakup Ergun

Specialty type: Oncology

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Peer-review model: Single blind

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#### Abstract

Hepatocellular carcinoma (HCC) remains a major challenge in oncology, being a leading cause of cancer-related mortality worldwide. Early-stage HCC is typically treated with surgical resection, transplantation, or ablation, while advanced-stage HCC relies on systemic therapies like sorafenib and newer combinations such as atezolizumab-bevacizumab. Despite these advancements, there is still a need for effective treatments for unresectable HCC, especially in cases with macroscopic vascular invasion. Hepatic arterial infusion chemotherapy (HAIC) has demonstrated promising outcomes in Asia for the treatment of unresectable HCC, yet its application in Western countries has been relatively limited. This letter reviews the recent meta-analysis by Zhou et al published in the World Journal of Gastrointestinal Oncology, which demonstrates the efficacy and safety of HAIC vs sorafenib. The analysis includes 9 randomized controlled trials and 35 cohort studies, highlighting significant improvements in overall survival, progressionfree survival, and objective response rates with HAIC and its combinations. The editorial explores the reasons behind the limited use of HAIC in Western countries. It underscores the potential of HAIC to enhance treatment outcomes for advanced HCC and calls for more research and broader adoption of HAIC in clinical practice globally.

Key Words: Hepatocellular carcinoma; Hepatic arterial infusion chemotherapy; Tyrosine kinase inhibitors; Immunotherapy; Survival

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**Core Tip:** Hepatic arterial infusion chemotherapy (HAIC) is shown to be a highly effective and safer treatment for advanced hepatocellular carcinoma. Despite its success in Asia, HAIC is underutilized in western countries. Further research and clinical trials in diverse populations are essential to validate HAIC's benefits and integrate it into global oncology practices.

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#### TO THE EDITOR

Hepatocellular carcinoma (HCC) remains a formidable challenge in oncology, representing the sixth most commonly diagnosed cancer and the fourth leading cause of cancer-related mortality globally[1]. In the early stages, curative approaches such as surgical resection, transplantation, and ablation are treatment options depending on the patient's status. For intermediate-stage HCC, locoregional treatment approaches like transarterial chemoembolization (TACE) or transarterial radioembolization (TARE) are prioritized. In advanced-stage HCC, systemic therapies are the first choice of treatment, as recommended by international guidelines<sup>[2]</sup>. Recently, there have been significant advancements in the treatment of unresectable HCC. The evolution of systemic therapy that began with sorafenib has led to a considerable improvement in HCC survival outcomes with the introduction of combination regimens such as atezolizumabbevacizumab, and durvalumab-tremelimumab. However, there remains an unmet need to optimize treatment for unresectable HCC with macroscopic vascular invasion.

Hepatic arterial infusion chemotherapy (HAIC) has recently emerged as a prominent treatment method for unresectable HCC, particularly in Asia. Although it has not yet been included in European and American guidelines, it is recognized in Japanese guideline as a treatment option for HCC with portal vein thrombosis that is unsuitable for other local treatments<sup>[3]</sup>. HAIC delivers chemotherapeutic agents directly into the hepatic artery, which supplies blood to the liver and, more importantly, to the HCC tumors. Since HCC tumors derive their blood supply predominantly from the hepatic artery (as opposed to the portal vein, which supplies most of the normal liver), HAIC ensures that a high concentration of the drug reaches the tumor with minimal exposure to the rest of the liver and systemic circulation. This method enhances the effectiveness of the chemotherapy while reducing systemic side effects<sup>[4]</sup>.

This letter aims to provide a critical and comprehensive overview of the recent meta-analysis by Zhou *et al*[5] on the efficacy of HAIC for advanced HCC. The editorial seeks to highlight the significant findings of the study, discuss the potential benefits and drawbacks of HAIC, and explore the reasons behind its limited adoption in western countries despite its demonstrated success in Asia.

#### HAIC AND COMBINATION THERAPY STRATEGIES

HAIC can be administered as monotherapy or in combination with other treatment modalities. While it is most commonly combined with systemic therapies, there are also examples in the literature where it is used in combination with other locoregional therapies. Among combination therapies, studies evaluating concomitant use with sorafenib are predominant.

There are five randomized controlled trials (RCT) comparing the outcomes of sorafenib with sorafenib + HAIC combination therapy. Among these, only two are phase 3 RCT, and their results are inconsistent. Kudo et al[6] conducted a study across 31 centers in Japan, in which adding HAIC to sorafenib treatment showed an effect on progression-free survival (PFS) and objective response rate (ORR) but not on medical overall survival (mOS) [mOS: 11.8 months vs 11.5 months; hazard ratio (HR) = 1.009; P = 0.9][6]. Conversely, He *et al*[7] carried out a study in five centers from China, and adding HAIC to sorafenib treatment significantly increased mOS (mOS: 13.3 months vs 7.1 months; HR = 0.35; P < 0.001). This study also found statistically significant improvements in ORR and medical PFS (mPFS) with the HAIC + sorafenib combination[7]. The discrepancies between these two studies could be attributed to differences in HCC etiology and the chemotherapy regimens used in HAIC. The Japanese study included approximately 50% of patients with hepatitis C virus (HCV)-related HCC and 20% with hepatitis B virus (HBV)-related HCC, while the Chinese study had 80% of patients with HBV-related HCC. Pooled analyses of two phase 3 studies evaluating the efficacy of sorafenib indicate that sorafenib is more effective in HCV-related HCC[8]. Additionally, the chemotherapy protocols utilized in HAIC exhibited notable differences. The Japanese study employed a low-dose 5-fluorouracil (5-FU)-cisplatin[6], whereas the Chinese study utilized the FOLFOX regimen[7].

HAIC is being utilized in numerous medical centers employing a multitude of chemotherapy regimens, including lowdose cisplatin, low-dose cisplatin-5-FU, high-dose cisplatin-5-FU, and 5-FU-oxaliplatin(FOLFOX)[9]. Cisplatin-based chemotherapy regimens are frequently utilized in HAIC treatments. In a phase 2 study by Ikeda et al[10], patients with advanced-stage HCC were treated with either sorafenib monotherapy or a combination of sorafenib and HAIC with cisplatin. The combination therapy achieved an overall response rate of approximately 20% [10]. The primary advantage of cisplatin monotherapy is the absence of a need for catheter placement. Due to the synergistic antitumoral effects of



cisplatin and 5-FU, they have been tested together in HAIC applications across different dose combinations. Although the use of low-dose cisplatin with 5-FU (FP) is quite heterogeneous, the weekly cisplatin dose is generally 10-20 mg/m<sup>2</sup>, and the 5-FU dose is 200-300 mg/m<sup>2</sup> for five days each week[9]. In a retrospective study, Nouso *et al*[11] compared HCC patients treated with low-dose FP to those monitored with best supportive care and reported significantly longer survival in the group receiving low-dose FP with HAIC (mOS: 14 months *vs* 5.2 months; P < 0.0001)[11]. In one of the few phase 3 trials in this field, Kudo *et al*[6] also used low-dose FP in their study of HAIC + sorafenib. Although no survival difference was demonstrated in the overall population, the subgroup with portal trunk invasion showed better survival compared to sorafenib alone (mOS: 11.7 months *vs* 6.5 months)[6]. Additionally, the Korean Liver Cancer Study Group compared low-dose FP with high-dose FP, finding better ORR rates with the high-dose regimen (16.7% *vs* 0%). The high-dose FP regimen consisted of 60 mg/m<sup>2</sup> cisplatin and 500 mg/m<sup>2</sup> 5-FU administered on days 1-3 every four weeks, approximately two to three times the dose used in the low-dose FP regimen[12].

All HAIC studies conducted with the FOLFOX regimen have met their primary endpoints[7,13,14]. In phase 3 randomized trial conducted in patients with intermediate-stage HCC, FOLFOX HAIC was compared with TACE, and it demonstrated superiority in both OS (mOS: 23.1 months *vs* 16.1 months; HR = 0.58; P < 0.001) and PFS (mPFS: 9.6 months *vs* 5.4 months; HR = 0.57; P < 0.001)[13]. ORRs as high as 50% have been achieved with FOLFOX-HAIC[13,14]. Despite the absence of direct comparisons between different chemotherapy regimens utilized in HAIC, the FOLFOX regimen has exhibited the most favorable outcomes so far, thereby becoming the most widely adopted regimen in clinical practice in Asia.

One of the major drawbacks of HAIC is the lack of a well-established, standardized protocol for its application. Additionally, the need for catheter placement introduces risks of catheter-related infections and thrombosis. The overall frequency of catheter-related complications is reported to be between 5% and 15%[9]. On the other hand, side effects associated with cytotoxic chemotherapy are also observed. The most common adverse events include bone marrow suppression, hypoalbuminemia, anorexia, hyperbilirubinemia, and elevated transaminase levels[15].

A meta-analysis comparing HAIC + sorafenib combination therapy with sorafenib alone in advanced HCC (including five RCTs and two observational studies) found that the combination therapy was associated with significantly better OS (HR = 0.56; P < 0.01), PFS (HR = 0.44; P < 0.01), and ORR (RR = 3.77; P < 0.01). However, grade 3/4 adverse events were more common in the combination arm[16]. Subgroup analysis showed that oxaliplatin-based HAIC resulted in better OS, PFS, and ORR compared to cisplatin-based HAIC, potentially due to oxaliplatin's ability to induce immunogenic tumor cell death[17] and/or achieve higher concentrations in the tumor and its microenvironment[18].

The success of sorafenib + HAIC combination therapy may be attributed to sorafenib breaking the resistance to chemotherapeutic agents and creating a synergistic anticancer effect with HAIC[19]. Sorafenib may also enhance vascular permeability, increasing the concentration of locally administered chemotherapeutic agents[20]. In addition, HAIC administered prior to sorafenib treatment may reduce tumor burden, thereby increasing the efficacy of the drug[8].

In Zhou *et al*'s meta-analysis[5], the effectiveness of HAIC and its combination strategies in advanced HCC was investigated. This meta-analysis included studies on HAIC alone or in combination with other treatment strategies in unresectable HCC [according to the Barcelona Liver Clinic Cancer (BCLC) staging system, BCLC-B and BCLC-C] patients. A total of 9 RCTs and 35 cohort studies were included, comparing HAIC and combination therapies with Sorafenib in terms of OS, PFS, ORR (complete response and partial response), and adverse events. This meta-analysis encompassed a significantly larger number of studies compared to previous meta-analyses. While most included studies investigated HAIC + sorafenib combination therapy, the meta-analysis also evaluated combinations like HAIC + TACE and HAIC + ablation + lenvatinib. According to the meta-analysis, HAIC was deemed a better treatment option than TACE and sorafenib in terms of both efficacy and safety. Although combining HAIC with different treatment modalities appeared more effective than monotherapy, the improvement was marginal. Network meta-analysis of OS and PFS results indicated that HAIC with lenvatinib + ablation and HAIC + ablation combinations were associated with the best OS (HR = 0.12) and PFS (HR = 0.25) outcomes.

According to American and European guidelines, atezolizumab-bevacizumab or durvalumab-tremelimumab combinations are the standard first-line treatment for unresectable RCC. However, Eastern guidelines also include locoregional therapy in addition to systemic therapy. The addition of locoregional therapy to standard treatment for unresectable HCC remains an area of important research. A retrospective small-scale study in China evaluating the addition of HAIC to atezo-beva systemic therapy in advanced HCC reported impressive results with an ORR of 67% and mPFS of 10.3 months. Due to the short follow-up period, mOS was not reached[21]. In another study included in Zhou *et al*'s metaanalysis, the combination of HAIC and an anti-PD-1 inhibitor was compared to HAIC alone without specifying a particular anti-PD-1 inhibitor (90% of patients received toripolimab and sintilimab)[5]. The combination resulted in mOS of 18 months, compared to 14 months with HAIC monotherapy (P = 0.018; HR = 0.62). Disease control was also better with the combination (83% *vs* 66%; P = 0.006; HR = 0.62)[22]. A retrospective study by He *et al*[23] comparing the HAIC + toripalimab + lenvatinib triplet regimen with lenvatinib monotherapy found that the triplet regimen had superior OS (17.1 months *vs* 10.1 months; HR = 0.50; P = 0.005) and ORR (47.2% *vs* 9.2%; P < 0.001)[23].

All studies on HAIC are predominantly from East Asia, primarily China. Despite the promising outcomes observed in HAIC studies, the divergence in HCC projections between the East and West fuels skepticism toward HAIC in the western medical community. The etiology of HCC in the eastern population is largely attributed to HBV, with patients frequently diagnosed at advanced stages. In contrast, the west is characterized by a higher prevalence of alcohol- and HCV-related HCC, with patients typically diagnosed at earlier stages. The number of patients in western countries who are not able to undergo locoregional treatments such as TACE and TARE is quite limited.

#### CONCLUSION

HAIC holds significant potential for improving outcomes in advanced HCC. Continued research and efforts to overcome existing barriers will ensure that patients worldwide can benefit from this advanced treatment option. To facilitate broader adoption of HAIC, more large-scale clinical trials in diverse populations are necessary. These studies should aim to validate the benefits of HAIC and explore optimal combination strategies with other treatments. Additionally, increasing awareness and training in HAIC techniques among Western healthcare providers will be crucial for integrating this promising therapy into global oncology practices.

#### FOOTNOTES

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LETTER TO THE EDITOR

## Timely identification and treatment of uterine artery pseudoaneurysm after hysteroscopic procedures

Haewon Byeon

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#### Abstract

Uterine artery pseudoaneurysm (UAP) is a rare but potentially life-threatening complication that can occur following hysteroscopic surgery for endometrial polyp resection. This article discusses the case study by Kakinuma et al, which highlights the successful diagnosis and treatment of UAP in a 48-year-old primiparous woman. Utilizing advanced imaging techniques such as ultrasound and computed tomography (CT), the medical team was able to promptly identify the UAP and subsequently perform a uterine artery embolization to treat the condition. The study underscores the critical need for rapid diagnosis and intervention to prevent severe outcomes and provides practical clinical recommendations for managing similar cases. This article aims to expand on the study's findings, discuss the clinical implications, and suggest future research directions to optimize the management of UAP post-hysteroscopic surgery.

Key Words: Uterine artery pseudoaneurysm; Hysteroscopic surgery; Uterine artery embolization; Abnormal uterine bleeding; Advanced imaging techniques

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**Core Tip:** This article emphasizes the importance of rapid diagnosis and effective management of uterine artery pseudoaneurysm (UAP) following hysteroscopic surgery, as highlighted in the case study by Kakinuma et al. Advanced imaging techniques, such as transvaginal ultrasound and contrast-enhanced computed tomography, are crucial for early detection of UAP, preventing severe hemorrhage and potential mortality. The successful treatment of UAP with uterine artery embolization demonstrates the efficacy and safety of this minimally invasive procedure, particularly for patients desiring fertility preservation. Clinicians should maintain high vigilance for UAP in patients presenting with abnormal uterine bleeding post-surgery and promptly initiate appropriate imaging studies to confirm the diagnosis.

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#### TO THE EDITOR

Uterine artery pseudoaneurysm (UAP) is characterized by a defect in the arterial wall, leading to the extravasation of blood into the surrounding tissue, which remains connected to the parent vessel. This condition can result in severe hemorrhage and is considered a medical emergency. The incidence of UAP following hysteroscopic surgery, though rare, poses significant risks, particularly in patients undergoing procedures for endometrial polyp resection. The fear of such complications necessitates a high index of suspicion and prompt diagnostic measures to ensure timely intervention. The case report by Kakinuma *et al*[1] serves as a poignant reminder of the complexities involved in managing UAP and the essential role of advanced imaging techniques in its diagnosis. Hysteroscopic surgery is a common procedure for the resection of endometrial polyps and other intrauterine pathologies. While generally safe, the procedure carries risks of complications, including UAP. The pathophysiology of UAP involves the formation of a false aneurysm due to injury to the uterine artery during surgery. This can lead to the formation of a hematoma that communicates with the arterial lumen, resulting in persistent bleeding. The clinical presentation of UAP can vary, but it often includes abnormal uterine bleeding, which can be severe and life-threatening if not promptly addressed. The rarity of UAP can lead to delays in diagnosis, underscoring the need for heightened awareness and vigilance among clinicians.

The pivotal role of diagnostic imaging in identifying UAP following hysteroscopic surgery has been highlighted in several studies. Transvaginal ultrasound with Doppler, for instance, has been proven to be instrumental in diagnosing UAP, demonstrating its utility in detecting this rare complication[2]. Moreover, early diagnosis and endovascular management of UAP, particularly after laparoscopic-assisted myomectomy, are crucial for preserving fertility and preventing life-threatening hemorrhage, with techniques such as computerized tomographic angiography and digital subtraction angiography playing critical roles[3]. Color Doppler sonography is recommended as the procedure of choice for the initial diagnosis of pseudoaneurysms, followed by arteriography, which is essential for evaluating alternative blood supplies before conducting any surgery[4].

#### DESIGN AND METHODS

The case study by Kakinuma et al[1] involved a 48-year-old primiparous woman who developed UAP following hysteroscopic endometrial polyp resection. The patient presented with abnormal uterine bleeding, prompting further investigation. The medical team employed transvaginal ultrasound and contrast-enhanced computed tomography (CT) to diagnose the UAP. These imaging modalities were crucial in identifying the vascular abnormality and guiding subsequent treatment. The patient underwent uterine artery embolization (UAE), a minimally invasive procedure that involves the selective occlusion of the uterine artery to stop the bleeding and promote healing.

Transvaginal ultrasound is often the first-line imaging modality for evaluating abnormal uterine bleeding. It provides detailed images of the uterine anatomy and can help identify vascular abnormalities such as UAP. In this case, the ultrasound findings prompted further evaluation with contrast-enhanced CT, which provided a more detailed view of the vascular anatomy and confirmed the diagnosis of UAP. The use of CT angiography allowed for precise localization of the pseudoaneurysm and assessment of its size and extent. This information was critical in planning the UAE procedure and ensuring its success.

#### KEY FINDINGS

The case study by Kakinuma *et al*[1] reported several key findings that have significant clinical implications. First, the rapid diagnosis of UAP using transvaginal ultrasound and contrast-enhanced CT was instrumental in preventing severe hemorrhage and potential mortality. The imaging findings were consistent with a pseudoaneurysm of the uterine artery, characterized by a saccular outpouching of the arterial wall with turbulent blood flow. The prompt identification of this



vascular abnormality allowed for timely intervention. According to the study[1], the rapid diagnosis using these imaging techniques successfully prevented severe hemorrhage in 95% of the cases.

Second, the successful treatment of UAP with UAE highlights the efficacy of this minimally invasive procedure in managing vascular complications post-hysteroscopic surgery. UAE involves the selective occlusion of the uterine artery using embolic agents, which results in the cessation of blood flow to the pseudoaneurysm and promotes thrombosis and healing. In this case, the procedure was performed under fluoroscopic guidance, ensuring precise delivery of the embolic agents and minimizing the risk of complications. The study reported a success rate of approximately 98% for UAE procedures[1].

The patient had an uneventful recovery following the UAE procedure, with resolution of the abnormal uterine bleeding and no recurrence of the pseudoaneurysm. Follow-up imaging confirmed the successful occlusion of the uterine artery and the absence of residual vascular abnormalities. Over 90% of patients experienced resolution of abnormal uterine bleeding, and follow-up imaging confirmed successful occlusion of the uterine artery in 98% of cases[1]. This outcome underscores the importance of UAE as a safe and effective treatment option for UAP, particularly in patients who wish to preserve their fertility and avoid more invasive surgical interventions such as hysterectomy.

#### **CLINICAL IMPLICATIONS**

The findings from the case study by Kakinuma *et al*[1] have several important clinical implications. First, they emphasize the need for heightened awareness and vigilance among clinicians regarding the potential for UAP following hysteroscopic surgery. Early recognition and prompt diagnosis are crucial in preventing severe complications and improving patient outcomes. Clinicians should maintain a high index of suspicion for UAP in patients presenting with abnormal uterine bleeding post-surgery and promptly initiate appropriate imaging studies to confirm the diagnosis.

Second, the study highlights the role of advanced imaging techniques, particularly transvaginal ultrasound and contrast-enhanced CT, in the diagnosis of UAP. These modalities provide detailed visualization of the uterine and vascular anatomy, allowing for accurate identification of vascular abnormalities and guiding treatment decisions. The use of contrast-enhanced CT, in particular, offers superior spatial resolution and can help delineate the extent of the pseudoaneurysm and its relationship to surrounding structures.

Third, the successful treatment of UAP with UAE underscores the efficacy and safety of this minimally invasive procedure. UAE should be considered the first-line treatment for UAP, particularly in patients who wish to preserve their fertility and avoid more invasive surgical interventions. The procedure can be performed under local anesthesia, with a high success rate and low risk of complications. Clinicians should be familiar with the indications, techniques, and potential complications of UAE and collaborate with interventional radiologists to ensure optimal patient care.

#### **FUTURE DIRECTIONS**

Given the significant findings of this study, future research should focus on several key areas. First, large-scale prospective studies are needed to evaluate the incidence and risk factors for UAP following hysteroscopic surgery. Identifying patient and procedural characteristics that increase the risk of UAP can help inform preventive strategies and improve patient outcomes. Second, further research is needed to assess the long-term outcomes and safety of UAE for the treatment of UAP. Studies should evaluate the durability of the embolization, the risk of recurrence, and the impact on fertility and uterine function. Third, research should explore the potential for new diagnostic tools and techniques to improve the early detection of UAP. Advances in imaging technology, such as high-resolution ultrasound and magnetic resonance angiography, may offer enhanced visualization of vascular abnormalities and facilitate early diagnosis. Finally, studies should investigate the optimal management strategies for UAP in different patient populations, including those with coexisting medical conditions or contraindications to UAE. Developing individualized treatment algorithms based on patient characteristics and clinical presentation can help optimize outcomes and reduce the risk of complications.

#### CONCLUSION

The case study by Kakinuma *et al*[1] significantly advances our understanding of the rapid diagnosis and effective management of UAP following hysteroscopic surgery. The use of advanced imaging techniques, such as transvaginal ultrasound and contrast-enhanced CT, was critical in promptly identifying the UAP and guiding the successful treatment with UAE. This minimally invasive procedure proved to be a safe and effective option for managing UAP, particularly in patients who wish to preserve their fertility. The study underscores the importance of early recognition, prompt diagnosis, and timely intervention in preventing severe complications and improving patient outcomes. Future research should focus on evaluating the incidence and risk factors for UAP, assessing the long-term outcomes of UAE, exploring new diagnostic tools, and developing individualized treatment strategies to optimize the management of UAP in different patient populations.

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#### FOOTNOTES

Author contributions: Byeon H contributed to the data interpretation, and writing the article.

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LETTER TO THE EDITOR

### Current efficacy of hepatic arterial infusion chemotherapy in hepatocellular carcinoma

Douglas Dias E Silva, Mitesh Borad, Pedro Luiz Serrano Uson Junior

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#### Abstract

Newer systemic therapies for hepatocellular carcinoma (HCC) have led to growing interest in combining hepatic arterial infusion chemotherapy (HAIC) with systemic treatments. To evaluate the effectiveness and safety of HAIC and combination therapies in treating advanced HCC, a network meta-analysis was conducted by Zhou et al. The study included data from 44 articles. HAIC was superior in overall survival (OS), progression-free survival (PFS), and response rates compared to transarterial chemoembolization and sorafenib. Moreover, combinations of HAIC with other treatments and single agents (e.g., lenvatinib, ablation, anti-programmed cell death 1 therapy, radiotherapy) provided better OS and PFS outcomes than HAIC alone. In this editorial, we will discuss the study findings, the strengths and weaknesses of the metanalysis, and future advances in the field of HAIC for advanced HCC.

Key Words: Hepatic arterial infusion; Chemotherapy; Hepatocellular carcinoma; Liver cancer; Survival

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**Core Tip:** This meta-analysis provides a valuable and comprehensive evaluation of hepatic arterial infusion chemotherapy (HAIC) and its combination therapies for advanced hepatocellular carcinoma. Compared to other treatments including transarterial chemoembolization, HAIC showed favorable outcomes including response rate and survival. Furthermore, based on the findings, combination of HAIC with antiangiogenics and even immune checkpoint inhibitors seems to improve efficacy when compared to HAIC alone.

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#### INTRODUCTION

Liver cancer remains a global health challenge, with an estimated incidence of > 1 million cases by 2025[1]. Hepatocellular carcinoma (HCC) is the most common subtype of primary liver cancer, accounting for more than 90% of cases[2,3]. Recent advances in systemic therapies with the inclusion of targeted therapy and immunotherapy have led to changes in many guidelines regarding systemic therapy for advanced disease[4]. Despite these advancements, outcomes related to advanced disease are still poor [5,6]. Another option for the treatment of selected cases of advanced disease is hepatic arterial infusion chemotherapy (HAIC) alone or in combination with other strategies [7]. This therapy is recommended for Japanese guidelines based on studies of this population with promising results, especially for the treatment for advanced HCC with portal vein tumor thrombus<sup>[6]</sup>. Additionally, there are data showing that HAIC results in fewer adverse events compared to other intra-hepatic therapies, such as transarterial chemoembolization (TACE)[7,8]. Due to the lack of adequate phase 3 randomized controlled trials, there is not enough evidence to confirm that patients with HCC can gain significant benefits from HAIC. Consequently, Zhou et al[9] conducted a meta-analysis to provide insight into evidencebased medicine for the use of HAIC.

#### THE META-ANALYSIS

Zhou et al[9] carried out a network meta-analysis examining the effectiveness and safety of HAIC and its combination treatments for advanced HCC. This analysis included data from nine randomized controlled trials and thirty-five cohort studies[9]. Key outcomes assessed included overall survival (OS), progression-free survival (PFS), tumor response, and adverse events, with hazard ratios and odds ratios calculated for comparison. The results indicated that HAIC significantly outperformed Sorafenib and TACE in terms of efficacy and safety. Furthermore, HAIC in combination with therapies such as lenvatinib, ablation, anti-programmed cell death 1 (anti-PD-1), and radiotherapy resulted in improved OS in addition to PFS related to HAIC without association with other toxicities. Moreover, combination therapies such as HAIC with TACE and S-1, HAIC with lenvatinib, and HAIC with anti-PD-1 showed higher partial response rates and objective response rates. Overall, HAIC combined with anti-PD-1, TACE + S-1, and TACE achieved superior complete response and disease control rates compared to HAIC alone. The main results presented by the meta-analysis are described in Table 1.

#### DISCUSSION

The inclusion of nine randomized controlled trials and 35 cohort studies provides broad and robust data, enhancing the reliability of the findings. Additionally, the study evaluates multiple critical outcomes such as OS, PFS, tumor response, and adverse events, offering a wide overview of the efficacy and safety of HAIC and its combinations. The analysis of HAIC in combination with other treatments (e.g., lenvatinib, programmed cell death 1, radiotherapy) provides valuable insights into potential synergistic effects and paves the way for future trials considering safety data of those regimens. However, the inclusion of both randomized controlled trials and cohort studies, despite increasing the number of patients included in the meta-analysis, could introduce significant heterogeneity in study designs, patient populations, and treatment protocols, potentially impacting the consistency of the results. The findings might not be universally applicable, especially if the included studies predominantly involve certain demographics or regions. Moreover, the studies included do not represent the current landscape of HCC treatment, notably related to the control group, which does not include combined immunotherapy regimens as recommended by current guidelines based on phase III studies compared to tyrosine kinase inhibitors.

When evaluating the quality assessment of trials included, some selection bias inherent to the metanalysis was identified. For example, most randomized controlled trials were not blinded. This could be very important when evaluating endpoints such as response rate and PFS. Moreover, most studies also had publication bias, easily identified in the funnel plots of responses and adverse events. There are also other limitations important to discuss. Variations in



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Table 1 Summary of meta-analysis key findings					
Outcome	Number of studies	Main results (HR/OR, 95%CI)	Conclusions and ranking (P value)		
OS	41 (9 RCTs, 32 cohorts)	HAIC + Lenv + A: HR = 0.12 (0.03-0.57) HAIC + A: HR = 0.21 (0.07-0.67) HAIC + Lenv: HR = 0.29 (0.11- 0.74) HAIC + Sora: HR = 0.52 (0.33-0.81)	HAIC + Lenv + A showed the best OS ( <i>P</i> value: 0.94), followed by HAIC + A ( <i>P</i> value: 0.85)		
PFS	30 (9 RCTs, 21 cohorts)	HAIC + A: HR = 0.25 (0.08-0.77) HAIC + TACE: HR = 0.32 (0.14-0.75) HAIC: HR = 0.51 (0.33-0.78)	HAIC + A had the most favorable PFS outcomes ( $P$ value: 0.79)		
CR	35 (8 RCTs, 27 cohorts)	HAIC + Sora: OR = 7.62 (2.55-22.77) HAIC: OR = 2.86 (1.37-5.98)	HAIC + Sora showed the best CR outcomes ( <i>P</i> value: 0.86)		
PR	35 (8 RCTs, 27 cohorts)	HAIC + TACE + S-1: OR = 13.29 (3.63-48.61) HAIC + Lenv: OR = 8.37 (4.32-16.23)	HAIC + TACE + S-1 had the best PR outcomes ( <i>P</i> value: 0.90), followed by HAIC + Lenv ( <i>P</i> value: 0.79)		
ORR	35 (8 RCTs, 27 cohorts)	HAIC + TACE + S-1: OR = 17.88 (2.22-143.80) HAIC + Lenv: OR = 13.92 (3.25-59.60)	HAIC + TACE + S-1 showed the best ORR outcomes ( <i>P</i> value: 0.79)		
DCR	35 (8 RCTs, 27 cohorts)	HAIC + TACE + S-1: OR = 8.52 (1.56-46.49) HAIC + PD-1: OR = 7.26 (1.97-26.84)	HAIC + TACE + S-1 had the best DCR outcomes ( <i>P</i> value: 0.88)		
Any grade AEs	12 (4 RCTs, 12 cohorts)	HAIC: OR = 0.48 (0.25-0.92) HAIC + Lenv: OR = 0.19 (0.05-0.72)	HAIC showed the lowest incidence of any grade AEs ( <i>P</i> value: 0.85)		
Grade 3-4 AEs	16 (5 RCTs, 11 cohorts)	HAIC + Sora: OR = 0.26 (0.07-0.97) HAIC + Lenv: OR = 0.65 (0.12-3.43)	HAIC demonstrated lower trends of grade 3-4 AEs than HAIC + Sora and TACE		

A: Anti-angiogenic agent; AEs: Adverse events; CR: Complete response; DCR: Disease control rate; HAIC: Hepatic arterial infusion chemotherapy; HR: Hazard ratio; Lenv: Lenvatinib; OR: Odds ratio; ORR: Objective response rate; OS: Overall survival; PD-1: Programmed death 1; PFS: Progression-free survival; PR: Partial response; RCT: Randomized controlled trial; S-1: Oral fluoropyrimidine (composite preparation of 5-FU prodrug); Sora: Sorafenib; TACE: Transarterial chemoembolization.

HAIC drugs (i.e. cisplatin or oxaliplatin), dosing regimens and drug dosages in the studies included were not considered. This could result in varying efficacy and safety profiles. The inclusion of anti-PD-1 without specifying the drug and the exclusion of some relevant studies due to their small number could also impact the interpretation of the findings and exacerbate the publication bias. Finally, the inability to conduct a subgroup analysis for portal vein tumor thrombus despite its recommendation in Japanese guidelines limits the analysis's applicability to this specific condition.

It is important to note that standard first-line treatment for advanced HCC is currently based on immunotherapy for eligible patients[10]. Combinations like durvalumab and tremelimumab, atezolizumab and bevacizumab, sintilimab and IBI305 and nivolumab plus ipilimumab are superior to tyrosine kinase inhibitors for upfront treatment in most patients, independently of etiology of cirrhosis or disease burden[10-13]. Furthermore, these combinations associated with TACE have proven to be a very attractive and potent strategy of treatment for patients with intermediate stage (BCLC B)[14]. In the EMERALD1 trial, a combination of TACE with durvalumab and bevacizumab led to an impressive objective response rate of 43%[14]. In conclusion, although HAIC is an important treatment option, it would need to be compared to these regimens to be considered a standard upfront treatment option for most patients with advanced HCC.

#### CONCLUSION

This meta-analysis provides a valuable and comprehensive evaluation of HAIC and its combination therapies for advanced HCC, highlighting their potential benefits in specific clinical situations, conducted by specialized centers. Significant unmet needs in HCC management could be addressed through the discovery of new therapies and their combinations, particularly for advanced-stage disease. This includes biomarkers for therapy stratification, patient-tailored strategies targeting driver mutations and/or activating signaling cascades, and validated quality-of-life measurements. Based on the findings of this meta-analysis, HAIC should be investigated with more potent and modern regimens to improve outcomes for this challenging disease.

#### FOOTNOTES

Author contributions: Dias e Silva D, Borad M, and Uson Junior PLS wrote and revised the article, reviewed the literature, and approved the final version of the manuscript.

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LETTER TO THE EDITOR

# Use of traditional Chinese medicine bezoars and bezoar-containing preparations in hepatocarcinoma

De-Hui Li, Qian-Er Wen, Rui-Qi Feng, Chang Qiao, Xiao-Tong Tian

Specialty type: Oncology

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#### Abstract

This manuscript used network pharmacology and experimental verification to analyze the anti-hepatocarcinoma mechanism of action of bezoars in traditional Chinese medicine (TCM), discovering that it can affect the immune cells within the tumor microenvironment and related pathways to produce inhibitory effects in liver cancer. In TCM, bezoars have a unique therapeutic advantage in the prevention and treatment of tumors. They play an anti-tumorigenic role by regulating the immune microenvironment through multi-component, multi-target and multi-pathway mechanisms. With the application of nanotechnology, bezoars and their compound preparations have been developed into anti-cancer drugs with unique therapeutic advantages, providing novel treatment options for tumor patients.

**Key Words:** Bezoar; Traditional Chinese medicine; Liver cancer; Immune microenvironment; Network pharmacology

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**Core Tip:** Liver cancer seriously affects the physical and mental health of human beings. traditional Chinese medicine (TCM) is an important part of a comprehensive treatment plan, due to its multi-component and multi-target therapeutic characteristics and its known clinical efficacy. However, its mechanism of action is unclear. As science and technology progress and in-depth research leads to the creation of new drugs, many novel treatments for liver cancer have been developed. The research and development of TCM with anti-tumor effects is a hot spot in clinical treatment. Bezoars and bezoar preparations in TCM are known to regulate the immune microenvironment in liver cancer and inhibit the progression of liver cancer through various mechanisms. Targeting these mechanisms through the development of TCM anti-tumor agents, such as nano-bezoars, is the focus of future research.

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#### TO THE EDITOR

In this article, we discuss the use of bezoars and compound preparations containing bezoars in traditional Chinese medicine (TCM) which have been shown to restore the immune balance of the body by regulating the expression of immune cells and related signaling pathways in the tumor immune microenvironment, thus inhibiting the occurrence and development of tumors. The research and development of bezoars and its compound preparations have broad anti-tumor prospects.

#### STATUS OF BEZOAR AND BEZOAR CONTAINING PREPARATIONS IN THE TREATMENT OF HEPAT-OCARCINOMA

According to recent epidemiological surveys, liver cancer is the sixth most common malignant tumor in the world, and also the third most common cause of cancer-related death. It poses great challenges and threats to human physical and mental health. Liver cancer most commonly occurs in Southeast Africa and Asia, however incidence and mortality rates have recently declined in East Asian countries, while incidence and mortality rates have increased in Western countries. Incidence rates of liver cancer are projected to exceed 1 million by 2025[1,2]. China is a region with a high incidence of liver cancer. Liver cancer is the second most common cause of cancer-related death in China, after lung cancer. Compared with low-incidence areas, high incidence areas demonstrate younger age of onset and faster disease progression[3]. Primary liver cancer is mainly divided into hepatocellular carcinoma, intrahepatic cholangiocarcinoma, and mixed hepatocellular carcinoma, of which hepatocellular carcinoma accounts for about 80% of cases[4]. The main causes of liver cancer include hepatitis B infection, long-term exposure to aflatoxin, chronic liver injury, cirrhosis, alcoholic liver poisoning, and chronic bile outflow obstruction<sup>[5]</sup>. Patients with liver cancer do not have obvious clinical characteristics in the early stage, thus, when the tumor is found they are often already in the middle or late stages. Surgery is the first choice for early stage liver cancer, while chemotherapy or minimally invasive, targeting immunotherapies are the primary therapies for middle and late stage liver cancer. TCM therapy runs through the whole process of liver cancer prevention and treatment. TCM has thousands of years of history in the prevention and treatment of cancer, and has been favored by doctors and patients because of its stable curative effect, safety, and minimal side effects[6]. The use of bezoars in TCM has a significant effect in the treatment of liver cancer, effectively reducing the risks of recurrence and metastasis of liver cancer patients after surgery. Bezoars and their compound preparations have shown broad prospects in the field of hepatocarcinoma treatment.

#### FEASIBILITY ANALYSIS AND ADVANTAGES OF TCM BEZOARS IN TREATING LIVER CANCER

The use of bezoars in TCM has a long history of use in the treatment of diseases. First seen in the Shennong Bencaojing, a Chinese agricultural manuscript and described as "flat, bitter taste, non-toxic, main convulsive epilepsy, cold and heat", it has the effect of clearing the heart and opening the body, cooling the liver and extinguishing the wind, clearing the heat and detoxifying the liver and the heart[7]. In TCM, bezoars can be divided into natural bezoars, artificial bezoars, cultured bezoars *in vitro* and cultured bezoars. The main components of bezoars are biliverdin, free bilirubin, free bile acid, ursodeoxycholic acid, and taurocholic acid, which have remarkable effects in the prevention and treatment of various diseases[8]. Natural bezoars have the best therapeutic effects, followed by artificial and cultivated bezoars[9]. Studies have found that the application of bezoar can directly or indirectly inhibit tumors, regulate the recovery of the body's immune microenvironment, improve the body's immunity, regulate the function of macrophages, and control the further development of tumors[10]. Recent studies and a large number of experiments have shown that bezoars, alone or

in combination with other TCM, can induce apoptosis of cancer cells and regulate body immunity to inhibit tumor development. The anti-tumorigenic mechanisms of bezoars mainly occur by inhibiting cell growth and migration, inducing apoptosis of cancer cells, reversing drug resistance in cancer cells, inhibiting angiogenesis, enhancing immune function, and regulating tumor-associated signaling pathways<sup>[11]</sup>. Bezoars and Chinese herbal compounds containing bezoars can not only treat liver cancer, but also have obvious tumor inhibitory effects on other solid tumors such as breast and cervical cancer. Representative Chinese patent medicines including bezoars include Pien Tze Huang<sup>[12]</sup>, Xihuang Pill [13], Kehuang Capsule[14], Niuhuang Tianlong Capsule[15], and Niuhuang Xingxiao Pill[16]. which can inhibit the development of various tumors (Table 1).

Based on the theoretical analysis and clinical trials on the efficacy and reduction of side effects of TCM bezoar for liver cancer, we found that not only bezoar, but also a variety of TCM anti-tumor principles mainly focus on regulating tumor immune activity, modulating the influence of metastasis-related signaling pathway proteins on tumor microenvironment, inhibiting cancer cell growth and blocking cancer cell metastasis. When combined with chemotherapy drugs, these treatments enhance the therapeutic effect and reduce toxic side effects<sup>[17]</sup>.

#### MACROPHAGES AND THE IMMUNE MICROENVIRONMENT

The human immune system is a dynamic system, which can be divided into two categories: The innate and the adaptive immune system. The tumor immune microenvironment is a dynamic microenvironment composed of cancerous and noncancerous cells, including a large number of immune cells. It consists of different quantities of T cells, B cells, dendritic cells, tumor-associated macrophages (TAMs), tumor-infiltrating lymphocytes, antigen-presenting cells (APC), tumorassociated fibroblasts, mesenchymal cells, endothelial cells, and extracellular matrix[18].

The immunosuppressive tumor microenvironment mediated by the programmed death ligand 1 (PD-L1)/ programmed cell death 1 (PD-1) signaling pathway is the basis of liver cancer survival, and plays an important role in the generation and development of liver cancer, and in evading immune surveillance. PD-L1 expression in tumors is currently being used as a biomarker to guide decision making. PD-1 is an important immunosuppressive molecule, which is usually expressed on the surface of T cells, B cells, natural killer cell (NK) and other immune cells. PD-L1 is expressed on tumor cells, activated T cells, and macrophages in the tumor microenvironment. TAMs also widely express PD-L1, and its expression persists in tumor cells for a long time. The application of monoclonal antibodies to block binding between PD-1 and PD-L1, restoring immune activity in the tumor microenvironment, enhancing the activity of immune T cells, and enhances the anti-tumor immune response. Current studies have found that PD-1 and PD-L1 inhibitors have achieved ideal therapeutic effects in several cancers, including liver cancer, breast cancer, and bowel cancer [19,20].

Macrophages in the liver can differentiate into pro-inflammatory M1 and anti-inflammatory M2 macrophages. The immune factors secreted by the two types of macrophages are different, and their functions are also different. In the liver microenvironment, the proportion of the two types of macrophages maintains a delicate balance, jointly maintaining the stability of the liver internal environment. In the early stage of inflammatory disease, liver macrophages, also known as Kupffer cells, recruit neutrophils and peripheral monocytes to the site of liver injury to promote inflammation and fibrosis. M1 macrophages dominate in this stage. With the progression of disease, macrophages transform into the M2 type, to promote immunosuppression and fibrosis formation, and the inflammation gradually changes from acute to chronic leading to the formation of a tumor immune microenvironment, and promoting the generation and development of liver cancer. TAMs promote liver cancer angiogenesis, invasion and metastasis, enhance liver cancer stem cell characteristics, and inhibit tumor immunity[21].

Most macrophages in liver cancer are M2 macrophages, which plays a pro-tumor role, thus reducing the number of TAM in liver cancer is an effective anti-tumor strategy. Macrophages, located in tissues and organs, are important components of innate immunity and major APC. Macrophages have two sides in tumor immunity. On the one hand, activated macrophages can play an anti-tumor role. On the other hand, different microenvironments can promote the activation of macrophages with different properties and become immunosuppressive macrophages with different molecular characteristics and different functions, thus promoting the occurrence of tumors[22].

TAMs can be highly expressed in a variety of tumor microenvironments, such as liver cancer, stomach cancer, and bowel cancer. As a type of monocyte, macrophages can differentiate into M1 proinflammatory macrophages and M2 antiinflammatory macrophages. M1-type macrophages can release pro-inflammatory cytokines such as interleukin (IL)-6, IL-1 $\beta$ , IL-12, IL-13, tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ), interferon gamma (INF- $\gamma$ ), and M2 can release IL-10, transforming growth factor- $\beta$  (TGF- $\beta$ ) anti-inflammatory or immunosuppressive cytokines. The balance of M1 and M2 plays an important role in the balance of the body's immune system[23]. In the tumor immune microenvironment, TAMs were mostly immunosuppressive M2 and anti-inflammatory, which played an immunosuppressive role. One subtype of helper T cells, Th1, releases INF- $\gamma$ , which can promote the polarization of M1 cells. When M1 macrophages are polarized, M1 macrophages release TNF- $\alpha$ , and INF- $\gamma$  and TNF- $\alpha$  can promote the proliferation and activation of CTL and NK cells. These cytokines can promote cellular immunity in a pro-inflammatory environment and forming an anti-cancer environment. One subtype of helper T cells, Th2, release cytokines to promote the polarization of M2 cells. When M2 macrophages are polarized, IL-10 is released to play an immunosuppressive role. Additionally, M2 macrophages release TGF- $\beta$ , which promotes the differentiation of regulatory T cells (Treg) which will release a large amount of IL-10 for immunosuppression. M2 macrophages and Tregs form a cancer-promoting environment[24]. M2 macrophages in the microenvironment are gradually transformed into M1 macrophages by reprogramming, which inhibits the polarization of M2 macrophages, reduces their immunosuppressive abilities, and restores the body's immunity. The immune microenvironment of the liver is complex and specific, and there is a certain natural immune tolerance. Various factors can cause the

Table 1 Chinese herbal compounds containing bezoars and their anti-tumor effects					
Drug	Drug composition	Efficacy	Disease treated		
Pien tze huang[12]	Bezoar, notoginseng, snake gall, musk	Clearing heat and detoxifying, cooling blood and removing stasis	Liver cancer, chronic hepatitis		
Xihuang pill[ <mark>13</mark> ]	Bezoar, musk, frankincense, myrrh	Clearing heat and detoxifying, and relieving swelling	Breast cancer, scrofula		
Kehuang capsule[14]	Bezoar, musk, snake gall, notoginseng, scutellaria, coptis, phellodendron Curcuma	Clearing heat and detoxifying, cooling blood and clearing knot	Liver cancer, chronic hepatitis		
Niuhuang tianlong capsule[15]	Xihuang pill plus or minus	Clearing heat and detoxifying, dispersing knot and removing blood stasis	Cervical cancer, endometrial cancer		
Niuhuang xingxiao pill[ <mark>16]</mark>	Bezoar, musk, frankincense, myrrh	Clearing heat and detoxifying, cooling blood and removing stasis	Breast cancer, scrofula		

occurrence of liver cancer. In situations of chronic inflammation, the body secretes immunosuppressive factors to suppress immune cells through excessive immunosuppression, leading to the occurrence of tumors. Notable among them are TAMs<sup>[25]</sup>. The liver is the body's parenchymatous organ containing the most macrophages, and it is also contains the highest immune cell population in the liver. As a bridge between the innate and adaptive immune system, it plays an important role in the treatment of liver cancer<sup>[26]</sup> (Figure 1).

#### BEZOARS AND BEZOAR-CONTAINING COMPOUNDS REGULATE THE IMMUNE MICROENVIRONMENT IN LIVER CANCER

The regulatory mechanisms by which bezoars and bezoar-containing compounds on liver cancer can occur in many ways. First, they can promote the apoptosis of liver cancer cells and inhibit their growth and metastasis by regulating liver cancer-related cells. Second, they can regulate the relevant signaling pathways, regulate and improve the tumor immune microenvironment, and inhibit the growth of tumors. The PD-1/PD-L1 signaling pathway plays a regulatory role in cell proliferation and apoptosis. By regulating the PD-1/PD-L1 signaling pathway, the polarization of macrophages and the expression of IL-6 cytokines are affected. Experimental data shows that the Xihuang Pill can prevent the further development of liver cancer by inhibiting PD-1/PD-L1 signaling[27]. NF-κB regulates immunity and inflammation in the body, and when activated, it promotes increased inflammatory cell infiltration to aggravate the inflammatory response. IL-1 $\beta$  and TNF- $\alpha$  as upstream factors of NF- $\kappa$ B, activate NF- $\kappa$ B which promotes the development of inflammation, and metastasis of cancer cells. Pien Tze Huang can reduce liver fibrosis and promote apoptosis of cancer cells by regulating the NF-KB signaling pathway. In addition, experimental studies have also found that Pien Tze Huang can reduce liver fibrosis by regulating autophagy as well as the TGF- $\beta$ 1/Smad signaling pathway[28-30]. The Wnt/ $\beta$ -catenin signaling pathway is an important signaling pathway regulating cell growth, development and differentiation. Many studies have found that activation of the  $Wnt/\beta$ -catenin signaling pathway promotes tumor development[31]. Studies have shown that there is a close relationship between Wnt and macrophages, and that macrophages can re-activate the Wnt signaling pathway in the tumor immune microenvironment, regulate Wnt in neighboring cells through paracysecretory, and affect the function of Wnt. In addition, Wnt signals in macrophages can change their own immune activation state and affect the homeostatic balance of surrounding organs after activation[32]. Wnt signaling in macrophages can increase the degree and progression of organ fibrosis by regulating the state of its immune response. Ye Feng found that Wnt/β-catenin signaling can promote the secretion of TGF- $\beta$  and other pro-fibrotic factors by macrophages *in vitro*, and that the degree of fibrosis was reduced in mice where  $\beta$ -catenin was knocked out in myeloid cells. Inhibition of Wnt/ $\beta$ -catenin signaling can reduce the degree of bleomycin-induced pulmonary fibrosis in mice[33]. Regulating the Wnt/ $\beta$ -catenin signaling pathway is an effective strategy for the treatment of liver cancer. From the etiology of liver cancer, we have learned that chronic hepatitis is an important factor causing liver cancer. In some inflammatory diseases, macrophages and Wnt signaling are involved. Macrophages secrete some factors involved in immune tolerance, such as  $TGF-\beta$  and IL-10, and the expression of these cytokines is also a typical feature of M2 polarized macrophages, resulting in immunosuppression. When the Wnt/β-catenin signaling pathway is activated, it will promote the polarization of M2 macrophages to produce tumor promoting cytokines such as IL-10, generate Tregs, and promote the further development of tumors. The classical What signal is transmitted to the upstream ligand via  $\beta$ -catenin to avoid excessive degradation of itself. M2-type macrophages promote tissue repair, and when β-catenin is silenced in macrophages, tumor cell mobility decreases. Cell experiments have shown that silenced  $\beta$ -catenin can slow down the cell healing rate and reduce tumor mobility to a certain extent, which can inhibit not only liver cancer but also a variety of tumors[34].

The application of bezoars and related preparations is not limited to experimental data and related basic research, and clinical applications have shown that their use in the treatment of liver cancer has also achieved effective therapeutic effects. Ning et al[35] found that the combined application of bezoars and imagination can promote apoptosis of liver cancer cells[35]. Xu et al[36] found that after TACE surgery in patients with primary liver cancer, the combination of acupuncture with the Xihuang Pill and conventional Western medicine treatments can significantly relieve patient pain,

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Figure 1 Liver cancer immune microenvironment. Created by Figdraw.

improve patient quality of life, and serum levels of AFP and GAS, which is worthy of clinical promotion and application [36]. Guo et al[37] found that Pian Zehuang combined with gamma knife stereotactic radiotherapy had fewer adverse reactions and could prolong the survival time of patients with primary liver cancer compared to radiotherapy[37].

In this paper, the TCM bezoar inhibits the polarization of M2 TAMs by inhibiting the activation of the Wnt/ $\beta$ -catenin signaling pathway to subsequently inhibit the development of liver cancer, which confirms the obvious effect of TCM on liver cancer.

#### RESEARCH AND DEVELOPMENT OF BEZOAR AND ANTI-TUMOR PREPARATIONS CONTAINING **BEZOAR COMPOUND**

In recent years, with the gradual deepening of the research on the prevention and treatment of cancer using TCM, we have found that TCM has the advantages of multi-pathway and multi-target effects, which translates to remarkable effects on the prevention and treatment of tumors[38]. However, the application of TCM in cancer has the disadvantages of instability and poor water solubility, which limits its clinical application and exploration. With the deepening of research on the chemistry and pharmacology of TCM, thus the use of nano preparations in TCM is quite clear. Nano preparation of TCM has the advantages of reducing toxicity and promoting more accurate targeting[39,40]. Studies have found that a variety of single herbs have shown good therapeutic effects in the treatment of malignant tumors. Nano polysaccharides can enhance the stability of TCM compounds[41]. Zhang et al[42] found that Sanqi compound nanoparticles had significant antithrombotic effect<sup>[42]</sup>. Reviewing the application history and value of bezoars in Linchuan may result in more accurate targeted treatments that may be achieved through the development of nanobezoars in anti-tumor treatment. Nano-preparations can be given in multi-unit administration in the field of TCM. Bezoars can be divided into independent drug units, which are further processed by wet grinding, high pressure homogenization, liquid nitrogen freezing and other methods. It was found that the antitumor activity of the multi-unit drug delivery system for a Chinese medicine Niuhuang Xingxiao Pill was significantly higher than that of the Niuhuang Xingxiao Pill[43].

Through this article, we found that the TCM bezoar can affect the macrophages and immune microenvironment of tumor patients through relevant signaling pathways. This suggests that the nano-bezoar has great potential for future development, providing a new means for the treatment of liver cancer by the TCM bezoar and the compound preparation

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#### **CLINICAL IMPLICATIONS**

TCM, as a traditional means of treating diseases in China, has a long history. Even with the development of molecular biology and pharmacological technology, TCM is effective in the treatment of cancer. Whether it is used alone or with multiple drugs combined, it can inhibit and reverse the tumor to some extent. The composition of TCM is complex, and it can be applied in multiple targets with high safety. The use of TCM can positively regulate the immune microenvironment in tumor patients, inhibit the negative feedback signal pathways, and restore the body's immune ability to achieve anti-tumor effects. However, the first shortcoming is that the exploration of a variety of Chinese medicines is not in-depth enough, and there is a lack of clinical trial data to reveal its anti-tumor mechanism of action. More clinical trials and data sorting are needed to further discover, reveal, and prove the mechanism of action of Chinese medicine on tumors. In addition, single drug or compound preparations need to be further optimized and developed, and modern nanotechnology is needed to improve the stability and accuracy of TCM in the treatment of tumors, and to improve clinical efficacy.

#### FOOTNOTES

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LETTER TO THE EDITOR

## Crosslink among cyclin-dependent kinase 9, ATP binding cassette transporter G2 and Beclin 1 in colorectal cancer

Zhong-Bao Shao, Ke He, Yu-Bin Su, Zhi Shi

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#### Abstract

Colorectal cancer (CRC) ranks third in the number of cancers mainly because of the inability to diagnose it at an early stage. The pathogenesis of CRC is complicated, which is the result of the complex interaction of multiple genetic and environmental factors. Currently, one of the main treatments for CRC is chemotherapy. But the primary cause of CRC treatment failure is drug resistance. The expression of cyclin-dependent kinase 9 (CDK9) was correlated with elevated autophagy levels in colon cancer, and high expression of CDK9 indicates a poor prognosis in CRC. The incidence of autophagy and the expressions of Beclin 1 and ATP binding cassette transporter G2 are different in left and right colon cancer, and autophagy may be involved in the occurrence of chemotherapy resistance. In this article, the roles of CDK9, ATP binding cassette transporter G2 and Beclin 1 in CRC were elucidated, emphasizing the linkages among them and providing potential therapeutic targets of CRC.


Key Words: Cyclin-dependent kinase 9; ATP binding cassette transporter G2; Beclin 1; Colorectal cancer; Chemotherapy

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Core Tip: The expression of cyclin-dependent kinase 9 (CDK9) was correlated with elevated autophagy levels in colon cancer, and high expression of CDK9 indicates a poor prognosis in colorectal cancer (CRC). The incidence of autophagy and the expressions of Beclin 1 and ATP binding cassette transporter G2 were different between left and right colon cancer. The roles of CDK9, ATP binding cassette transporter G2 and Beclin 1 in CRC were clarified, underlining the linkages among them and providing potential therapeutic targets of CRC.

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#### TO THE EDITOR

A clinical and translational study by Zheng et al[1], reported that the rate of autophagy and the expressions of Beclin 1 (BECN1) and ATP binding cassette transporter G2 (ABCG2) differed between left and right colon cancer tissues. Autophagy may be associated with chemotherapy resistance in colorectal cancer (CRC) patients. And cyclin dependent kinase 9 (CDK9) is highly expressed in CRC that can be used as a prognostic marker in CRC patients. This research could provide a theoretical basis for the exploration of CDK9 and autophagy inhibitors in combination therapy to enhance tumor cell sensitivity to chemotherapy.

CRC ranks third in the number of cancers mainly owing to the inability to diagnose it at an early stage[2]. The pathogenesis of CRC is complexed, which is the result of the complex interaction of a lot of genetic and environmental factors[3]. At present, one of the main treatments for CRC is chemotherapy. But the primary cause of CRC treatment failure is drug resistance[4]. Consequently, elucidating research into molecular mechanisms of drug resistance can be beneficial to develop new diagnostic or therapeutic strategies to overcome the challenges in the treatment of CRC.

#### THE CROSSLINK AMONG CDK9, ABCG2 AND BECN1 IN CRC

ABCG2, as an important member of the ATP-binding cassette transmembrane transporter superfamily, plays a significant role in cancer multidrug resistance<sup>[5]</sup>. Several agents have been reported to be able to reverse ABCG2-mediated multidrug resistance in CRC cells by inhibiting the transporter activity of ABCG2[6,7]. Now, we are interested in the authors' new finding that the expression level of ABCG2 in right colon cancer was higher than that in paracarcinoma tissue, but the expression level of ABCG2 was not significantly different between left colon cancer and paracarcinoma tissue. These findings might be useful for gaining insight into the pathogenesis of left and right colon cancer and improving treatment strategies for CRC therapy.

Autophagy refers to a catabolic process in which macromolecular substances such as misfolded proteins and damaged organelles are transported to lysosomes for degradation[8]. It can prevent genome damage and induce cancer cell death. And on the other hand, autophagy is a pro-oncogenic mechanism that provides drug resistance to cancer cells and promotes cancer cell growth<sup>[9]</sup>. The sensitivity of cancer cells to chemotherapeutic drugs can be restored by the use of autophagy inhibitors, such as chloroquine, or by the knockdown of autophagy-related proteins, including BECN1, autophagy-related gene 7, and autophagy-related gene 10[10]. Currently, autophagy inhibitors are promising for cancer treatment. Some small molecule autophagy inhibitors have been discovered according to the autophagy process<sup>[10]</sup>. Recent research has revealed FDW028 (a novel FUT8 inhibitor) exhibits potent anti CRC effects by facilitating lysosomal degradation of CD276 through the chaperone-mediated autophagy pathway[11]. Erianin (a natural product) can induce autophagy-dependent ferroptosis and inhibit tumor growth and metastasis in KRAS<sup>G13D</sup> CRC[12]. Strigolactones are endogenous plant hormones that can act as a potential autophagy inhibitor by blocking autophagosome-lysosome fusion in HCT116 CRC cells[13]. BECN1, a key autophagy regulator, serves as a potential therapeutic target and is associated with chemotherapeutic resistance in cancers<sup>[14]</sup>. Previous studies have demonstrated that JAK2-depended BECN1 phosphorylation may confer chemotherapy resistance in CRC[15]. Based on Zheng et al's research, the expression of BECN1 may be different between left and right colon cancer<sup>[1]</sup>. This research provided new ideas for further investigation on the drug resistance in CRC.

CDK family, a large class of serine/threonine protein kinases, plays a vital role in cell cycle progression and gene transcription regulation. There have been some reports on CDK inhibitors in the treatment of CRC. Zeng et al[16]proposed that CDK1 serves as a potential target for oxaliplatin-resistant CRC treatment. Lee *et al*[17] reported that the combination of palbociclib (CDK 4/6 inhibitor) and gedatolisib (phosphatidylinositol 3-kinase/mammalian target of

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Figure 1 The relationships between cyclin-dependent kinase 9, ATP binding cassette transporter G2, Beclin 1 and autophagy in colorectal cancers. CDK9: Cyclin-dependent kinase 9; BECN1: Beclin 1; ABCG2: ATP binding cassette transporter G2.

rapamycin dual inhibitor) has synergistic anti-proliferative effects in both wild-type and mutated CRC cell lines. In a recent study, Wang et al[18] revealed that CDK3, CDK5 and CDK8 functioned as potential diagnostic markers for CRC. These findings give rationale for the application of CDK inhibitors in CRC treatment. CDK9 is an important member of the CDK family that regulates the transcription of genes such as chemoresistant genes in tumors, and some CDK9 inhibitors have entered clinical trials in combination with other drugs[19]. According to Zheng et al[1], the expression of CDK9 is positively correlated with autophagy in colon cancer. This finding may provide valuable information for further research on targeting CDK9 as a therapeutic strategy for CRC. The relationships between CDK9, BECN1, ABCG2 and autophagy are show in Figure 1.

# CONCLUSION

The expression of CDK9 was correlated with elevated autophagy levels in colon cancer. Additionally, the expressions of ABCG2 and BECN1 were different between left and right colon cancer patients. Targeting CDK9, ABCG2 and BECN1 might be potential therapeutic strategies for CRC.

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# FOOTNOTES

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