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Novel therapy for advanced gastric cancer

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Abstract

Gastric cancer (GC) is a common lethal malignancy. Gastroesophageal junction and gastric cardia tumors are the fastest rising malignancies due to increasing prevalence of obesity and acid reflux in the United States. Traditional chemotherapy remains the main treatment with trastuzumab targeting human epidermal growth factor receptor 2 positive disease. The median overall

survival (OS) is less than one year for advanced GC patients; thus, there is an urgent unmet need to develop novel therapy for GC. Although multiple targeted agents were studied, only the vascular endothelial growth factor receptor inhibitor ramucirumab was approved recently by the United States Food and Drug Administration because of its 1.4 mo OS benefit (5.2 mo vs 3.8 mo, $P = 0.047$) as a single agent; 2.2 mo improvement of survival (9.6 mo vs 7.4 mo, $P = 0.017$) when combined with paclitaxel in previously treated advanced GC patients. It is the first single agent approved for previously treated GC and the second biologic agent after trastuzumab. Even with limited success, targeted therapy may be improved by developing new biomarkers. Immune therapy is changing the paradigm of cancer treatment and is presently under active investigation for GC in clinical trials. More evidence supports GC stem cells existence and early stage studies are looking for its potential therapeutic possibilities.

Key words: Gastric cancer; Novel therapy; Targeted therapy; Immune therapy; Gastric cancer stem cell

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Core tip: Advanced gastric cancer (GC) has very poor outcome with chemotherapy remains the main treatment. There is an urgent unmet need to develop novel therapy for GC. Limited success is achieved for targeted therapy after trastuzumab for human epidermal growth factor receptor 2 positive disease. Ramucirumab was recently approved by Food and Drug Administration as a single agent or combined with paclitaxel in refractory advanced GC patients. Immune therapy and GC stem cell research are on the horizon.

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INTRODUCTION

Gastric cancer (GC) is a common malignancy and the second leading cause of cancer death worldwide^[1]. In the United States, there were approximately 22220 new cases and 10990 death in 2014^[2]. With overweight and obesity being a more serious epidemiologic issue in the United States, gastroesophageal junction and gastric cardia adenocarcinoma have been the fastest rising cancer. Majority of GCs are present at advanced stages with either metastatic or extensive local/regional disease. It is a group of heterogeneous diseases with different anatomy, epidemiology, etiology, pathogenesis, and behavior. Chemotherapy using fluoropyrimidine or platinum as backbone is the main treatment for advanced GCs. The median survival is limited to 7 to 12 mo in clinical trial setting^[3,4]. There is an urgent demand for new therapy to improve its treatment and outcome.

DIFFICULTY AND PROGRESS IN TARGETED THERAPY

Targeted therapy has been the main focus in clinical trials, even though majority of the targeted agents were tested in an unselected "off target" patient population and there was a lacking of biomarkers. It has led to the failure of multiple large phase III clinical trials in different pathways. Trastuzumab is approved for human epidermal growth factor receptor 2 (HER2) positive GCs. Ramucirumab has recently gained its label as a single agent or in combination with paclitaxel for refractory GCs patients following fluoropyrimidine or platinum containing chemotherapy.

Epidermal growth factor receptor targeting therapy

Epidermal growth factor receptor (EGFR) has been studied extensively. EXPAND and REAL 3 are the two recent phase III clinical trials with EGFR antibodies: cetuximab and panitumumab. Both of them failed to show survival benefit and were concerning for worse toxicity in the EGFR inhibitor study arms. In the EXPAND trial, median progression-free survival (PFS) (4.4 mo vs 5.6 mo, $P = 0.32$) and overall survival (OS) (9.4 mo vs 10.7 mo, $P = 0.95$) favored the chemotherapy only group, overall response rates (RR) were similar 30% vs 29%^[5]. Grade 3-4 toxicities were substantially higher in the cetuximab-containing regimen than in the control regimen^[5]. REAL 3 trial demonstrated inferior OS in the panitumumab study group when compared to control group (11.3 mo vs 8.8 mo, $P = 0.013$) with more toxicities^[6]. Biomarker was not used to select patient in both studies. Only 6% screened patients were positive for Kirsten rat sarcoma viral oncogene homolog (KRAS) mutation, a potential association of benefit was found in KRAS mutated group although not significant^[6]. This result is contrary to KRAS mutated colon cancer^[7].

Phosphatidylinositol 3-kinase/Akt/ mammalian target of rapamycin targeting therapy

The phosphatidylinositol 3-kinase/Akt/mammalian target

of rapamycin signaling pathway was studied with everolimus in 656 previous treated advanced GC patients in a phase III trial: GRANITE-1. Primary endpoint was not reached (OS: 5.4 mo vs 4.3 mo, $P = 0.12$), even though PFS was improved (1.7 mo vs 1.4 mo, $P < 0.001$)^[8]. No biomarker was required for this study entry.

HER2 targeting therapy

HER2 overexpression by immunohistochemistry or gene amplification by fluorescence *in situ* hybridization was required for patients' recruitment for the phase III ToGA trial. This pivotal trial led to trastuzumab approval with all the outcomes better in the study group (median OS: 13.8 mo vs 11.1 mo, $P = 0.0046$; PFS: 6.7 mo vs 5.5 mo, $P = 0.0002$; RR: 47% vs 35%, $P = 0.0017$)^[9]. A post-hoc analysis grouped HER2 status and suggested that larger survival benefit in patients with tumor HER 2 IHC 3+ or 2+ and FISH positive group (OS: 16.0 mo vs 11.8 mo, $P = 0.036$)^[9]. Lapatinib is a dual tyrosine kinase inhibitor (TK) inhibitor of HER2 and EGFR. It failed to meet OS benefit in two large phase III trials: TRIO-013/Logic in the first line and TyTan in the second line settings (TRIO-013/Logic: 12.2 mo vs 10.5 mo, $P = 0.35$; TyTan: 11.0 mo vs 8.9 mo, $P = 0.1044$)^[10,11]. Lapatinib failure in GC trials might partially relate to its EGFR inhibition effect. Pertuzumab is another humanized monoclonal antibody that binds HER2. Its combination with trastuzumab and chemotherapy is established as first line treatment for metastatic HER2 positive breast cancer^[12]. This combination is being evaluated in a phase III clinical trial for HER 2 positive advanced GCs (NCT01774786). Trastuzumab emtansine (T-DM1) is an antibody-drug conjugate with monoclonal antibody trastuzumab lined to cytotoxic agent emtansine. A randomized phase III trial is ongoing with T-DM1 vs taxane for previously treated advanced GCs (NCT01641939).

Antiangiogenic pathway targeting therapy

Vascular endothelial growth factor (VEGF) pathway (angiogenesis) is of great interest in advanced GCs with recent success in ramucirumab, although VEGF-A neutralizing antibody bevacizumab did not reach its primary endpoint in phase III AVAGAST trial (OS: 12.1 mo vs 10.1 mo, $P = 0.1002$; PFS: 6.7 mo vs 5.3 mo, $P = 0.0037$; RR: 46% vs 37.4%, $P = 0.0315$)^[13]. Ramucirumab is a vascular endothelial growth factor receptor 2 (VEGFR2) monoclonal antibody inhibiting VEGF binding. Two pivotal phase III clinical trials REGARD and RAINBOW have led to the approval of ramucirumab in 2014 for advanced GCs after progression on fluoropyrimidine or platinum containing chemotherapy. In REGARD trial, ramucirumab was compared to placebo in previously treated advanced GC patients. Survival was significant better as a single agent (OS: 5.2 mo vs 3.8 mo, $P = 0.047$)^[14]. Ramucirumab was investigated in combination with paclitaxel compared to paclitaxel alone in RAINBOW trial. It demonstrated survival benefit again (OS: 9.6 mo vs 7.4 mo, $P = 0.017$)^[15]. Advanced GC patients in both trials have been treated previously

and the OS benefits were impressive. Ramucirumab has become the standard second line treatment for advanced GC. In the first line setting, ramucirumab was studied together with FOLFOX in a phase II trial. It did not add much improvement (PFS: 6.4 mo vs 6.7 mo, $P = 0.89$; OS: 11.7 mo vs 11.5 mo)^[16]. No biomarker has been established for ramucirumab either. A global phase III trial RAINFALL (NCT 02314117) is ongoing comparing fluropyrimidine/Cisplatin with or without ramucirumab in HER2 negative advanced GC patients as first line treatment^[17]. Apatinib is an oral small molecular TKI of VEGFR-2. In a phase III clinical trial of advanced GC patients who failed second-line chemotherapy, the OS was significantly prolonged in the apatinib group when compared to the placebo group (6.5 mo vs 4.7 mo, $P < 0.016$; PFS: 2.6 mo vs 1.8 mo, $P < 0.0001$; RR 2.84% and 0.00%)^[18]. This study further confirmed the efficacy of VEGFR-2 inhibitor for the patients with advanced GC^[18]. Regorafenib, an oral multi kinase inhibitor with antiangiogenic effect by VEGFR-2 inhibition, showed PFS benefit over placebo for refractory advanced GC patients in a global phase II trial (INTEGRATE, PFS: 11.1 wk vs 3.9 wk, $P < 0.0001$; OS: 25 wk vs 19.4 wk, $P = 0.11$)^[19]. Another phase II PaFLO trial (NCT 01503372) examined chemotherapy with or without the antiangiogenic TKI pazopanib as first line in HER2 negative patients. The study did not meet its predefined PFS rate of minimum of 40% at 6 mo (PFS rate: 31.4% vs 25.9%). Marginal efficacy in the pazopanib group was observed with median PFS 5.1 mo compared to 3.9 mo in the control group (HR: 0.93, 95%CI: 0.56-1.54)^[20].

Mesenchymal-epithelial transition factor receptor/hepatocyte growth factor targeting therapy

Mesenchymal-epithelial transition factor receptor (c-MET) and its ligand hepatocyte growth factor (HGF) were also evaluated. Rilotumumab is an antibody to HGF, and it was tested in the frontline with chemotherapy in MET-positive advanced GC patients in two phase III clinical trials RILOMET-1 (NCT01697072) and RILOMET-2 (NCT02137343) based on the positive phase II study^[21]. Chemotherapies with or without the drug were examined. These studies have to stop early due to increased fatal adverse events for advanced GC patients. RILOMET-1 study recently reports significantly worse OS in the study group (OS: 9.6 mo vs 11.5 mo, HR: 1.37, $P = 0.016$)^[22]. Onartuzumab is an antibody against c-MET being studied in combination chemotherapy in advanced GC patients with HER2-negative, MET-positive disease (MetGastric) in the frontline setting (NCT01662869). The study was negative with the addition of onartuzumab to chemotherapy favored placebo group (OS ITT: 11.3 mo vs 11.0 mo, $P = 0.24$; OS: MET 2+/3+ 9.7 mo vs 11.0 mo, $P = 0.062$)^[23].

Poly (ADP-ribose) polymerase targeting therapy

Poly (ADP-ribose) polymerase (PARP) inhibitor in combination with paclitaxel was studied in a second

line phase II advanced GC study (NCT01063517). The study was enriched for patients with low ATM tumors by IHC based on preclinical data of responsiveness of GC cell lines to olaparib association with low ATM protein level. Of the 124 randomized patients, olaparib plus paclitaxel was well tolerated. Although the primary endpoint of PFS was not met (All patients: 3.9 mo vs 3.6 mo, $P = 0.261$; ATM patients: 5.3 mo vs 3.7 mo, $P = 0.35$), the OS was statistically significant improved in the study for both all patients and ATM patients (All patients: 13.1 mo vs 8.3 mo, $P = 0.010$; ATM patients: NC vs 8.2 mo, $P = 0.003$)^[24]. A large phase III study is ongoing in Asian patients (NCT01924533).

Hedgehog pathway targeting therapy

Hedgehog pathway inhibitor vismodegib combined with FOLFOX was examined in a phase II study for advanced GC patients. Hedgehog pathway is over-expressed in GE tumors and pre-clinical data suggested hedgehog inhibitors control tumor growth, cell motility and invasiveness. Median PFS was 11.5 mo vs 9.3 mo ($P = 0.34$) and median OS was 12.2 mo vs 13.9 mo ($P = 0.48$)^[25]. It is another negative trial in an unselected advanced GC population.

Fibroblast growth factor receptor targeting therapy

Fibroblast growth factor receptor (FGFR) pathway is required for driving growth and survival of GC carrying *FGFR2* gene amplification. Dovitinib (TKI258) and AZD4547 are evaluated in this pathway for GCs. Dovitinib is currently being studied as monotherapy or combined with docetaxel in the second or third line setting. One trial (NCT01719549) required patients to have *FGFR2* gene amplification and the other two trials (NCT01576380, NCT01921673) were performed in the unselected patient population. The SHINE study (NCT01457846) of AZD4547 monotherapy vs paclitaxel for patients with *FGFR2* polysomy or gene amplification recently reported to be negative. The PFS was 1.8 mo in the AZD group compared to 3.5 mo in the paclitaxel group^[26].

No biomarkers except HER2 are available for clinical practice. The difficulty to identify predictive biomarkers for targeted therapy remains, and warrants further investigation. Majority of the above mentioned large phase II or III trials were done in unselected patient populations with negative results. The cancer genome atlas project recently proposed to divide GC into four subtypes: Epstein-Barr virus positive tumor, microsatellite unstable tumors, genomically stable tumor, and chromosomally unstable tumor^[27]. This classification is based on comprehensive molecular characterization. The advance in technology and understanding of its heterogeneity will potentially lead to identify key targets and pathways for treatments. The laboratory testing to establish positive markers need to be standardized. Future clinical trial design should consider both predictive and prognostic biomarkers to direct targeted therapies.

ERA OF IMMUNE THERAPY

Immune therapy has gained tremendous interest in cancer research and starts a new era for cancer treatment in recent years. Immune checkpoint pathway has made significant progress with several new agents approved for clinical use recently. Suppressing this pathway allows T cell activation and use human immune system to attack tumor cells. High RR and possible durable response have been seen in melanoma and lung cancer with relative low toxicities^[28-31]. There are two classes of agents which are under evaluation including inhibitors for cytotoxic T-lymphocyte associated antigen 4 (CTLA-4) and program cell death 1 (PD-1) or its ligand (PD-L1) inhibitors. Multiple agents are in early development and some have been tested in clinical trials. CTLA-4 inhibitors such as ipilimumab (MDX-010) and tremelimumab (CP-675,206) regulate the amplitude of early stage T cell activation. PD-1 and PD-L1 inhibitors such as nivolumab (ONO-4538), pembrolizumab (MK-3475), MEDI4736 and MPDL3280A act on the T cell activity in the peripheral tissues. Seven GC patients were included in a safety study for anti-PD-L1 antibody BMS 936559^[32]. Multiple early phase clinical trials are presently ongoing to evaluate their safety and efficacy in advanced solid tumors including GC (for example: NCT01375842, NCT01693562).

CTLA-4 inhibitor tremelimumab was studied in 18 advanced GC patients as a second line treatment. One patient achieved partial response (PR) and four patients had stable disease (SD). Improved survival was observed in patients experiencing a post treatment carcinoembryonic antigen proliferative response (OS: 17.1 mo vs 4.7 mo, $P = 0.004$) despite the objective RR was low^[33]. Another phase II trial of sequential ipilimumab vs best supportive care as a second line therapy has completed with results pending (NCT01585987).

PD-1 inhibitor pembrolizumab (MK-3475) demonstrated encouraging results in the phase 1b KEYNOTE-012 study for GC with 67% patients received ≥ 2 prior therapies. PD-L1+ was used as the biomarker with 65 out of 162 (40%) screened patient being positive, and 39 patients enrolled eventually. ORR was 22% by central review and 33% by investigator review^[34]. Median time to response was 8 wk with a median response duration of 24 wk. The 6-mo PFS and OS rate were 24% and 69%^[34]. Four patients experienced high-grade drug-related adverse events: peripheral sensory neuropathy, fatigue, decreased appetite, hypoxia, and pneumonitis^[34]. This promising result has led to further investigation. A phase II KEYNOTE-059 (NCT02335411) study has been launched with pembrolizumab monotherapy or in combination with cisplatin plus 5-fluorouracil for advanced GC. Phase III KEYNOTE-061 (NCT02370498) is planned with pembrolizumab vs paclitaxel after the first line therapy with platinum and fluoropyrimidine. Another phase III study with nivolumab (ONO-4538) is recruiting patients with advanced GC (NCT02267343) in Asian countries and PD-L1 positivity

was not required.

Combining checkpoint pathway inhibitors are studied in advanced solid tumors with the hope to generate stronger immunogenicity. A phase I b/II study is ongoing to assess the safety and efficacy of PD-L1 inhibitor MEDI4736 in combination with CTLA-4 inhibitor tremelimumab vs monotherapy for patients with advanced GC (NCT02340975). Another Phase I b/II study of advanced solid tumor included GC is evaluating nivolumab monotherapy vs nivolumab combined with ipilimumab (NCT01928394).

Immune therapy is currently opening a new page for cancer treatment. Harness human immune system to fight for GC may become a reality very soon. Many obstacles and challenges warrant further investigation such as standardization of laboratory testing, biomarkers, tumor immune response criteria, management of immune related adverse events, safety and efficacy of re-exposure.

GC STEM CELL

Hematopoietic stem cell transplant has been well established and widely used in clinical practice to save lives. With more accumulative evidence in recent years, the questionable solid tumor stem cells hypothesis becomes more believable. GC stem cells are thought to be responsible for tumor self-renewal, metastasis, chemotherapy resistance and tumor recurrence^[35]. *In vitro* sphere-forming assays and *in vivo* tumor formation in immune-deficient mice have been employed for solid tumor stem cell research. The gastric stem cell was thought to be existed in gastric epithelium initially. Bone marrow derived cells were also identified in mouse models of Helicobacter-induced GC^[36,37]. However majority of the studies are still *in vitro* or using mice model^[38]. One oral first in class cancer stemness inhibitor called BBI608 was studied plus weekly paclitaxel in a phase I b trial in refractory solid tumors. Two out of the five refractory GC patients had a partial response (48% and 45% regressions), one had stable disease (25% regression) and two had prolonged stable disease ≥ 24 wk^[39]. A phase III clinical trial is ongoing (BRIGHTER: NCT02178956) with this cancer cell stemness inhibitor for previously treated advanced GC patients^[40]. One GC patient demonstrated minor regression or SD ≥ 16 wk in another phase I cancer stem cell inhibitor BBI503 trial (NCT01781455)^[41].

FUTURE PERSPECTIVE

GC is a common malignancy with poor outcomes. There is an urgent unmet need to improve treatment and outcome for this lethal disease. Understanding the heterogeneous nature of this cancer and incorporate genomic atlas to develop biomarkers as well as newer target agents are important. Develop precision medicine and tailor optimal therapies to individual patient based on

Table 1 Summary of selected targeted agents for advanced gastric cancer

Target	Study agent	Trial	Treatments	Phase	Biomarker	Results primary end point
EGFR	Cetuximab	EXPAND NCT00678535	Arm1: CX + cetuximab Arm 2: CX	III	No	Negative PFS: 4.4 mo vs 5.6 mo ($P = 0.32$)
EGFR	Panitumumab	REAL3 NCT00824785	Arm1: EOC+ Panitumumab Arm2: EOC	II / III	No	Negative OS: 8.8 mo vs 11.3 mo ($P = 0.013$)
mTOR	Everolimus	GRANITE-1 NCT00879333	Arm1: Everolimus Arm2: Placebo	III	No	Negative OS: 5.4 mo vs 4.3 mo ($P = 0.124$)
HER2	Trastuzumab	ToGA NCT01041404	Arm1: CF + Trastuzumab Arm 2: CF	III	Yes HER2	Positive OS: 13.8 mo vs 11.1 mo ($P = 0.0046$)
HER2/EGFR	Lapatinib	TRIO-013/Logic NCT00680901	Arm1: CX + Lapatinib Arm2: CX	III	Yes HER2	Negative OS: 12.2 mo vs 10.5 mo ($P = 0.35$)
HER2/EGFR	Lapatinib	TyTAN NCT00486954	Arm1: Paclitaxel + Lapatinib Arm2: Paclitaxel	III	Yes HER2	Negative OS: 11.1 mo vs 8.9 mo ($P = 0.1044$)
HER2	Pertuzumab	JACOB NCT0177486	Arm1: CF + Trastuzumab + Pertuzumab Arm2: CF + Trastuzumab	III	Yes HER2	Ongoing
HER2	T-DM1	GATSBY NCT01641939	Arm1: Taxane Arm2: T-DM1 2.4 mg/kg once a week Arm3: T-DM1 3.6 mg/kg every 3 wk	II / III	Yes HER2	Ongoing
VEGF	Bevacizumab	AVAGAST NCT00548548	Arm1: CF + Bevacizumab Arm2: CF	III	No	Negative OS: 12.1 mo vs 10.1 mo ($P = 0.1002$)
VEGFR	Ramucirumab	REGARD NCT00917384	Arm1: Ramucirumab Arm2: Placebo	III	No	Positive OS: 5.2 mo vs 3.8 mo ($P = -0.047$)
VEGFR	Ramucirumab	RAINBOW NCT01170663	Arm1: Paclitaxel + Ramucirumab Arm2: Paclitaxel	III	No	Positive OS: 9.6 mo vs 7.4 mo ($P = 0.017$)
VEGFR	Ramucirumab	RAINFALL NCT02314117	Arm1: CF + Ramucirumab Arm2: CF	III	Yes HER2 negative	Ongoing
VEGFR	Apatinib	NCT0152745	Arm1: Apatinib Arm2: Placebo	III	No	Positive OS: 6.5 mo vs 4.7 mo ($P < 0.016$), PFS: 2.6 mo vs 1.8 mo ($P < 0.0001$)
VEGFR (multi-kinase)	Regorafenib	INTEGRATE	Arm1: Regorafenib Arm2: Placebo	II	No	Positive PFS: 11.1 wk vs 3.9 wk ($P < 0.0001$)
VEGFR, PDGFR, c-Kit	Pazopanib	PaFLO	Arm1: FLO + Pazopanib Arm2: FLO	II	Yes HER2 negative	Negative PFS rate at 6 mo 31.4% vs 25.9% (Did not meet predefined 40%)
MET/HGF	Rilotumumab	RILOMET-1 NCT01697072	Arm1: ECX + Rilotumumab Arm2:	III	Yes MET	Terminated due to increased death signal Negative (Detrimental) OS: 9.6 vs 11.5 mo (HR 1.37, $P = 0.016$)
MET/HGF	Rilotumumab	RILOMET-2 NCT02137343	Arm1: CX + Rilotumumab Arm2: CX	III	Yes MET	Terminated due to increased death signal
MET	Onartuzumab	METGastric NCT01662869	Arm1: FOLFOX Arm2: FOLFOX + Onartuzumab	III	Yes MET+, HER2-	Negative ITT OS: 11.3 mo vs 11.0 mo ($P = 0.24$) MET2+/3+ OS: 9.7 mo vs 11.0 mo ($P = 0.06$)
PARP	Olaparib	NCT01063517	Arm1: Paclitaxel + Olaparib Arm2: Paclitaxel	II	Yes ATM	Negative PFS: 3.9 mo vs 2.6 mo ($P = 0.261$) All patients PFS: 5.3 mo vs 3.7 mo ($P = 0.315$) ATM- patients Positive for secondary endpoints OS: 13.1 mo vs 8.3 mo ($P = 0.010$) All Patients OS: NR mo vs 8.2 mo ($P = 0.003$) ATM- patients
PARP	Olaparib	NCT01924533	Arm1: Paclitaxel + Olaparib Arm2: Paclitaxel	III	No	Ongoing
Hedgehog	Vismodegib	NCT00982592	Arm1: FOLFOX + Vismodegib Arm2: FOLFOX	II	No	Negative PFS: 7.3 mo vs 9.0 mo ($P = 0.64$)
FGFR	Dovitinib	NCT01719549	Dovitinib monotherapy	II	Yes FGFR	Ongoing
FGFR	Dovitinib	NCT01576380	Dovitinib monotherapy	II	No	Completed, waiting for result
FGFR	Dovitinib	NCT01921673	Docetaxel + Dovitinib	I / II	No	Ongoing
FGFR/VEGFR	AZD4547	SHINE NCT1457846	Arm1: AZD4547 Arm2: Paclitaxel	II	Yes FGFR	Negative PFS: 1.8 (AZD) vs 3.5 mo

EOC: Epirubicin, oxalilatin, capecitabine; CF: Fluoropyrimidine, cisplatin; T-DM1: Trastuzumab emtansine; ECX: Epirubicin, cisplatin, capecitabine; CX: Cisplatin, capecitabine; FOLFOX: 5-Fluorouracil, folinic acid, oxaliplatin; NR: Not reached; FLO: 5-FU, leucovorine, oxaliplatin; EGFR: Epidermal growth factor receptor; mTOR: Mammalian target of rapamycin; HER2: Human epidermal growth factor receptor 2; VEGF: Vascular endothelial growth factor; VEGFR: Vascular endothelial growth factor receptor; PDGFR: Platelet-derived growth factor receptor; MET: Mesenchymal-epithelial transition factor; HGF: Hepatocyte growth factor; PARP: Poly ADP-ribose polymerase; FGFR: Fibroblast growth factor receptor.

information including molecular study results will be the future focus. With the recent breakthrough in immune therapy in other solid tumors and promising early phase clinical trial results in GC, immune checkpoint pathway inhibitors are undergoing evaluation. In order to generate stronger immunogenicity, combining different checkpoint pathway inhibitors or chemotherapy or targeted therapy might be needed. GC stem cell research was initially cluttered with skepticism until more evidence accumulated recently. It is an exciting field warrants further evaluation.

CONCLUSION

Ramucirumab is the second biologic agent after trastuzumab approved with statistically significant but marginal survival benefit for GC patients in spite of multiple negative phase III clinical trials of other targeted agents (as summarized in Table 1). Better understanding and use of genomic atlas/biomarkers will potentially lead to development of targeted agents with better efficacy. Immune therapy especially checkpoint pathway inhibition is a promising field and being studied in multiple clinical trials. GC stem cell therapy is finally moving from bench work to early phase clinical investigation. Targeted therapy, immune therapy and cancer stem cell therapy are promising fields and may meet the urgent demand for novel therapy to treat GC in near future.

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2015 Advances in Colorectal Cancer

Autophagy in colorectal cancer: An important switch from physiology to pathology

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Abstract

Colorectal cancer (CRC) remains a leading cause of cancer death in both men and women worldwide. Among the factors and mechanisms that are involved in the multifactorial etiology of CRC, autophagy is an important transformational switch that occurs when a cell shifts from normal to malignant. In recent years, multiple hypotheses have been considered regarding the autophagy mechanisms that are involved in cancer. The currently accepted hypothesis is that autophagy has dual and contradictory roles in carcinogenesis, but the precise mechanisms leading to autophagy in cancer are not yet fully defined and seem to be context dependent. Autophagy is a surveillance mechanism used by normal cells that protects them from the transformation to malignancy by removing damaged organelles and aggregated proteins and by reducing reactive oxygen species, mitochondrial abnormalities and DNA damage. However, autophagy also supports tumor formation by promoting access to nutrients that are critical to the metabolism and growth of tumor cells and by inhibiting cellular death and increasing drug resistance. Autophagy studies in CRC have focused on several molecules, mainly microtubule-associated protein 1 light chain 3, beclin 1, and autophagy related 5, with conflicting results. Beneficial effects were observed for some agents that modulate autophagy in CRC either alone or, more often, in combination with other agents. More extensive studies are needed in the future to clarify the roles of

autophagy-related genes and modulators in colorectal carcinogenesis, and to develop potential beneficial agents for the prognosis and treatment of CRC.

Key words: Colorectal cancer; Autophagy; Gene; Protein; Carcinogenesis

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Core tip: This review describes the role of autophagy in cancer, focusing on the involvement of autophagy in colorectal cancer (CRC). Initially, we describe the steps and components of autophagy, and we then further highlight the dual role of autophagy in cancer, where it can potentially act as both a promoter and an inhibitor during the transformation from normal to malignant cell. In particular, we emphasize the major autophagy genes involved in CRC pathogenesis along with autophagy-modulating agents and their modes of action in the context of CRC therapy.

Burada F, Nicoli ER, Ciurea ME, Uscatu DC, Ioana M, Gheonea DI. Autophagy in colorectal cancer: An important switch from physiology to pathology. *World J Gastrointest Oncol* 2015; 7(11): 271-284 Available from: URL: <http://www.wjgnet.com/1948-5204/full/v7/i11/271.htm> DOI: <http://dx.doi.org/10.4251/wjgo.v7.i11.271>

INTRODUCTION

Despite advances in diagnosis and treatment, colorectal cancer (CRC) remains one of the major causes of cancer death in both sexes worldwide: It is the third most common diagnosed cancer in males and the second most common in females^[1]. It is well known that many risk factors, including multiple genes and environmental influences, are involved in malignant transformation. Recent research provides new data regarding the complex mechanisms involved in colorectal carcinogenesis. Among these mechanisms, autophagy is important in the switch from normal to malignant colorectal cells. The involvement of autophagy in cancer appears to be context specific, with evidence suggesting that it can have a dual role in both tumor suppressing and tumor promoting activities. Moreover, autophagy performs important functions in different processes that are connected to carcinogenesis, including inflammation, immune response and genome stability.

Here, we describe the involvement of autophagy in carcinogenesis, with a particular emphasis on CRC. We summarize the components and steps of macroautophagy (herein referred to as autophagy), and we emphasize the conflicting roles of autophagy in cancer, indicating that it has both promoter and suppressor mechanisms during malignant transformations. The

second part of this study is focused on the autophagy genes and proteins that are associated with CRC. Finally, the effects of autophagy-based drugs in CRC treatment are discussed.

AUTOPHAGY STEPS AND REGULATION

Autophagy is an evolutionarily conserved catabolic process that is characterized by cellular self-digestion and the removal of excessive, long-lived or dysfunctional organelles and proteins^[2]. Autophagy occurs as a physiological process in normal cells at a basal level to assure cellular homeostasis, or as a strategic survival mechanism that recycles energy and nutrients under special conditions. Hypoxia, stress and nutrient deprivation trigger autophagy as a critical adaptive response during starvation^[3]. Three morphologically distinct forms of autophagy can be distinguished: macroautophagy, microautophagy and chaperone-mediated autophagy^[4]. Macroautophagy is identified by the presence of double membrane vesicles known as autophagosomes, which engulf cytoplasmic components that include damaged organelles and deliver them to lysosomes for degradation. The other two forms, microautophagy and chaperone-mediated autophagy, involve a direct membrane invagination to engulf damaged proteins and the translocation of soluble cytosolic proteins by chaperone-dependent selection across the lysosomal membrane, respectively^[5,6].

Autophagy-related genes (ATGs) play a critical role in facilitating the regulation of well-orchestrated autophagy. To date, thirty-six ATGs have been identified^[7]. Autophagosome formation is initiated by unc-51-like kinase (ULK) and class III phosphatidylinositol 3-kinase (PI3K) complexes. The ULK complex consists of ATG13, ATG101, ULK1/2 and family-interacting protein FIP200^[8,9]. Under normal growth conditions, the mammalian target of rapamycin (mTOR) complex inhibits the formation of the ULK complex, in effect blocking autophagy, and the ULK components are dissociated. Various stimuli (*e.g.*, hypoxia, starvation) inhibit mTOR, allowing the ULK kinase complex to be activated, which initiates the formation of an isolation membrane (Figure 1) called a phagophore^[10,11]. The origin of phagophores has not been explained, but the plasma membrane, endoplasmic reticulum, Golgi apparatus and mitochondria are all possible sources^[12]. The completion of this critical step is driven by vacuolar sorting protein 34, a class III PI3K that is bound to beclin-1, and other ATG proteins (*e.g.*, ATG14), which generate PI3K, the second complex, that catalyzes the production of phosphatidylinositol-3-phosphate^[10,13].

Autophagosome elongation and closure steps and the further conversion to a nascent closed autophagosome are controlled by two ubiquitin-like conjugates. First, ATG12 forms a conjugate with ATG5 under the control of ATG7 and ATG10, which have E1 and E2-like enzyme activity, respectively. The resulting ATG12-ATG5

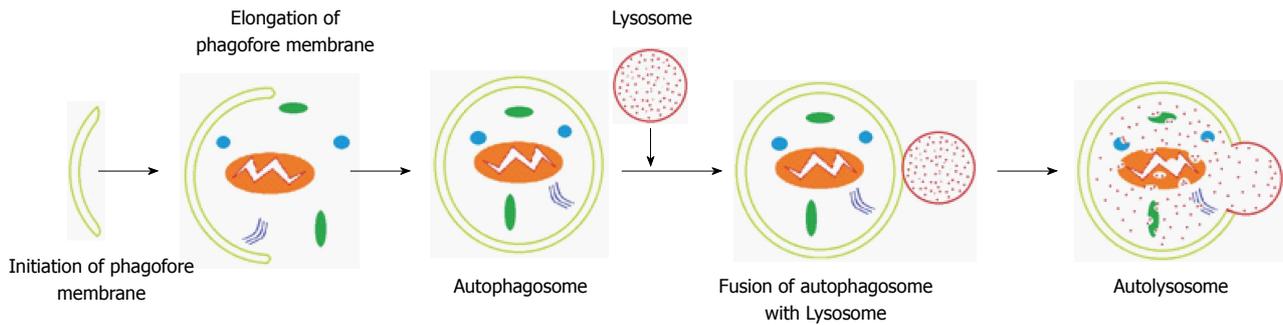


Figure 1 Morphological steps of the autophagy process. Autophagy is initiated with the formation of a phagophore, which sequesters cellular material in a double-membrane vesicle called an autophagosome. The autophagosome fuses with lysosomes to form an autolysosome.

complex interacts with ATG16L1 to form a multimeric ATG12-ATG5-ATG16L1 conjugate that is located on the outer surface of the autophagosomal membrane. It will dissociate from the membrane upon completion of the autophagosome^[14,15]. The second ubiquitin-like pathway involves the conjugation of the microtubule-associated protein 1-light chain 3 (LC3- I) to the lipid phosphatidylethanolamine (PE) by ATG7 and ATG3, which is an E2-like enzyme, to form the membrane-bound LC3- II. LC3 is initially synthesized as a precursor protein, proLC3, and is immediately processed to LC3- I by ATG4 through cleavage of its C-terminal amino acid. The membrane-bound form of LC-3, LC-3 II, is recruited to both sides of the autophagosomal membrane^[16,17]. After fusion with lysosomes, LC3- II on the cytoplasmic face of the autolysosome can be delipidated by ATG4 and recycled, whereas proteins located on internal surface of the autophagosome are processed for degradation by lysosomal enzymes in autolysosomes. During the maturation process, lysosomal-associated membrane protein 2 and the Ras-related protein Rab-7a facilitate autophagosome fusion with endocytic and lysosomal compartments to form an autolysosome. Autophagic cargo is then degraded through the activity of lysosomal proteases^[18-21].

AUTOPHAGY: AN IMPORTANT SWITCH IN CANCER PATHOGENESIS

Autophagy plays crucial roles in the pathogenesis of various human diseases, including cancer, neurodegenerative diseases, infection, and cardiovascular, metabolic, and pulmonary diseases, and aging^[22]. The currently accepted hypothesis is that autophagy has dual, contradictory roles in carcinogenesis (Figure 2). First, autophagy is a surveillance mechanism in normal cells, where it acts to protect cells from malignant transformations by removing damaged organelles and aggregated proteins and reducing DNA damage, reactive oxygen species (ROS) and mitochondrial abnormalities. However, autophagy also supports tumor formation by providing access to nutrients that are critical to the metabolism and growth of tumor cells, and by inhibiting

cellular death and increasing drug resistance^[7,23]. The response of cells to autophagy during cancer metastasis is stage dependent. Autophagy may help to reduce cancer metastasis in the early steps of tumor cell dissemination by promoting inflammatory responses against tumors. Furthermore, autophagy limits tumor necrosis and the expansion of dormant cancer cells into micrometastases, in tandem with impairing oncogene-induced senescence^[24]. Autophagy seems to support metastasis during advanced stages of cancer by increasing the survival of detached metastatic cells in the absence of extracellular matrix, and by supporting the dissemination of cancer cells to distant organ sites by triggering tumor cells that lack a connection with the extracellular matrix in the new environment to shift to a dormant state until appropriate conditions occur^[24,25].

Autophagy as a suppressor during early stages

Autophagy can prevent the transformation from normal to malignant through several suppressive mechanisms. An appropriate autophagic response is necessary for genome stability and for the clearance of mutagens because it acts to prevent the accumulation of the genetic defects that accompany malignant transformations. Damaged mitochondria and the redox-active aggregates of ubiquitinated proteins are removed by autophagy, resulting in avoidance of the overproduction of highly genotoxic ROS^[26]. Inhibition of autophagy switches off this protection and can expose cells to ROS cytotoxicity, which promotes the activation of oncogenes^[27,28]. In addition to mitophagy, autophagy supports genomic stability by enabling the discarding of micronuclei that are produced by cell cycle anomalies^[29], and it may also promote autophagic cell death, known as type II programmed cell death, under certain conditions^[30,31].

The impact of autophagy on tumor progression exhibits a significant degree of context dependence^[23]. BECN1 gene studies in hormone-related cancers unmasked, for the first time, the possible tumor suppressing role of autophagy^[32,33]. There remains significant debate regarding the role of BECN1 as a tumor suppressor due to the proximity of BECN1 to BRCA1, a well-known tumor suppressor gene. Both of these genes are located on

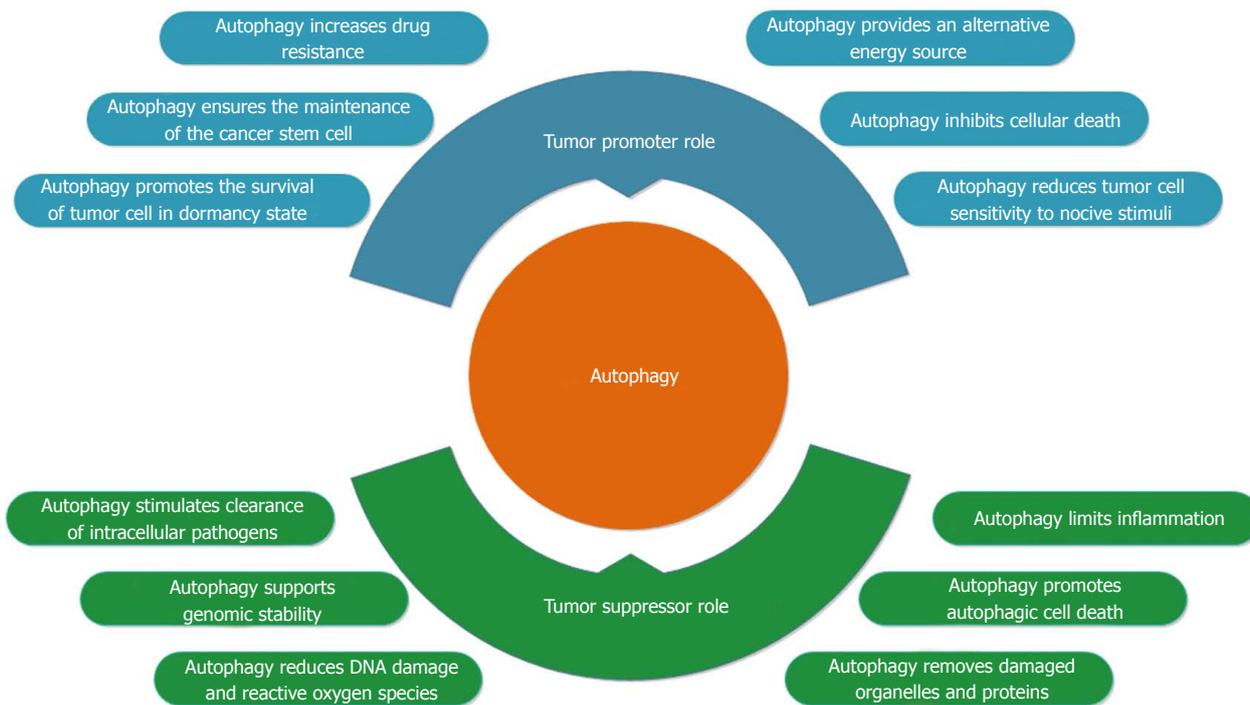


Figure 2 The dual and contradictory roles of autophagy in cancer. Autophagy can potentially act as either a promoter or an inhibitor during the transformation from normal cell to malignant cell. Autophagy supports tumor formation by providing an alternative energy source, increasing drug resistance, inhibiting cell death, promoting the survival of tumor cells in a dormant state and ensuring the maintenance of cancer stem cell compartments. Autophagy protects normal cells from malignant transformation by removing damaged organelles and proteins, reducing DNA damage and reactive oxygen species, supporting genomic stability, promoting autophagic cell death, limiting inflammation and stimulating the clearance of intracellular pathogens.

human chromosome 17q21^[34]. The role of autophagy as an important tumor suppressive process that has been demonstrated in murine experiments. Lack of BECN1 gene in embryoid bodies leads to embryonic death^[35], and mice with a heterozygotic deletion of BECN1 demonstrate increased susceptibility to tumorigenesis in multiple tissues^[36,37]. Similarly, mice deficient for ATG5 and ATG7 died after birth^[38,39], while mice with mosaic deletion of ATG5 and liver-specific ATG7-deficient mice developed only benign liver adenomas^[40]. Mice lacking autophagy genes ATG5 or ATG7 acquired premalignant pancreatic cancer, while the progression to pancreatic cancer driven by KRasG12D was blocked^[41]. ATG7 deletion in a murine model (BrafV600E-induced lung cancer) initially accelerated the proliferation of tumor cells, but at later stages of tumorigenesis it reduced tumor burden, blocked conversion to a more malignant phenotype and increased the life spans of experimental mice^[42]. In the absence of autophagy, the advance to cancer can be arrested, resulting in protection from conversion into malignant cells. Progression to a malignant phenotype may require additional genetic alterations^[43].

In addition, autophagy is involved in both innate and adaptive immune responses, by which it prevents the establishment and proliferation of malignant cells^[44]. Malignant transformation can be stimulated by an inflammatory microenvironment, which contains high amounts of potentially genotoxic ROS as well as various

mitogenic cytokines^[45]. Autophagy limits inflammation by efficiently disposing of inflammasomes, thereby inhibiting the pro-inflammatory signals that are delivered by some pattern recognition receptors, such as RIG-I-like receptors^[46], and limiting the abundance of B-cell CLL/lymphoma 10, a protein that is involved in pro-inflammatory NF-κB signaling^[47]. Autophagy ensures a well-coordinated and appropriate response, enabling crucial cells in the immune system to develop properly and to produce interferon, secrete antimicrobial peptides or present antigens to stimulate adaptive immunity. Dying malignant cells may determine innate and/or adaptive antitumor immune responses by recruiting antigen-presenting cells and other cellular components of the immune system. Thus, defects in autophagy may prevent the host immune system from properly recognizing and eliminating premalignant and malignant cells. Moreover, autophagy mediates potent anti-inflammatory effects^[48,49].

Autophagy plays a key role in the first line of defense against pathogens and thus has anticarcinogenic effects that combat viral and bacterial infections. A xenophagic response is required for the stimulation of pathogen-specific immune responses and for the rapid clearance of intracellular pathogens^[48]. Some of these processes are associated with digestive cancers (*e.g., Helicobacter pylori*, which is associated with gastric carcinoma, or *Streptococcus bovis*, which may cause colorectal carcinoma)^[50,51].

Autophagy as a promoting factor during late stages

Autophagy seems to promote malignant progression and resistance to therapy following the initiation of tumor growth^[2,27]. As a conserved cellular survival mechanism, tumor cells can use autophagy to provide a backup energy source for survival and expansion^[52]. During the progression of tumors, malignant cells are under metabolic stress as a result of a high proliferation rate and exposure to hypoxia, and nutrient deprivation due to inadequate blood supply or selective pressure from therapeutic intervention^[53]. Tumor cells usually have a high proliferation rate, which demands more energy and resources than normal cells, and both ATP and metabolites can be obtained by increasing autophagy^[54]. Although angiogenesis does occur in tumors, the availability of glucose and glutamine is reduced in some tumor regions due to the leakiness of tumor-associated vessels and continued hypovascularization^[55].

Autophagy is activated in the hypoxic areas of tumors, and the inhibition of autophagy by AKT activation or by monoallelic disruption of BECN1 promotes cell death specifically in those regions. These results support hypothesis that tumor cells can use autophagy as a surveillance mechanism under metabolic stress conditions, to provide an alternative energy source for the survival and proliferation of malignant cells^[52].

The pro-malignant role of autophagy has been demonstrated in tumor studies in which the inhibition of autophagy was linked to reduced tumor processes. Moreover, down-regulating the expression of essential autophagy proteins impaired tumor growth and led to the accumulation of abnormal mitochondria and reduced oxygen consumption, and autophagy was necessary to support the growth of Ras-driven tumors^[56]. However, increased autophagy has also been associated with poor outcomes and short disease-free periods in human pancreatic cancers^[57]. *In vitro* studies have shown that the survival of Ras-driven cancer cells requires autophagy and that gaining autophagy results in a marked increase in the survival of malignant cells under conditions of metabolic stress^[28]. Inhibiting autophagy by deleting ATG5 prevents the progression of premalignant lesions to cancer in either a p53-independent or p53-dependent manner^[41,58]. Furthermore, deletion of ATG7 decreases the tumor growth rate and induces nonmalignant tumor formation. In addition, non-Ras-driven tumoral cell types also need autophagy for survival, and the loss of autophagy has been shown to inhibit malignant tumor development. For example, FIP200 deletion significantly reduced proliferation and suppressed mammary tumor initiation and progression in a mouse model of breast cancer driven by the PyMT oncogene^[59]. In a Palb2 knockout mouse model, heterozygous deletion of the autophagy gene BECN1 reduced Palb2-associated mammary tumorigenesis in a p53-dependent manner, indicating that in the presence of DNA damage and oxidative stress, autophagy can support tumor development by suppressing p53^[60].

Autophagy can improve the resistance of cancer

cells to detachment from the basal membrane, resulting in transformed cells that are less sensitive to therapy-induced cell death. Moreover, this activity sustains the survival of cancer cells that enter a state of dormancy or senescence in response to therapy and ensures the maintenance of the cancer stem cell compartment^[23].

Autophagic responses favor the growth and progression of established tumors by reducing their sensitivity to different stimuli that would normally promote their death^[61]. KRasG12D-driven pancreatic adenocarcinoma cells that enter a state of dormancy in response to oncogene ablation have recently been shown to activate autophagy to efficiently counteract metabolic stress^[62], demonstrating the functional and phenotypic features of cancer stem cells. In addition, mammary cancer stem cells are often characterized by elevated autophagic flux, and their ability to efficiently form tumors *in vivo* appears to rely on autophagy, as tumor formation can be abolished through the genetic inhibition of BECN1 or ATG4A^[63,64]. Thus, autophagy may also sustain tumor progression by preserving the viability of the cancer stem cell compartment and/or by promoting the persistence of dormant cancer cells.

Moreover, autophagy is required not only for the emission of immunostimulatory signals by malignant cells succumbing to specific anticancer agents but also for the activation of tumor-targeting innate and adaptive immune responses^[49]. Cancer cells that have been isolated from established tumors where autophagy was inhibited were less resistant to exogenous stimuli than their wild-type counterparts^[61]. In line with these data, autophagy-deficient tumors are often more sensitive to several chemotherapeutic agents and radiation therapy than their autophagy-proficient counterparts^[65,66]. Cancer cells that are exposed to therapeutic interventions can also undergo senescence. Although senescent cells do not proliferate, they may support disease relapse by releasing a wide panel of pro-inflammatory and mitogenic cytokines into the microenvironment^[67].

AUTOPHAGY GENE SWITCHES TO CRC

The autophagy machinery involves multiple genes and proteins that have critical functions in complex autophagic pathways, and these genes may be involved in the important switch from normal to colorectal pathology under specific conditions (Table 1).

LC3 gene

The LC3 gene family encodes three isoforms (LC3A, LC3B, and LC3C) and is the mammalian homologue of yeast ATG8^[68]. The isoform LC3B is cleaved into the soluble form LC3B-I, which is conjugated with PE to generate the lipidated form (LC3B-II). LC3B-II accumulates specifically on nascent autophagosomes and is one of the most widely and reliably used markers for autophagy^[69]. LC3 was the first autophagy marker proposed to be involved in human CRC^[70]. LC3-II is overexpressed in CRC compared to normal tissue,

Table 1 Autophagy-related genes in colorectal cancer

Gene/protein	Expression level in colorectal cancer
LC3/LC3- II	Higher expression, especially in advanced stages ^[20] Higher expression associated with aggressiveness ^[71] Higher perinuclear expression associated with positive prognosis ^[77] Higher levels in DLD-1 and SW480 CRC lines treated with autophagy inhibitors ^[72] Higher levels in CRC cell lines treated with 5-FU ^[73] Higher levels in CRC cell lines treated with 5-FU and radiotreated ^[74] Lower levels associated with good outcome and treatment response ^[75,76] Negative expression associated with poor clinical outcome and survival ^[87]
BECN1/ Beclin-1	Higher expression, negatively linked to metastasis ^[82] Higher expression associated with favorable outcome ^[83] Higher expression associated with longer survival in patients treated with 5-FU ^[84] Higher expression associated with a worse survival in patients treated with 5-FU ^[85] Higher expression associated with metastasis and worse prognosis ^[86] Lower levels associated with increased survival in advanced CRC patients treated with cetuximab ^[75,76] Lower levels associated with poor clinical outcome and survival ^[87] Lower levels associated with a good response after chemoradiation in patients with rectal cancer ^[88]
ATG5	Higher levels associated with lymphovascular invasion ^[92] Lower levels ^[91] Lower expression associated with poor clinical outcome survival ^[87] Lower expression enhanced sensitivity to oxaliplatin ^[93]
ATG10	Higher expression associated with tumor lymph node metastasis and poor survival ^[95]
ATG16L1	ATG16L1T300A polymorphism improved overall survival in human CRC patients ^[116]
BCL2/Bcl-2	Higher levels associated with migration and invasion ^[105] Higher levels associated with resistance to paclitaxel ^[106]
Bif-1	Lower levels ^[109]

LC3: Microtubule-associated protein 1 light chain 3; CRC: Colorectal cancer; 5-FU: 5-fluorouracil; Bif-1: Bax-interacting factor 1; BECN1: Beclin 1; ATG5: Autophagy related 5; BCL2: B-cell CLL/lymphoma 2.

especially in advanced stages^[20]. Zheng *et al.*^[71] reported that LC3B- II was overexpressed in cancer cells and that autophagy enhanced the aggressiveness of CRC. LC3B expression in the peripheral areas of CRC tissues was correlated with tumor differentiation, growth pattern at the tumor margin, pN and pStage, as well as vessel and nerve plexus invasion. An increased level of LC3- II protein was found in DLD-1 and SW480 CRC-derived cell lines that were treated with a combination of autolysosome inhibitors. Association with 3-methyl adenine (3-MA), an inhibitor of PI3K, blocks autophagosome formation and led to increased apoptosis in treated CRC cell lines^[72]. The treatment of CRC cell lines with 5-fluorouracil (5-FU) activated the autophagic process as a protective mechanism in cancerous cells, increased LC3-II levels and reduced the rate of apoptosis compared with untreated cell lines, and an increase in the apoptotic rate was induced by adding 3-MA to 5-FU^[73]. Similar results were reported by Schonewolf *et al.*^[74], who reported that both 5-FU treated and radiotreated CRC cell lines showed an increase in autophagy. After adding chloroquine (CQ) to the treatment, these authors reported an increase in the sensitivity of malignant cells to apoptosis. However, in early stages, LC3- II expression levels were decreased compared with normal tissue^[20]. A low LC3 value has been associated with a good response to treatment and a good survival prognosis, especially in patients with advanced CRC^[75,76]. Perinuclear LC3A expression has been shown to be a positive predictor in patients with stage II A-III colorectal adenocarcinomas who

were treated with only surgery, whereas an increased autophagic response was linked to metastasis and a worse prognosis^[77].

BECN1 gene

BECN1, the mammalian orthologue of yeast ATG6, encodes the beclin-1 protein, which exerts its biological activities through three identified structural domains: A Bcl-2 homology domain, a central coiled-coiled domain and an evolutionarily conserved domain^[78]. Beclin-1 plays a pivotal role in autophagy as a component of the autophagy class III PI3K complex. By interacting with different factors, it regulates autophagy pathways, resulting in the gain (*e.g.*, AMBRA 1, UVRAG) or loss (*e.g.*, Bcl-2) of autophagy. Moreover, beclin-1 dysfunction has been linked to immune disorders, neurodegenerative diseases and cancer^[79].

BECN1 plays a controversial role in colorectal carcinomas in that it supports tumorigenesis^[80] but may also inhibit CRC cell growth^[81]. Higher expression levels of BECN1 have been reported in malignant colorectal tissue than in normal colorectal mucosa^[82], with overexpression being especially associated with advanced stages of CRC^[75,83-85]. Using immunohistochemistry, Ahn *et al.*^[80] showed increased BECN1 expression in 95% of colorectal carcinoma samples compared to normal mucosal epithelial tissue, but they found no significant association with invasion, metastasis or stage. High BECN1 expression has been linked to a good prognosis and longer survival in patients with stage IIIB colorectal carcinoma^[83]. Consistent with these findings, an

increased level of BECN1 expression was strongly associated with longer 5-year survival in patients with locally advanced colon carcinomas who were treated with 5-FU chemotherapy for six months after surgery^[84]. Overexpression of BECN1 in patients with resected stage II and III colon carcinomas who were treated with 5-FU-based adjuvant therapy was associated with worse overall survival, supporting a role for autophagy in drug resistance^[85]. Moreover, in a meta-analysis, overexpression of BECN1 was associated with a poor prognosis and metastasis in patients with CRC^[86]. Furthermore, low levels of BECN1 were correlated with a longer survival in advanced CRC patients who were treated with cetuximab-containing chemotherapy^[75,76]. Supporting this hypothesis, a lack of the expression of the autophagy-related proteins LC3B, ATG5 and beclin-1 is associated with poor clinical outcomes and poor survival in CRC patients^[87]. Rectal adenocarcinoma patients exhibiting low expression levels of BECN1 were more likely to experience a good response to chemoradiation than patients with increased expression levels of BECN1^[88]. Moreover, the expression levels of BECN1 were reduced in a panel of human neoplasms, including brain tumors and gastric and colorectal carcinomas^[89].

ATG5 gene

ATG5 protein is encoded by the *ATG5* gene and forms a complex with ATG12 that participates in autophagosome membrane elongation^[22]. Mutations in the *ATG2B*, *ATG5*, *ATG9B*, and *ATG12* genes have been associated with CRC and gastric cancer^[90]. An association between mutations in the *ATG5* gene and reduced levels of ATG5 protein expression has been shown in gastrointestinal cancers, including CRC^[91]. ATG5 expression was down-regulated in 95% of CRC patients and, interestingly, increased ATG5 expression was associated with lymphovascular invasion^[92]. Other research showed that ATG5 is down-regulated in colorectal carcinoma, in both tissue samples and cell lines, and that down-regulation of ATG5 in CRC enhanced sensitivity to oxaliplatin^[93]. Heterozygous deletion of *ATG5* predisposed mice to intestinal adenoma growth and enhanced the antitumor effect of interferon gamma. In CRC mouse models, treatment with ursolic acid promoted autophagic cell death through a path mediated by ATG5^[94].

ATG10 gene

The *ATG10* gene has been mapped to chromosome 5 and encodes an E2 ubiquitin ligase-like enzyme that has essential functions in vesicle elongation, where it catalyzes the conjugation of ATG5 and ATG12^[22]. *ATG10* was found to be upregulated in CRC tissues and high protein expression of *ATG10* was associated with tumor lymph node metastasis and invasion. Moreover, the presence of *ATG10* was correlated with poor survival, indicating that *ATG10* may be a potential prognostic marker for CRC^[95].

AMBRA1 gene

The *AMBRA1* gene encodes the activating molecule in beclin-1-regulated autophagy (Ambra1) protein, which has roles in autophagy, cell growth, cell death, embryonic development and carcinogenesis^[96]. *AMBRA1* is mutated in a subset of colorectal neoplasms^[97].

UVRAG gene

The UV radiation resistance-associated gene (UVRAG) encodes a tumor suppressor protein that induces autophagy by interacting with BECN1. In addition to its function in autophagy, UVRAG is also involved in endocytic trafficking, DNA damage repair and apoptosis^[98]. UVRAG, in association with BECN1, supports the maintenance of genomic stability by protecting established CRC cells against radiation-induced DNA damage^[99]. UVRAG is heterozygous mutated in a high proportion of gastric and colonic tumors^[100,101].

BCL2 gene

The *BCL2* gene encodes the antiapoptotic B-cell lymphoma 2 (Bcl-2) protein, which inhibits autophagy by directly binding to the BH3 domain of beclin-1 and blocking its activity^[102]. A recent report suggested that the prosurvival Bcl-2 protein modulates autophagy only indirectly, by inhibiting the apoptosis mediators Bax and Bak^[103]. Bcl-2 has been associated with migration and invasion of malignant cells and with the prevention of apoptosis in pT3 CRC patients^[104,105]. In addition, the overexpression of Bcl-2 in CRC was correlated with resistance to paclitaxel^[106]. Furthermore, the role of Bcl-2 in modulating autophagy has been investigated in different cancer cell lines, including colon carcinoma, where the deletion of the BH4 domain in the Bcl-2 protein in HT29 colon carcinomas was not found to affect tumorigenicity^[107].

Bif-1 gene

The *Bif-1* gene encodes Bax-interacting factor (Bif-1), also known as endophilin B1, which is involved in the control of membrane dynamics in cytosolic organelles, such as the Golgi complex and mitochondria, as well as in autophagosomes. Bif-1 induces the formation of autophagosomes and modulates autophagy-enhancing PI3K lipid kinase activity by interaction with beclin-1 through UVRAG^[108]. The expression of Bif-1 was found to be reduced in colorectal carcinomas and the loss of Bif-1 suppressed programmed cell death and promoted colon adenocarcinomas. Bif-1 null mice developed normally, with the exception of an enlarged spleen, but they had an increased incidence of spontaneous tumor formation: 82.8% of Bif-1 null mice developed lymphoma compared with 14.3% of their wild-type counterparts^[109].

IBD susceptibility genes

Autophagy has also been linked to CRC through inflammatory bowel disease (IBD). In the complex pathogenesis leading to colitis-associated cancer, the

severity of inflammation is a risk factor for CRC^[110]. Cytokines released by epithelial and immune cells play an important role, and autophagy can affect the regulation of both inflammation and immune system functions^[22]. Autophagy contributes to intestinal homeostasis by ensuring intracellular defenses against microbes, by maintaining the integrity of secretory granules in Paneth cells, and by regulating the inflammasome or mediating antigen presentation^[111]. Genome-wide association studies provided the first link between autophagy and IBD by showing that the ATG16L1 T300A polymorphism is associated with an increased risk of Crohn's disease (CD)^[112-114]. In addition, IRGM, NOD2, and LRRK2 have been identified as additional markers of CD risk, and autophagy and DAP1 were associated with ulcerative colitis^[115]. Recently, the ATG16L1T300A polymorphism was found to improve overall survival in human CRC patients and to enhance the production of type I interferon^[116].

AUTOPHAGY DRUGS IN CRC

Recent data indicate that only tumors that utilize excessive levels of autophagy, even in nutrient-rich conditions and in the absence of stressful stimuli, respond to autophagy inhibitors *in vivo*^[117]. This suggests that only a fraction of cancer patients may benefit from the administration of autophagy inhibitors. Along similar lines, autophagy has been shown to underlie, at least in part, the therapeutic activity of some anticancer regimens^[118,119].

Autophagy promotes cancer cell survival under stressful conditions or nutrient deprivation and thus may contribute to chemoresistance. The drugs targeting various autophagy pathways can either induce gain or loss of autophagy. The exaggerated and sustained autophagy that is triggered by anticancer therapies can lead to type II cell death in various cancers, including CRC. Increased autophagy in the early stages of cancers can induce protection by suppressing tumorigenesis, necrosis, and chronic inflammation^[13]. On the contrary, inhibition of autophagic influx may accelerate the initial steps of tumorigenesis and reduce protein degradation, and as a consequence, the reduced protein turnover might induce the early tumor progression.

In advanced stages, tumor cells use autophagy to survive cellular metabolic stress and to provide essential nutrients to tumor cells that are experiencing ischemia. Therefore, inhibiting autophagy in late-stage cancers can suppress tumor progression by blocking this prosurvival mechanism in nutrient-deprived tumor cells and by preventing protein recycling and cellular growth^[120]. On the other hand, inhibition of autophagy can also lead to a decrease in the antitumorigenic activity achieved by promoting non-apoptotic cell death.

This prosurvival autophagy mechanism can be overcome by inhibition. Autophagy-inhibiting compounds include lysosomotropic agents^[121]. These agents target acidic compartments, such as lysosomes, but are not

specific to tumor cells and therefore have a range of effects on other cells. Lysosomotropic agents cross the lysosomal membrane and are then protonated within the acidic vesicle^[122]. This results in an increased pH, which prevents cellular degradation and indirectly inhibits autophagy. Preclinical studies have demonstrated the effects of lysosomotropic agents, including CQ, which include the indirect modulation of late-stage autophagy^[123]. Furthermore, CQ inhibits phospholipase A2 and lysophospholipid acylhydrolase, enzymes that are required for the acidification of lysosomes^[124].

Treating human colon carcinoma HT29 cells with CQ sensitized mouse colon cancers to antiangiogenic and cytotoxic therapy^[93]. Moreover, the combination of CQ and 5-FU displayed a significant advantage over treatment with 5-FU alone in inhibiting tumor growth in colon 26 cells, which are a CRC cell line^[125]. A combination of the autophagy inhibitor CQ and vorinostat, a histone deacetylase inhibitor, was shown to significantly reduce tumor growth and induce apoptosis in a colon cancer xenograft model^[126]. Notably, the combination of CQ with saracatinib, an inhibitor of Src nonreceptor tyrosine kinase, enhanced apoptotic cell death and resulted in 64% tumor growth inhibition compared with saracatinib alone^[127]. Autophagy inhibitors shown synergy with proteasome inhibitors; for example, the simultaneous use of bortezomib and CQ in a colon cancer xenograft model decreased tumor growth to a greater extent than the use of either of these drugs alone^[128].

Interestingly, treatment of human HCT-15 colon adenocarcinoma culture cells with B-group soyasaponins induced autophagy and suppressed proliferation through a marked increase in autophagic cell death^[129]. In addition to its effects on cell viability and anchorage-independent growth inhibition, the flavonoid quercetin induced autophagic processes in Ha-Ras transformed human colon cells and has been proposed to have anticancer properties^[130]. Vitamin D can trigger autophagy by enhancing BECN1 expression and inducing PI3KC3 expression^[131]. Cetuximab (an antibody for EGFR) generates autophagy and it is currently used to treat *K-Ras* mutation-negative, EGFR-expressing, metastatic CRC^[121]. Moreover, MS-275, a synthetic benzamide derivative of HDAC, promoted Atg7 protein expression and induced autophagy to switch to apoptosis through the modulation of p38 in human colon cancer cells^[132].

Curcumin is a natural polyphenolic compound that is isolated from the plant *Curcuma longa*. In addition to apoptosis, curcumin also promotes autophagic cell death type II^[133] by inhibiting the Akt/mTOR/p70S6K pathway or by activating the ERK1/2 pathway^[134]. The proliferation of HT-29 and HCT-15 human colon cancer cell lines was inhibited by curcumin treatment, which arrested the cell cycle in the G2/M phase with no detected apoptosis^[135]. Curcumin administered in combination with 5-FU plus oxaliplatin resulted in increased inhibition of growth and enhanced apoptosis

in HCT-116 and HT-29 colon cancer cells compared to each of these drugs alone, and these effects were attained mainly through the attenuation of the EGFR and IGF-1R signaling pathways^[136]. The induction of autophagy activation and ROS production was observed in HCT116 human colon cancer cells that were treated with curcumin, and they showed higher mRNA and protein LC3 levels^[137].

Autophagy facilitates cancer cell resistance to chemotherapy treatments, and the inhibition of autophagy may resensitize resistant tumor cells to anticancer therapy, thus enhancing the efficacy of the treatment. For example, imatinib induces nonapoptotic autophagic cell death, while the inhibition of autophagy enhances its cytotoxicity, but only at a late stage^[138]. Autophagy activation was observed in colon cancer stem cells by analysis of the expression of the intestine-specific transcription factor Cdx1, which plays a crucial role in chemoresistance to paclitaxel^[106]. Similarly, autophagy increased resistance to photodynamic therapy-induced apoptosis in CRC stem-like cells^[139]. However, this report did not address whether the protective autophagy that was induced in cancer stem cells was due to a drug-mediated response to stress or to the inherent ability of cancer stem cells to maintain a high threshold for autophagy. Suppression of protective autophagy by 3-MA was reported to enhance the therapeutic efficacy of cisplatin and 5-FU in digestive cancers, including colon cancer^[140].

Many mTOR inhibitors with effective antitumor activity have been developed. However, they also have downstream effects that include the activation of autophagy, which is linked to prosurvival mechanisms in tumor cells through the recycling of damaged cellular contents. The addition of an autophagy inhibitor could solve this complication by excluding this alternate recovery pathway and sensitizing malignant cells to anticancer therapies^[141,142].

Taken together, these observations suggest that autophagy supports the progression of established neoplasms through several mechanisms and that pharmacological inhibitors of autophagy may exert robust antineoplastic effects, at least in some settings.

Future research aimed at exploring the context specific role of autophagy in particular cancer types can provide new opportunities to develop personalized therapeutic strategies based on the regulation of autophagy, and autophagy modulators may become a targetable option for enhancing the efficacy of anticancer therapies used alone or, more likely, in combination with other chemotherapeutic drugs^[120].

CONCLUSION

Multiple genes and proteins are involved in the complex steps of autophagy. Recent evidence has suggested that autophagy plays an important role in all stages of carcinogenesis, by influencing initiation, progression and metastatic capacity in tumors. The precise mechanisms

that involve autophagy in cancer are not yet defined, and they seem to be context dependent, having both promoting and inhibiting roles. During the first steps of cancer, autophagy may have a suppressive effect, whereas it may alternatively act as tumor promoter during advanced cancer stages. It is necessary to determine how these dual roles of autophagy in CRC are regulated and identify the signals, molecules, and mechanisms that enable autophagy to play a dominant pro-malignant role in one situation and the opposite role in another. The most important research on CRC has been focused on several molecules, mainly LC3, BECN1, ATG5, and these studies have produced conflicting results. Several therapeutic agents that modulate autophagy in CRC have been developed and show promising results supporting their use either alone or, more likely, in combination with other drugs. Further research is required to better understand the relationship between CRC and autophagy, and to produce potentially beneficial agents for the prognosis and therapy of CRC.

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2015 Advances in Gastric Cancer

Breakthrough therapy for peritoneal carcinomatosis of gastric cancer: Intraperitoneal chemotherapy with taxanes

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Abstract

The effect of chemotherapy on peritoneal carcinomatosis (PC) of gastric cancer remains unclear. Recently, the intraperitoneal (IP) administration of taxanes [*e.g.*, paclitaxel (PTX) and docetaxel (DOC)] during the perioperative period has shown promising results. Herein, we summarized the rationale and methodology for using IP chemotherapy with taxanes and reviewed the clinical results. IP administered taxanes remain in the IP space at an extremely high concentration for 48-72 h. The drug directly infiltrates peritoneal metastatic nodules from the surface and then produces antitumor effects, making it ideal for IP chemotherapy. There are two types of perioperative IP chemotherapy with taxanes: neoadjuvant intraperitoneal and systemic chemotherapy and sequential perioperative intraperitoneal chemotherapy (SPIC). In SPIC, patients receive neoadjuvant IP chemotherapy and the same regimen of IP chemotherapy after cytoreductive surgery (CRS) until disease progression. Usually, a taxane dissolved in 500-1000 mL of saline at ordinary temperature is administered through an IP access port on an outpatient basis. According to phase I studies, the recommended doses (RD) are as follows: IP DOC, 45-60 mg/m²; IP PTX [without intravenous (IV) PTX], 80 mg/m²; and IP PTX (with IV PTX), 20 mg/m². Phase II studies have reported a median survival time of 14.4-24.6 mo with a 1-year overall survival of 67%-78%. A phase III study comparing S-1 in combination with IP and IV PTX to S-1 with IV cisplatin started in 2011. The prognosis of patients who underwent CRS was better than that of those who did not; however, this was partly due to selection bias. Although several phase II studies have shown promising results, a randomized controlled study is needed to validate the effectiveness of IP chemotherapy with taxanes for PC of gastric cancer.

Key words: Taxane; Paclitaxel; Docetaxel; Carcinoma;

Gastric cancer; Intraperitoneal infusions; Cytoreduction surgical procedures

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Core tip: Herein, we provided an overview on the recent advances in intraperitoneal (IP) chemotherapy using taxanes (*e.g.*, paclitaxel and docetaxel) for peritoneal carcinomatosis of gastric cancer. In particular, we focus on the rationale of IP chemotherapy with taxanes, treatment methodology, and results of current clinical studies. Intraperitoneally administered taxanes remain in the IP cavity for a long time, and they directly infiltrate the peritoneal metastatic nodule from the surface. Therefore, the repeated intra-abdominal administration of taxanes through an IP access port is needed to increase the antitumor effect of IP chemotherapy.

Yamaguchi H, Kitayama J, Ishigami H, Kazama S, Nozawa H, Kawai K, Hata K, Kiyomatsu T, Tanaka T, Tanaka J, Nishikawa T, Otani K, Yasuda K, Ishihara S, Sunami E, Watanabe T. Breakthrough therapy for peritoneal carcinomatosis of gastric cancer: Intraperitoneal chemotherapy with taxanes. *World J Gastrointest Oncol* 2015; 7(11): 285-291 Available from: URL: <http://www.wjgnet.com/1948-5204/full/v7/i11/285.htm> DOI: <http://dx.doi.org/10.4251/wjgo.v7.i11.285>

INTRODUCTION

Gastric cancer is the fourth most common cancer worldwide, and it is the second leading cause of cancer-related deaths^[1]. Gastric cancer may disseminate along the inside surface of the peritoneal cavity, leading to peritoneal carcinomatosis (PC). PC is the most frequent mode of metastasis and recurrence in patients with gastric cancer. According to the national registry database of Japan, PC accounted for 51% of deaths in 355 patients with non-curable primary gastric cancer^[2]. The same database also revealed that PC was the most frequent cause of death in 13002 patients who underwent gastrectomy for primary gastric cancer^[2]. Yoo *et al*^[3] reported that in 508 patients who underwent radical gastrectomy for gastric cancer, the first recurrence site was the peritoneum (43.9%) and then a local site (32.5%) followed by the liver (16.9%).

Despite recent advances in chemotherapy regimens for gastric cancer, the effect of systemic chemotherapy on PC remains unclear. Clinical trials on methotrexate + 5-fluorouracil (5-FU), FOLFOX-4, and continuous 5-FU for PC of gastric cancer showed that the median survival time (MST) was 5.2-10.6 mo, and the 1-year overall survival (OS) was 16.2%-40.7%^[4-7].

In alternative treatment modalities, cytoreductive surgery (CRS) combined with hyperthermic intraperitoneal chemotherapy (HIPEC) has been used for treating PC of gastric cancer. Reportedly, the MST and

1-year survival were 9.2-11.5 mo and 35.5%-48.1% respectively^[8-11]. However, CRS + HIPEC should be performed in specialized facilities, because these demanding procedures are associated with a high mortality and morbidity^[12].

The intraperitoneal (IP) administration of anticancer drugs is a reasonable method for treating PC, because an IP administered cytotoxic drug acts directly on the peritoneal metastatic nodules at a high concentration. In HIPEC procedures, mitomycin C (MMC) and/or cisplatin (CDDP) dissolved in heated saline at 42 °C-43 °C are usually administered into the peritoneal cavity^[13].

Recently, the IP administration of taxanes such as paclitaxel (PTX) or docetaxel (DOC) without heating them at the ordinary temperature during the perioperative period in gastric cancer patients with PC has been performed mainly in Japan. Several clinical trials using IP chemotherapy with taxanes have shown promising results^[14-18].

Based on the literature published in the last decade, we summarized the rationale for using IP chemotherapy with taxanes, methodology used for IP chemotherapy, and clinical results of IP chemotherapy in gastric cancer patients with PC.

RATIONALE FOR USING IP CHEMOTHERAPY WITH TAXANES

Taxanes such as PTX and DOC produce cytotoxic effects by inducing excessive polymerization of tubulin and dysfunctional microtubules, which leads to mitotic arrest and cell death^[19,20]. PTX and DOC are water insoluble, and for clinical use, they are solubilized with Cremophor EL (Taxol®; Bristol-Myers Squibb Co.) and Polysorbate 80 (Taxotere®; Aventis Pharma SA), respectively.

Since taxanes are hydrophobic, high-weight molecular materials, IP administered taxanes are gradually drained from the peritoneum through lymphatic stomata that open directly into the pleural space^[21,22]. In contrast, hydrophilic, low-weight molecular materials such as MMC or CDDP are rapidly absorbed through the peritoneal mesothelial layer and into the capillary vessels.

The area under the curve ratios of the intra-abdominal space to the plasma after IP administration of the drug are about 1000 for PTX, 207-552 for DOC, 10-24 for MMC, and 12-21 for CDDP^[23-28]. The prolonged retention of IP administered taxanes within the IP space allows the taxanes to directly penetrate into peritoneal disseminated tumors^[23,29-31], which leads to the destruction of peripheral microvessels of tumor nodules^[32]. However, the depth of infiltration from the surface of the peritoneal disseminated nodules after the one time IP administration of a taxane is limited^[33,34]. In a previous study, we showed that the distance of PTX infiltration reached approximately 100-200 μm from the surface of the tumor^[35]. Therefore, to improve the antitumor effects of taxanes against PC, repeated IP administration is necessary.

Table 1 Phase I studies on intraperitoneal chemotherapy using taxanes for the treatment of gastric cancer with peritoneal carcinomatosis

Ref.	<i>n</i>	Intraperitoneally administered taxanes	Initial dose (mg/m ²)	MTD (mg/m ²)	RD (mg/m ²)	DLT
Kodera <i>et al</i> ^[42]	4	PTX	60	-	-	-
Fushida <i>et al</i> ^[26]	24	DOC	25	60	45	Abdominal pain and diarrhea
Ishigami <i>et al</i> ^[45]	9	PTX	20	30	20	Febrile neutropenia and diarrhea
Fujiwara <i>et al</i> ^[43]	12	DOC	40	-	60	-
Kurita <i>et al</i> ^[44]	18	PTX	40	90	80	Leukocytopenia
Fushida <i>et al</i> ^[16]	12	DOC	35	50	45	Febrile neutropenia and diarrhea

MTD: Maximum tolerated dose; RD: Recommended dose; DLT: Dose-limiting toxicities; PTX: Paclitaxel; DOC: Docetaxel.

From the perspective of pharmacokinetics and tissue penetration, taxanes are ideal drugs for IP chemotherapy. Moreover, even if taxanes are repeatedly administered intraperitoneally, they rarely cause adhesion of organs in the peritoneal cavity because of their antiproliferative effect. Thus, the distribution of IP administered taxanes across the intra-abdominal space is not hampered by drug-induced peritonitis.

METHODOLOGY OF USING IP CHEMOTHERAPY WITH TAXANES

Perioperative IP chemotherapy with taxanes

There are two types of perioperative IP chemotherapy with taxanes for treating PC of gastric cancer: neoadjuvant intraperitoneal and systemic chemotherapy (NIPS)^[36] and sequential perioperative intraperitoneal chemotherapy (SPIC)^[37]. In NIPS, patients receive 1-6 courses of IP chemotherapy with a taxane as a neoadjuvant therapy; however, they do not receive IP chemotherapy after CRS^[17,38,39]. In SPIC, patients receive several courses of IP chemotherapy preoperatively, and they receive the same regimen of IP chemotherapy after CRS until disease progression^[14-16].

Peritoneal access port system

In most reported studies, a peritoneal access port system was used for IP chemotherapy. However, this device was not used when patients received a single IP administration during staging laparoscopy^[28,39], or if patients received IP administration two times *via* a catheter as neoadjuvant chemotherapy^[17]. A peritoneal access port is implanted into the subcutaneous space of the lower abdomen, and a catheter is placed usually in the pelvic cavity. Taxane dissolved in 500-1000 mL of saline at the ordinary temperature is administered through the peritoneal access port. Thus, using this method, taxanes can be repeatedly administered on an outpatient basis.

Complications associated with the port system occurred in 20.6% of 131 patients at our institution^[40]. Inflow obstruction and infection were the main complications that occurred in 7.6% and 6.9% of patients, respectively. The median period of IP chemotherapy

using the peritoneal port system was 12.9 mo (range, 0.8-61.5 mo). Compared to previous studies on ovarian cancer^[41], the course of IP chemotherapy performed at our institution was much longer, but the complication rate was lower.

The use of a peritoneal port system can facilitate IP administration and reduce the patients' burden of receiving IP chemotherapy. Moreover, the device can provide another benefit to patients, because the peritoneal lavage sample, which is essential for evaluating the effect of IP chemotherapy on PC, can be obtained noninvasively through the peritoneal access port.

CLINICAL STUDIES ON IP CHEMOTHERAPY WITH TAXANES

Phase I study

The findings from six phase I studies on IP chemotherapy with taxanes are summarized in Table 1. PTX was used for intraperitoneally administering agents in three studies, and DOC was used in the other three studies. PTX or DOC was IP administered without other anticancer drugs in two studies^[26,42], DOC was IP administered with S-1 in two^[16,43], PTX was IP administered with S-1 in one^[44], and intravenous (IV) PTX and S-1 was administered in one^[45].

The recommended dose (RD) of DOC IP administration was 45-60 mg/m². The RD of PTX IP administration was 80 mg/m² when PTX was not IV administered, and it was 20 mg/m² when PTX was IV administered. Although the RD of 20 mg/m² in our phase I study was relatively low because we used a combination of IV PTX, the IP PTX concentration remained extremely high for > 72 h.

Dose-limiting toxicities of these phase I studies included grade 3 febrile neutropenia, leukopenia, and diarrhea for the PTX IP regimen; and grade 3 febrile neutropenia, abdominal pain, and diarrhea for the DOC IP regimen.

Phase II study

The findings of six phase II studies on IP chemotherapy with taxanes are summarized in Table 2. PTX was used for IP administered agents in three studies^[14,15,39], and DOC was used in the other three studies^[16,17,38]. The

Table 2 Phase II studies on intraperitoneal chemotherapy using taxanes for the treatment of gastric cancer with peritoneal carcinomatosis

Ref.	n	Method	Intraperitoneally administered agents	MST (mo)	1-yr OS (%)	2-yr OS (%)	5-yr OS (%)
Yonemura <i>et al</i> ^[38]	61	NIPS	DOC (40 mg) + CBDCA (150 mg)	14.4	67		
Ishigami <i>et al</i> ^[14]	40	SPIC	PTX (20 mg/m ²)	22.6	78		
Fujiwara <i>et al</i> ^[17]	18	NIPS	DOC (40-60 mg/m ²)	24.6	76	54	
Imano <i>et al</i> ^[39]	35	NIPS	PTX (80 mg/m ²)	21.3	69	46	14
Yamaguchi <i>et al</i> ^[15]	35	SPIC	PTX (20 mg/m ²)	17.6	77	45	
Fushida <i>et al</i> ^[16]	27	SPIC	DOC (35-50 mg/m ²)	16.2	70	33	

MST: Median survival time; OS: Overall survival; DOC: Docetaxel; CBDCA: Carboplatin; PTX: Paclitaxel; NIPS: Neoadjuvant intraperitoneal and systemic chemotherapy; SPIC: Sequential perioperative intraperitoneal chemotherapy.

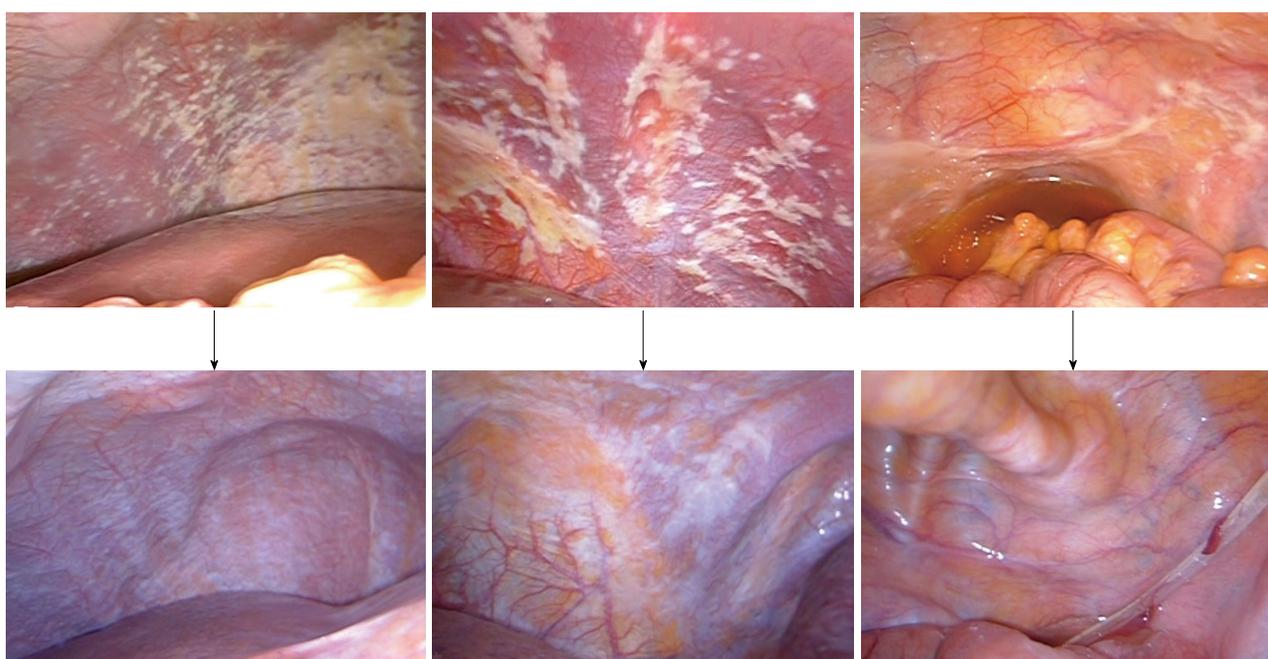


Figure 1 Laparoscopy before and after treatment. Staging laparoscopy (upper) showing peritoneal metastatic nodules in the right subphrenic peritoneum (left), left subphrenic peritoneum (middle), and Douglas pouch (right). The second laparoscopy (lower) revealing that the metastatic nodules have disappeared after 12 courses of the intravenous and intraperitoneal administration of paclitaxel and oral S-1 chemotherapy.

overall response rate among these phase II studies ranged from 55%-71%. The MSTs and 1-year OS were 14.4-24.6 mo and 67%-78%, respectively. The main toxicities were hematologic (e.g., anemia, neutropenia, and leukopenia), and the non-hematological toxic effects were relatively mild. Regarding CRS, gastrectomy with D2 dissection was usually performed. In addition to D2 gastrectomy, peritonectomy was performed only by Yonemura *et al*^[38]. Post-operative complications, ranging 9%-22%, were reported in four studies^[16,17,38,39]. Surgery-related mortality was found in one patient, and the cause of death was sepsis from an abdominal abscess^[38].

In three of six phase II studies, patients received 1-6 courses of NIPS. The MSTs of patients who underwent CRS after NIPS were 20.4-29.8 mo. In the other phase II studies, patients received SPIC. In 2010, we reported on a phase II study on SPIC in 40 gastric cancer patients with PC, which included six cytology positive (CY1)

and macroscopically negative (P0) patients^[14]. Sixteen patients underwent CRS. According to recently updated survival data, the MST was 23.6 mo and the 1-, 2-, and 5-year OS were 78%, 50%, and 18%, respectively.

We performed another phase II study with the same regimen in 35 gastric cancer patients with PC^[15]. However, in this study, CY1P0 patients were excluded, because they may have a better prognosis compared to macroscopic PC (P1) patients. CRS was performed in 21 patients. Patients with peritoneal cancer index (PCI) scores ≥ 20 had a lower survival rate than those with PCI scores < 20 . According to recently updated data, the MST was 18.0 mo, and the 1-, 2-, and 4-year OS were 77%, 42%, and 10%, respectively. The findings from staging laparoscopy and second-look laparoscopy are shown from a representative case (Figure 1).

Fushida *et al*^[16] performed a phase I/II study on SPIC with IP DOC in 27 patients. Fourteen patients underwent CRS and received postoperative IP chemotherapy.

The 1- and 2-year OS of patients who underwent CRS were 92.8% and 62.5%, respectively.

Phase III study

In Japan, a randomized, multicenter, phase III trial (the PHOENIX-GC trial, UMIN000005930) compared S-1 in combination with IV and IP PTX to S-1 with IV CDDP in 180 gastric cancer patients with P1. This study began in 2011, and the final analysis will be obtained in November 2015.

IP chemotherapy with taxanes combined with CRS

If PC can be controlled by IP chemotherapy with a taxane, gastrectomy as CRS is considered to be a reasonable treatment. Because IP chemotherapy as a localized therapy for peritoneal cavity may not have intensive antitumor effects on primary gastric tumors and metastatic lymph nodes. Other than the aforementioned phase II studies, two studies have reported on the treatment results of IP chemotherapy combined with CRS.

Kitayama *et al.*^[18] treated 64 gastric cancer patients with PC who had malignant ascites with IP and IV PTX combined with S-1. CRS without peritonectomy was performed in 34 patients. After CRS, chemotherapy with the same regimen was continued (*i.e.*, SPIC). The MST of these patients and the 1-year OS were 26.4 mo and 82%, respectively. Those of the 30 patients who did not undergo gastrectomy were 12.1 mo and 26%, respectively.

Yonemura *et al.*^[46] performed NIPS with IP DOC and CDDP combined with S-1 in 96 patients. After two cycles of NIPS, 82 patients underwent CRS (gastrectomy with D2 dissection and peritonectomy). Complete cytoreduction was achieved in 58 patients. The MST and 1-year OS of patients who underwent CRS was 14.4 mo and 61%, respectively. The MST of patients who underwent complete cytoreduction and those who did not undergo CRS were 21.1 mo and 9 mo, respectively.

In these reports, the prognosis of patients who underwent CRS was better than that of those who did not. However, this survival difference was partly due to a strong selection bias since CRS was performed only in good responders. A randomized controlled study will need to be performed in order to determine the significance of CRS.

DISCUSSION

It is important whether IP chemotherapy with taxanes is needed after CRS. Yonemura *et al.*^[46] reported that 22 of 61 patients who received NIPS with complete CRS had recurrence in the peritoneum. Fujiwara *et al.*^[17] suggested that IP chemotherapy may have been needed in their patients, because 8 of 14 patients who had curative surgery following NIPS died from peritoneal recurrence. It is reasonable to consider that IP chemotherapy with a taxane should be continued as long as possible even

after CRS to suppress the development of microscopic cancer cells that may still exist in the whole peritoneal cavity. Therefore, we consider that SPIC is better suited for treating PC of gastric cancer.

Another important issue is how the criteria for performing CRS are determined. If patients do not respond to IP chemotherapy, CRS should not be performed. We have performed CRS in patients who have met the following criteria: (1) no distant metastasis, except in the peritoneum; (2) a negative peritoneal lavage cytology; and (3) a second-look laparoscopy reveals that the peritoneal metastatic nodules are reduced. To select eligible patients for CRS more precisely, novel and useful biomarkers that reflect a good response to IP chemotherapy are needed.

Phase III studies on IP chemotherapy with taxanes have been reported in the gynecological field, especially for PC of ovarian cancer. IP PTX with systemic chemotherapy for PC of ovarian cancer showed a significant survival benefit^[47]. Based on the findings from these phase III studies^[47-49], the National Cancer Institute has recommended IP chemotherapy in patients with optimally debulked ovarian cancer^[50].

Regarding the treatment of PC from gastric cancer, there are promising findings from several phase II studies with IP chemotherapy using taxanes. However, it is difficult to draw any definitive conclusions about the overall clinical usefulness of this treatment method until we obtain the findings from the PHOENIX-GC phase III trials.

In conclusion, IP administered taxanes remain in the IP cavity for a long period, and they produce antitumor effects by infiltrating peritoneal metastatic nodules from the surface. In addition, repeated IP administration of taxanes through an IP access port before and after CRS seems necessary for improving the effect of IP chemotherapy. Lastly, IP chemotherapy with taxanes for PC from gastric cancer is safe and feasible. Although several phase II clinical studies have shown promising results, further randomized phase III clinical trials are needed to validate IP chemotherapy with taxanes for gastric PC.

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2015 Advances in Gastric Cancer

Individualized treatment of gastric cancer: Impact of molecular biology and pathohistological features

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Abstract

Gastric cancer is one of the most common malignancies worldwide. The overall prognosis remains poor over the last decades even though improvements in surgical outcomes have been achieved. A better understanding

of the molecular biology of gastric cancer and detection of eligible molecular targets might be of central interest to further improve clinical outcome. With this intention, first steps have been made in the research of growth factor signaling. Regarding morphogens, cell cycle and nuclear factor- κ B signaling, a remarkable count of target-specific agents have been developed, nevertheless the transfer into the field of clinical routine is still at the beginning. The potential utility of epigenetic targets and the further evaluation of microRNA signaling seem to have potential for the development of novel treatment strategies in the future.

Key words: Gastric cancer; Molecular biology; Targeted therapy; Personalized medicine; Signaling pathway

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Core tip: Advanced gastric cancer remains a frequent malignancy with poor prognosis despite multimodal treatment options. Surgery alone has been demonstrated not to be the optimal strategy and is predominantly limited to cases without distant metastases. About one half of gastric cancer patients cannot be cured. Due to its individual heterogeneity on the molecular level these tumors frequently do not respond to systemic treatment. The implementation of the growing knowledge about the molecular behavior of gastric cancer in the development or improvement of target-specific treatment strategies might be one of the major challenges for the next decades.

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GENERAL CLINICAL ASPECTS

Gastric cancer is still one of the leading oncologic challenges due to its frequent occurrence as well as its poor prognosis^[1]. The ongoing improvement of surgical techniques and perioperative care over the past decades have not only extended the repertoire of treatment options with curative intent but also have contributed to the reduction of perioperative morbidity. Thus, currently about 50% of all gastric cancer patients can be treated curatively and the majority of these patients undergo the surgical treatment without severe complications^[2]. But still one half of all gastric cancer patients have to be regarded as palliative cases with no chance for long term survival and even the curatively resected patients face an overall recurrence rate of 50%^[3].

In view of this development it can be assumed that further evolvement of surgical treatment will not improve tumor-related survival substantially. The molecular biology of the individual tumor might be one important key to a better understanding of the disease and an advancement in the prognosis of gastric cancer patients.

The knowledge about the molecular biology of gastric cancer is of high interest for several reasons: (1) aberrations at the genomic as well as at the proteomic level might be useful as biomarkers for exact classification; (2) molecular markers may further improve and refine tumor staging; (3) knowledge about the individual molecular signature may enable a personalized and target specific treatment; and (4) molecular presentation of the tumor and target specific treatment may lead to an improved prognosis.

UNDERSTANDING OF THE MOLECULAR BIOLOGY: GENERAL CHALLENGES

The understanding of molecular biology of gastric cancer is crucial for the appraisal of its clinical behavior and to control the tumor growth with all its consequences. As in almost all other tumor entities the following characteristics may challenge the establishment of an effective treatment: (1) every individual tumor presents with a unique pattern of molecular variance, comparable with an individual fingerprint; (2) in a certain manner every tumor can be regarded as an autonomous organism which in fact means that tumors do not consist of a homogenous tissue mass but show a regional heterogeneity; (3) over time every tumor changes spontaneously in its molecular biological behaviour; and (4) every tumor reacts in a distinct manner to treatment attempts.

These aspects are basically important in un-targeted treatment approaches as the application of conventional cytostatic substances or surgery but are even more important for target-specific treatment strategies. In view of the multidimensional complexity of molecular tumor biology it becomes clear that it is unlikely to find "the single one agent" to achieve a safe and sustainable

tumor control.

CURRENT STATE OF THE ART IN MOLECULAR TARGETED TREATMENT

Growth factors, growth factor receptors and downstream features

Epithelial growth factor: To date, four different types of epithelial growth factor receptors (EGFR) have been identified, also called as ErbB1-4^[4]. Once activated, they form homo- or heterodimers and then become internalized within the cell. From there three different pathways (MAP-kinase pathway, STAT pathway and PI3K pathway) can be activated, subsequently leading to the transmission of the signal into the nucleus and specific regulation of gene expression by activated cyclinD1, iNOS, B-myb, COX2 and Aurora kinase 2. With the exception of ErbB2, in addition to the original epidermal growth factors multiple other ligands can bind and activate EGFR: transforming growth factor alpha, epiregulin, amphiregulin and β cellulin. ErbB2 in contrast, can not be activated directly by any growth factor, but can be heterodimerized by other members of the EGFR family^[5].

It has been reported that EGFR overexpression occurs in 60% to 70% of gastric cancer cases, however gene amplification seems to be rather uncommon^[6,7]. EGFR2 measured by fluorescence *in situ* hybridisation was detected in 22% of gastric cancers^[8,9], while it was more frequent in intestinal than in diffuse type gastric cancer according to the Lauren classification (32% and 20%)^[9,10]. EGFR overexpression in gastric cancer was related to poorer survival and poorer response to chemotherapy^[11].

Due to its central role in epithelial signaling as well as its biological properties EGFR became an interesting target for molecular-based treatment and thus there is now a remarkable variety of EGFR-targeted molecules available.

Three main target points have been proposed: the inactivation of the receptor, the stimulation of antibody-dependent cell cytotoxicity and the inhibition of the tyrosine kinase activity by multityrosin kinase inhibitors.

To date, seven monoclonal antibodies targeting EGFR are available: cetuximab, trastuzumab, matuzumab, panitumumab, nimetuzumab, perluzumab and T-DM1^[10].

Cetuximab inhibits the binding of EGF and TGF α to EGFR, furthermore it promotes the internalization of the receptor^[12]. The application of cetuximab is well established in stage 4 colorectal cancer (with k-ras wild type)^[13] and in several head and neck malignancies^[14,15].

Several phase 2 and 3 trials showed a positive effect of the administration of cetuximab combined with standard chemotherapy protocols as a first line therapy with response rates up to 58% and 69% in advanced gastroesophageal junction and gastric cancer (overall survival up to 9.5 mo)^[10,16]. In contrast, cetuximab in combination with cisplatin or irinotecan as a second line

therapy revealed only a marginal benefit on the overall survival (7.1 mo)^[17]. Moreover, cetuximab as a single-agent administration for second line therapy resulted in even lower impact on the overall survival (3.6 to 4 mo) with poor response (9%)^[18].

Cetuximab in combination with several cytostatic substances for neoadjuvant chemotherapy showed response rates up to 70%^[19,20].

Trastuzumab is known to have a broad variety of molecular effects: Binding to the extracellular part of the *her-2/neu* molecule and thus suppressing the intracellular localised tyrosine kinase activity, antibody dependent cell toxicity (ADCC)^[21], activation of natural killer cells, inhibition of angiogenesis and the phosphoinositol-3-kinase signaling pathway (PI3K) as well as cell cycle arrest^[22-24]. The administration of trastuzumab as adjuvant treatment has been approved for node positive breast cancer^[25].

The most important study with respect to gastric cancer is the ToGA trial. It has been shown that those patients who were positive for the *her-2/neu* receptor (22% of all cases) had a significant improvement in tumor response and overall survival when standard chemotherapy was combined with trastuzumab (47% vs 34%, 13.8 mo vs 11.1 mo)^[26]. An innovative and promising further development of trastuzumab, named T-DM1 is currently undergoing clinical testing. In the T-DM1 molecule the trastuzumab antibody is coupled to maytansine, a microtubule polymerization inhibitor which unfolds its effect after internalization of the antibody-receptor complex within the cytosol^[27].

Recently it has been published that *in vitro* the cytotoxic effect of trastuzumab on gastric cancer cell lines significantly increased when the cancer cells were pre-treated by incubation with reovirus serotype 3^[28].

Matuzumab is an IgG1 antibody with ADCC. Unlike cetuximab and nimotuzumab it is a fully humanized molecule. Unfortunately, it has been shown that combination treatment of matuzumab with cytostatic substances is not beneficial for overall survival and response rates^[29].

Panitumumab is an IgG2 antibody. It is routinely used in the treatment of metastatic colorectal cancer. The comparison of combined chemotherapy with or without panitumumab yielded disappointing results with a poorer outcome in the panitumumab group in terms of overall survival and overall response rate (8.8 mo vs 11.3 mo and 42% vs 46%, respectively). Surprisingly, in the subgroup of patients with severe rash the overall survival of patients who received panitumumab-including treatment was significantly improved (10.2 mo vs 4.3 mo)^[30].

Nimotuzumab is similar to matuzumab a fully humanized antibody, known to exhibit ADCC. There is some evidence in the literature that nimotuzumab in combination with cytostatic substances might be effective in squamous cell carcinoma of the esophagus and in glioma. To date, there are two studies available investigating the effect of nimotuzumab plus cytostatic

substances in metastatic gastric cancer. In one study, the overall response rate was improved (63% vs 50%) with similar progression free survival, the other study showed the progression free survival to be slightly improved with similar response rates (5.5 mo vs 3 mo)^[10].

Pertuzumab is an inhibitor of homo - as well as heterodimerization of the EGF receptor. Therefore, it seems to be reasonable to combine pertuzumab with different EGF receptor antagonists like trastuzumab. It is also known to exhibit ADCC. The administration of pertuzumab is approved for metastatic breast cancer^[31]. The combination of pertuzumab and trastuzumab seems to be effective in advanced gastric cancer with overall response rates up to 86%^[32].

Vascular endothelial growth factor: The recruitment of new blood vessels for the supply of the growing tumor with nutrients and oxygen is known to be one of the crucial steps in tumor progression, especially in the development of distant metastases^[33]. Although neoangiogenesis in the tumor environment and physiological angiogenesis partly have similar pathways there are remarkable differences in vessel architecture, vascular permeability as well as a different interplay of endothelial cells and perivascular cells. In this context, vascular growth factors play an crucial role. Vascular growth factors are expressed when tissue hypoxia is present. Several other changes can result in vascular endothelial growth factor (VEGF) up-regulation too, e.g., low pH or silenced tumor suppressor genes like p53^[34].

To date, we know five important factors of angiogenesis: VEGF A-D and placenta derived growth factor. Furthermore, three targets for these growth factors have been detected: vascular endothelial growth factor receptor (VEGFR) 1-3. VEGFR2 seems to be the most important subtype. It is localized on the cell surface of endothelial cells and bone marrow derived endothelial progenitor cells^[35]. VEGFR2 binds to VEGF A, C and D, leading to activation of the PI3K signaling pathway as well as MAP kinase signaling pathway^[36]. Some of the most important down stream effects are the inhibition of apoptosis, the proliferation of endothelial cells and increased endothelial cell migration^[35]. The binding of the mediator molecule to its receptor is substantially increased in the presence of the co-receptors neuropilin 1 and 2. The application of these co-receptors as possible targets for molecular based treatment is currently under development^[37].

Overexpression of VEGF and its downstream molecules is common in numerous malignancies. Interestingly, Takahashi *et al.*^[38] already demonstrated in 1996 that VEGF is more frequently dysregulated in intestinal type than in diffuse type gastric cancer (36% and 16%, respectively). Two different antibodies targeting the VEGF signalling pathway have been shown to be effective and eligible in the treatment of advanced gastric cancer: Bevacizumab and ramucirumab.

Bevacizumab binds to VEGF-A and thus interrupts

the activation of VEGFR1 and VEGFR2^[33]. Whereas different phase 1 and 2 trials revealed promising effects of bevacizumab on gastric cancer progression, the results of phase 3 studies were disappointing. Although in the AVAGAST study overall median survival was slightly longer in patients who received bevacizumab plus standard chemotherapy, these results did not reach a statistically significant level (12.1 mo and 10.1 mo, $P = 0.1002$). Merely progression free survival was significantly longer in the intervention group (6.7 mo and 5.3 mo, $P = 0.0301$)^[39]. The subsequently performed AVATAR study did not show any benefit of treatment with bevacizumab in combination with standard chemotherapy as compared to standard chemotherapy only (median overall survival 10.5 and 11.4 mo, progression free survival 6.3 and 6.0 mo)^[40]. Based on these results bevacizumab currently is not routinely used in the treatment of advanced gastric cancer.

Ramuzirumab is a competitive inhibitor of VEGFR2 with a 8fold higher affinity to the receptor as compared to natural ligands^[41]. Two phase 3 studies revealed ramucirumab to have positive effects on the containment of gastric cancer progression. The REGARD study investigated the impact of ramucirumab as a second line therapy on advanced gastric cancer. In comparison to the placebo group as well overall survival, disease control rate and overall response rate were significantly better (3.8 mo vs 5.2 mo, 49% vs 23%, 3.4% vs 2.6%). Interestingly, among male patients these effects were even more distinct^[42]. The RAINBOW study compared the outcomes after administration of paclitaxel with or without ramucirumab to a similar target audience. Overall survival and disease control rate both were better in the intervention group (9.6 mo vs 7.4 mo, 80% vs 64%)^[43].

In summary, currently ramucirumab seems to be the only one option to treat advanced gastric cancer with a VEGF-R specific antibody.

Platelet derived growth factor receptor: The Platelet derived growth factor (PDGF) family consists of 4 homodimers A-D and the heterodimer AB. Due to its dimeric structure it binds to receptor molecules which subsequently activate each other. Two different subtypes of PDGF receptors have been identified (alpha and β)^[44]. Under physiological conditions PDGF is released when platelets are damaged. Furthermore, PDGF signalling is known to play an important role in the embryonic development of kidney, blood vessels, lung and several components of the central nervous system^[45,46].

In several aspects the importance of the PDGFs as well as its corresponding receptors have to be regarded as being closely connected with the VEGF system. Whereas activation of VEGF signalling leads to recruitment of new blood vessels, one important downstream effect of PDGF signaling is the maintenance of microvessels. The regulation of the tumor environment - especially activities of fibrocytes and pericytes - as well

is partly realized by the PDGF signalling pathway^[46].

Up-regulation of PDGF signaling has been demonstrated for prostate cancer, breast cancer, lung cancer as well as colorectal cancer. In gastric cancer it has been shown that PDGF is frequently overexpressed in tumor cells whereas its corresponding receptor is overexpressed in several cell types of the microenvironment. It has been postulated that the tumor cell derived PDGF signal selectively leads to the up-regulation of PDGFR expression in environmental non-tumour cells^[46].

To date, there are no PDGF specific antibodies available for clinical use regarding gastric cancer.

Fibroblast growth factor: The fibroblast growth factor family consists of 23 molecule subtypes, targeting four different FGF receptor subtypes. In addition, several co-factors like Klotho-type co-receptors and heparan sulfat proteoglycans are involved in the initiation of the FGF signaling pathway^[47]. Binding of the growth factor to its receptors leads to autophosphorylation of the receptor molecule which subsequently activates different signal cascades. Activation of the MAP kinase or WNT signaling pathway terminally regulates the transcription programming, whereas PI3K-AKT, Hedgehog, Notch and noncanonical WNT signaling pathway promote the epithelial-mesenchymal transition. Overall, the FGF signaling is involved in numerous biological processes, such as stemness, anti-apoptosis, proliferation, drug resistance, angiogenesis and invasion^[47].

As for many other tumor entities, overexpression of FGF components has been described for gastric cancer, too. The FGFR-2 for instance is known to be up-regulated in 2%-9% of all gastric cancer cases, but is overexpressed in 50% in poorly differentiated and diffuse type gastric cancer^[48].

Currently, there are several experimental studies in progress which evaluate the impact of monoclonal antibodies against FGF-19, FGFR-2 and FGFR-3 at the level of animal models.

Hepatocellular growth factor: Under physiological conditions, Hepatocellular growth factor (HGF) and its corresponding receptor MET play a central role in the embryonic development, wound healing and organ regeneration. Therefore, HGF is normally secreted by surrounding mesenchymal cells^[49,50]. The physiological HGF signal can be altered by numerous molecular disorders, such as gene amplification, mutation and abnormal gene splicing^[51]. Aberrant HGF signaling can be observed in a broad variety of different tumors, among them lung cancer, colorectal cancer, hepatocellular cancer and - as well - gastric cancer. The receptor is activated by receptor dimerization which is induced by binding of HGF. Activation of MAPK and PI3K-AKT signalings are typical subsequent downstream features which lead to cell proliferation, prolonged cell survival and cell mobilisation^[52]. Whereas overexpression of MET seems to be a common feature in gastric cancer (22%-24%), gene amplification is infrequent (2%-10%). Aberrant

HGF signaling is related to poorer overall survival^[53].

Currently, three different monoclonal antibodies targeting the HGF system are available: onartuzumab, rilotumumab and ficlatuzumab^[52].

Onartuzumab has been demonstrated to be beneficial on the level of case reports but did not influence the clinical course in unselected patient populations.

Gastric cancer patients treated with rilotumumab in combination with chemotherapy following the ECX protocol showed a better overall survival as compared with those who received ECX only (5.7% and 4.2%)^[54]. Global phase 3 studies dedicated to the impact of onartuzumab and rilotumumab on advanced gastric cancer are currently underway^[52].

The benefit of ficlatuzumab combined with chemotherapy has been investigated for non-small cell lung cancer but did not have a statistically significant effect on overall survival^[52].

Targeting the growth factor pathways by small molecules

During the last decades two main molecular approaches have been asserted to target growth factor receptors which in fact are complex proteins: Monoclonal antibodies which bind to selected regions on the molecule surface and receptor tyrosine kinase inhibitors (RTKI) which are small molecules. These molecules mimic a metabolite that binds to the active center of the kinase. Two main categories of RTKI can be (more or less) distinguished: RTKIs which bind selectively to one or more related receptor types, and so-called multi-tyrosine kinase receptor inhibitors which have a more pluripotent spectrum of potential receptor targets.

Essentially, RTKI are available for every growth factor receptor. However, clinical outcomes in particular regarding advanced or metastasized gastric cancer show at best moderate improvements in terms of tumor control and survival.

For EGFR gefitinib, erlotinib, lapatinib and dacomitinib have been developed. Gefitinib showed moderate improvement of overall survival in several phase 2 studies. Administration of erlotinib in combination with cytostatic substances led to significant improvement of tumor control in two phase 2 studies. Lapatinib did not show any improvement when administered to patients with advanced, unresectable or metastasized gastric cancer. The benefit of dacomitinib is not clearly evaluated to date^[10].

For VEGFR apatinib is a selective inhibitor. Several studies showed a significant improvement for overall and progression free survival in patients with heavily pre-treated unresectable gastric cancer (OS 6.5 mo vs 4.7 mo, $P = 0.01$)^[12].

Imatinib is a RTKI which targets PDGFR. It is well established in the treatment of gastrointestinal stroma tumors for over 10 years now. A phase 1 study in 2012 showed that imatinib was well tolerated in patients with advanced gastric cancer but did not show significant

clinical improvement regarding survival and tumor control. Dasatinib, a novel PDGFR specific molecule is effective in the treatment of chronic lymphatic leukaemia, the benefit of dasatinib in the treatment of solid tumours is currently investigated^[46].

For the FGFR family a broad variety of small molecules is presented in the literature: dovitinib, brivanib, intendantib and ponatinib to name only a few. However, none of them is established in the treatment of gastric cancer at present^[47].

HGF specific small molecules can be subdivided in three categories: Type 1, 2 and 3.

Type 1 inhibitors are most specific to HGFR, for instance crizotinib. Type 2 inhibitors target a wider spectrum of receptors (AXL, RON, VEGFR2): foretinib, cabozantinib. Type 3 inhibitors bind as well to multiple receptor subtypes and different sites of the respective receptor: tivantinib. For gastric cancer only foretinib reached the level of a phase 2 study but unfortunately without significant benefit on an unselected patient group regarding HGFR expression^[52].

Proteinase-activated receptors

Proteinase-activated receptors (PAR) is a subgroup in the family of G-protein-coupled receptors. Receptor activation is realized by specific serine-proteases, such as trypsin and thrombin, which subsequently leads to further activation of the PI3K signaling pathway. Interestingly, one downstream effect of upregulated PAR2 signaling is the trans-activation of EGF receptors with the known subsequent effects. There is some evidence that prostaglandin-2 may inhibit the PAR2 signaling pathway which could be a potential target for specific molecular treatment approaches, but to date there is no PAR-associated treatment introduced in to the clinical routine^[55].

Morphogens and embryonic signaling pathways

Sonic hedgehog signaling: The Sonic hedgehog signaling (SHH) signaling pathway is one of the key players in the embryonic development, especially in defining body axes and segmental forming. The SHH signal is transduced within the cell *via* patched (PTCH), a transmembranous receptor which subsequently leads to the activation of smoothened and further to the deactivation of a protein complex which normally abolishes Gli, a nuclear factor that can initiate the expression of components of different other pathways, such as WNT, bone morphogenic protein (BMP) and Transforming growth factor β (TGF- β)^[56].

Vismodegib, sonidegib and saredegib are small molecule drugs which inhibit smoothened and thus interrupt the intracellular transmitted SHH signal. Thereby, these molecules mimic the effect of cyclopamine, a naturally occurring SHH inhibitor. The effectiveness of vismodegib in targeted treatment has been described for different tumor entities: With a pilot study on metastatic pancreatic cancer patients it was shown that

vismodegib down-regulates the SHH activity but without statistical significance on survival so far^[57]. Vismodegib has been proven as the very first SHH antagonist for the treatment of basal cell carcinoma in 2013^[58].

Phase 1 studies to verify the clinical eligibility of sonidegib are currently underway. The evaluation of saridegib is at present in the stage of experimental studies.

Another interesting molecular approach towards SHH signaling might be the application of HMG reductase inhibitors, such as statins. The attachment of a cholesterol residue to the SHH molecule is known to be essential to initiate the SHH signaling pathway by SHH. Although to date there are no clinical trials available which introduced statins to clinical use for certain tumor entities, there is some evidence that statins influence the clinical and biological behavior of malignant tumors. Recently, it has been published that statins significantly decrease cancer-specific mortality, particularly in colorectal, prostate and breast cancer.

WNT signaling

WNT signaling is known to be evolutionary highly conserved. During the embryonic development it is mainly involved in cellular differentiation. But also in adults WNT signaling is indeed important, particularly in the stem cell niches of the gastrointestinal tract. Likewise the SHH signaling pathway, the WNT signal starts by binding of WNT ligands to its receptor frizzled which in turn co-acts with LRP and transduces the signal towards the cytosol. To date four different subpathways have been described. In the classical or also called the canonical WNT pathway a multiprotein complex consisting of Axin, GSK3B and APC is being destabilized. This multiprotein complex normally abolishes β -catenin by phosphorylation. The disintegration of the multiprotein complex in turn leads to an accumulation of active non-phosphorylated β -catenin, which subsequently moves to the nucleus and binds to components of transcription (TCF-LEF complex). Interestingly, WNT signaling is coupled to EGFR signaling by at least two mechanisms: First the activation of EGFR signaling leads to internalization of E-cadherin- β -catenin complexes which in turn promotes WNT-dependent gene expression and second E-cadherin inhibits EGFR signaling by preventing receptor dimerization^[59,60].

The following targets have been defined to be eligible to suppress WNT activity: Porcupine (an enzyme that modifies the WNT ligands which is essential for their activity), the frizzled-LRP-dishevelled complex, axin, cyclooxygenase-2, GSK3 β and the TCF- β -catenin complex. Different small molecules targeting porcupine are currently under experimental evaluation, most of them act as competitive ligands to porcupine. They are also called "inhibitors of WNT production"^[61].

Aberrant WNT signaling is frequently observed in gastric cancer. β -catenin is overexpressed in up to 30% of gastric cancer cases, whereas the loss of APC function

occurs in 20% of all gastric cancer cases. SFRP loss, a physiological down-regulation of WNT signaling, is as well frequently to be found in gastric cancer tissue^[62,63].

At the moment there is no WNT associated treatment available for clinical routine, in particular not for gastric cancer.

Notch signaling

As another morphogenic signaling pathway Notch is known to be involved in embryonic organ development as well as in adult stem cell niche regulation. Notch promotes its cellular effects *via* regulation of proliferation, differentiation and apoptosis. The basic molecular mechanism is that one membrane-bound ligand (two subgroups: Jagged 1-2 and Delta like 1-4) binds to its receptor which is membrane-bound, too, but is belonging to a different cell. Thereafter the intracellular component of the receptor is cleaved. The Notch intracellular domain then moves to the nucleus and up-regulates expression of several genes, among them c-myc (oncogene), cyclin D1 (cell cycle promotion), p21 (cell cycle arrest) and bcl-2 (apoptosis)^[64-66].

Notch activity has been described to be involved in several tumor entities and among them in gastric cancer. Particularly Notch 1, Jagged 1 and DLL 4 were found to be frequently dys-regulated in gastric cancer tissues. Furthermore, there were statistically significant differences in the incidence of their up-regulation when stratifying tumor tissues to the classification according to Lauren as well as tumor location and tumor size^[66].

To date, there are no substances available which target at the Notch signaling pathway.

TGF- β and BMP

TGF- β and BMP constitute a super family of morphogens and regulate a broad variety of cellular activities. Up-regulation of the signal cascade may result in antitumor biological effects: At early tumor stages cell differentiation and apoptosis are promoted whereas proliferation is inhibited, leading finally to anti-tumor signals. On the other hand, the up-regulation of TGF- β and BMP in advanced tumor stages may result in the promotion of tumor angiogenesis, cell motility and aberrant interplay with the interstitium^[67-69].

Several subtypes of the TGF- β /BMP family are frequently up-regulated in gastric cancer, for instance BMP7 can be verified in 55% of specimen, whereas BMP2 is up-regulated in almost all cases of gastric cancer and BMP4 up-regulation is a frequently occurring event in un-differentiated gastric cancer.

Dalantercept is an inhibitor of BMP9 and BMP10 which has been shown to suppress effectively tumor angiogenesis. It has been proven to be eligible in a phase 1 study and is now under evaluation as a palliative second line treatment for renal cell carcinoma. DMH-1, a novel small molecule which inhibits the intracellular component of BMP-1 has been shown to have anti-tumor effects in the animal model^[70].

Nuclear factor κ B and interleukin receptors

Nuclear factor κ B (NF- κ B) as well as interleukin signaling are known to be involved in cancer development and cancer progression. NF- κ B can be regarded as a quick time transcription factor that regulates immune reaction as well as proliferation and apoptosis. Extracellular signals like bacterial or viral antigens, interleukin 1 β and tumor necrosis factor initiate a signal which enters the nucleus within few minutes. This is realized by storing NF- κ B in the cytosol which there is inactivated by forming a complex inhibitor of NF- κ B (I κ B). IKK, the I κ B kinase inactivates I κ B, which leads to a NF- κ B release. Rapid movement of NF- κ B to the nucleus in turn leads to up-regulated expression of different genes like cytokines, chemokines and adhesion molecules.

Upregulated NF- κ B signaling in gastric cancer is associated with elevated proliferation, genomic instability and drug resistance.

Two different molecular approaches targeting NF- κ B signaling are at the present time available: Phytochemicals: silibinin (*Silybum marianum*): Prostate cancer; resveratrol (red grapes, red wine): Prostate cancer, mesothelioma; catechins (green tea): Prevention against numerous tumor entities.

The abovementioned agents are partly a domain of alternative medicine but not an integral part of the clinical routine. Systematic studies and randomized trials are needed to shed more light on the actual clinical impact of these treatment options.

Denosumab is an inhibitor of RANKL (receptor activator of NF- κ B) and thus can down-regulate NF- κ B signaling. It has been shown to be effective in giant cell tumor of bone in pre-clinical studies.

To our knowledge currently there is no molecular treatment available targeting the NF- κ B signaling pathway in gastric cancer.

Furthermore, there is an abundance of inflammatory-associated molecular markers which are up-regulated in gastric cancer, including those which are associated with significantly poorer survival, such as different interleukins, HIF-1 α , chemokine receptors as well as matrix metalloproteases (MMP-3, -7, -9, -11).

Components and regulators of cell cycle

Cell cycle up-regulation is one of the most central mechanisms of tumor cell proliferation and tumor growth. It is strictly regulated by different controlling factors. The cell cycle can be sectioned into different cell cycle phases which only can be entered by passing the respective checkpoints. Under physiological conditions the entry of a cell into the cell cycle needs growth factors, whereas in tumor cells the cell cycle can be started at lower levels of growth factors or even at their complete absence^[71,72]. Cyclin D1 and 2 as well as CDK 4 and 6 are the most important factors that promote the entry into the S phase of the cell cycle. Cyclin D1 and 2 are frequently up-regulated in gastric cancer.

Furthermore, cyclin D is an important downstream target of different signaling pathways, such as SHH, WNT and Notch. In 15% of gastric cancer cases an up-regulated cyclin E can be observed^[62,73,74]. The protein complexes formed by cyclin plus its corresponding CDK are inhibited by different factors, such as p21, which is down-regulated in 60% of gastric cancer cases^[75].

Another major cell cycle associated key player is p53, the so-called "guardian of the genome", which is responsible for arresting the cell when DNA is severely damaged. Over 50% of all malignant tumors show a loss of p53, in gastric cancer these are at least 40%. Loss of p53 is known to be particularly frequent in advanced stages of gastric cancer and in those cases when tumor differentiation is low^[76,77].

Cell cycle and its regulators are investigated intensively for several decades to find clinical eligible bonds which inhibit cell cycle activity and promote cycle arrest or apoptosis.

Flavopiridol (also known as alvocidib) as well as roscovitine (also known as seliciclib) can be regarded as CDK inhibitors of the first generation, both of them being relatively unspecific.

After promising results of phase 1 studies with inhibitory effects on multiple different CDK subtypes, the clinical outcomes in phase 2 studies were disappointing failing significant clinical activity. After all, there was a measurable clinical activity in some haematological neoplasms, such as chronic lymphatic leukaemia and mantle cell lymphoma.

Roscovitine, a purine based molecule failed to have clinical effects in as well phase 1 and phase 2 studies^[78,79].

Dinaciclib as a CDK inhibitor of the second generation revealed remarkable activity on numerous tumor cell lines as well as in several tumor mouse models. In the subsequent phase 1 studies dinaciclib resulted in stable disease in different solid tumors, but again the positive results could not be confirmed with phase 2 studies with the exception of palliative treatment in refractory chronic lymphatic leukaemia, so that now a phase 3 study in this field is underway^[78].

The impact of down-regulation of cyclin D1 by using adenoviral vectors is currently explored.

Currently the abovementioned drugs are not approved for clinical use in the treatment of gastric cancer.

SOME FUTURE PERSPECTIVES

Beside the further development of target-specific molecules against components of the abovementioned signaling pathways two categories of molecular tumor biology might be of interest: the clinical importance of micro RNAs and effectors of epigenetic regulation.

MicroRNAs are small molecules without coding function and with a usual length of 18 to 25 nucleotids. To date, more than 2000 different sequences have been detected in the human genome. It is postulated that microRNA molecules are involved in 30% of gene expression. Interestingly they are frequently to be found

at so-called fragile chromosomal sites and typically in intergenic regions. The signature of microRNAs changes from normal tissue to malignant tumor tissue. Micro RNAs can as well be down- and up-regulated.

For example miR-139 has been shown to be frequently down-regulated in gastric cancer. In contrast, overexpression leads to inhibited cell proliferation in gastric cancer cell lines. It seems to be involved in the regulation of the chemokine receptor CXCR4.

The individual signature of microRNAs might be used as a biomarker in predicting the biological behavior of tumors. Furthermore, antagonization of oncogenic microRNAs and the restoration of down-regulated microRNAs with tumorsuppressive activity might be promising targets in the future^[80].

To a certain degree, the function of microRNA molecules is associated to epigenetic mechanisms, another challenging future perspective towards better understanding of the molecular biology of gastric cancer. Epigenetics means methylation of the DNA strand as well as different modifications of the histone molecules. DNA methylation is realized by DNMT 1 and 2 which place the methyl residues predominantly at so-called CpG rich regions. Hypermethylation of promoter regions upstream of tumor suppressor genes is a commonly observed phenomenon in different solid tumors. Histone molecules can be acetylated by HAT and deacetylated by HDACs at lysine sites, furthermore lysine as well as arginine sites can be methylated or demethylated. A broad variety of dys-regulated histone modification has been described for gastric cancer, for instance the hyperacetylation of histones neighboring the myc oncogene. Restoration of dyregulated histone and DNA modification might be another promising target to anticancer treatment^[81].

Considering the variety of target specific therapeutics in relation to the clinical impact on the population of gastric cancer patients and the individual complexity of the "cancer organism" it becomes clear, that molecular targeted approaches generate their best effects on respective subgroups which harbour the suitable molecular signature. Therefore, the knowledge about the individual presence of molecular markers might become essential and of paramount interest in the future.

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2015 Advances in Gastric Cancer

Gastric cancer: The times they are a-changin'

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Abstract

Gastric cancer is the third leading cause of cancer death worldwide. Even though during these last decades gastric cancer incidence decreased in Western countries, it remains endemic and with a high incidence in Eastern countries. The survival in advanced and metastatic stage of gastric cancer is still very poor. Recently the Cancer Genoma Atlas Research Network identified four subtypes with different molecular profiles to classify gastric cancer in order to offer the optimal targeted therapies for pre-selected patients. Indeed, the key point is still the selection of patients for the right treatment, on basis of molecular tumor characterization. Since chemotherapy reached a plateau of efficacy for gastric cancer, the combination between cytotoxic therapy and biological agents gets a better prognosis and decreases chemotherapeutic toxicity. Currently, Trastuzumab in combination with platinum and fluorouracil is the only approved targeted therapy in the first line for c-erbB2 positive patients, whereas Ramucirumab is the only approved targeted agent for patients with metastatic gastric cancer. New perspectives for an effective treatment derived from the immunotherapeutic strategies. Here, we report an overview on gastric cancer treatments, with particular attention to recent advances in targeted therapies and in immunotherapeutic approach.

Key words: Targeted therapy; Chemotherapy; Gastric cancer; Immunotherapy

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Core tip: Gastric cancer, despite its decrease in West Countries, remains one of the most common malignancies worldwide. The prognosis in the advanced setting is often poor even with a multidisciplinary approach, which aims to increase the patients' survival. The molecular classification of four subtypes of gastric adenocarcinomas (The Cancer Genome Atlas project) allowed a better stratification of patients in clinical trials for targeted

therapies. Biologic agents, modulating the immune checkpoints, seem to be the best promising therapeutic approach, opening new perspective for advanced gastric cancer treatment.

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INTRODUCTION

During these last decades gastric cancer incidence decreased, but it still remains the third most frequent cause of cancer-related mortality worldwide^[1,2]. At diagnosis, about half of gastric cancer patients show an advanced disease, with a 5-year survival rate lower than 30%^[3,4]. Even though gastric cancer incidence decreased in Western countries, it remains endemic and with a high incidence in Eastern countries. The incidence in Eastern Asia was 24.2/100000; in Latin America and Caribbean was 15.8-23.7/100000; in Africa and Northern America there was the lowest incidence (<http://globocan.iarc.fr>, accessed on 16/01/2015). In the United States the estimated number of new cases of gastric cancer in 2014 overtook 22000 cases^[2], with differences among several ethnic groups. In Europe gastric cancer holds the 5th place for male sex and the 6th place for female sex for incidence^[5,6].

Gastric cancer can be hereditary and associated to specific mutations^[7]. Often Gastric cancer are sporadic and depends on progressive accumulations of genotypic and phenotypic modifications due to different etiological factors such as wrong diets, presence of gastritis, infection by *H. pylori*, smoking, obesity, elevated body mass index (BMI) and reflux^[8,9]. Indeed, combinations of smoking, elevated BMI, and reflux may account for almost 70% of total cases^[10,11]. Untreated gastritis induces a chronic mucosal inflammation, that causes structural changes of gastric mucosa, leading to metaplastic transformation and structural changes of the glandular tissue, that can undergo to a neoplastic differentiation^[9,12].

Many efforts have been done in order to prevent gastric cancer: recognition and treatment of *Helicobacter pylori* (*H. pylori*) infections; diet changes like lower use of salted foods, and the use of refrigerators are factors which contributed to reduce the incidence of gastric cancer^[13]. Nonetheless, the incidence of the cancers of gastroesophageal junction (GEJ) and gastric cardia increased in western country^[14]. To explain these epidemiological data there are several interpretations, such as problems related to a correct subdivision among esophageal, junctional and cardia adenocarcinomas, that may have cloud the issue leading to a misclassification^[14,15].

MOLECULAR CLASSIFICATION: "THERE'S A BATTLE OUTSIDE AND IT IS RAGING"

The most common classification systems, such as the Laurén and the World Health Organization classifications, are essential for therapeutic decision, but are unable to predict response to targeted therapies. Recent studies on molecular profiling of upper gastrointestinal (GI) tumors increased our knowledge on the biology of gastric cancer and developed a molecular classification, identifying dysregulated pathways in different subgroups of gastric cancer.

The Cancer Genoma Atlas (TCGA) analysis uncovered four main genotypes of gastric cancer based on the molecular characterization of 295 primary adenocarcinomas^[16]: Epstein-Barr virus (EBV) positive; microsatellite unstable (MSI); genomically stable (GS); and tumors with chromosomal instability (CIN). The EBV-associated tumors are about 10% of the cancers; they display CDKN2A promoter hypermethylation and in 80% of the cases they have PIK3CA mutations and amplification of JAK2 and CD274 and PDCD1LG2. This subset of gastric cancer can benefit of targeted immunotherapy. MSI tumors represent approximately the 20% of the cases and show mutations in PIK3CA, HER2, HER3, and EGFR. GS gastric tumors represent about 20% of the adenocarcinomas, they show newly described mutations in RHOA, which are relevant to control actin-myosin-dependent cell contractility and motility. Almost 50% of gastric tumors showed CIN, with a marked aneuploidy and focal amplification of receptor tyrosine kinases, such as VEGFA. This subtype is frequently found in GEJ cancer. This study provides a guide to test new agents against new molecular targets specific for a gastric cancer subtype, enabling clinicians to make a better selection of patients for future trials with targeted therapy and immunotherapy in gastric cancer.

SURGICAL TREATMENT

Radical surgery is still the only one curative treatment, but gastric cancer is mostly diagnosed in local advanced or metastatic stage, when the survival still remains poor^[17]. Surgical resection for gastric or GEJ cancer combined with D1/D2 lymph node dissection should be performed by experienced team to reduce mortality and morbidity^[18]. Surgery with curative intent has to provide free-margin and at least D1 resection combined with removal at minimum of 15 lymph nodes^[19]. The extent of lymph node dissection is a significant surgical procedure that specifies the lymph node involvement, because preoperative lymph node staging is considered highly unreliable. The results of many randomized studies have not agreed to demonstrate superiority of D2 resection vs the D1 resection; to conclude the standard recommended surgery could be at least D1 resection, while D2 resection could be indicated in some

particular young patients^[20-22].

A combine approach of surgery and chemotherapy can improve outcomes of gastric cancer patients, with potentially resectable tumors. The Magic trial conducted in United Kingdom^[23] and the ACCORD trial conducted in France^[24] showed a statistically significant longer 5-year survival for patients treated with perioperative chemotherapy. Decisions were less clear for adjuvant setting: chemotherapy alone or with radiotherapy should be recommended for patients underwent to a less than optimal lymph node resection, R1 or with lymph node involvement^[25].

CYTOTOXIC CHEMOTHERAPY: "YOUR OLD ROAD IS RAPIDLY AGING"

The only treatment for patients with metastatic disease is the systemic chemotherapy. Currently there is no first-line standard single chemotherapeutic regimen but cisplatin based regimens, which able to improve the overall survival (OS) because a cytotoxic combination is superior to a single-agent regimen^[26]. The physician's choice of platinum-based doublets or triplets is taken after careful assessment of the patients' performance status. Currently, standard first-line options include FOLFOX [5-fluorouracil (5-FU, oxaliplatin)], S1/cisplatin or 5-FU/cisplatin, DCF (docetaxel, cisplatin, and 5-FU), ECF/EOX (epirubicin, cisplatin/oxaliplatin, and 5-FU/capecitabine). In the platinum-based doublets oxaliplatin could substitute cisplatin, while capecitabine and S1 are equivalent in terms of effectiveness to 5-FU^[27,28].

A third drug, usually epirubicin or taxotere, can be added with the aim to obtain a high response rate (RR) and a better control of the disease^[29,30].

Although most patients receive a first-line chemotherapy, in clinical practice only less than half of patients progressing after treatment receive a salvage treatment, mostly in western countries. Only recently a second-line chemotherapy has shown to be superior to the best supportive care in advanced disease: Two distinct trials proved that irinotecan and docetaxel, in monochemotherapy, control the metastatic disease^[31,32].

It's evident that chemotherapy reached a plateau of efficacy for gastric cancer, thus in an attempt to improve it, getting a better prognosis and decreasing chemotherapeutic toxicity, the combination between cytotoxic therapy and biological agents is useful. Indeed, results of ToGA trial allow to approve the first biologic drug for stomach cancer. Today, trastuzumab is indicated for first-line in patients HER2-positive in combination with 5-FU or capecitabine and cisplatin^[33].

Even more recently, two randomized trials demonstrated that Ramucirumab, a monoclonal antibody directed against VEGFR-2, is effective both alone or in combination with a second line chemotherapy with paclitaxel, in patients with metastatic gastric cancer^[34,35].

BIOMARKERS FOR GASTRIC CANCER

Since chemotherapy is not effective in all patients, who are resistant to cytotoxic treatment, it's mandatory to develop new anticancer regimens and to identify biomarkers able to predict the patients' responses to different cytotoxic drugs in gastric cancer. One of the molecules currently under investigation is the alpha-1 Microglobulin/Bikunin Precursor (AMBP), because its high level in serum could predict poor response to paclitaxel- capecitabine regimen^[36]. Thus AMBP could be a potential biomarker to identify patients who would benefit from this specific chemotherapeutic regimen.

Forkhead box transcription factor 1 (FoxM1) could be an other potential biomarker and target for gastric cancer. Indeed, FoxM1 overexpression is correlated with the pathogenesis of a variety of human malignancies such as breast cancer, non-small-cell lung cancer and ovarian cancer, and it is a critical molecule for chemoresistance to a microtubule-stabilizing anticancer agent as docetaxel^[37-42]. FoxM1 overexpression was significantly associated with resistance in chemotherapy of docetaxel in addition to 5-FU, S-1 and cisplatin (CDDP) for patients with advanced gastric cancer^[43,44]. Taken together, these results suggest that FoxM1 is involved in the mechanisms of resistance to cytotoxic drugs and its inhibition might be a promising therapeutic strategy for is a pleiotropic protein affecting a wide range of molecular and cellular processes.

Accumulating data, derived by different studies on the role of ANXA2 in tumorigenesis, suggest that ANXA2 is aberrantly expressed in a wide spectrum of tumors, affecting tumor cell adhesion, proliferation, apoptosis, invasion, metastasis and the interaction between immune cells and cancer cells in the microenvironment^[45,46]. The expression of ANXA2 in gastric cancer tissue is associated to a poor prognosis^[47,48]. A recent study reported that ANXA2 might be a good diagnostic and predictive marker for response to chemotherapy, indeed the chemotherapy-unresponsive patients show higher serum ANXA2 levels than the chemotherapy-responsive ones^[49].

Several studies have consistently demonstrated that miRNAs, short noncoding RNA molecules involved in post-translational regulation of gene expression, contribute significantly to human carcinogenesis by modulating the expression of both proto-oncogenes and tumor suppressor genes^[50]. Studies on gastric cancer allowed to identify up- and down-regulated miRNAs, which can be associated to clinical-pathological features of gastric cancer^[51,52]. Moreover, many data report that the expression of different miRNA patterns is also associated with premalignant stages or even risk conditions to develop gastric cancer, such as *H. pylori* infection^[53,54].

TARGETED THERAPY: "FOR THE LOSER NOW, WILL BE LATER TO WIN"

Advances in knowledge of the cancer biology led to the

discover of specific oncogenic signalling pathways of different driver mutations, resulting in the development of many new target agents. The prevalence of genomic alterations in gastric cancer patients has been recently assessed. Indeed, five distinct gastric cancer patient subgroups have been identified, according to the genomic alterations: FGFR2 (9% of tumours), KRAS (9%), epidermal growth factor receptor (EGFR) (8%), ERBB2 (7%) and MET (4%). Therefore, about 37% gastric cancer patients could be treated with anti-RTK/RAS agents^[55]. Many new target therapies were tested in clinical trials in gastric cancer patients, but without great results, thus we need further molecular studies to identify right patients for the right drugs.

EGFR1 inhibitors

EGFR is a trans-membrane glycoprotein receptor expressed in about 60% of gastric cancer patients. A meta-analysis on 1600 gastric cancer patients evaluated the survival according to the EGFR expression, showing that positive EGFR expression does not significantly predict the poor survival of gastric cancer^[56].

Cetuximab is an immunoglobulin G1 type chimeric monoclonal antibody targeting EGFR. Thanks to the successes achieved by the cetuximab in colorectal cancer, it was also tested in gastric cancer in combination with chemotherapy in phase II studies: FOLFIRI^[57], cisplatin plus docetaxel^[58], oxaliplatin plus 5-FU^[59,60] with encouraging results regarding ORR in all trials. However, the expected results from the combination of chemotherapy and cetuximab were not confirmed by the phase III EXPAND study (cetuximab in combination with capecitabine and cisplatin), that failed both in terms of OS and of progression-free survival (PFS)^[61]. The analysis of potential biomarkers such as KRAS mutations, EGFR expression, HER2 expression, did not identify the patients group responsive to cetuximab.

The REAL3 randomised study tested the efficacy of panitumumab in combination with EOX (epirubicin, oxaliplatin, capecitabine). In October 2011, trial recruitment was halted and panitumumab withdrawn because did not show any benefit at interim analysis. In multivariate OS analysis with performance status and disease stage, both KRAS mutation and PIK3CA mutation were negatively prognostic. No prognostic effect was associated with HER2 or PTEN status, and no BRAF mutations were identified^[62].

The phase III COG trial evaluated Gefitinib vs placebo in patients with metastatic esophageal or types I / II junctional adeno or squamous cell carcinoma, progressing after prior chemotherapy. This study did not improve OS; however, there was significant improvement in PFS, quality of life and palliation of symptoms^[63].

Some trials of several novel EGFR agents are still ongoing. The phase III ENRICH trial of nimotuzumab in combination with irinotecan in the second-line setting is pre-selecting patients with high EGFR expression (NCT01813253). Finally, before defining EGFR inhibitors

as ineffective in gastric cancer, we absolutely identify predictive biomarker for response, in order to avoid repeating the mistakes done with gefitinib in lung cancer^[64,65].

HER2 inhibitors

All members of the HER family of receptor tyrosine kinases, whose members include HER1 (or EGFR), HER2, HER3, and HER4, are expressed in gastric cancer. HER2 is a protooncogene encoded by ERBB2 found on chromosome 17. The percentage of gastric cancer patients positive to HER2 ranges from 7% to 42% due to tumor heterogeneity and the different methods and scoring systems used for evaluating HER2^[66]. HER2-positivity also depends on histologic type: It is frequent in patients with intestinal histology (34%), rare in those with diffuse-type histology (6%); it also depends on disease site: It's frequent in GEJ (32%) and rare in gastric cancer (18%)^[67]. It remains unclear whether HER2 positivity is a negative prognostic factor because there are studies both for and against this hypothesis^[68,69]. The ToGA trial is a randomized Phase III study which brought to the approval of Herceptin as the only targeted agent for patients with HER2 positive metastatic gastric and GEJ cancer. Three thousand six hundred patients were assessed for HER2 positivity, and the 594 patients HER2-positive were recruited in the clinical trial^[33], which evaluated efficacy of anti-HER2 trastuzumab in combination with 5-FU or capecitabine and cisplatin vs chemotherapy alone in HER2 patient. Median OS in control arm was 11.1 mo compared with 13.8 mo in experimental arm with a statistically significant increase in RR. Every 3 wk for six cycles, the treatment was administered, whereas trastuzumab was continued every 3 wk until disease progression, or unacceptable toxicity, or withdrawal of consent. One of the most interesting result of this study was that the survival advantage was greatest in patients with IHC 3+ tumors (HR = 0.66, 95%CI: 0.50-0.87), less effective in patients with IHC 2+ tumors (HR = 0.78, 95%CI: 0.55-1.10), and ineffective in those with HER2 gene-amplified, but not protein expressing (IHC 0 or 1+) tumors. Grade 3 or 4 adverse events (AEs) occurred in similar percentages in both arms. Now all patients with advanced or metastatic gastric or GEJ cancer, and suitable for combination chemotherapy with fluoropyrimidine and cisplatin, should be assessed for the expression of HER2 and therefore can be treated with additional trastuzumab.

The phase III HELOISE trial, combining trastuzumab with cisplatin and capecitabine (NCT01450696), and the TEX regimen, combining trastuzumab with Taxotere, Eloxatin and Xeloda as treatment for HER2 positive non-resectable cancer (NCT01295086) are ongoing to improve the efficacy of combination chemotherapy. Heloise trial aims to assess whether trastuzumab maintenance is able to increase the gastric cancer patients' survival. The second trial evaluates the safety

and efficacy of three drugs combination in addition to trastuzumab.

Development of resistance to trastuzumab urged investigators to test new drugs target HER2, but not all HER2-targeting agents have had such an unequivocal success.

The dual HER2/EGFR inhibitor lapatinib (Tykerb) is an orally drug. Lapatinib is a very interesting TK1 inhibitor, able to interfere with cell proliferation, to sensitize gastric cancer cells to the irinotecan metabolite SN-38^[70] and to have a synergic effect combined with chemotherapy^[71].

Lapatinib was evaluated in the first setting in combination with capecitabine/oxaliplatin (LOGiC trial). 545 patients were randomized and 487 had HER2+ centrally confirmed, but combination treatment failed to improve the median OS (12.2 mo vs 10.5 mo, HR = 0.91, 95%CI: 0.73-1.12) compared with chemotherapy alone. No correlation was found between intensity of staining for HER2 by IHC and outcomes. However, the LOGiC trial did suggest that Asian patients and those under age 60 years might benefit of this combination^[72].

The TyTAN trial is a phase III study second-line therapy of paclitaxel. Investigators enrolled 261 HER2-amplified Asian patients and they observed statistically significant improvements in OS and PFS among a pre-specified subgroup of patients with strong HER2 positivity. However, addition of lapatinib did not produce any significant benefit on PFS (5.4 mo vs 4.4 mo) or OS (11.0 mo vs 8.9 mo) with significant gastrointestinal (diarrhoea 20%) and bone marrow toxicity (febrile neutropenia, 7%)^[73]. Several other HER2-targeting agents were also evaluated in clinical trials, including trastuzumab emtansine (T-DM1; Kadcyla) and pertuzumab (Perjeta).

T-DM1 is a conjugate molecule that combine a cytotoxic agent with an antibody targeted specific tumor cells. Due to positive results in breast cancer (EMILIA trial)^[74], is now ongoing a randomized, multicenter, adaptive phase II/III study to study the efficacy and safety of trastuzumab emtansine (T-DM1) vs taxane (docetaxel or paclitaxel), in patients with previously treated locally advanced or metastatic HER2-positive gastric cancer, including adenocarcinoma of the GEJ (GATSBY trial, NCT01641939). Another phase I/II study was designed to assess T-DM1 in combination with capecitabine in patients with metastatic gastric cancer (NCT01702558). The ongoing phase III JACOB trial is evaluating the combination of pertuzumab, trastuzumab, and chemotherapy (NCT01774786). The combination of two antibodies aims to amplify the trastuzumab antitumor efficacy in HER2-positive patients. Again with the aim of overcoming resistance to trastuzumab, it is also ongoing a phase II trial with afatinib, an irreversible panHER TK1 (NCT01522768). A better and more accurate knowledge of the mechanisms of cellular resistance to trastuzumab is essential for the future. Certainly, the intra-tumor heterogeneity in HER2 expression/amplification is very important, but other mechanisms have been implicated as PI3K/Akt pathway, m-TOR inhibitors, MET-inhibitors (when c-MET

is overexpressed), overexpression of IGF-1 receptor (IGF-1R), SRC inhibitors. From these pre-clinical studies will emerge the right molecules to be tested in the next clinical trials.

Another HER2-directed strategy is represented by vaccines. Despite the great success of HER2 vaccine strategies in animal models, effective clinical results have not yet been obtained^[75].

HER2 vaccines, DNA or peptide-based, are studied mainly for breast cancer, often in combination with other HER2 targeted therapies^[76]. Regional treatments are another possible application. Radio-immunotherapy is now evaluating 212Pb immunoconjugates with trastuzumab in intraperitoneal treatment^[77].

Angiogenesis inhibitors

Angiogenesis is crucial for tumor growth, thus anti-angiogenic drugs are now a standard of care for many solid tumors of the adult. In gastric cancer VEGF is overexpressed in 40% and VEGFR in 36% of cases. Some studies reported that VEGF overexpression correlates with advanced and aggressive disease^[78-80]. We recently showed that even though VEGF serum levels were higher in gastric patients than in controls, they were not correlated to the OS^[81].

Bevacizumab is a recombinant humanized monoclonal antibody anti-VEGF-A, a strong driver of angiogenesis in tumorigenesis. Phase II studies conducted with bevacizumab in chemotherapy combination, showed encouraging RR, time to disease progression (TTP), and OS^[82,83], but not confirmed by phase III trials. The phase III trial AVAGAST evaluated effects of bevacizumab in combination with cisplatin and capecitabine as a first-line therapy in 774 patients with advanced gastric carcinoma^[84]. Addition of bevacizumab failed to improve OS, with median OS 12.1 mo vs 10.1 mo, even though it achieved a significant increase in PFS (6.7 mo vs 5.3 mo) and overall RR (46.0% vs 37.4%). To evaluate the hypothesis that angiogenic markers may be predictive for bevacizumab efficacy, correlations between pre-specified biomarkers (VEGF-A, protein expression of neuropilin-1, and VEGFR-1 and VEGFR-2) and clinical outcomes were assessed too. High plasma VEGF-A levels and low expression of neuropilin-1 showed a trend toward improved OS. These are strong biomarker candidates that aim to predict the response to bevacizumab in gastric cancer patients from non-Asian regions^[85]. Moreover, the sub-group analysis by geographical regions, tumor site and histology concluded that the highest survival benefits are for non-Asian patients with distal gastric non-diffuse type cancer (OS 11.4 mo vs 7.3 mo).

MAGIC-B trial with bevacizumab in combination with chemotherapy (ECX regimen) in perioperative setting is ongoing^[86]. The study results could provide relevant information on antiangiogenic efficacy in the early stages of disease.

In this complex and rather disappointing background,

results of ramucirumab in the treatment of advanced gastric cancer have been published. Ramucirumab (IMC-1121B) is a fully human IgG1 monoclonal antibody direct against VEGFR-2. The phase III REGARD trial was conducted to assess efficacy and safety of ramucirumab as second-line treatment vs supportive care in advanced gastric cancer. Three hundred and fifty-five patients were enrolled. Ramucirumab significantly improved OS (OS 5.2 mo vs 3.8 mo) and PFS (2.1 mo vs 1.3 mo), with good tolerability. Most frequent grade 3-4 AEs were hypertension (7.3% in experimental arm vs 2.6% in placebo arm), anemia (6.4% vs 7.8%), abdominal pain (51.% vs 2.6%), ascites effusion (4.2% vs 4.3%), asthenia (42.% vs 3.5%), hyponatremia (3.4% vs 0.9%) and anorexia (3.4% vs 3.5%). No grade 4 hypertension has been observed^[34].

The phase III RAINBOW was conducted in 665 patients with the aim to evaluate efficacy and safety of ramucirumab plus paclitaxel combination in second-line treatment in advanced gastric cancer patients. The study reached its primary objective of increasing OS, indeed the combination resulted superior in median OS (9.7 mo vs 7.3 mo), median PFS (4.4 mo vs 2.8 mo) and RR (28% vs 16%). Hypertension, fatigue and neutropenia were the most frequent toxicities in experimental arm, whereas febrile neutropenia had comparable incidence.

Gaining the results of ramucirumab in second-line, we would have expected a good success also in first-line. However, the study combination of FOLFOX6 plus ramucirumab has not demonstrated to increase OS and PFS in patients with metastatic gastric cancer (23%), GEJ (31%) and esophageal (46%). 168 patients were enrolled, median PFS 6.4 mo vs 6.7 mo, OS 11.7 mo vs 11.5 mo. Addition of RAM to FOLFOX6 showed PFS difference at 3 mo and improved disease control rate (DCR); longer PFS in RAM vs placebo was observed in gastric/GEJ cancer patients^[87].

Apatinib is a tyrosine kinase inhibitor (TKI) agent targeting VEGFR-2 (VEGFR). A phase II randomised trial tested apatinib vs placebo in 144 pre-treated gastric cancer patients. Apatinib was taken orally in two different ways: 850 mg once and 450 mg twice a day. Median OS times were 2.50 mo (in the placebo arm), 4.83 mo (apatinib 850 mg once a day arm) and 4.27 mo (apatinib 450 mg twice a day arm). Median PFS times were 1.40 mo, 3.67 mo, and 3.20 mo, respectively. The differences between apatinib and placebo groups were statistically significant for both PFS ($P < 0.001$) and OS ($P < 0.001$ and 0.0017). Toxicities were tolerable and manageable^[88]. The multicenter, randomized, double-blind, placebo-controlled phase 3 trial tested Apatinib 850 mg, po, qd, 28 d as one cycle or matching placebo. The study was planned to enroll 270 cases, stratified to the number of metastatic sites (≤ 2 or > 2). Median overall survival (mOS) was significantly prolonged in the apatinib group compared with in the placebo group. The results confirmed the efficacy and safety of apatinib in the patients with advanced gastric cancer^[89].

Sunitinib and sorafenib are multi-target TKIs also studied in order to suppress angiogenesis in gastric cancer. Phase II open-label randomized trial evaluated the combination of sunitinib plus docetaxel vs docetaxel monotherapy in second-line treatment in 107 patients with metastatic gastric cancer. Sunitinib arm was associated with a significantly higher ORR (41.1% vs 14.3%), but there was no significant difference in TTP (3.9 mo vs 2.6 mo)^[90].

Sorafenib targets BRAF, VEGF, and PDGFR^[91]. Combination of sorafenib plus chemotherapy (docetaxel and cisplatin) was assessed in a phase II trial, first-line setting, in 44 patients with metastatic gastric cancer. The combination demonstrated a PFS of 5.8 mo, median OS of 13.6 mo, and ORR 41%; grade 3-4 EAs toxicity was neutropenia^[92].

Pazopanib is an oral second-generation multitargeted TKI, which showed antiangiogenic and antitumor activity. There are two phase II trials now ongoing in order to evaluate efficacy and safety of pazopanib as first-line treatment in metastatic gastric cancer. The first one, a phase II PaFLO trial, wants to examine FLO (5-FU, leukovorin and oxaliplatin) + pazopanib used in combination for advanced gastric cancer (ClinicalTrials.gov Identifier: NCT01503372). The second one, a phase II non-randomized open label trial, evaluates Pazopanib in combination with Capecitabine and Oxaliplatin in patients with advanced gastric cancer. The primary end-point is RR, the second end-points are PFS, OS and metabolic response rate by PET-CT (ClinicalTrials.gov Identifier: NCT01130805).

Hepatocyte growth factor-mesenchymal-epithelial transition factor axis

Mesenchymal-epithelial transition factor (c-MET) is the TK receptor of hepatocyte growth factor (HGF)^[93]. c-MET expression or amplification was documented in many solid tumors and was correlated with poor prognosis in gastric cancer too. IHC analysis in gastric cancer specimens showed c-MET expression in 65% of cases with high-intensity staining in about 20% of cases^[94]. However, the real activation of c-MET mutations and its resulting amplification, is a rare event: c-MET amplification occurs in 5%-10% of cases^[95]. This discrepancy between expression and amplification of c-MET has important consequences when we design clinical trials with HGF-c-MET pathway inhibitors.

Rilotumumab (AMG 102) is human monoclonal antibody (IgG2) against HGF. A phase II double-blind randomized study, evaluated the efficacy and safety of rilotumumab with ECX regimen in gastric cancer patients in first-line treatment. Rilotumumab associated to chemotherapy improved the median PFS from 4.2 to 5.6 mo, and the OS from 8.9 to 11.1 mo. In the rilotumumab plus ECX arms, the most common adverse observed events were: neutropenia, anemia, peripheral edema, thrombocytopenia, and deep vein thrombosis^[96]. MET protein levels and gene copy

numbers were measured in archival tumor samples by immunohistochemistry (IHC) and fluorescence *in situ* hybridization, respectively. Rilotumumab in combination with ECX improved the median OS from 5.7 to 11.1 mo in patients with gastric tumors with high MET expression.

The RILOMET-01 phase III trial evaluated the efficacy and safety of Rilotumumab + ECX in MET-pos by IHC, previously untreated G/GEJ cancer. Primary endpoint was OS. 609 patients were randomized, but the study was stopped early because an imbalance in deaths (data cutoff: Nov 2014). OS, PFS and ORR were statistically worse in the experimental arm. The subgroup with higher percentages of cells with $\geq 1+$ MET expression does not seem to benefit with ramucirumab. PK and MET biomarker analyses are pending, thus we don't know whether they will offer any answers to this failure^[97].

Onartuzumab is a humanized, monovalent (one-armed) monoclonal antibody against MET. One phase III trial (randomized multicenter double-blind placebo-controlled studies), currently ongoing (but it's not recruiting participants) is evaluating the efficacy and safety of onartuzumab (MetMab) in combination with mFOLFOX6 in patients with metastatic HER2-negative and Met-positive adenocarcinoma of the stomach or GEJ (NCT01662869).

Crizotinib is a small MET kinase inhibitor. Phase I study showed promising activity in c-MET amplified gastric cancer patients^[98].

Tivantinib is a selective non-ATP competitive small-molecule inhibitor of c-MET. Phase II single-arm study evaluated the efficacy of tivantinib monotherapy in Asian patients with previous treatment for MGC (ARQ-197). Tivantinib was administered orally daily. The primary end-point was the DCR. Thirty patients were enrolled and no objective responses were observed, and DCR was 36.7%. There was not relationship between efficacy and gene amplification of c-MET, expression of c-MET, p-MET and HGF^[99]. New clinical trials with c-MET inhibitors were restricted to patients defined as a "MET positive" to identify selected patients for a special genetic/molecular profile. However, the HGF/c-MET axis is involved in multiple pathways that operate at different levels^[100]. The anti-HGF compounds may not be sufficient to completely inhibit HGF/c-MET axis^[101]. Hereafter it will be necessary to define with much more precision what "MET positive" gastric cancer means.

m-TOR inhibitors - PI3K pathway inhibition

m-TOR regulates angiogenesis, cellular metabolism, proliferation, and cell growth. Its activation is done through the PI3K pathway (*via* Akt/protein kinase B and tuberous sclerosis complex). In gastric cancer, mTOR and p-mTOR (its activated form) overexpression were respectively 50.8% and 46.5%. Overexpression of total mTOR protein significantly correlated with tumor differentiation, T1/T2 tumors, and stage I / II / III disease. p-mTOR overexpression significantly correlated

with lymph node metastasis and all stage disease^[102].

Everolimus is an oral m-TOR inhibitor, approved for the treatment of renal cell carcinoma, breast cancer, and progressive NET of pancreatic origin. A phase II study, in 53 patients with previously treated metastatic gastric cancer, reported a median PFS of 2.7 mo and OS of 10.1 mo. Common grade 3/4 AEs included anemia, hyponatremia, increased gamma-glutamyltransferase, and lymphopenia. Grade 1/2 pneumonitis was reported in 15.1% of patients^[103]. Another phase II trial assessed the efficacy and safety of combination regimen of capecitabine plus everolimus in patients with refractory gastric cancer who have failed at least two cytotoxic regimens. Forty seven patients were enrolled in this trial. Everolimus in combination with capecitabine achieved an ORR of 10.6% and a DCR of 48.9%, with respectively a median PFS and OS of 2.3 mo and 5.1 mo^[104]. The phase III GRANITE-1 evaluated everolimus or BSC plus placebo in 656 previously treated advanced gastric cancer patients. The results of this trial showed median OS of 5.39 mo in the everolimus arm and an OS of 4.3 mo in the placebo arm, with an advantage in PFS statistically significant but clinically irrelevant (1.7 mo vs 1.4 mo)^[105]. Phase III study in advanced gastroesophageal adenocarcinoma patients comparing everolimus combined with paclitaxel vs paclitaxel alone (NCT01248403) is ongoing.

IGF family

The IGF family plays an important role in growth and metabolism. Deregulation of IGFs/IGF-1R system promotes metastases diffusion, proliferation and invasion in gastric cancer. A number of antibodies targeting IGF-1R have been studied. Ganitumab (AMG 479) and figitumumab (CP 751) have been evaluated in phase I study in patients with solid tumors, including gastric cancer. They showed promising results^[106].

PARP inhibitors

PARP inhibitors (Poly-ADP-Ribose-Polymerase) have been studied in breast cancer with a know history of deficient BRCA1/2. The activity of PARPS inhibitors is improved in presence of drugs that cause double-strand breaks in DNA such as platinum compounds.

Olaparib activity has been proven in a phase II trial with paclitaxel (Bang YJ *Im SA J ClinOncol* 2013 31(sup)). The study failed to increase the PFS, but it improved OS. A randomized phase III with paclitaxel in gastric cancer patient second-line is ongoing (NCT019245337).

IMMUNOTHERAPY: "...AND KEEP YOUR EYES WIDE"

Until few years ago, the more validated hypothesis was that epithelial tumors originate from tissue stem cells. A large intra-tumoral heterogeneity exists and cancer stem cells are part of it, indeed they are in the primary tumors, but they also disseminate to different

organs, remaining dormant or originating metastases and often are responsible to chemo-resistance^[107,108]. To date, it's evident that tumor growth depends on the interactions among cancer cells, microenvironment and immune system cells. Tumor and cancer stem cells express receptors for antigens on specific cell type, thus determining the capability of one tumor to metastasize to a specific organ, such as for breast, lung and prostate cancer which commonly metastasize to bone^[109-112]. The importance of tumor microenvironment in promoting cancer progression is even more recognized, because its cellular components release a series of factors which constitute a favourable soil for cancer cell homing and growth^[113,114]. Looking at the immune system, a variable number of immune cells infiltrate tumors: mast cells, lymphocytes, macrophages and myeloid derived suppressor cells (MDSCs), with a deep impact on tumor progression^[115]. For instance, MDSCs are a heterogeneous population of immature myeloid cells driving the progression of cancer disease by suppressing both the innate and adaptive immune response. Indeed they suppress CD4 and CD8 T cell populations, and promote the activation and expansion of regulatory T cells, which mediate immunosuppression^[116-118].

A strong rationale exists to adopt the immunotherapy for gastric cancer, because inflammation has been recognised as an hallmark of cancer^[119] and gastric cancer, particularly the upper GI tumors are an inflammatory-mediated disease^[120]. Here we will describe the last frontiers of immunotherapy in gastric cancer treatment, but a comprehensive overview of immunotherapy in gastric cancer has been recently published by Murphy *et al*^[121].

Encouraging results derive from the combination of cellular immunotherapy and chemotherapy, that improves the quality of life and might prevent the recurrence in patients with advanced gastric carcinoma^[122]. The TCGA network identified elevated programmed death ligand-1 (PD-L1) expression in the EBV subtype in gastric cancer^[16]. PD-1 is an immune checkpoint, involved in tumor suppression and in tumor microenvironment, because it regulates T cell pathways. New frontiers of immunotherapy are focalized on targeting the immune checkpoints, in order to remove inhibitory pathways that block an effective T cell response against the tumor^[123]. Two antibodies against PD-1 (Pembrolizumab and Nivolumab) have been approved in 2014 form United States Food and Drug Administration. The checkpoint therapy could be useful for gastroesophageal cancer, which express PD-L1 in 18% to 42 % of cases^[124]. Phase II and phase III clinical trials involving either single agent PD-1/PD-L1 inhibition or combined with CTLA-4 inhibitors (ipilimumab) are ongoing. In KEYNOTE-012 trial 39 patients PD-L1-positive with advanced gastric cancer received pembrolizumab, which showed a positive anti-cancer activity with an objective response of 22.2%, the median time to response was 8 wk (range 7-16 wk), with a median duration of response of 24 wk (range 8+ to 33+ wk). At 6 mo, 24% of patients showed no

signs of disease progression, and 69% remained alive; the median PFS reached 1.9 mo. The most common AEs included fatigue (17.9%), decreased appetite (12.8%), hypothyroidism (12.8%), and arthralgia (10.3%). Four patients showed severe AEs associated with pembrolizumab, particularly, one of these patients died for treatment-associated hypoxia^[125]. The OS data were presented at 2015 ASCO Annual meeting: The 6-mo OS rate was 69%. These results support the ongoing development of pembrolizumab for gastric cancer^[126]. The phase II KEYNOTE-059 study will soon be initiated to evaluate pembrolizumab as monotherapy or in combination with cisplatin and 5-FU in patients with advanced gastric or GEJ adenocarcinoma^[127].

On May 2015 the phase III KEYNOTE-061 study started. This is a Randomized trial of Pembrolizumab vs Paclitaxel in Advanced Gastric or GEJ adenocarcinoma patients who progressed after first-line therapy with platinum and fluoropyrimidine (NCT02370498).

In the near future, ipilimumab and nivolumab, two immunostimulatory monoclonal antibodies with antineoplastic effects, might offer new therapeutic options for patients with advanced gastric cancer^[128]. In particular, Nivolumab, a fully human IgG4 anti-PD-1 monoclonal antibody, resulted active and generally well tolerated in patients with advanced solid tumors in a phase I trial^[129,130]. A Japanese randomized phase III study started in october 2014 to evaluate Nivolumab (ONO-4538) vs BSC in patients with unresectable advanced or recurrent GC patients (NCT02267343).

CONCLUSION: "...AS THE PRESENT NOW, WILL LATER BE PAST"

Gastric cancer is one of the most common causes of cancer death in the world. Healing can only be guaranteed by an optimal surgery and still in the early stages of the disease. However, especially in Western countries, diagnosis is too late and the survival of patients with metastatic disease rarely exceeds 12 mo of diagnosis.

The multidisciplinary approach is always mandatory: The perioperative treatment, when indicated, has shown to be effective in increasing the survival of these patients and, in advanced disease, the total care by nutritionist, surgeon and oncologist has positive impact on the quality of life of these patients.

Chemotherapy in metastatic disease is the only chance of cure, but brings with it side effects also important and poor response rates. "... Your old road is rapidly aging" sang Bob Dylan (www.bobdylan.com), but it is true that at the moment that is the way we know best. Perhaps times are changing. As for lung and colorectal cancer, the targeted therapies are revolutionizing the clinical practice, but we also learned that to achieve maximum efficacy of these new molecules we have to change tumors classification.

New drugs and new classification: the genomic and molecular classification given by TCGA network will help

us to characterize with greater precision our patients. "... There's a battle outside and it is raging" but we will be armed with new knowledge.

Some clinical trials have led to the registration of drugs such as trastuzumab and ramucirumab. For EGFR inhibitors, lapatinib or everolimus, the phase III studies represented a setback.

However, the key is still patients selection on basis of molecular tumor characterization. Gefitinib in lung cancer reminds us "... for the loser now, will be later to win".

Which is the best cytotoxic combination for target therapies? Which is the best setting for using the new molecules? We do not know yet. In deed, it's possible that gastric cancer during progression disease and under evolutionary pressure of cytotoxic treatment can transform molecularly into a different phenotype.

Moreover, ethnic differences may cause different responses to the same molecules. Even this finding will lead to a personalized cancer medicine.

Finally, immunotherapy opens a vast and fascinating scenery for gastric cancer treatment. Some etiological factors such as viral and bacterial infections *via* EBV and *H. pylori* suggests that gastric cancer can be treated with new drugs such as immunotherapy checkpoint inhibitors.... And keep your eyes wide.

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2015 Advances in Gastric Cancer

Clinical significance of MET in gastric cancer

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Abstract

Chemotherapy has become the global standard treatment

for patients with metastatic or unresectable gastric cancer (GC), although outcomes remain unfavorable. Many molecular-targeted therapies inhibiting signaling pathways of various tyrosine kinase receptors have been developed, and monoclonal antibodies targeting human epidermal growth factor receptor 2 or vascular endothelial growth factor receptor 2 have become standard therapy for GC. Hepatocyte growth factor and its receptor, c-MET (MET), play key roles in tumor growth through activated signaling pathways from receptor in GC cells. Genomic amplification of *MET* leads to the aberrant activation found in GC tumors and is related to survival in patients with GC. This review discusses the clinical significance of MET in GC and examines MET as a potential therapeutic target in patients with GC. Preclinical studies in animal models have shown that MET antibodies or small-molecule MET inhibitors suppress tumor-cell proliferation and tumor progression in *MET*-amplified GC cells. These drugs are now being evaluated in clinical trials as treatments for metastatic or unresectable GC.

Key words: MET; Gastric cancer; Genomic amplification; Immunohistochemistry; Clinical trial

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Core tip: MET protein overexpression or *MET* gene amplification was associated with tumor progression and survival in gastric cancer (GC), although the definition of MET overexpression remains to be standardized. In preclinical studies, MET antibodies or small-molecule MET inhibitors suppressed cell proliferation and tumor progression in *MET*-amplified GC cells. Therefore, MET-targeting therapy is promising, and MET overexpression might be a useful biomarker of the response to chemotherapy inhibiting MET. Some clinical trials of MET inhibitors were conducted in metastatic GC, but sufficient benefits have not been demonstrated yet.

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INTRODUCTION

Gastric cancer (GC) is the fourth most common cancer, with 989600 cases newly diagnosed in the world in 2008, accounting for about 8% of all newly diagnosed cancers^[1]. The effectiveness of chemotherapy remains very limited in patients with unresectable or metastatic GC, and overall survival (OS) was 10 to 13 mo in patients who received combination chemotherapy with multiple cytotoxic agents^[2,3].

Receptor tyrosine kinases (RTKs) are growth factor receptors associated with various physiological responses to embryogenesis and homeostasis. RTK activity is strictly regulated in normal cells, although dysregulation or constitutive activation of RTKs has been found in various types of cancer cells^[4]. Aberrant or oncogenic activation of RTKs augments tumor-cell proliferation, anti-apoptosis, vascularization, metastasis, and resistance to anticancer agents. RTKs are the most intensively pursued target molecules for anticancer drugs, because tumor cells with activated RTK signaling pathways are sensitive to appropriate RTK inhibitors^[5]. Trastuzumab, a monoclonal antibody against p185 human epidermal growth factor receptor 2 (HER2), was first used clinically to treat GCs with HER2 overexpression. However, only 12% of patients who received trastuzumab had tumors that overexpressed HER2 in that trial^[6]. Ramucirumab is a monoclonal antibody against vascular endothelial growth factor receptor 2 (VEGFR2). Second-line treatment with ramucirumab significantly prolonged survival in two phase III trials in GC^[7,8]. Many inhibitors of RTKs have been investigated to identify potential targets for the treatment of GC.

Proto-oncogene c-MET (MET), a member of the RTK family, is a known hepatocyte growth factor (HGF) receptor that is encoded by the *MET* gene. MET has a primary single-chain precursor protein made of alpha and beta subunits, the latter of which contains a cytoplasmic kinase domain and a docking site^[9]. Binding of HGF to the extracellular domain activates the kinase activity that phosphorylates the tyrosines at the carboxy terminal docking site. Phosphorylated MET (p-MET) can recruit a variety of proteins, including growth factor receptor-bound protein 2 (GRB2), GRB2-associated binding protein 1 (GAB1), phospholipase C (PLC)-gamma, SRC, and SHP2, and activates downstream signaling molecules such as phosphatidylinositol-3-kinase (PI3K)/AKT and extracellular signal-regulated kinase (ERK)/mitogen-activated protein kinase (MAPK) pathways^[10,11]. Similar to other RTKs, MET plays key roles in tumor survival, growth, angiogenesis, and metastasis. The aberrant signaling of MET by overex-

pression or gene amplification has been detected and correlated with tumor progression or patients' survival in GC^[12-15]. Alternative activation of the MET pathway is considered an important mechanism causing resistance to treatments targeting HER family members^[16,17]. Unfortunately, a phase III study of rilotumumab, an HGF monoclonal antibody inhibiting MET pathway, has been recently discontinued because of high treatment-related mortality. However, inhibition of MET must undoubtedly be an important treatment for GC.

In this article, we reassess the clinical significance of MET in GC and summarize currently available results of preclinical studies and clinical trials of MET inhibitors.

CLINICAL OUTCOMES OF MET EXPRESSION IN GC

Protein expression on immunohistochemistry

Studies examining the relation between MET protein expression and clinical outcomes in GC specimens are summarized in Table 1. MET protein expression on immunohistochemistry (IHC) is predominantly detected in cytoplasm of tumor cells, but is also found in the cell membrane^[12,18-20]. Lee *et al.*^[12] assessed membranous MET expression according to a standardized technique, similar to that used to evaluate HER2 expression. MET expression was observed even in stromal cells in tumors^[18]. Moreover, MET overexpression was more frequently detected in dysplasia and precancerous gastric lesions than in intestinal metaplasia^[21].

MET overexpression has frequently been found in intestinal type or differentiated type cancers^[12,14,22,23], although one study reported a correlation with diffuse type^[13]. Retterspitz reported that MET was overexpressed in 51% (45 of 88) of diffuse type tumors^[24]. MET overexpression has been significantly associated with tumor invasion depth^[12,13,23], lymph-node metastasis^[12,13,19,20,25,26], distant metastasis^[12,13,25], tumor stage^[12,20,23,26], and recurrence^[14], although several studies found no relation to any clinicopathological factors^[24,27,28]. MET overexpression correlated with liver metastasis only in stage IV disease^[29]. Some studies showed that MET overexpression was an independent prognostic factor that was significantly related to poor survival^[12-14,19,20,25,26,30-32].

In one study, p-MET was detected in 59% (72 of 121) of GC tumors and was significantly associated with lymph-node metastasis, disease stage, and outcomes^[20]. In another study, however, only 7% (2 of 30) of tumors overexpressed p-MET in spite of the fact that 63% (24 of 38) overexpressed MET^[22]. In another study using a new technique, collaborative enzyme enhanced reactive-immunoassay, p-MET was detected in 24% (103 of 434) of GC tumors, including 31% of intestinal type, 24% of diffuse type, and 0% of mixed type^[33].

Gene expression

Studies assessing *MET* gene expression are summarized

Table 1 MET protein expressions on immunohistochemistry and clinical outcomes in gastric cancer

	<i>n</i>	Definition of overexpression	%	Relation to clinicopathological factors	Relation to survival	Ref.
Usual IHC	495	2+/3+, > 10%	22	Intestinal type, recurrence	Worse ³	[14]
	170	Cytoplasmic, 2+/3+	13	ND	ND	[38]
	121	≥ 5%	66	N, stage	Worse	[20]
	114	> 30%	74	NA	Worse ³	[30]
	98	Intensity and extensity scoring system	59	N, M	Worse	[25]
	50		78	NA	NA	[28]
	38	2+/3+, ≥ 25%	63	Intestinal type	ND	[22]
	94 ¹	≥ 50%	50	NA	NA	[24]
	121 ²	Any staining	98	Liver metastasis	ND	[29]
	TMA	438	Membranous, 2+/3+, > 10%	24	T, N, M, stage, intestinal type	Worse
436		Intensity and extensity scoring system	44	T, N, M, diffuse type	Worse ^{3,4}	[13]
215		Cytoplasmic, > 10%	69	NA	NA	[27]
212		2+/3+	12	ND	Worse ³	[32]
182		Intensity and extensity scoring system	66	N, intestinal type, differentiated type	Worse	[19]
163		Cytoplasmic 2+/3+ ≥ 10%, and positive > 75%	4	ND	Worse ³	[31]
124		Cytoplasmic, 3+	71	T, stage, intestinal type	ND	[23]
114		Intensity and extensity scoring system	82	N, stage	Worse	[26]
35			43	ND	Likely worse	[18]

¹Limited to diffuse or mixed type; ²Only stage IV; ³An independent prognostic factor on multivariate analysis; ⁴Only IHC3+. IHC: Immunohistochemistry; TMA; Tissue micro array; T: Tumor invasion depth; N: Lymph-node metastasis; M: Distant metastasis; ND: Not described; NA: Not associated.

Table 2 MET mRNA expressions and clinical outcomes in gastric cancer

	<i>n</i>	Overexpression		Relation to clinicopathological factors	Relation to survival	Ref.
		Cut-off value	%			
Tumor	100	Value determined by nonparametric receiver operating characteristics	11	M	Worse	[34]
	100	ND	24	ND	ND	[43]
	45			N, stage, differentiated type	ND	[35]
	43	Value of mean + 2 SD in noncancerous tissue	70	NA	ND	[36]
	15			Intestinal type	ND	[22]
Serum	52	Detected	62	T, N, M, stage, recurrence, v	Worse	[37]

T: Depth of tumor invasion; N: Lymph-node metastasis; M: Distant metastasis; v: Venous invasion; ND: Not described; NA: Not associated.

in Table 2. *MET* mRNA expression in GC tissue has been reported to significantly correlate with lymph-node metastasis, distant metastasis, and disease stage^[34,35], although one study found no clinical significance^[36]. Higher levels of *MET* mRNA expression were frequently detected in intestinal or differentiated type cancers^[22,35]. Serum *MET* mRNA expression in peripheral blood has been detected and was significantly associated with tumor progression and short survival^[37].

Studies of *MET* gene alterations are summarized in Table 3. On fluorescence *in situ* hybridization (FISH) or silver *in situ* hybridization, *MET* gene amplification was detected in 3.4% to 7.1% of tumors^[12,32,38]. In a study of esophagogastric adenocarcinoma, *MET* amplification was observed in 2.2% (10 of 460) of patients^[39]. However, overexpression has been defined according to two patterns, *i.e.*, both amplification and high polysomy, or amplification alone. Gene amplification has been found to be significantly related to distant metastasis and tumor stage^[12,39]. On copy number assay using reverse transcription polymerase chain reaction (RT-PCR), *MET* gene amplification was observed in 1.5% to 30% of

tumors, although the definition of *MET* amplification somewhat differed among studies^[15,18,40-42]. In a study using single nucleotide polymorphism array, *MET* amplification was detected in 3% to 4% of patients^[43,44]. Wang *et al.*^[43] reported that *MET* amplification was found in 7% (3 of 41) of intestinal type cancers, but not in other types.

In many studies using FISH or RT-PCR, patients with *MET*-amplified tumors had significantly poorer survival than those with non-amplified tumors^[12,15,18,32,39,41,42]. Only a Japanese study, with the lowest incidence of gene amplification, reported no relation of *MET* amplification to survival or any clinicopathological characteristic^[40].

Gene mutation

A mutation of *MET* exon 14 coding for the juxta-membrane domain with a regulatory site was detected, and all other mutations were found in *MET* exons 16 to 20^[45]. *MET* exon 2 skipping was found in 30% (82 of 272) of GC cases and was associated with increased *MET* gene expression. In addition, novel variants of *MET* exon 18 and/or 19 skipping were observed in 42% (47

Table 3 MET gene alterations and clinical outcomes in gastric cancer

	<i>n</i>	Definition of positive expression	%	Relation to clinicopathological factors	Relation to survival	Ref.
FISH	460 ¹	GA	2.2	Stage	Worse	[39]
	196	GA	6.1	ND	Worse	[32]
	170	GA or HP	15 (GA7.1 HP7.6)	ND	ND	[38]
SISH	381	GA or HP	19 (GA3.4, HP16)	Intestinal (HP), M (GA), stage (GA)	Worse ² (GA)	[12]
RT-PCR	472	> 4 copies	21	NA	Worse ²	[33]
	266	> 4 copies	1.5	NA	NA	[40]
	216	≥ 5 copies	10	Unknown	Worse ²	[41]
	128	≥ 4 copies	30	T, stage	Worse ²	[42]
	45	≥ 7 copies	7	ND	Worse	[18]
SNP array	193	GA	4	ND	ND	[44]
	100	GA	3	ND	ND	[43]
Polymorphism analysis	34 (tumor)	Any alterations	59	T, N, M	ND	[47]
	34 (serum)	Any alterations	41	N, M	ND	[47]

¹Esophagogastric adenocarcinoma; ²An independent prognostic factor on multivariate analysis. FISH: Fluorescence *in situ* hybridization; SISH: Silver *in situ* hybridization; RT-PCR: Reverse transcription polymerase chain reaction; SNP: Single nucleotide polymorphism; GA: Gene amplification; HP: High polysomy; ND: Not described; NA: Not associated; T: Tumor invasion depth; N: Lymph-node metastasis; M: Distant metastasis.

of 272) of GC patients^[46]. In another study, alterations of the *MET* gene were detected in both cancer tissue and peripheral blood of GC patients, and such alterations significantly correlated with tumor depth, lymph-node metastasis, and distant metastasis^[47]. *MET* polymorphism (A/G or G/G genotype of *MET* rs40239) was significantly associated with favorable survival in a Japanese cohort, although no significant association was found in American or Austrian cohorts^[48].

PRECLINICAL STUDIES OF MET INHIBITORS FOR GC

Several GC cell lines (Hs746T, GTL16, MKN45, SNU5, SNU620, HSC58, 58As9, and 58As1) have *MET* amplification and were used in preclinical studies of MET inhibition.

Selective tyrosine kinase inhibitors for MET

Volitinib (HMPL-504/AZD6094) is a small, potent adenosine triphosphate (ATP)-competitive tyrosine kinase inhibitor (TKI) of MET. Volitinib showed higher anti-proliferative activity against GC cell lines with gains of *MET* gene copy number (SNU5, Hs746T, SNU620, GTL16, *etc.*) than against those without such gains (MKN1, MKN74, AZ521, KATO III, AGS, *etc.*). The expressions of p-MET, phosphorylated AKT (p-AKT), and phosphorylated ERK (p-ERK) were down-regulated by volitinib in Hs746T cells. In a GC patient-derived tumor xenograft model with *MET* amplification, volitinib inhibited tumor growth; furthermore, the antitumor activity of volitinib was enhanced by concurrent treatment with docetaxel^[38].

SU11274 is a small molecule TKI of MET. SU11274 blocked HGF-induced epithelial-mesenchymal transition, inducing down-regulation of Snail-2 and vimentin and up-regulation of E-cadherin in MKN45 cells, but not in non-amplified GC cells (MKN74). SU11274 suppressed

proliferation of tumor cells regardless of the presence of HGF and also inhibited migratory potential. In a mouse model of peritoneal dissemination established from MKN45, SU11274 reduced the numbers and sizes of peritoneal tumors^[34]. SU11274 treatment combined with SN38 synergistically suppressed proliferation of GC cells (side population cells of OCUM-2M) and tumor volume in a xenograft model^[49].

PHA-665752 is a specific TKI for MET. In GTL16 cells, PHA-665752 inhibited growth in soft agar as well as cell proliferation and induced apoptosis regardless of the presence of HGF. PHA-665752 treatment decreased expression of MET-dependent signaling pathways, including p-MET, p-AKT, p-ERK, phosphorylated focal adhesion kinase (p-FAK), p-PLC-gamma, or phosphorylated signal transducer and activator of transcription, in GTL-16 or MKN45 cells^[50,51]. Inhibition efficacy was higher in MKN45 cells than in non-amplified GC cells (MKN1, MKN28, and AGS)^[51]. PHA-665752 significantly inhibited an increase in tumor volume in a GTL16 xenograft model^[50]. PHA-665752 induced autophagy, and combined treatment with PHA-665752 and an autophagy inhibitor acted synergistically in GTL16 cells^[52]. Furthermore, PHA-665752 restored growth inhibition in GC cells (SNU216) resistant to lapatinib (anti-EGFR and HER2)^[16].

SGX523 is a selective, ATP-competitive MET inhibitor. Tyr 1248 is essential for high-affinity binding of SGX523 to MET. SGX523 inhibited p-MET and downstream signal pathways (p-GAB1, p-AKT, and p-ERK) in GTL16 cells. SGX523 inhibited tumor growth in a GTL16 xenograft model^[53].

BAY-853474 is a highly selective, ATP-competitive MET inhibitor. It suppressed tumor growth in an Hs746T xenograft model and reduced plasma biomarkers, such as soluble MET ectodomain and IL-8^[54].

KRC-408 is a small-molecule TKI that inhibits MET by occupying the ATP binding site. KRC inhibited p-MET and its constitutive downstream effectors (p-AKT, p-MEK,

p-ERK, phosphorylated mammalian target of rapamycin (mTOR), and p-p70S6K in MKN45 cells. KRC-408 induced apoptosis as represented by increased levels of caspase-3 and PARP. MKN45 cells in G2/M phase accumulated and those in S phase decreased after KRC-408 treatment. KRC-408 significantly delayed tumor growth in an MKN45 xenograft model, accompanied by decreased expression of p-MET, p-AKT, p-ERK, and CD34^[55].

AMG 337 is a small-molecule ATP-competitive TKI of MET. Treatment with AMG 337 affected the viability of only two GC cell lines (SNU5 and Hs746T). Administration of AMG 337 resulted in dose-dependent antitumor efficacy in MET-amplified GC xenograft models^[56].

Multikinase TKI

Crizotinib (PF-2341066) is an ATP-competitive, small-molecule TKI of MET and anaplastic lymphoma kinase. Crizotinib inhibited GTL16 cell growth and induced apoptosis in GTL16 cells. Crizotinib treatment reduced p-MET expression and inhibited tumor growth in a GTL16 xenograft model. These effects were accompanied by a decrease in tumor mitotic index (Ki67 expression), induction of apoptosis (caspase-3 expression), and a reduction in microvessel density (CD31 expression)^[57]. Crizotinib induced apoptosis and reduced expression of p-AKT and p-ERK in *MET*-amplified GC cells (SNU5, HSC58, 58As9, and 58As1), but not in non-amplified GC cells (MKN28 and MKN1). Crizotinib treatment up-regulated the expression of a proapoptotic member of the Bcl-2 family (BIM), whereas it down-regulated the expression of members of the inhibitor of apoptosis protein (IAP) family, such as survivin, X-linked IAP, and c-IAP1. Crizotinib exhibited marked antitumor activity in 58As9 and SNU5 xenografts, but not in other xenografts derived from non-amplified GC cells (AZ521 and MKN28)^[58]. In another study, crizotinib effectively inhibited the growth of *MET*-amplified GC cells (SNU620, SNU5, Hs746T, and GLT16) or *MET*-overexpressed GC cells (SNU638). *MET*-positive patient-derived GC xenografts responded to crizotinib and showed down-regulation of p-MET, p-AKT, and p-ERK^[32].

Foretinib (GSK1363089) is an ATP-competitive multikinase inhibitor of MET, RON, AXL, tunica internal endothelial cell kinase 2 (TIE2), and VEGFR2. Foretinib inhibited the growth of MKN45 cells and FGFR2-amplified GC cells (KATO-III) more strongly than that of non-amplified GC cells (MKN1, MKN7, and MKN74). Foretinib suppressed phosphorylation of EGFR, HER3, and FGFR3 *via* MET inhibition in MKN45 cells, while it inhibited phosphorylation of EGFR, HER3 and MET *via* FGFR2 inhibition in KATO-III cells^[59].

Cabozantinib (XL184) is an ATP-competitive, small-molecule multikinase inhibitor against MET, VEGFR2, and RET. SNU5 and Hs746T cells markedly responded to cabozantinib^[60].

S49076 is a potent ATP-competitive multikinase

inhibitor of MET, AXL/MER, and FGFR1-3. S49076 decreased p-MET expression and cell viability in GTL16 cells. S49076 down-regulated p-MET, p-AKT, and phosphorylated p70S6K and inhibited tumor growth in a GTL16 xenograft model^[61].

T-1840383 is a potent inhibitor that targets MET, VEGFR1-3, RET, RON, RSE, TIE2, and TRKA. T-1840383 inhibited tumor growth in association with reduced p-MET, p-AKT, and p-ERK expression in an MKN45 xenograft model. In a peritoneal dissemination model generated from GC cells (NUGC4 expressing luciferase), T-1840383 treatment significantly prolonged survival in mice^[62].

MK-2461, an ATP-competitive multitargeted inhibitor of activated MET, FGFR2, and platelet-derived growth factor receptor, potently inhibited the phosphorylation of three tyrosine residues of MET (Y1003 in the juxta-membrane domain, and Y1349 and Y1365 in the COOH-terminal docking site) in GTL16 cells. The anti-proliferative potencies of MK-2461 were higher in GC cells with amplification of *MET* or *FGFR2* (GTL16, SNU5, SNU16, KATO III) than in non-amplified GC cells (MKN74, AGS, SNU1, *etc.*). In GTL16 xenograft models, MK-2461 effectively suppressed MET signaling and tumor growth^[63].

Other drugs

K252a is a potent small molecule inhibitor of the TRK family and reduced MET-driven proliferation in GTL16 cells. After K252a treatment, GTL16 cells lost the ability to form lung metastases in mice^[64].

Oridonin, a diterpenoid isolated from the plant *Rabdosia rubescens*, has been used in traditional Chinese medicine for the treatment of human cancer, such as esophageal and prostate carcinomas. Oridonin potently inhibited MET phosphorylation and MET-dependent cell proliferation in SNU5 cells. Oridonin inhibited tumor growth and down-regulated p-AKT, p-ERK, p-c-RAF in an SNU5 xenograft model. Expression levels of Ki67 and CD31 on IHC also decreased in that model^[65].

Resistance to MET inhibitors

HER kinase activation has been shown to play a role in the acquisition of resistance to MET inhibitor in GC cells. Phosphorylation of EGFR and HER3, which are activated *via* MET-driven receptor cross-talk, were suppressed by a MET inhibitor (PHA-665752) in GTL-16 and MKN-45 cells. However, EGF or heregulin-beta1 (HRG) treatment activated MET-independent EGFR or HER3 and restimulated PI3K/AKT or MEK/MAPK pathway. EGF or HRG treatment increased expression of cyclin D1, which had been reduced by a MET inhibitor, and promoted the cell cycle from arrest phase to synthetic phase. Therefore, combined treatment with a MET inhibitor plus an MEK or AKT inhibitor suppressed cell proliferation that had been promoted by HER family activation^[66]. In the other study, activation of HER family members induced resistance to MET inhibitor.

Table 4 Development of MET-targeting agents for gastric cancer

Type	Agent	Other targets	Phase	Line	Combined therapy	Results or status	Ref.
MET selective non-ATP competitive TKI	Tivantinib (ARQ197)	None	II	2 nd /3 rd	None	No CR/PR Median PFS 1.4 mo	[72]
MET-selective ATP-competitive TKI	AMG 337	None	II	Any	None	Ongoing	[74]
			I	2 nd /3 rd	None	1 CR and 4 PR in 10 patients with MET -amplified tumor	[73]
Multitargeted ATP-competitive TKI	Foretinib (GSK1363089)	VEGFR2, RON, AXL, TIE2	II	1 st (95%)	Docetaxel, Cisplatin	No CR/PR Median OS 7.4	[75]
	Crizotinib (PF-2341066)	ALK	I			Tumor shrinkage in 2 patients with PFS 3.5 and 3.7 mo	[39]
MET mAb	Onartuzumab (MetMab)	None	III	1 st	mFOLFOX	Ongoing	[77]
HGF mAb	Rilotumumab (AMG 102)	None	III	1 st	ECX	Suspended	[79]
		None	III	1 st	CX	Suspended	[80]
		None	II	1 st	ECX	Median PFS 4.2 mo Median OS 5.6 mo	[78]

ATP: Adenosine triphosphate; TKI: Tyrosine kinase inhibitor; mAb: Monoclonal antibody; VEGFR: Vascular endothelial growth factor receptor; ALK: Anaplastic lymphoma kinase; TIE: Tunica internal endothelial cell kinase; CR: Complete response; PR: Partial response; RFS: Relapse-free survival; OS: Overall survival; FOLFOX: Folinic acid + fluorouracil + oxaliplatin; ECX: Epirubicin + oxaliplatin + capecitabine; CX: Oxaliplatin + capecitabine.

GTL16 cells that had acquired constitutive activation of EGFR by EGFR-L858R mutation did not respond to anti-MET treatment, such as MET silencing or MET inhibitor (PHA-665752). mRNA levels of HER family members significantly increased in the resistant GTL16 cells^[67]. Qi *et al.*^[68] reported two mechanisms of resistance to the MET inhibitors PHA-665752 and PF-2341066. One mechanism was the activation of EGFR signaling. In GC cells acquiring resistance to MET inhibitors, EGFR signaling (EGFR, AKT, and ERK) was activated *via* an increase in transforming growth factor alpha. The other mechanism involved a gene mutation in the MET activation loop (Y1230). That mutation destabilizes the autoinhibitory conformation of MET on structural analysis and abrogates interaction with the inhibitor^[68]. Increased copy numbers of *MET* or *KRAS* and increased expression of p-ERK or p-AKT were detected in GTL16 cells resistant to the MET inhibitor PHA-665752^[69]. In addition, a novel *SND1-BRAF* fusion was detected in GTL16 cells that were resistant to the MET inhibitor RF-04217903 and was proven to be responsible for the resistance^[70].

CLINICAL STUDIES OF MET INHIBITORS IN GC

Published and ongoing clinical studies of MET inhibitors in GC are summarized in Table 4. Tivantinib (ARQ197) is a non-ATP-competitive, selective MET inhibitor. In a phase I trial in 51 patients with GC, 14 patients had stable disease (SD) for 4 mo or longer, and circulating endothelial cells decreased in 58% (25 of 43) of patients. Tivantinib decreased p-MET, MET, and phosphorylated focal adhesion kinase and increased terminal deoxynucleotidyl transferase-mediated deoxyuridine triphosphate-biotin nick-end labeling (TUNEL) staining in tumor biopsy specimens^[71]. In a phase II study of tivantinib as second- or third-line therapy in GC, no

objective response was observed in the 30 patients enrolled; the disease control rate was 37%, and median progression-free survival (PFS) was only 43 d. Tivantinib seemed to have modest antitumor efficacy and mild toxicity. As for adverse effects, severe (grade 3 or higher) neutropenia and anemia were most common, each occurring in 13% (4 of 30) of the patients^[72].

Recently, favorable outcomes of treatment with ANG 337 have been reported in a phase I study in 10 patients with MET-amplified esophago GC^[73]. One patient had a complete response, and 4 had partial responses, even when ANG 337 was given as second-line or subsequent chemotherapy. An ongoing phase II study is expected to explore whether the levels of MET amplification and expression or the presence of mutation in tumor specimens correlates with the response to AMG 337^[74].

Foretinib lacked efficacy against metastatic GC in a phase II study enrolling 74 patients. The best response was SD in 23% (10 of 44) of patients who received intermittent dosing and 20% (5 of 25) of those who received daily dosing. Only 4% (3 of 67) of the patients had *MET* amplification in tumor specimens, and one of them had SD. OS was 7.4 mo with intermittent dosing and 4.3 mo with daily dosing. Severe (grade 3 or higher) treatment-related adverse events occurred in 44% (21 of 48) of the patients who received intermittent dosing and 35% (9 of 26) of those who received daily dosing. Elevated aspartate aminotransferase levels (10%) and fatigue (15%) were the most frequent adverse events in patients who received intermittent dosing and daily dosing, respectively. Plasma levels of MET, HGF, VEGFR2, and VEGF-A were measured at baseline and during treatment, but these markers did not correlate with response^[75].

Crizotinib was administered to 4 patients with *MET*-amplified esophagogastric adenocarcinomas in part of a phase I study. Two patients had tumor shrinkage (16% and 30%) with PFS of 3.5 and 3.7 mo, respectively^[39].

Onartuzumab (formally called MetMab and PRO 143966) is an anti-MET receptor monoclonal antibody. In a phase I clinical trial, one patient with metastatic GC had a complete response for approximately 2 and a half years^[76]. A phase III study of onartuzumab combined with modified FOLFOX (5-fluorouracil + leucovorin + oxaliplatin) is ongoing^[77].

Rilotumumab (AMG 102) is a monoclonal antibody against HGF. In a phase I b/II study of rilotumumab combined with epirubicin, cisplatin, and capecitabine (ECX) as first-line chemotherapy, 121 patients were randomly assigned to treatment (40 to rilotumumab 15 mg/kg; 42 to rilotumumab 7.5 mg/kg; 39 to placebo). Median PFS was significantly longer in both rilotumumab groups combined than in the placebo group (5.7 and 4.2 mo, respectively). The response rate was 39%, and the disease control rate was 80% in the combined rilotumumab group. MET status was evaluated on IHC in that study, and MET positivity was defined as at least 25% membrane staining of tumor cells at any intensity. In the MET-positive group, median OS was much longer in the combined rilotumumab group than in the placebo group (10.6 mo vs 5.7 mo). In the MET-negative group, patients had better survival than those in the MET-positive group, and rilotumumab was not significantly effective. As for adverse effects, severe (grade 3 or higher) venous thromboembolism occurred in 20% (16 of 81) of the patients^[78]. However, the management of thromboembolism might be the most critical issue. Two phase III trials of rilotumumab plus ECX and rilotumumab plus cisplatin and capecitabine have been suspended because of increased treatment-related mortality^[79,80].

CONCLUSION

Many studies have suggested that MET protein overexpression or *MET* amplification plays a critical role in the progression of GC and negatively affects survival in patients with GC. However, the criteria used to define overexpression of MET protein have differed among many studies, and the assessment of MET protein expression is unlikely to be standardized as strictly as that of HER2 or EGFR. It remains unclear whether staining intensity of the membrane or the cytoplasm of tumor cells should be assessed. Differences in staining intensity associated with the use of different antibodies and different IHC procedures used to assess MET expression remain a problem that must be solved before techniques for assessing MET status can be standardized. The use of different assessment techniques by different investigators is another problem. The evaluation of p-MET expression might provide the most objective measure of MET status; however, the fact that different antibodies recognize different phosphorylated sites might be a major obstacle to the standardization of techniques for assessing p-MET expression. On the other hand, *MET* amplification on FISH may be appropriate for standardized assessment,

similar to *HER2* amplification. Several studies have used consistent criteria to define *MET* amplification on FISH, and it is more objective assessment than that of protein expression on IHC, although the cost- and time-effectiveness of gene analysis may be poor. Deng *et al.*^[44] reported that *MET* amplification was mutually exclusive from amplification of other genes, such as *EGFR*, *HER2*, *FGFR2*, and *KRAS*. Therefore, MET-targeting therapy is considered a promising treatment for GC with *MET*-amplification as well as GC with amplification of other RTKs.

Preclinical studies have suggested that MET inhibitors are most promising against *MET*-amplified or MET-overexpressed cancers. Various MET inhibitors have been developed and studied in clinical trials; however, several trials showed insufficient efficacy and unexpected outcomes. These results might have been caused by lack of identification of specific biomarkers. Methodological differences in the evaluation of MET status remain an important problem in conducting clinical trials. In an ongoing study of monoclonal antibodies of MET, patients with MET expression on IHC are being recruited^[77]. As mentioned above, the assessment of MET protein expression on IHC remains to be standardized. The same procedure for assessment of MET status on IHC is needed for clinical studies. Many TKIs of MET have produced favorable results in *MET*-amplified GC in many preclinical studies, and AMG 337 and crizotinib were effective in some patients with *MET*-amplified GC in preliminary clinical studies^[39,73]. MET TKIs thus may be a promising treatment for patients with *MET*-amplified GC.

Resistance to MET inhibitors is another critical issue. Several lines of evidence from preclinical studies suggest that activation of the HER family is involved in resistance to MET inhibitors, and treatment against HER family pathways may overcome this issue. Owing to the diversity of RTKs, treatment with a multitargeted TKI or combined therapy with single-targeted TKIs might be a promising approach to enhance efficacy. However, potential benefits of treatment with multiple inhibitors of RTKs have yet to be demonstrated in clinical trials in GC.

MET is considered a promising target in GC, although the results of phase III trials of rilotumumab have been disappointing. It is essential to identify specific subgroups of patients most likely to benefit from treatment with MET inhibitors. Future studies should attempt to define biomarkers that would optimize the selection of patients who respond to MET inhibitors.

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Polymorphisms in mucin genes in the development of gastric cancer

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Abstract

Gastric cancer (GC) is the third leading cause of cancer-related death worldwide. In areas of high prevalence, such as Japan, South Korea and China, most cases of GC are related to *Helicobacter pylori* (*H. pylori*), which involves well-characterized sequential stages, including infection, atrophic gastritis, intestinal metaplasia, dysplasia, and GC. Mucins are the most abundant high-molecular-weight glycoproteins in mucus, which is the first line of defense and plays a major role in blocking pathogenic factors. Normal gastric mucosa shows expression of MUC1, MUC5AC and MUC6 that is specific to cell type. However, the specific pattern of MUC1, MUC5AC and MUC6 expression is changed in gastric carcinogenesis, accompanied by *de novo* expression of secreted MUC2. Recent studies have provided evidence that variations in these mucin genes affect many steps of GC development, such as *H. pylori* infection, and gastric precancerous lesions. In this review, we focus on studies of the association between polymorphisms in mucin genes and development of GC. This information should be helpful for the early detection, surveillance, and treatment of GC.

Key words: Gastric cancer; *Helicobacter pylori*; Genetic polymorphism; Mucin; Risk; Association study; Atrophic gastritis

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Core tip: *Helicobacter pylori* (*H. pylori*) infection is the single most important risk factor in the development of gastric cancer (GC), however the etiology of GC involves host and other environmental factors. Genetic and biological evidence highlights the important roles of variations in mucin genes in the development and progression of GC. In this review, we summarize studies

of the association between polymorphisms in *MUC1*, *MUC5AC*, *MUC6* and *MUC2* and development of GC, which should be helpful for the early detection, surveillance, and treatment of GC.

Wen R, Gao F, Zhou CJ, Jia YB. Polymorphisms in mucin genes in the development of gastric cancer. *World J Gastrointest Oncol* 2015; 7(11): 328-337 Available from: URL: <http://www.wjgnet.com/1948-5204/full/v7/i11/328.htm> DOI: <http://dx.doi.org/10.4251/wjgo.v7.i11.328>

INTRODUCTION

Although gastric cancer (GC) incidence and mortality rates are declining in most countries, it is still the fifth most common cancer and the third leading cause of cancer-related death worldwide^[1]. Epidemiological studies have shown that a high intake of salt, tobacco smoking, and *Helicobacter pylori* (*H. pylori*) infection increase the risk of GC^[2-4]. In areas of high prevalence of GC, such as Japan, Korea and China, most cases of GC are related to *H. pylori*. GC is the result of a long complex multifactorial and multistep process that involves well-characterized sequential stages. The initial lesion is inflammatory and is usually caused by *H. pylori* infection, which results in chronic superficial gastritis. The following pathological model of GC progression includes atrophic gastritis, intestinal metaplasia, dysplasia and GC^[5,6]. *H. pylori* infection is the most important risk factor for GC and it was classified as a class I carcinogen by the World Health Organization in 1994, nevertheless, the etiology of GC also involves host and other environmental factors. This is demonstrated by the fact that only 1%-3% of patients with *H. pylori* infection develop GC^[7,8]. The hypothesis that genetic susceptibility or predisposition plays an important etiological role in GC is supported by many case-control studies and genome-wide association studies (GWASs)^[9-14].

H. pylori initiates colonization of the gastric mucosa by crossing the gastric mucus layer and adhering to the gastric epithelium^[15]. Mucus is the first line of defense and plays a major role in blocking pathogenic factors, and mucins are the major components in mucus and are responsible for its biochemical and biophysical properties^[16]. The mucin family comprises 21 members. The mucins are high-molecular-weight glycoproteins characterized by a heavily O-glycosylated tandem repeat region rich in proline, threonine and serine, which is encoded by a variable number of tandem repeats (VNTRs)^[17-20]. Mucins are categorized into two subgroups according to their physiological and structural characteristics: membrane-bound, such as *MUC1*, and secreted, including *MUC2*, *MUC5AC* and *MUC6*^[17]. *In situ* hybridization and immunohistochemistry have demonstrated the cell-type-specific expression of mucins in epithelial tissues^[21,22]. Normal gastric mucosa shows

cell-type-specific expression of *MUC1*, *MUC5AC* and *MUC6*^[21-23]. Apical *MUC1* is expressed in the gastric mucosa in the superficial and foveolar epithelium and mucous neck zone cells^[24]. Secreted mucin *MUC5AC* is detected in the superficial epithelium, whereas *MUC6* is found in the deep glands^[25,26]. This specific pattern of *MUC1*, *MUC5AC* and *MUC6* expression is changed in gastric carcinogenesis, accompanied by *de novo* expression of secreted *MUC2*^[26-30]. Recent genetic and biological evidence highlights the important roles of variations in these mucin genes in the development and progression of GC. In this review, we focus on studies of the association between polymorphisms in *MUC1*, *MUC5AC*, *MUC6* and *MUC2* genes and development of GC (Table 1). Details of the studied single nucleotide polymorphisms (SNPs) in mucin genes are described in Table 2.

POLYMORPHISMS IN *MUC1* IN THE DEVELOPMENT OF GC

MUC1 is a highly polymorphic membrane-associated mucin that is often aberrantly expressed in cancer^[31]. *MUC1* gene is located on chromosome 1q21 and contains a highly conserved VNTR of 20 amino acids, varying from 25 to 125 repeats, depending on the allele^[32]. In recent decades, some studies were performed to investigate the potential roles of genetic variations in *MUC1* in gastric carcinogenesis, but most of them were focused on the VNTRs, with inconsistent results. Costa *et al.*^[33] observed that polymorphism in the *MUC1* VNTRs influenced the binding of *H. pylori* to gastric cells. Vinall *et al.*^[28] reported that small *MUC1* VNTR alleles were correlated with *H. pylori*-associated gastritis in European populations. Two studies from Portugal (which has the higher risk of GC in Europe) showed that small *MUC1* VNTR alleles were significantly associated with gastric carcinoma^[34], as well as chronic atrophic gastritis and incomplete intestinal metaplasia, which are two well-established precursor lesions of GC^[35]. However, another study from Denmark indicated that small *MUC1* VNTR alleles are more frequent in the Danish population (which has the lower risk of GC in Europe) than in Portugal^[36].

GWASs have recently been important in identifying potential genetic variations related to cancer susceptibility. In 2010, Abnet *et al.*^[37] conducted a GWAS in 1625 patients with GC and 2100 controls. They identified a significant SNP of rs4072037 A/G in the *MUC1* gene for GC. The A allele was correlated with increased susceptibility to GC in Chinese patients during initial scanning, however, this association was not maintained in the second phase, or when the results of the two phases were combined. A GWAS on GC in Japan revealed the top 10 SNPs that were significantly related to the diffuse type of GC, which included two located in chromosome 1q22^[38]. Subsequently, Saeki *et al.*^[39] performed high-density mapping to explore the

Table 1 List of association studies between polymorphisms in mucin genes and development of gastric cancer

Gene	Ref.	Population	Disease	Study design	Sample (case/control)	Polymorphism	Association
MUC1	Vinall <i>et al</i> ^[28]	European	<i>H. pylori</i> related gastritis	Case-control study	57 gastritis patients	VNTR	Yes
	Carvalho <i>et al</i> ^[34]	Portuguese	GC	Case-control study	159/324	VNTR	Yes
	Silva <i>et al</i> ^[35]	Portuguese	CAG, IM	Case-control study	174 patients	VNTR	Yes
	Abnet <i>et al</i> ^[37]	Chinese	GC	GWAS	1625/2100	rs4072037	Yes
					Replication: 615/1202		No
					Combined: 2240/3302		No
	Saeki <i>et al</i> ^[39]	Japanese	DGC	Case-control study	606/1264/304/1465	rs4072037, rs2070803	Yes
		Japanese			452/372	rs4072037, rs2070803	Yes
		South Korean					Yes
	Xu <i>et al</i> ^[40]	Chinese	GC	Case-control study	138/241	rs4072037	Yes
	Jia <i>et al</i> ^[43]	Polish	GC	Case-control study (tag SNP approach)	273/377	rs6427184	Yes
						rs4971052	Yes
						rs4276913	Yes
						rs4971088	Yes
						rs4971092	Yes
						rs4072037	Yes
	Jia <i>et al</i> ^[43]	Polish	<i>H. pylori</i> infection	Case-control study (tag SNP approach)	320/57	rs6427184	No
						rs4971052	No
						rs4276913	No
						rs4971088	No
						rs4971092	No
						rs4072037	No
	Zhang <i>et al</i> ^[44]	Chinese	GC	Case-control study	1681/1858	rs4072037	Yes
	Palmer <i>et al</i> ^[45]	Caucasian	GC	Case-control study	596/587	rs4072037	Yes
	Li <i>et al</i> ^[46]	Chinese	GC	Case-control study	300/300	rs2070803	Yes
	Zhang <i>et al</i> ^[47]	Chinese	Non-cardia GC	Case-control study (tag SNP approach)	288/281	rs4072037	No
						rs2990245	No
						rs9628662	No
					rs9426886	No	
Zhang <i>et al</i> ^[47]	Chinese	<i>H. pylori</i> infection	Case-control study (tag SNP approach)	122/159	rs4072037	No	
					rs2990245	No	
					rs9628662	No	
					rs9426886	No	
Frank <i>et al</i> ^[48]	German	CAG	Case-control study	533/1054	rs4072037	No	
Marin <i>et al</i> ^[49]	Spanish	GCPLs	Case-control study (tag SNP approach)	387 patients	rs3814316	No	
					rs9426886	No	
					rs1045253	No	
Sun <i>et al</i> ^[50]	Hispanic American	GC	Case-control study	132/125	rs4072037	No	
Duan <i>et al</i> ^[51]	-	GC	Meta-analysis	4220/6384	rs4072037	Yes	
Zheng <i>et al</i> ^[52]	-	GC	Meta-analysis	6580/10324	rs4072037	Yes	
Mocellin <i>et al</i> ^[42]	Asian	DGC	Meta-analysis	7279 subjects	rs2070803	Yes	
MUC5AC	Jia <i>et al</i> ^[43]	Polish	GC	Case-control study (tag SNP approach)	273/377	rs1541314	No
					rs2014486	Yes	
					rs2075859	No	
					rs2672785	No	
					rs2735733	Yes	
					rs7118568	No	
					rs868903	Yes	
					rs4963049	No	
Jia <i>et al</i> ^[43]	Polish	<i>H. pylori</i> infection	Case-control study (tag SNP approach)	320/57	rs1541314	No	
					rs2014486	No	
					rs2075859	No	
					rs2672785	No	
					rs2735733	No	
					rs7118568	No	
					rs868903	No	
					rs4963049	No	
Zhou <i>et al</i> ^[61]	Chinese	Non-cardia GC	Case-control study (tag SNP approach)	288/281	rs3793966	No	
					rs7118568	No	
					rs868903	No	
					rs3793964	Yes	
					rs3750919	No	
					rs5743942	No	
					rs4963062	No	
					rs885454	Yes	
					rs6578810	No	
					rs11040869	Yes	
					rs7118481	No	
					rs7105198	No	

MUC6	Zhou <i>et al</i> ^[62]	Chinese	<i>H. pylori</i> infection	Case-control study (tag SNP approach)	122/159	rs3793966	No	
						rs7118568	No	
						rs868903	No	
						rs3793964	No	
						rs3750919	No	
						rs5743942	No	
						rs4963062	No	
						rs885454	No	
						rs6578810	No	
						rs11040869	No	
						rs7118481	No	
						rs7105198	No	
		Wang <i>et al</i> ^[63]	Chinese	GC	Case-control study	230/328	VNTR	Yes
		Nguyen <i>et al</i> ^[68]	-	<i>H. pylori</i> infection	Case-control study	92/68	VNTR	Yes
		Garcia <i>et al</i> ^[69]	Portuguese	GC	Case-control study	157/376	VNTR	Yes
	Kwon <i>et al</i> ^[70]	South Korean	GC	Case-control study	470/1103	VNTR	Yes	
	Jia <i>et al</i> ^[43]	Polish	GC	Case-control study (tag SNP approach)	273/377	rs1128413	No	
MUC2						rs4077293	No	
						rs7483870	No	
						rs7943115	No	
						rs11602663	No	
						rs11605303	No	
						rs10902076	No	
						rs2071174	No	
						rs11245936	No	
						rs10794359	No	
						rs7112267	No	
						rs12574439	No	
						rs7119740	No	
						rs11601642	No	
		Jia <i>et al</i> ^[43]	Polish	<i>H. pylori</i> infection	Case-control study (tag SNP approach)	320/57	rs1128413	No
							rs4077293	No
						rs7483870	No	
						rs7943115	No	
						rs11602663	No	
						rs11605303	No	
						rs10902076	No	
						rs2071174	No	
						rs11245936	No	
						rs10794359	No	
						rs7112267	No	
						rs12574439	No	
						rs7119740	No	
						rs11601642	No	
	Marin <i>et al</i> ^[49]	Spanish	GCPLs	Case-control study (tag SNP approach)	387 patients	rs4076950	No	
						rs7481521	No	
						rs11246384	No	
						rs6597947	No	
						rs9794921	No	
	Frank <i>et al</i> ^[48]	German	CAG	Case-control study	533/1054	rs7481521	No	
	Jeong <i>et al</i> ^[72]	South Korean	GC	Case-control study	455/457	VNTR	Yes	
	Marin <i>et al</i> ^[49]	Spanish	GCPLs	Case-control study (tag SNP approach)	387 patients	rs10902073	Yes	
						rs10794281	Yes	
						rs2856082	No	
						rs2071174	Yes	
						rs7396030	No	
						rs11245936	No	
						rs7944723	Yes	
						rs6421972	No	
						rs10794293	Yes	
						rs11245954	No	
						rs7480563	No	
						rs7126405	No	
						rs3924453	Yes	
						rs4077759	Yes	
	Frank <i>et al</i> ^[48]	German	CAG	Case-control study	533/1054	rs2856111	No	
						rs11825977	No	

CAG: Chronic atrophic gastritis; DGC: Diffuse gastric cancer; GCPLs: Gastric cancer precursor lesions; *H. pylori*: *Helicobacter pylori*; IM: Intestinal metaplasia; SNP: Single nucleotide polymorphism; GC: Gastric cancer.

Table 2 Description of the studied single nucleotide polymorphisms in mucin genes

Gene	Chromosome	SNPs	Wild alleles	Mutated alleles	Contig position ¹	Location ²		
MUC1	1q21	rs4072037	A	G	12007689	T22T		
		rs2070803	C	T	12000652	3' flanking region		
		rs6427184	A	G	11965720	3' flanking region		
		rs4971052	C	T	11968955	3' flanking region		
		rs4276913	A	G	11974610	3' flanking region		
		rs4971088	T	A	11985820	3' flanking region		
		rs4971092	T	C	11986883	3' flanking region		
		rs2990245	T	C	12043084	5' flanking region		
		rs9628662	T	G	12051963	5' flanking region		
		rs9426886	T	A	11994691	3' flanking region		
		rs3814316	C	T	11992655	3' flanking region		
		rs1045253	T	C	12046857	5' flanking region		
		MUC5AC	11p15.5	rs1541314	G	A	1182293	3' flanking region
				rs2014486	A	G	1177573	3' flanking region
rs2075859	C			T	1169258	3' flanking region		
rs2672785	C			T	1165711	3' flanking region		
rs2735733	C			T	1180410	3' flanking region		
rs7118568	C			G	1162850	3' flanking region		
rs868903	T			C	1161460	3' flanking region		
rs4963049	A			G	1155197	3' flanking region		
rs3793966	C			T	1221718	3' flanking region		
rs3793964	C			T	1220752	3' flanking region		
rs3750919	G			A	1211601	3' flanking region		
rs5743942	C			T	1232798	3' flanking region		
rs4963062	G			A	1245411	3' flanking region		
rs885454	C			T	1162161	3' flanking region		
rs6578810	T	G	1209349	3' flanking region				
rs11040869	G	A	1203382	3' flanking region				
rs7118481	G	C	1267108	3' flanking region				
rs7105198	G	C	1086133	5' flanking region				
MUC6	11p15.5	rs1128413	C	T	950694	3' flanking region		
		rs4077293	C	T	936522	3' flanking region		
		rs7483870	C	T	916019	3' flanking region		
		rs7943115	G	A	913885	3' flanking region		
		rs11602663	C	T	960778	Intronic		
		rs11605303	G	A	978110	5' flanking region		
		rs10902076	G	C	1006044	5' flanking region		
		rs2071174	C	T	1013712	5' flanking region		
		rs11245936	G	A	1026266	5' flanking region		
		rs10794359	C	T	991715	5' flanking region		
		rs7112267	C	T	996981	5' flanking region		
		rs12574439	G	C	997948	5' flanking region		
		rs7119740	C	G	1000419	5' flanking region		
		rs11601642	C	A	1002509	5' flanking region		
rs4076950	C	T	955021	Intronic				
rs7481521	G	A	967811	V619M				
rs11246384	C	T	970448	Intronic				
rs6597947	G	T	977029	5' flanking region				
rs9794921	G	T	979867	5' flanking region				
MUC2	11p15.5	rs10902073	C	A	1000934	5' flanking region		
		rs10794281	C	T	1003149	5' flanking region		
		rs2856082	C	G	1011562	5' flanking region		
		rs2071174	C	T	1013712	5' flanking region		
		rs7396030	C	T	1025368	Intronic		
		rs11245936	G	A	1026366	G832S		
		rs7944723	C	G	1039802	P1832P		
		rs6421972	G	A	1042586	I2154T		
		rs10794293	C	T	1045031	Intron		
		rs11245954	A	G	1047170	V2459V		
		rs7480563	G	A	1047741	T2524P		
		rs7126405	G	A	1049388	Q2653P		
		rs3924453	G	A	1051898	3' flanking region		
		rs4077759	C	T	1052068	3' flanking region		
rs2856111	T	C	1015747	L58P				
rs11825977	A	G	1015920	V116M				

¹Based on contig NT_004487.20 for *MUC1* gene, and contig NT_009237.19 for *MUC5AC*, *MUC6* and *MUC2* genes; ²SNP location relative to each gene in the region. SNPs: Single nucleotide polymorphisms.

susceptibility locus of GC at chromosome 1q22 and reported that two SNPs of rs2070803 and rs4072037 were significantly related to susceptibility to diffuse GC in Japan, and the results were validated in other Japanese and Korean studies. SNP rs4072037 is located in exon 2 of the *MUC1* gene and controls alternative splicing at the boundary between exons 1 and 2^[39-41]. This SNP affects promoter activity and disrupts the physiological function of *MUC1*^[41,42]. The rs4072037 G allele is correlated with higher VNTRs and the A allele with lower VNTRs^[41]. However, the VNTRs are unlikely to be the causal polymorphism for GC susceptibility because the TRs are not translated in normal or malignant gastric epithelial cells^[39]. This suggests that the VNTRs are a tagging polymorphism for other genetic variations, such as rs4072037, related to risk of gastric carcinogenesis. It is particularly interesting that rs4072037 A is a major allele in Chinese, Japanese and Korean populations, which have a high incidence of GC, but a minor allele in Caucasians, who have a low incidence of GC. SNP rs2070803 G/A is downstream of the *MUC1* and *TRIM46* genes and its functional effects are unknown. *MUC1* is located downstream of the *TRIM46* gene. These two genes are part of a cluster, which also includes *KRTCAP2*, *THBS3*, *MTX1*, *PKLR* and *HCN3*, located in a region of strong linkage disequilibrium (LD) and are transcribed in opposite directions^[42]. *TRIM46* is not expressed in gastric mucosa^[39], therefore, SNP rs2070803 might also be a tag for variants in other genes located in this LD region, such as *MUC1*, which are involved in gastric carcinogenesis.

In addition to GWASs, the association of *MUC1* SNPs with GC has been investigated in many case-control studies using a candidate gene approach. An association study in China showed that patients with rs4072037 AA genotype had a significantly increased risk of GC^[40]. Jia *et al.*^[43] conducted a population-based, case-control study in the Polish population. Each of the tested tag SNPs (including rs6427184, rs4971052, rs4276913, rs4971088, rs4971092 and rs4072037) across the *MUC1* region had significant associations with increased risk of GC. This association remained significant after adjusting for multiple tests, which also demonstrated that rs4072037 AA genotype was related to increased risk of GC. However, the study showed that *MUC1* tag SNPs were not associated with *H. pylori* infection, suggesting that the effects of *MUC1* polymorphisms on risk of GC are not mediated by *H. pylori* infection. The association between rs4072037 A allele and increased GC risk was further replicated in Chinese and Caucasian populations^[44,45]. Another study demonstrated that rs2070803 GA/AA genotypes were protective against GC, with > 50% risk reduction in Chinese individuals^[46]. However, other studies have shown conflicting results. A case-control study conducted by our group showed that four tag SNPs (including rs4072037) in *MUC1* were not associated with the risk of non-cardia GC, or *H. pylori* infection in the Han population in Northwest China^[47]. Another study showed no association between

rs4072037 and risk of chronic atrophic gastritis, a well-defined precursor of GC in the German population^[48]. Marín *et al.*^[49] reported that three tag SNPs (rs3814316, rs9426886 and rs1045253) in *MUC1* were not associated with precursor lesions of GC in a high-risk area of Spain. Another study demonstrated that rs4072037 was not associated with GC risk in Hispanic Americans^[50]. To clarify the current limited and conflicting evidence, and to establish the true impact of *MUC1* variations on gastric carcinogenesis, several meta-analyses have been performed. Duan *et al.*^[51] conducted an analysis of 10 case-control studies comprising 4220 cases and 6384 controls. They found that rs4072037 G allele was associated with a decreased risk of GC progression, especially in Asians. This result is consistent with the study of Zheng *et al.*^[52] of 6580 cases and 10324 controls, which suggested the involvement of *MUC1* rs4072037 polymorphism in gastric carcinogenesis among Asian individuals. A further meta-analysis showed that the rare rs2070803 A allele was associated with reduced risk of diffuse-type GC^[42]. All the evidence suggests that *MUC1* polymorphisms, such as rs4072037, are promising biological markers for predicting GC risk, especially in Asian populations.

POLYMORPHISMS IN *MUC5AC* IN THE DEVELOPMENT OF GC

MUC5AC is a major secreted mucin in healthy gastric mucosa and is the major receptor for *H. pylori* in the human stomach. BabA and SabA adhesins on *H. pylori* bind to Lewis B blood group antigens on *MUC5AC*, facilitating colonization^[53-55]. In chronic *H. pylori* infection, normally expressed *MUC5AC* and *MUC5AC*-producing cells may gradually decrease^[56,57]. *MUC5AC* is located on chromosome 11p15.5^[58], which often has loss of heterozygosity in patients with GC^[59,60]. Studies on the association between *MUC5AC* polymorphisms and GC development are limited at present. Jia *et al.*^[43] investigated the relationship between eight tag SNPs of *MUC5AC* and GC in a Polish study. The three tag SNPs rs868903, rs2014486 and rs2735733 in the 3' flanking region of *MUC5AC* were related to the risk of GC. Their minor allele homozygotes were significantly associated with increased risk of GC. However, none of the eight tested tag SNPs were associated with risk of *H. pylori* infection. Our group also performed a case-control study to evaluate the association of 12 tag SNPs of *MUC5AC* with risk of non-cardia GC in the Han population in Northwest China. We observed that three tag SNPs, rs3793964, rs11040869 and rs885454, were significantly associated with the risk of non-cardia GC. The minor allele homozygotes of rs3793964 and rs11040869, as well as the heterozygote of rs885454 had a protective effect on risk of non-cardia GC^[61]. These three tag SNPs are all located in the 3' flanking region of *MUC5AC*. The discrepancies between the

two studies may have been due to racial differences in variant frequencies. However, few biological studies on genetic variations in *MUC5AC* have been reported. Similarly, our results also suggested that polymorphisms of *MUC5AC* gene were not associated with the risk of *H. pylori* infection, suggesting *MUC5AC* polymorphisms are involved in other processes besides bacterial binding in developing GC^[62]. Wang *et al*^[63] conducted a case-control study in the Chinese population, which reported that some variations in an upstream repetitive region of *MUC5AC* were associated with GC susceptibility and progression. Their findings highlight the importance of *MUC5AC* polymorphisms in risk of GC.

POLYMORPHISMS IN *MUC6* IN THE DEVELOPMENT OF GC

The secreted mucin, *MUC6*, is highly expressed in normal gastric mucosa. One study has shown that *MUC6* has antimicrobial properties against *H. pylori*. Unique glycan residues on *MUC6* inhibit biosynthesis of major cell wall component cholesteryl- α -D-glucopyranoside^[64]. *MUC6* is aberrantly expressed in response to *H. pylori* infection^[65], and *MUC6* expression is lower in GC compared with normal mucus^[66]. *MUC6* is also located on chromosome 11p15.5, which is a region rich in recombination^[59]. *MUC1* and *MUC6* have a large number of VNTRs^[67]. Several studies have focused on the relationship between VNTR polymorphisms of *MUC6* and GC development. In one of these, small VNTR alleles of *MUC6* gene were associated with increased risk of *H. pylori* infection^[68]. Others showed that small *MUC6* VNTR alleles were more frequent in patients with GC than in healthy blood donors^[69], and short rare *MUC6* minisatellite 5 alleles had an effect on susceptibility to GC by regulating gene expression^[70]. However, Jia *et al*^[43] investigated the relationship between *MUC6* polymorphisms and GC, using a tag SNP approach. Fourteen of the tag SNPs tested across the *MUC6* region were not associated with risk of GC or *H. pylori* infection. The authors inferred that VNTR polymorphisms had many alleles, which might have divided the study population into several classes, thus making statistical analysis difficult. Similarly, Marín *et al*^[49] observed that five tag SNPs in *MUC6* were not associated with GC precursor lesions. Furthermore, Frank *et al*^[48] investigated the association between polymorphism in *MUC6* and the risk of chronic atrophic gastritis, using a candidate SNP approach. However, there was no association between the putative functional SNP rs7481521 (*MUC6* V619M) and chronic atrophic gastritis. Further studies are needed to elucidate the roles of *MUC6* polymorphisms in the gastric carcinogenesis pathway.

POLYMORPHISMS IN *MUC2* IN THE DEVELOPMENT OF GC

Normal gastric mucosa shows little or no expression

of *MUC2*. However, in intestinal metaplasia and GC, the level of *MUC2* is increased^[27,29,30]. *MUC2* might be activated by proinflammatory cytokines expressed after *H. pylori* infection, leading to its overexpression^[71]. *MUC2* gene is clustered on chromosome 11p15.5 with *MUC5AC*, *MUC5B* and *MUC6*^[58]. Only three studies have evaluated the relationship between *MUC2* polymorphisms and development of GC. Jeong *et al*^[72] reported that the short rare minisatellite 6 alleles of *MUC2* gene are associated with GC. Marín *et al*^[49] have investigated the association of 14 tag SNPs in *MUC2* with evolution of GC precursor lesions in 387 patients with 12.8 years follow-up. According to the diagnosis at recruitment and after follow-up, the patients were divided into three groups, that is, those with no change in lesions, progression of lesions, and regression of lesions. The results indicated that three SNPs (rs10794293, rs3924453 and rs4077759) at the 3' moiety in *MUC2* were associated with a decreased risk of lesion progression. In contrast, another four SNPs (rs10902073, rs10794281, rs2071174 and rs7944723) at the 5' moiety were significantly associated with lesion regression. The association of SNPs with GC precursor lesions was stronger in patients with *H. pylori* infection. However, it was also shown that functional SNP rs11825977 (V116M) in *MUC2*, which might influence *MUC2* mRNA expression^[73], as well as the potentially functional SNP rs2856111 (L58P), were not associated with the risk of chronic atrophic gastritis^[48].

CONCLUSION

GC is the third leading cause of cancer mortality and a serious global problem. Many studies have tried to identify the factors responsible for GC, but the exact sequence of molecular events involved in the development of GC remains unclear. In areas of high GC prevalence, most cases are related to *H. pylori* infection, and GC develops through several stages, including infection, gastric atrophy, intestinal metaplasia and dysplasia. There is a lot of evidence to support the key role of mucins in development of GC. This review focused on studies of the association between polymorphisms in mucin genes and development of GC. The strength of such an association varied among the studies. The diversity in study populations and lifestyle, as well as sample size may account for this inconsistency. For example, functional SNP rs4072037 in *MUC1* gene may affect the development of GC, but the effects seem to be stronger in Asian populations. Future association studies need global collaboration to expand sample size and identify more susceptibility polymorphisms. However, lifestyle factors should be taken into account to ensure accurate and significant results. Such studies will identify useful biomarkers for early detection of GC, with the potential for better disease prevention through selective treatment and surveillance of individuals harboring high-risk genetic profiles.

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Immunotherapeutic approaches in biliary tract carcinoma: Current status and emerging strategies

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Abstract

For biliary tract carcinoma (BTC), complete surgical

resection of tumor is only feasible in a minority of patients, and the treatment options for patients with unresectable or metastatic disease are limited. Advances in cancer immunology have led to identification of tumor-infiltrating immune cells as indicators of prognosis and response to treatment in BTC. This has also facilitated development of immunotherapy that focuses on enhancing the immune system against biliary tumors. This includes peptide- and dendritic cell-based vaccines that stimulate *in-vivo* immune responses against tumor-specific antigens. Adoptive immunotherapy, which entails the *ex-vivo* expansion of tumor-infiltrating immune cells for subsequent reintroduction, and cytokine-based therapies have been developed in BTC. Clinical studies indicate that this type of therapy is generally well tolerated. Combination therapy with dendritic cell-based vaccines and adoptive immunotherapy has shown particularly good potential. Emerging strategies through discovery of novel antigen targets and by reversal of tumor-associated immunosuppression are expected to improve the efficacy of immunotherapy in BTC. Collaborative efforts by integration of targeted immunotherapeutics with molecular profiling of biliary tumor will hopefully make a positive impact on advancing towards the goal of developing precision treatment of patients with this highly lethal disease.

Key words: Adoptive immunotherapy; Cancer vaccines; Biliary tract carcinoma; Cholangiocarcinoma; Gallbladder carcinoma; Immunotherapy; Precision treatment

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Core tip: Advances in cancer immunology have led to development of novel therapeutics that focuses on enhancing the immune system against biliary tract cancer. These include peptide- or dendritic cell-based vaccines, adoptive immunotherapy, and immunostimulatory cytokines. Immunotherapy is generally well tolerated with good potential for developing into treatment. The efficacy of immunotherapy may be improved by

reversal of tumor-associated immunosuppression and through discovery of novel antigen targets. Integration of targeted immunotherapeutics with molecular profiling of biliary tumor is expected to make a positive impact on advancing towards the goal of developing precision treatment of patients with this highly lethal disease.

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INTRODUCTION

Cholangiocarcinoma and gallbladder adenocarcinoma are the most common primary malignancies of the biliary tract. Collectively referred to as biliary tract carcinoma (BTC), these diseases are a cause of substantial morbidity and mortality. Each year in the United States alone, approximately 11000 patients are diagnosed with BTC and 3700 lives are claimed by the disease^[1].

Until recently, the treatment options available to patients with BTC primarily involved surgery, radiation, and systemic chemotherapy. Complete surgical resection is potentially curative, but it can only be achieved in the 10% of patients who present with localized disease without vascular invasion^[2]. Patients with BTC that is locally advanced, metastatic, or recurrent are typically offered single agent or combination chemotherapy, depending upon performance status. Typical regimens consist of gemcitabine, 5-fluorouracil, and platinum-based agents^[3]. Despite these interventions, clinical outcomes in BTC are generally poor. Fewer than 5% of patients with cholangiocarcinoma^[2] and 13% with gallbladder cancer^[4] survive longer than two years following diagnosis.

Advances in cancer immunology and immunotherapy have facilitated the development of additional treatment options that bring new hope to patients with BTC. This new generation of therapeutics seeks to strengthen the patient's immune system in combating malignancy, typically by priming it against tumor-specific antigens. Such treatments are more selective against malignant cells and therefore tend to be less toxic than traditional chemotherapy. Furthermore, by exerting an antitumor effect indirectly through the immune system rather than *via* direct activity against malignant cells, these therapeutic approaches can produce durable responses that persist long after the drug itself has been metabolized.

In this article, we concisely review cancer immunology as it relates to malignancies of the biliary tract. The immunotherapeutic approaches that are being investigated for use in BTC will be described, along with the data from clinical trials that have been completed thus far. We will also discuss ongoing clinical trials and

emerging strategies for immunotherapy in BTC.

CANCER IMMUNOLOGY IN BILIARY TRACT CANCER

Focusing and enhancing the antineoplastic effects of the immune system as treatment for BTC has only recently become a subject of concerted investigation. Evidence suggests that at the earliest stages of tumor development, the host immune system is capable of both detecting and controlling the disease. Over time, however, this generates evolutionary pressure that favors the proliferation of cancer cells that are less immunogenic or otherwise capable of suppressing the host immune response^[5-9]. Despite this, there often persists a small cohort of immune cells that remain able to identify and invade the tumor. The characteristics of this immune infiltrate are of prognostic value in a variety of malignancies, including BTC^[10,11]. The frequency and clinical significance of tumor infiltration by the cellular mediators of the host immune response is summarized in Table 1.

Tumor infiltration by the innate immune system

The innate immune system, consisting of the complement cascade, natural killer (NK) cells, granulocytes, and phagocytes, mounts an initial non-specific defense against infections and malignancy. The frequency of tumor infiltration by the cellular components of the innate immune system is highly variable. While fewer than half of biliary tumors are penetrated by NK cells^[12,13] or mast cells^[13], macrophages are observed in the majority of BTC^[13].

Despite correlating with outcomes in a host of other malignancies^[16-20], infiltration of BTC by the innate immune system appears to be of little clinical significance. Neither the presence of intratumoral NK cells nor mast cells is correlated with clinical outcomes^[12]. The density of tumor-infiltrating macrophages, however, appears to increase as lesions progress from pre-malignant precursors to invasive malignancy and later to metastatic disease^[13]. This is believed to be the result of activated macrophages releasing pro-inflammatory and pro-angiogenic cytokines that facilitate tumor growth. These include tumor necrosis factor- α , vascular endothelial growth factor A, and granulocyte macrophage colony-stimulating factor^[21,22].

Tumor infiltration by the adaptive immune system

The adaptive immune response is initiated by the consumption of foreign material by antigen presenting cells, most often dendritic cells. After processing the antigen for presentation, dendritic cells migrate to lymph nodes where they stimulate the proliferation of antigen-specific lymphocytes and recruit CD4⁺ T-helper cells. Activated CD4⁺ cells release cytokines that induce the differentiation of B-lymphocytes into antibody-releasing plasma cells, and activate cytotoxic CD8⁺

Table 1 Cellular mediators of innate and adaptive immune system in biliary tract carcinoma

Cell type	Frequency of infiltration	Clinical significance	Ref.
Natural killer cells	19.1%-33% overall 20% of ICC, 21% of ECC, 16% of GBC	No correlation with disease stage, grade, or survival	[12,13]
Mast cells	2% of ICC, 2.5% of ECC, 8.5% of GBC	No correlation with survival	[13]
Macrophages	87% of ICC, 70% of ECC, and 71% of GBC	Associated with more advanced disease	[13]
Dendritic cells	Not determined	Associated with improved survival	[12,14]
CD4 ⁺ helper T-lymphocytes	43% of ICC, 30% of ECC, and 34%-51% of GBC	Associated with reduced probability of metastases and improved survival in ECC	[12,13]
CD8 ⁺ cytotoxic T-lymphocytes	46% of ICC, 49%-55% of ECC, and 38%-51% of GBC	Associated with reduced probability of metastases and improved survival in ECC	[12,13,15]
B-lymphocytes / plasma cells	4.5% of ICC, 6.7% of ECC, and 10.1% of GBC	Associated with improved survival	[13]

ECC: Extrahepatic cholangiocarcinoma; GBC: Gallbladder carcinoma; ICC: Intrahepatic cholangiocarcinoma.

T-lymphocytes (CTL). After clearing the antigen, both CD4⁺ and CD8⁺ T cells may differentiate into memory T-cells that organize an expedited secondary immune response if the offending antigen is encountered again. It is these memory cells that form the physiologic basis for vaccination.

Like the innate immune system, there is considerable variability in the frequency of tumor infiltration by cells of the adaptive immune system. Although the exact percentage of BTC that contains dendritic cells is not clear, their presence appears to be nearly universal in both GBC^[12] and cholangiocarcinoma^[14]. Approximately 30%-50% of BTC is infiltrated with CD4⁺ or CD8⁺ T-lymphocytes^[12,13]. Tumor infiltration by B-lymphocytes or plasma cells is seldom observed^[13], which may be attributed to the tendency for these cells to rarely migrate outside of lymph nodes.

Tumor infiltration by the cellular mediators of the adaptive immune response is generally correlated with improved outcomes in BTC. The presence of dendritic cells^[12,14], CD4⁺ T-cells^[12], CD8⁺ T-cells^[12,15], or plasma cells^[13] within a biliary tumor is predictive of improved OS. This trend towards more favorable prognosis is consistent with findings in other malignancies, such as colorectal^[23] and esophageal carcinoma^[24]. Though it has not been reported in BTC, the subset of CD3⁺ T-cells in colorectal cancer suggests that these cells are possibly involved in vitamin D-mediated immunoprevention^[25].

IMMUNOTHERAPEUTIC APPROACHES IN BTC

While the endogenous immune response is initially successful in slowing the growth of BTC, the malignancy eventually becomes capable of evading the immune system. This occurs through intense evolutionary pressure that confers a survival advantage to cancer cells that lack foreign antigens, secrete immunosuppressive substances, or otherwise limit the effectiveness of the host immune system^[5-9]. Several approaches for potentiating or redirecting the immune response to BTC are being investigated. Vaccines based upon either peptides or dendritic cells seek to sensitize the immune

system against tumor-specific antigens. The extraction, amplification, and reintroduction of a patient's own tumor-infiltrating immune cells *via* adoptive immunotherapy is being evaluated. Treatment using immunostimulatory cytokines has been attempted.

Targets of vaccination

Through the controlled presentation of a particular antigen, vaccination primes the immune system to respond swiftly and accurately to repeat exposures in the future. This occurs, in part, through the production of memory T-cells that orchestrate this secondary response. As a result, the effectiveness of vaccination is a function of both the immune system's strength and the selection of a proper target antigen. Ideally, the target should be highly specific to malignant cells and strictly conserved within the tumor. This ensures that collateral damage to normal tissues will be minimized, while also reducing the likelihood that an antigen-negative cancer cell will arise to repopulate the tumor.

One antigen that largely fulfills these criteria is Wilm's Tumor protein 1 (WT1)^[10], a transcription factor that is normally involved in urogenital development. This protein also functions as a tumor suppressor through interactions with platelet derived growth factor receptor, epithelial growth factor receptor, c-MYC, and B-cell lymphoma 2^[26]. Approximately 68%-80% of biliary tumors harbor mutations of WT1^[26]. While the clinical significance of mutated WT1 in BTC remains unclear, similar mutations are known to correlate with poor prognosis in testicular cancer^[27], breast cancer^[28], and squamous cell carcinoma of the head and neck^[29].

Another potential target for immunization is the glycoprotein, mucin protein 1 (MUC1)^[10]. Consisting of a large and heavily glycosylated extracellular domain, MUC1 forms the hydrophilic barrier that is characteristic of BTC and other types of adenocarcinoma. This mucinous shell repels hydrophobic chemotherapeutics and obstructs immune cells, while also allowing the tumor to immerse itself in growth factors^[30]. MUC1 is over-expressed in 90% of gallbladder carcinoma^[31] and 59%-77% of cholangiocarcinoma^[31-34]. Excessive production of MUC1 in BTC is typically indicative of more

advanced disease^[32] and impaired OS^[31-33].

Peptide-based vaccines and personalized peptide vaccination

Peptide-based vaccines are among the most investigated class of cancer immunotherapy. The vaccine typically contains one or more antigens that are heavily expressed by malignant cells and often emulsified in Freund's adjuvant to increase immunogenicity. The goal of immunization is to stimulate mass-production of memory lymphocytes that can generate a strong secondary immune response against cancer cells that bear the particular antigen.

The efficacy of any single peptide-based vaccine is intrinsically limited, however, by the heterogeneity of BTC. Although the overall expression of certain antigens, such as WT1 and MUC1, is often increased within biliary tumors, the distribution of these antigens is non-uniform. While some cells over-express the antigen, there are often others from which it is entirely absent. Furthermore, the tenacity with which the immune system responds to these antigens varies widely between patients, even among those with similar HLA types^[35]. This is due, in part, to differences in the number of lymphocyte precursors that are maximally sensitive to the particular antigen^[36].

Personalized peptide vaccination seeks to overcome these limitations by immunizing patients against multiple antigens simultaneously. While it is likely that a tumor will harbor cells that lack any single antigen, the odds are exponentially less that any single cell will lack each of 3 to 4 antigens that are individually quite common. This has the additional benefit of theoretically counteracting the pressure of selection for tumor cells that lack the target antigens^[35]. To bypass individual differences in sensitivity to particular antigens, it is possible to measure the frequency of antigen-sensitive CTL precursors within each patient. They may then be vaccinated against only the antigens to which they will most likely respond^[36].

Dendritic cell-based vaccines

Similar to their peptide-based counterparts, dendritic cell-based vaccines expose the immune system to an antigen with the goal of generating memory lymphocytes that will produce a robust secondary immune response. Rather than simply introducing a peptide that requires subsequent processing and presentation to the adaptive immune system, these vaccines contain dendritic cells that are already loaded with antigen. These vaccines may be prepared against a particular antigen or more generally against a tumor lysate. While the latter approach stimulates the immune system against a larger number of antigens and theoretically produces a greater antitumor response, it may also carry a risk of autoimmunity. While the use of dendritic cells-based vaccines against BTC remains in its infancy, the success of sipuleucel-T in treating prostate cancer^[37]

demonstrates the promise that these therapeutics may someday fulfill.

Adoptive immunotherapy

Unlike the treatments described previously, adoptive immunotherapy is not intended to produce an *in-vivo* immune response. Instead, a patient's own tumor-infiltrating lymphocytes are extracted, modified, and induced to clonally proliferate *ex-vivo*. This expanded population of tumor-specific immune cells is then reintroduced, and they migrate back to the tumor and continue to combat its growth. The effectiveness of this treatment may be further increased by depleting the patient's existing lymphocyte population with cytotoxic chemotherapy in advance of returning the grafted lymphocytes. This is believed to prolong the lifespan of the transplanted cells.

Immunostimulating cytokines

The cytokine, interleukin-2 (IL2) is a potent anti-neoplastic agent due to its ability to stimulate the proliferation and cytotoxic effects of CD8⁺ T-lymphocytes^[38-40]. Administering IL2 as a monotherapy or in combination with adoptive immunotherapy is an effective treatment for certain malignancies, such as melanoma^[41,42] and renal cell carcinoma^[42,43]. Treatment with IL2 is associated with a substantial side effect profile that includes nephrotoxicity, extravasation of fluid secondary to increased vascular permeability, and rarely transient myocarditis^[40,41].

CLINICAL STUDIES OF IMMUNOTHERAPY IN BTC

Each type of immune-based approach described above has been evaluated for therapeutic efficacy in patients with BTC. Many of these agents have been studied as monotherapy as well as in combination with traditional chemotherapy or targeted therapeutics. The completed clinical trials of immunotherapy in BTC are described below and the compiled data are summarized in Table 2.

Peptide-based vaccines

To date, most clinical studies of immunotherapy in BTC have focused on peptide-based vaccines, often targeted against WT1 or MUC1. This type of treatment is generally well tolerated; however it appears to exert only a modest anti-neoplastic effect when administered as monotherapy.

Vaccines against WT1 are often administered in combination with gemcitabine based chemotherapy. Preclinical studies suggest that gemcitabine upregulates the expression of WT1, thereby theoretically enhancing the effect of immunization^[53]. In a phase I trial, anti-WT1 vaccination and gemcitabine were administered to patients with unresectable gallbladder cancer, cholangiocarcinoma, or pancreatic adenocarcinoma^[44]. This regimen increased the number of WT1-specific

Table 2 Trials of immunotherapy in biliary tract carcinoma

Immunotherapy	Treatment regimens	Phase	n	Types of BTC	OS (mo)	PFS (mo)	Ref.
Peptide-based vaccine (WT1)	Peptide vaccine + gemcitabine	I	25	Pancreatic, GBC, ICC, ECC	9.3	--	[44]
Peptide-based vaccine (WT1)	Peptide vaccine monotherapy	I	9	Pancreatic, CC	--	--	[45]
Peptide-based vaccine (NUF2, CDH3, KIF20A)	Peptide vaccine triple therapy	I	9	GBC, ICC, ECC	9.7	3.4	[46]
Peptide-based vaccine (LY6K, TTK, IGF2BP3, DEPDC1)	Peptide vaccine quadruple therapy	I	9	GBC, ICC, ECC	12.3	5	[47]
Peptide-based vaccine (Many)	Personalized peptide vaccination +/- chemotherapy	II	25	GBC, ICC, ECC	6.7	--	[48]
Dendritic cell-based vaccine (MUC1)	Dendritic cell vaccination +/- chemotherapy +/- radiotherapy	I / II	12	Pancreatic, CC	26	--	[49]
Dendritic cell-based vaccine (WT1, MUC1)	Peptide vaccine +/- chemotherapy	--	65	GBC, ICC, ECC	--	--	[50]
Dendritic cell-based vaccine, adoptive immunotherapy	Surgery + dendritic cell vaccine + T-cell transfer <i>vs</i> surgery alone	--	36	ICC	31.9	18.3	[51]
Interleukin-2	Induction cisplatin + gemcitabine, consolidation capecitabine + radiation, and maintenance IL-2 + 13-cis-retinoic acid	II	54	Pancreatic, GBC, CC	> 27.5	16.2	[52]

CC: Cholangiocarcinoma; OS: Overall survival; PFS: Progression-free survival; WT1: Wilm’s tumor 1; NUF2: Cell division cycle associated protein 1; CDH3: Cadherin 3; DEPDC1: DEP domain containing 1; ECC: Extrahepatic cholangiocarcinoma; GBC: Gallbladder cancer; ICC: Intrahepatic cholangiocarcinoma; IGF2BP3: Insulin-like growth factor-II mRNA binding protein 3; KIF20A: Kinesin family member 20A; LY6K: Lymphocyte antigen 6 complex locus K; MUC1: Mucin 1.

lymphocytes in circulation, but it did not improve clinical outcomes or increase toxicity over that which is expected from gemcitabine monotherapy. At the present time, a phase II study of WT1 vaccination as an adjunct to combination chemotherapy with gemcitabine plus cisplatin is underway^[53]. This study aims to establish the 1-year OS rate for patients receiving treatment.

Similar to WT1, peptide-based immunization against MUC1 is well tolerated but it lacks definite proof of clinical efficacy. In a phase I trial of nine patients with advanced stage cholangiocarcinoma or pancreatic adenocarcinoma, monotherapy with peptide-based vaccines against MUC1 produced only a single instance of stable disease^[45]. Despite failing to influence outcomes, vaccination did generate a robust anti-MUC1 IgG response in 78% of patients with negligible toxicity. In the future, vaccination against MUC1 could fill a niche in addition to gemcitabine or fluorouracil-based chemotherapy. This is because preclinical studies have found that these agents increase the expression of MUC1 in cholangiocarcinoma cells^[53]. Further research is indicated to determine the safety and efficacy of such regimens.

The prospect of combination therapy with multiple peptide-based vaccines has been explored. Triple therapy with vaccines against cell division cycle associated protein 1 (NUF2), cadherin 3 (CDH3), kinesin family member 20A in patients with GBC, ICC, and ECC was investigated in a phase I clinical trial^[46]. This treatment stimulated peptide-specific T-cell responses in all patients and 55% achieved stable disease. A four vaccine regimen against lymphocyte antigen 6 complex locus K (LY6K), TTK protein kinase, insulin-like growth factor-II mRNA binding protein 3, and DEP domain containing 1 has also been tested in a phase I trial of

nine patients with BTC^[47]. Peptide specific T-cell responses were generated in 78% of patients receiving this regimen and clinical responses were observed in 67%. In both trials of combination therapy with peptide-based vaccines, the presence of an injection site reaction correlated with OS^[46,47]. This underscores the reliance of this treatment upon provoking a strong immune response to generate an anti-tumor effect. Aside from these local dermatologic reactions, treatment-associated toxicity was minimal.

The efficacy of combination vaccination may be refined by individualizing the process by which targets are selected. This approach of personalized peptide-based vaccination was assessed in a phase II trial of 25 patients with either gallbladder adenocarcinoma or cholangiocarcinoma^[48]. Patients received as many as 4 of 31 possible vaccines in addition to systemic chemotherapy, if their performance status could support such treatment. This regimen produced stable disease in 80% of patients and negligible toxicity beyond that which is typically associated with chemotherapy.

Dendritic cell-based vaccines

Immunotherapy with antigen-pulsed dendritic cells is exceptionally well tolerated, and it appears to be efficacious against BTC. In a combined phase I / II trial, 12 patients with BTC or pancreatic adenocarcinoma received an anti-MUC1 dendritic cell-based vaccine following tumor resection and, in some instances, chemoradiation^[49]. A median OS of 26 mo was observed, while 33% of patients survived longer than 50 mo without evidence of disease recurrence. While this study was not designed to differentiate between durable responses that occur due to vaccination and those that arise from complete surgical resection, it is conceivable

Table 3 Ongoing clinical trials of immunotherapy in biliary tract carcinoma

Agent	Treatment regimen	Phase	Estimated date of completion	Sponsoring Institution	Identification number
Cytokine induced killer cells	Cytokine induced killer cell monotherapy	I / II	May, 2016	Siriraj Hospital	NCT01868490
Tumor infiltrating lymphocytes	Tumor infiltrating lymphocytes + IL-2 + cyclophosphamide + fludarabine	II	December, 2019	National Cancer Institute	NCT01174121
Poly-ICLC	Cyclophosphamide + radiation therapy + TACE + poly-ICLC	I / II	July, 2014	Rutgers, the State University of New Jersey	NCT00553683

IL-2: Interleukin-2; Poly-ICLC: Polyinosinic-polycytidylic acid polylysine carboxymethylcellulose; TACE: Transcatheter arterial chemoembolization.

that the combination of adjuvant chemotherapy, radiation therapy, and immunotherapy eliminated microscopic residual disease after surgery.

In another trial, dendritic cell-based vaccines against WT1 and/or MUC1 in combination with chemotherapy was evaluated in 65 patients with unresectable, metastatic, or recurrent BTC^[50]. This regimen was well tolerated and 15% of patients had stable disease following 6 mo of treatment. Although the response rate did not differ between patients who were vaccinated against one or both targets, the correlation between post-immunization fever and improved survival does suggest the responses generated by this regimen may be at least partially attributed to immune activation.

Adoptive immunotherapy

Direct transfer of cellular immunity *via* adoptive immunotherapy has also been investigated for use in BTC. In a study of 36 patients with intrahepatic cholangiocarcinoma, surgery alone was compared to surgery followed by combination adoptive immunotherapy with tumor-lysate pulsed dendritic cells and transfer of activated T-cells^[51]. Patients who received adjuvant immunotherapy experienced nearly double the OS of those treated with surgery alone with minimal toxicity. Among the 16 patients who produced the largest injection site reaction, median OS was 95.5 mo.

Similar durable and dramatic responses to combined immunotherapy with dendritic cell-based vaccines and activated T cell transfer have been described in case reports of patients with cholangiocarcinoma^[54] and gallbladder cancer^[55]. Anecdotal evidence also suggests that combining T-cell based adoptive immunotherapy with cetuximab may have activity against malignant ascites and peritoneal carcinomatosis due to metastatic cholangiocarcinoma^[56].

IL2 maintenance therapy

The use of IL2 as a maintenance therapy was explored in a multicenter phase II trial of 54 patients with pancreatic adenocarcinoma or BTC^[52]. These patients initially received 3 cycles of combination chemotherapy with cisplatin and gemcitabine as induction therapy. Patients who remained progression-free were subsequently treated with concurrent capecitabine and radiotherapy as consolidation, followed by maintenance

IL2 and 13-cis-retinoic acid. The progression-free survival (PFS) and overall survival (OS) for all patients enrolled in this study was 6.8 and 12.1 mo, respectively. Outcomes were notably better when considering only the subset of patients who were able to complete the entire course of treatment, however, with median PFS of 16.2 mo and OS that had not yet been reached after a median follow-up of 27.5 mo. Further investigation will be needed to determine whether this differential survival is truly due to a response to treatment, or if those patients simply had more indolent disease independent of therapy.

ONGOING CLINICAL TRIALS OF IMMUNOTHERAPY IN BTC

Currently, several clinical trials of immunotherapy in malignancies of the biliary tract are ongoing and as listed in Table 3. These studies utilize different immunotherapeutic approaches. In one study, cytokine induced killer cells are employed as monotherapy. In another study, adoptive transfer of tumor-infiltrating lymphocytes is combined with IL2 and chemotherapy. In attempt to reverse systemic immunosuppression, the immunomodulatory agent, polyinosinic-polycytidylic acid polylysine carboxymethylcellulose, is used in combination with chemotherapy and radiation therapy. In those two studies involving chemotherapy, low-dose metronomic cyclophosphamide is used to eliminate the immunosuppressive regulatory T lymphocytes (T_{reg}) and prevent tumor-associated angiogenesis.

CONCLUSION

Immunotherapy in BTC has been under active investigation and tremendous opportunities exist for developing it into a safe and effective treatment of patients with this disease. Clinical studies indicate that this type of therapy is generally well tolerated. The efficacy of immune-based treatment of BTC is improving as the complex interactions between the immune system and biliary tumors are better understood. Combination therapy with dendritic cell-based vaccines and adoptive immunotherapy has shown particularly good potential. Several directions for future investigation of immunotherapy that may improve the clinical

outcomes of patients with this disease are described as follows.

Preliminary studies suggest that the distribution and types of immune cells that infiltrate biliary tumors may be used to predict the likelihood that an individual tumor will respond to a particular chemotherapy regimen^[57]. Further characterizing these associations could be clinically beneficial, as it would provide a physiologic basis for selecting therapy as an adjunct to the current paradigm that relies upon tumor histology and stage. On the other hand, application of mass spectrometry and genomic sequencing to discover new antigens^[58] may help facilitate development of novel strategies for targeted immunotherapy in BTC. Furthermore, evidence suggests that increased inflammatory signaling *via* IL6 is associated with reduced response to vaccination^[36,48]. The hypothesis that addition of the IL6 receptor antagonist tocilizumab enhances the effects of vaccination remains to be tested.

Besides, tumor evasion of the immune system is often mediated by cytotoxic T-lymphocytes associated antigen 4 (CTLA4) or the interaction between programmed cell death 1 (PDCD1, also known as PD1 or CD279) and its ligand (PDCD1LG1, also known as PDL1 or CD274)^[9]. It will be important to investigate the potential of blocking these immunosuppressive pathways with monoclonal antibodies in conjunction with the currently used immunotherapeutic approaches in BTC. The anti-CTLA4 antibody ipilimumab has shown great promise in other malignancies such as melanoma^[59], but it has not yet been studied in BTC. Similarly, pembrolizumab and nivolumab, monoclonal antibodies that target PD1/CD279 signaling have been found to improve anti-tumor T-cell response and induce tumor regression in subsets of patients with melanoma, renal cell carcinoma, and non-small-cell lung cancer^[8,60,61]. Preclinical studies suggest that immunohistochemical analysis for PDL1/CD274 in biliary tumors may help identify the patients who are likely to benefit from such therapeutics^[62].

The synergistic relationships between cytotoxic chemotherapy and immunotherapy deserve further investigation for treatment of BTC. In one study, gemcitabine, which is a mainstay of treatment in BTC, was found to enhance cell-mediated immunity *via* increased expression of HLA on malignant cells^[63]. Platinum-based agents have a similar effect on HLA expression, while also reducing PDL2/CD273-mediated suppression of antigen-specific T-lymphocytes^[64]. It is plausible that the addition of gemcitabine and cisplatin to immunotherapy could further improve the treatment responses.

Ultimately, the goal is to combine the advances in cancer immunotherapy with those of targeted therapy and molecular profiling to develop precision treatment for improving the clinical outcomes of patients with this highly lethal disease.

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Current status of familial gastrointestinal polyposis syndromes

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Abstract

Because of the rarity of familial gastrointestinal cancer-predisposing syndromes, their exploration in literature

is not extensive. In this review, an update of the clinicopathological and molecular criteria of gastrointestinal familial polyposis syndromes with potential malignant transformation is performed. In addition, a guide for screening and surveillance was synthesized and a distribution of gene mutations according to the specific syndromes and geographic distribution was included. The following inherited polyposis syndromes were analyzed: familial adenomatous polyposis, the hamartomatous familial polyposis (Juvenile polyposis, Peutz-Jeghers syndrome, Cowden syndrome, Bannayan-Riley-Ruvalcaba syndrome, hereditary mixed polyposis syndrome, Gorlin syndrome, Birt-Hogg-Dube syndrome, neurofibromatosis type I and multiple endocrine neoplasia syndrome 2B), Li-Fraumeni syndrome, and MUTYH-associated adenomatous polyposis. For proper medical care, subspecialization of gastroenterologists, pathologists, and geneticists in the field of familial diseases should be introduced in the medical curriculum.

Key words: Inherited polyposis syndromes; Hereditary cancer; Stomach; Intestine; Colorectal

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Core tip: In this review the clinicopathological and histological aspects of inherited polyposis syndromes of the gastrointestinal tract are explored in detail. In addition, a guide for surveillance is proposed.

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INTRODUCTION

The familial cancer-predisposing syndromes of the

gastrointestinal tract are heterogeneous groups of diseases with the lifetime risk of gastrointestinal cancer generally low but their associated morbidities should be very attentively examined for developing specific programs of familial screening. Because these syndromes are relatively rare in the daily activity, management of their diagnosis and therapy is difficult.

These syndromes include, in particular, the following inherited polyposis syndromes: familial adenomatous polyposis (FAP), hamartomatous polyposis syndromes (Juvenile polyposis, Peutz-Jeghers syndrome, Cowden syndrome, Bannayan-Riley-Ruvalcaba syndrome, hereditary mixed polyposis syndrome, Gorlin syndrome, Birt-Hogg-Dube syndrome, neurofibromatosis type I, and multiple endocrine neoplasia syndrome 2B), Li-Fraumeni syndrome, and *MUTYH*-associated adenomatous polyposis. They are usually diagnosed from the stomach to the rectum, the esophagus and anal canal being only secondarily involved^[1-30]. Although Cronkhite-Canada- and Proteus syndrome^[22] are also polyposis syndromes of the gastrointestinal tract, they do not present familial predisposition and are not included in this paper.

In this review, an update of clinicopathological criteria used for diagnosis of the inherited cancer-predisposing syndromes of the gastrointestinal tract and identification of eligible families was performed, followed by revision of criteria of screening and surveillance in the daily practice. A synthesis of data regarding the molecular profile of hereditary syndromes and their geographic particularities are synthesized in Table 1, based on our experience and literature data^[1-36].

CLINICOPATHOLOGICAL AND MOLECULAR FEATURES

FAP

FAP is a rare autosomal dominant syndrome (1:8300 live births), that is characterized by the presence of hundreds to thousands of adenomatous polyps scattered throughout colorectal mucosa^[36] (Figure 1). It is produced through mutations of the adenomatous polyposis coli (*APC*) gene that was firstly described in 1991^[1]. The risk for rectal adenocarcinomas is 87% up to 45 years of age and rise by 100% in older ages, but other colorectal segments can also be affected^[1,28]. FAP-related colorectal cancer (CRC) represent < 1% of all CRC cases^[36].

Other extracolonic associated lesions include small bowel, periampullary and gastric adenomatous polyps, adrenal adenomas and carcinomas^[32]. The lifetime risk of occurrence of duodenal polyps is almost 100%^[28]. The second and third portion of duodenum, including the periampullary region, are more predisposed to present adenomas^[28].

Regarding the stomach, the adenomatous polyps were reported to occur in 12%-84% of patients with FAP but less than half of them are focally dysplastic

and below 1% present malignant transformation^[2,3]. They are located mostly in the antrum, followed by gastric fundus^[2,28]. However, fundic gland polyps can also occur sporadically not only within FAP^[2]. The reported incidence of sporadic fundic gland polyps is about 1%-2% of all middle-aged healthy females who underwent upper endoscopy, more rare in males (30% of all cases) while the familial ones are usually multiple, occur at younger ages, and have an equal gender distribution^[3]. Microscopically, the fundic gland polyps consist of cystically dilated oxyntic glands lined by parietal cells, chief cells, and neck cells, with apical mucin bubbles^[2,4,5]. Dysplasia occurs in the covering neck cells and/or foveolar epithelium and dysregulation of epithelial proliferation is immunohistochemically (IHC) proved by loss of the normal inverse topographic distribution of Ki-67 proliferation marker and the cyclin-dependent kinase inhibitor p21 (*WAF1/CIP1*)^[2,4-6]. In these cases, for unknown reasons, a more increased risk for gastric intestinal-type adenocarcinomas have been reported in Japanese and Korean populations (four-fold) while no significant risk, when compared with the general population, was encountered in the Western countries (two-fold)^[2,4-6]. Although FAP syndrome is not rare in Romanian patients, we did not have cases with associated gastric lesions (personal communication).

Gardner's syndrome is a variant of FAP characterized by *APC* mutation-related gastrointestinal polyps and associated osteomas, dental abnormalities (supranumerary teeth), epithelial and mesenchymal tumors of the skin (epidermoid cysts, lipoma, fibroma, leiomyoma), desmoid tumors (most frequently in the abdominal wall or intra-abdominal), congenital hypertrophy of the retinal pigment epithelium and tumors of the thyroid gland^[28,32,34]. Congenital hypertrophy of the retinal pigment epithelium is the commonest extracolonic manifestation of FAP that occurs in 70%-80% of patients^[28]. It is characterized by occurrence of gray-brown round lesions in the retina, the clinical significance being not known yet^[28].

In Turcot's syndrome, the FAP is associated with tumors of the central nervous system, especially medulloblastoma^[32].

The attenuated FAP (AFAP) is a less severe form of FAP that is characterized by predominance of proximally located polyps of the colon (10-99 adenomatous polyps), a later age of onset and a lower risk (lifetime cumulated risk < 70%) for developing CRC^[7,32].

MUTYH-associated polyposis

It is an autosomal recessive syndrome produced through mutations of the *mutY* homolog (*MUTYH*) gene that was firstly described in 2002 in three members of a British family^[27,28,35]. *MUTYH*-associated polyposis (MAP) is clinically similar to the AFAP, being characterized by the early-onset of multiple adenomatous polyps of the colorectal segments (10-99 adenomatous or serrated polyps), with risk for malignant transformation,

Table 1 The molecular profile and geographic particularities of inherited gastrointestinal cancer-predisposing syndromes^[1-36]

Name of the syndrome	Mutated genes	Type of mutation	Geographic particularities
FAP	APC: Exon 15 - first half (54% of patients with FAP)	Classic phenotype: mutations between codons 178 and 309, and between 409 and 1580 (exons 5-8 and 9-14) Germline truncation (C > T), especially at codons 1309 and 1061: Nonsense mutations (28%) Small insertions (10%) Small deletions (46%)	NS
	APC: Chromosome arms 5q, 8p, 17p and 18q	LOH	NS
	β -catenin: Exon 3 (15%)	NS	NS
	APC/ β -catenin (28%)	NS	NS
	K-ras: Codon 12 (3%) - associated mutation	GGT to TGT/GTT	NS
Gardner syndrome	APC: Long arm of chromosome 5	Interstitial deletion	NS
	APC: Patients with congenital hypertrophy of the retinal pigment epithelium	Truncating mutations between codons 311 and 1465	NS
	APC: Patients with desmoid tumor	Downstream codon 1400 (1445-2011)	NS
	APC: Patients with gastro-duodenal adenomas	Mutations at the 3' before codon 1395 and between codons 564 and 1493	NS
	APC: Patients with hepatoblastomas	Mutations at the 5' to the mid region between codons 141 and 1751	NS
AFAP	APC: Patients with thyroid tumors	Mutations between codons 140 and 1309	NS
	APC	Somatic G:C→T:A	NS
	APC: Exons 3 and 4 (5' end of the gene), exon 9, and the very 3' end of the gene beyond codon 1595	Truncating mutation	NS
MUTYH-associated polyposis	APC: Variants	Missense mutations I1307 K N1026S E1317Q	I1307K: almost exclusively in Ashkenazi Jewish descendants - detected in 6% of all family members, with 10%-20% lifetime risk of developing CRC N1026S: Identified in one Spanish AFAP family (all members) E1317Q: NS
	MUTYH: Located on the chromosome 1p34.3-p32.1, contains 16 exons	Germline biallelic inactivation	Absent in Asia (Japan, Taiwan, South Korea)
		Missense mutations: p.Y179C - exon 7 (c.536A > G; p.Tyr179Cys) p.G396D - exon 13 (c.1187g > A; p.Gly396Asp)	Specific for Eastern, Southern, and Central Europe, North America, European inhabitants from Canada, and Sephardi Jews
		Missense mutation p.Ala385ProfsX23 p.E410GfsX43 Missense mutation p.Y104X Missense mutation p.E480X	Absent in Finland, India, Pakistan, Tunisia, Singapore, and Ashkenazi Jewish
	MUTYH variants	Heterozygous mutations	Specific for Northern Europe Specific for Tunisia Specific for Pakistan Specific for India Asia (Japan, Taiwan, South Korea): p.Arg19; p.Arg109Trp; p.Gly286Glu Southern Europe: p.Glu480del Pakistan: p.Tyr104 India: p.Glu480
Juvenile polyposis syndrome (pure type)	K-ras: Codon 12 - associated mutation (64%), usually in patients with sessile serrated adenomas	c.34G > T	NS
	MADH4/SMAD4/DPC4: Chromosome 18q21.1 (30%)	NS	NS
	BMPR1A: Chromosome 10q23 (20%-30%) Other genes (49%) ENG: exons 11, 12 PTEN: chromosome 10q23.3	Large deletions NS	NS NS
Juvenile polyposis + hemorrhagic telangiectasia	MADH4/SMAD4/DPC4: Chromosome 18q21.1	NS	NS
	STK11: Chromosome 19p13.3 or 19q13.4 (50%-94%)	NS	NS
Peutz-Jeghers syndrome	TGF- β PTEN: Chromosome 10q23.3	NS	NS

Peutz-Jeghers syndrome + primary pulmonary hypertension	<i>ALK1/ACVRL1</i>	NS	NS
Cowden syndrome	<i>PTEN</i> : Chromosome 10q23.3 (13-85%)	Nonsense mutations missense mutations frameshift mutations Large deletions	NS
Bannayan-Riley- Ruvalcaba syndrome	<i>PTEN</i> : Chromosome 10q23.3 (60%-65%)	NS	NS
Hereditary mixed polyposis syndrome	<i>BMPRIA</i> : Chromosome 10q23 <i>GREM1</i>	NS	NS
Li-Fraumeni syndrome – classic type	<i>p53</i> : Exons 4-9 (23%-50%)	NS	NS
Unclassified/ unexplained polyposis syndromes (50%)	<i>PTEN</i> : Chromosome 10q23.3 Other genes: <i>BMPR2</i> , <i>ACRV1</i> , <i>SMAD1</i> , <i>SMAD2</i> , <i>SMAD3</i> , <i>SMAD5</i> , <i>SMAD7</i> (22%)	Nonsense mutations missense mutations frameshift mutations NS	NS

FAP: Familial adenomatous polyposis; BMPR: Bone morphogenetic protein receptor; CRC: Colorectal cancer; ENG: Endoglin; FAP: Familial adenomatous polyposis syndrome; LOH: Loss of heterozygosity; NS: Non-specified; TGF: Transforming growth factor.



Figure 1 Macroscopic aspect of the colonic mucosa in a 43 years old male with classic Familial adenomatous polyposis.

and infrequent extracolonic manifestations^[25-28]. The phenotype of MAP is less severe than classic FAP^[36]. In some of the cases, MAP-related CRC can be developed without the polyposis background, the differential diagnosis with Lynch syndrome being difficult^[35].

Juvenile polyposis syndrome

It is a rare autosomal dominant hereditary syndrome (1:100000-160000 live births) characterized by identification of 1-100 hamartomatous polyps throughout the gastrointestinal tract, mostly in the colorectal segments, diagnosed in young patients^[8-12]. Microscopically, these polyps are covered by normal columnar epithelium and present mucus-filled tortuous dilated glands lined by columnar epithelium in the lamina propria; the dense stroma is edematous and rich in inflammatory infiltrate predominantly composed of plasma cells^[8,11,13]. The clinical diagnosis is based on at least one of the following Jass's modified criteria^[6,12]: (1) Multiple juvenile polyps throughout the gastrointestinal tract; (2) At least five colorectal juvenile polyps; or (3) Any number of juvenile polyps identified in patients with a family history of juvenile polyps. These polyps can present malignant transformation, the lifetime risk being about 34%-38% for colorectal segments and 21% for stomach^[9,10,12]. Juvenile polyposis-related gastric cancers are rather produced through *SMAD4* than *BMPRIA* mutation genes^[12]. Association with hereditary

hemorrhagic telangiectasia also known as Osler-Weber-Rendu syndrome have been reported in about 20% of the cases; protein-losing enteropathy can also be associated^[9,13].

Peutz-Jeghers syndrome

This syndrome is a rare autosomal dominant inherited disorder (1:8300-200000 live births) associated with a lifetime hazard for cancer up to 93%, which occurs as a consequence of a germline mutation in the *STK11* gene^[12,14-16]. It is characterized by familial gastrointestinal hamartomatous polyposis and 1-5 mm mucocutaneous melanic spots around the mouth, in the buccal mucosa, on the fingertips and toes, and, infrequently, on the eyelid and sole of the foot^[16]. The spots occur in first years of life; the skin spots spontaneously disappear at puberty but mucosal spots remains visible per life^[16].

Regarding the polyps, the upper jejunum is most frequently involved (78%), followed by colon and stomach (24%)^[15-19]. Solitary gastric polyps can occur rarely, less than 30 cases being reported to 2012^[17]. Microscopically, the gastrointestinal hamartomatous polyps, that can undergo focal or total malignant transformation, are characterized by hyperplastic mucosal glands with periglandular proliferation of smooth muscle fibers^[16,17]. Arborizing pattern of smooth muscle proliferation is characteristic^[15,16]. In solitary polyps of the stomach, it was suggested that the branching of

the muscularis mucosae are not so well developed in the subsequent layers^[15,17]. Gallbladder, bronchi, urinary bladder, and the ureter can also present hamartomatous polyps with similar histological architecture and further possible malignization^[12].

Multiple synchronous or metachronous colonic and extra-colonic carcinomas of different organs like breast (54%), pancreas (36%), stomach (29%), ovary (21%), small bowel (13%), or other organs (cervix, uterus, testes, lung, appendix), can be associated in the same patient or his first-degree relatives, with a cumulative risk over 90%^[12,15-18]. Associated lymphomas and sex-cord tumors were also encountered^[16].

For a final diagnosis, one of the following criteria should be filled^[12,14-19]: (1) At least two histologically proved Peutz-Jeghers polyps; (2) At least one histologically proved Peutz-Jeghers polyp in a patient with specific mucocutaneous spots; (3) Identification of at least one Peutz-Jeghers polyp in a patient with at least one relative with confirmed diagnosis of Peutz-Jeghers syndrome; and (4) Specific mucocutaneous spots in a patient with at least one relative with confirmed diagnosis of Peutz-Jeghers syndrome.

Cowden syndrome

It is an autosomal dominant hereditary syndrome that occur in 1:200000 live births (more frequent in Asian population). It is characterized by synchronous or metachronous tumors in multiple organs that occur in one patient or in members of his family. This familial gastrointestinal hamartomatous polyposis occurs as a result of mutations in the phosphatase and tensin (*PTEN*) gene.

The clinical diagnosis is based on the following International Cowden Consortium major criteria, modified by the National Comprehensive Cancer Network Cowden syndrome^[9,12,14,19,20]: macrocephaly (75%-97% of the cases - 58 cm for women and 60 cm for men), multiple (at least 3) gastrointestinal hamartomas including ganglioneuromas but excluding hyperplastic polyps (50%), dysplastic gangliocytomas of the cerebellum associated with seizures, tremors, and disorders of coordination (Lhermitte-Duclos syndrome), breast cancer (37%), nonmedullary (follicular) thyroid carcinoma (16%), endometrial cancer, and macular pigmentation of the glans penis. The mucocutaneous lesions are considered as pathognomonic (major criteria) only if the following associations are identified^[12,20]: At least three trichilemmomas (at least one being biopsically proved), at least three acral keratoses, at least three mucocutaneous neuromas, or oral papillomas (at least three without biopsy or at least one biopsically proved). The minor criteria are presence of benign lesions of the breast (fibrocystic change, benign epithelial tumors), thyroid (multinodular goiter, adenoma, papillary carcinoma), single lesion of the gastrointestinal tract (adenoma, lipoma, hamartoma), at least three lipomas, testicular lipomatosis, malformations or tumors of the

urogenital tract, vascular malformations, and mental retardation ($IQ \leq 75$)^[12,19,20]. Recently, the autism spectrum disorders, colon/renal cancer, and esophageal glycogenic acanthosis (at least three) were included in the minor criteria^[12]. For a final diagnosis, the following associations are necessary: at least three major criteria [at least one being macrocephaly, Lhermitte-Duclos syndrome (in adults), or gastrointestinal hamartomas], two major and three minor, or three minor criteria^[12,19,20]. Absence of one of the associated criteria allows the diagnosis of the "Cowden syndrome-like family"^[19].

Gastrointestinal hamartomas occur in 50% of patients with Cowden syndrome, being currently considered the second most common feature, after macrocephaly^[19]. The estimated lifetime risk for malignancy at the age of 70 is 85% for any cancer, 77%-85% for breast and 35%-38% for thyroid cancer, 33% for renal cancer, 28% for endometrial, 7%-15% for CRC and 6% for melanoma^[12,15,20,21]. Gastric malignancy is rarely associated, 1/100 patients with Cowden syndrome being affected^[20].

Other hamartomatous polyposis syndromes

Besides Cowden syndrome, *PTEN* gene mutations were described in patients with Bannayan-Riley-Ruvalcaba and hereditary mixed polyposis syndrome^[7,12].

Bannayan-Riley-Ruvalcaba syndrome is an autosomal dominant disorder characterized by hamartomatous polyps of the small intestine and colon (25% of the cases) along with genital spots, macrocephaly, subcutaneous/visceral lipomas including lipomatosis of the glans penis, hemangiomas, and mental retard^[7].

In some cases, identification of the specific genetic syndrome is very difficult, the recommended diagnosis being hereditary mixed polyposis syndrome. In this category, association of atypical juvenile polyps, hyperplastic polyps, sessile serrated adenomas, and adenomatous polyps can be associated with increased risk for CRC^[7].

Other very rare familial hamartomatous syndromes that can include hamartomatous polyps of the gastrointestinal tract are the following^[7,12]: Gorlin syndrome (consequence of *PTCH1* mutations), characterized by hyperkeratosis of palms, soles, and jaw, skeleton abnormalities, macrocephaly, frontal bossing, and associated medulloblastoma and basal-cell carcinomas; multiple endocrine neoplasia syndrome 2B (consequence of *RET* mutations), characterized by neuromas of the lips and tongue, and associated pheochromocytoma and medullary thyroid cancer; neurofibromatosis type I (consequence of *NF1* mutations), characterized by café au lait spots, axillaries and inguinal freckling, and associated neurofibromas, gliomas, malignant peripheral nerve sheath tumors, and tumors of the breast; and Birt-Hogg-Dube syndrome (consequence of *FLCN* mutations), characterized by spontaneous pneumothorax and associated fibrofolliculomas of the skin, and renal tumors.

Li-Fraumeni syndrome

It is an autosomal dominant hereditary cancer syndrome characterized by mutations in the *p53* gene that determines occurrence of leukemia, carcinomas of the breast and adrenal glands, brain tumors, sarcomas of the soft tissues and bone, *etc*^[19-21,23-26]. The classic Li-Fraumeni syndrome criteria of eligible families include one family member diagnosed with sarcoma before 45 years of age, a first-degree relative with any type of cancer before 45 years of age, and a first/second relative with any cancer diagnosed before 45 years of age or a sarcoma at any age^[19,20]. Similar to Cowden syndrome, absence of one of the associated criteria allows the diagnosis of the "Li-Fraumeni syndrome-like family"^[19,23,24].

Gastric carcinoma, preponderantly located in the proximal stomach, is reported to occur in about 2%-5% of carriers with *p53* mutations at the median age of 36 years, ranging between 12 and 74 years^[24]. Association of early-onset gastric carcinoma and CRC can involve in 10%-28% of the families with classic Li-Fraumeni syndrome, but carcinomas of the lung, melanomas, lymphomas, and germ cell tumors have also been reported^[24]. The incidence of Li-Fraumeni-related gastric cancer is higher in Asian population (Japan and South Korea), when compared with people from United States, being supposed that *p53* mutation could enhance the carcinogenic effect of *H. pylori*^[24].

GENETIC COUNSELING AND CRITERIA FOR SURVEILLANCE

In patients with *FAP* and *FAP-variants* including *Gardner syndrome*, *Turcot syndrome*, and *AFAP*, the main goal of surveillance is to detect the CRC in early stages^[28], combining molecular and clinical approaches^[33].

The clinico-genetic screening should be performed in all first degree relatives of a patient with *FAP* and should be started, when it is possible, from the mid adolescence^[28].

The genetic screening consists in attentively examination of the *APC* gene, according to the particularities presented in Table 1, after a proper genetic counseling of the patient who should be asked for the informed consent. The gold standard method is the full sequencing of the *APC* gene, to examine all the 15 exons^[28]. The mutation cluster region (mutational hotspot of *APC* gene) is the 5'part of exon 15 from codon 1250 to 1464^[28]. If no mutations are detected, the current guidelines recommend to continue testing for large gene rearrangements^[28,35].

From colonoscopy point of view, it is worthy noticing that the small polyps are mostly limited to the recto-sigmoid at the time of adolescence and only thereafter increase in size and number^[28]. However, because half of patients develop adenomatous polyps before puberty and 95% by 35 years, sigmoidoscopy screening is recommended starting at age 12-14 years old

and performed every two years in mutation carriers. Identification of adenomas is an indicator for annually total colonoscopy, with biopsies from the suspect areas, until colectomy will be performed, depending on the individual endoscopic features^[1,28]. Prophylactic colectomy is recommended for multiple ulcerated polyps larger than 1 cm that shows high-grade dysplasia^[28]. The type of resection depends on the patient's age and personal decision, number and extension of polyps, and also by the macroscopic aspect of the tumors^[28].

At risk family members carrying germline mutations near codon 1300 can present early-onset CRC in their childhood and colonoscopy surveillance should also begin before puberty^[32,33]. On the other hand, if the carrying germline mutations suggest risk for *AFAP*, screening should be carried out every two years from the age of 18-20 years, with focused attention on identification of the right-sided distribution of adenomas. Once adenomatous polyps are identified, endoscopic polypectomy followed by annually total colonoscopy is recommended, followed by colectomy in case of large ulcerated polyps with high-grade dysplasia^[28,32]. Postoperative endoscopic follow-up is necessary in patients with rectal remnant, to detect the possible carcinoma of the ileo-anal pouch^[28].

For classic *FAP*, flexible sigmoidoscopy remains the standard of care, whereas in patients with *FAP* variants the proximal colon should also be explored through total colonoscopy. Modern imagistic methods such as capsule endoscopy and/or entero-CT-scan or entero-MRI can also be used for complex investigations. Because duodenal cancer is the second cause of death of patients with *FAP*, with 5% lifetime risk^[28], gastrointestinal endoscopy is recommended to be carried out every 5 years after identification of the colorectal polyps^[28].

Besides the risk for gastrointestinal cancer, the protocol of surveillance should also take into account the extraintestinal manifestations, including papillary carcinoma of the thyroid (the third commonest tumor in patients with *FAP*, with a risk of about 160 times higher than in general population, and a male to female ratio of 1:17), pancreatic carcinoma but also the central nervous system tumors and neuroblastomas^[14,28], based on the genetic particularities shown in Table 1.

Annually thyroid palpation, eventually completed by cervical ultrasonography, is recommended starting at the age 25 years^[28,36]. Because patients with *FAP* present 1000-fold increased risk developing desmoid tumor, compared to the general population^[34], diagnosis of such tumors, mostly in the abdominal wall, should be followed by a total colonoscopy, especially in young people. Although benign, due to highly recurrence rate, desmoids tumor represents one of the main causes of death of patients with *FAP*^[28].

For patients diagnosed with *MAP*, the surveillance is identically to those used for *AFAP*. The colonoscopy surveillance begins at 18-20 years old being carried out every two years and annually after adenomas detection. Upper endoscopy is also recommended every five years

starting at the age of 25-30 years old, to explore the duodenal segments^[28,36]. Screening for extra-intestinal manifestations is not recommended. Biallelic *MUTYH* gene mutations should be suspected and explored in patients with colorectal polyposis diagnosed before the age of 50 years, especially in associated serrated adenomas. In first degree relatives the two most common mutations, p.G396D and p.Y179C, should be determined. Identification of at least one of the two missense mutations should be followed up by full gene sequencing^[28]. Sequencing should also be done in non-Caucasian suspected patients, focusing on the specific geographic and ethnic particularities shown in Table 1.

For juvenile polyposis syndrome, annual upper and lower endoscopies are recommended to be performed in the *MADH4/SMAD4* carriers by the mid-teens or at the time of initial symptoms, most of the cases being diagnosed around the age of 40 years^[8-13]. Modern imagistic methods such as capsule endoscopy and/or entero-CT-scan or entero-MRI can also be used^[37].

In the bioptic specimens of gastrointestinal polyps, loss or partial loss of the epithelial expression of SMAD4 protein, with or without retained stromal expression, can be a first sign of suspected *SMAD4* mutation^[11]. Proctocolectomy or subtotal colectomy should be considered in patients with multiple polyps, severe symptoms, and/or history of familial CRC, but a specific guideline does not exist^[12]. According to the British Society of Gastroenterology and Association of Coloproctology for Great Britain and Ireland, in asymptomatic family at-risk members, including the proved *SMAD4/ BMPR1A* mutations, every 1-2 years colonoscopy is recommended from age 15-18 years until age 70 years and gastroduodenoscopy from the age of 25 years^[12,29].

In *SMAD-4* mutation-carriers, investigation for a possible associated hereditary telangiectasia is also recommended^[13]. Because severe gastrointestinal bleeding can be associated in these syndromes, long-time intravenous using of low doses of the antiangiogenic (anti-VEGF) drugs such as bevacizumab (2 mg/kg per course, every 3 wk) have been recently proposed^[30]. Identification of a pulmonary associated vascular malformation and a dilated thoracic aorta is mandatory to avoid bleeding complications^[12].

Decreased SMAD4 expression can also activate the transforming growth factor- β and, as a consequence, breast epithelial malignant proliferation can occur, as in one of the previously reported cases^[31]. Duodenal and pancreatic tumors can also occur in these patients^[14].

In patients with Peutz-Jeghers syndrome, surveillance for tumors of the colorectum, small intestine, breast, pancreas, and sex-cord tumors should be performed^[12,14]. Endoscopic examination of the gastrointestinal tract is recommended to be performed every 3 years beginning from the age of 18 years (and every 1-2 years after the age of 50 years) while suspicion for breast cancer should be excluded based on annual ultrasound examinations from the age of 25-30 years completed by

annual mammography from the age of 50 years^[12,15]. In symptomatic children, periodic gastrointestinal endoscopy should be done^[12]. In patients with Peutz-Jeghers syndrome, the capsule endoscopy proved to have a higher diagnostic sensitivity than the Barium-contrast X-Ray and entero-MRI but the size and location of polyps are difficult to be evaluated^[37].

No guidelines for screening of other cancers have been implemented to date.

For Cowden syndrome, being known that breast cancer and thyroid cancer occurs in 25%-50% of females and 3%-10% of all patients, respectively, a personal and familial cancer surveillance for these associated malignancies and also for endometrial cancer in females would be necessary^[12,19]. Currently, the gastrointestinal tract surveillance is not routinely recommended below 50 years of age, although an earlier endoscopic colonic and gastric surveillance beginning at the age of 30-35 years with follow-up every 1-2 years was recently suggested, especially for Asian population^[20]. However, annual mammogram and vaginal ultrasound with endometrial sampling should be done from age 30 years for women and biannual colonoscopy and renal ultrasound examination from age 35-40 years in both males and females are recommended in the most recent studies^[12]. Annual thyroid examination should begin from age 18 or 5-10 years before the earliest thyroid tumor in the family^[12].

For the other previously nominated hamartomatous polyposis syndromes, the childhood surveillance should take into account the gastrointestinal and extra-gastrointestinal complications such as bleeding, severe anemia, intussusception, whereas the adults should be examined to detect malignancies in early stages, similar to patients with Cowden syndrome^[7,12].

In patients with Li-Fraumeni syndrome, although germline *p53* mutations can be identified in the family members, it is difficult to establish the rules of surveillance, because tumors can occur in every organs^[19]. In these "p53 families", screening program is recommended to begin at earlier ages including investigations for breast, colorectal, and gastric cancer detection^[19]. However, the guidelines of the National Comprehensive Cancer Network Surveillance recommend colonoscopy as part of the surveillance protocol in these carriers^[20].

Because some of the inherited polyposis syndromes remain unexplained/unclassified, the genetic screening should take into account, after a meticulous histological examination, a minimal number of gene mutations, respectively the genes *SMAD4*, *BMPR1A*, *STK11*, and *PTEN*^[14]. The surveillance protocol should also take into consideration the other nontumor complications such as intussusceptions, ileus, gastrointestinal hemorrhage, and anemia^[21].

CONCLUSION

Despite the well-conducted screening programs worldwide, the accurate diagnosis of inherited cancer-

predisposing syndromes of gastrointestinal tract remains difficult. Lack of experience of both gastroenterologists and pathologists, due to rare occurrence of these syndromes, increases the difficulty. Subspecialization in the field of familial malignancies and founded of specialized medical centers in this field is essential for future proper medical care.

Because of geographic and ethnic particularities of gene mutations, national and international guidelines of screening and surveillance in these risk families should be elaborated. Development of the IHC markers that could predict specific gene mutation is a cheaper method that can be routinely used to detect these familial cases. Although rare, association of multiple tumors in the same patient is a time- and money-consuming management, the reason why a proper screening and surveillance could benefit both the patient and medical care system.

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Observational Study

Colorectal cancer screening in an academic center compared to the national average

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Abstract

AIM: To investigate if the increased emphases on training and education on current colorectal cancer (CRC) screening guidelines has resulted in improved national CRC screening rates in an internal medicine training program, and to determine if the doctor's post graduate year (PGY) level of training affected CRC screening rates.

METHODS: We conducted a cross sectional study of every patient who presented to the outpatient clinic of New York Methodist Hospital, Brooklyn, NY, over the span of six continuous weeks in 2011. A questionnaire was integrated into every patient's medical interview that helped determine that patient's current CRC screening status, screening mammography status if applicable, Papanicolaou smear status if applicable, and current pneumococcal vaccination status. At the same time, patient demographics were also obtained. All of the questionnaire data was collected at the end of each medical visit and was compiled by a designated researcher. After all the data points were collected, it was ensured that the patient has been seen by his or her continuity care resident at least twice in the past. Data was then compiled into a secure, encrypted database to then be analyzed by our statistician.

RESULTS: Data from 547 consecutive clinic visits were obtained. Of these, we reviewed 483 charts that met all of the inclusion criteria and did not meet the exclusion criteria. The data was then analyzed for differences between PGY levels, patient's sex, race, and educational level. The study population consisted of 138 men and 345 women. 35 patients were white (7.40%), 174 were black (39.79%) and 264 were Hispanic (55.81%). Our CRC screening rates were: 66% for PGY-1's, 72% for PGY-2's and 77% for PGY-3's. There was no statistical difference noted between the three groups ($P \leq 0.05$) or was there any difference sex, insurance status or educational level. Overall CRC screening rate was 72% which was not different from the New York State average ($P < 0.05$). There was a statistically significant higher rate of CRC screening amongst Hispanics 76% ($P = 0.034$) and in people within the ages of 70-79, 82% ($P = 0.015$).

CONCLUSION: Patients that are followed by internal medicine residents at our urban outpatient teaching clinic did not receive higher rates of CRC screening nor did rates of screening vary with their PGY level.

Key words: Screening; Colorectal cancer; Post graduate year; Colorectal cancer; Residency; Urban

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Core tip: It is assumed that greater seniority and experience amongst medical residents can equal improved colorectal cancer screening percentage in an outpatient academic center. We not only compare screening rates between different post graduate years but also compare the medical resident's screening rates to the national average.

Gonzalez MO, Sadri LM, Leong AB, Mohanty SR, Mehta P. Colorectal cancer screening in an academic center compared to the national average. *World J Gastrointest Oncol* 2015; 7(11): 356-360 Available from: URL: <http://www.wjgnet.com/1948-5204/full/v7/i11/356.htm> DOI: <http://dx.doi.org/10.4251/wjgo.v7.i11.356>

INTRODUCTION

Despite established screening guidelines, national colorectal cancer (CRC) screening rates vary between 54%-75% of the at risk population^[1]. CRC is the third leading cause of cancer-related deaths in the United States when men and women are considered separately, and the second leading cause when both sexes are combined^[2]. CRC is expected to cause approximately 49700 deaths during 2015^[2]. The American Cancer society estimates that there will be 93090 new cases of colon cancer and 39610 new cases of rectal cancer in 2015^[2]. When diagnosed early, CRC is typically curable. Screening guidelines have been developed to

help reduce the mortality of CRC. For a person without increased risk factors, starting at the age of 50 years, it has been generally accepted that a colonoscopy every 10 years, flexible sigmoidoscopy (FS) every 5 years or annual fecal occult blood test (FOBT) would be considered a sufficient screening technique^[3].

Despite these screening strategies and increased efforts by governing bodies to increase awareness of CRC screening in both the medical community and general public, in 2010 only 54.1%-75.2% of the United States population responded that they were "up to date" with their CRC screening, with the state of New York averaging 69%-75.2%^[1].

It is assumed that clinical guidelines are observed and followed more often in an academic training setting like a residency program due to the fact that there is more emphasis on education in an academic setting and the medical residents are under constant supervision. However, we have observed that a majority of resident training involves acute disease management in the inpatient setting and little research has attempted to assess the quality of ambulatory education and resident competence especially for disease prevention and health maintenance^[4].

We assessed the CRC screening rates at New York Methodist Hospital in 2010 and compared them to the 2010 New York state screening rates as recognized by the Center for Disease Control (CDC). Furthermore, we wanted to try to recognize possible barriers to CRC screening in our community hospital and try to identify ways that we could improve our CRC screening rates. We felt it was important to ascertain if current efforts to educate physicians in training are effective and to help identify ways to improve education efforts.

MATERIALS AND METHODS

Ambulatory care resident education

The New York Methodist Hospital internal medicine residency program is a traditional, accredited 3 year program consisting of both inpatient and ambulatory based training. At the time of this study there were 106 medical residents providing longitudinal care for patients in the ambulatory clinic. All resident physicians provide patient care in the ambulatory clinic two half days every week throughout all three years of their training. Additionally, residents do 4 to 5 mo solely of ambulatory care without any inpatient responsibilities. During those 4 to 5 mo, residents have a weekly morning rotation in the clinic's gastroenterology clinic and work under the supervision of board certified gastroenterologist. Formal lectures addressing preventive care cancer screening are interspersed throughout the academic year including one lecture focused on colorectal cancer screening in the average risk patient. Throughout their training, residents are given monthly exams; in two of which the primary focus is to test the resident's knowledge on primary prevention and screening strategies.

Table 1 Study population breakdown

Population	Number of patients	Percentage of patients
PGY-level		
PGY-1	170	35.20%
PGY-2	160	33.13%
PGY-3	153	31.68%
Sex		
Female	345	71.43%
Male	138	28.57%
Race		
Blacks	174	36.02%
Whites	35	7.25%
Hispanics	264	54.66%
Other	10	2.07%
Highest educational level		
Elementary school	28	5.80%
Middle school	63	13.04%
High school	186	38.51%
College or University	43	8.90%
Unknown	163	33.75%
Insurance type		
Medicare/Medicaid	288	59.63%
Private Insurance	32	6.63%
Unknown	163	33.75%
Age of patient (yr)		
50-59	179	37.06%
60-69	177	36.65%
70-79	90	18.63%
80-89	34	7.04%
90-99	3	0.62%

PGY: Post graduate year.

Study population

A cross sectional study was taken from patients who received their care at the internal medicine clinic of New York Methodist Hospital over a 6 wk period. Residents were given a questionnaire and integrated it into their clinical data gathering during the patient’s clinic visit session. Data was collected after every clinic encounter throughout the six weeks. Exclusion criteria included patients under the age of 50, patients with an increased risk for developing colorectal cancer (family or personal history of adenomatous polyps, CRC, or polyposis syndromes) patients who had previous CRC screening in last 5 years and patients who have been followed by an internal medicine resident for less than 8 mo and had less than 2 clinic visits in which the patient had been seen by their designated resident.

Data collection

Data from 547 consecutive office visits in the internal medicine resident ambulatory clinic over a span of 6 wk was collected. Four hundred and eighty-three of those charts met the inclusion criteria and were selected and reviewed in further detail. The investigators confirmed that there had been a minimum of two clinic visits with their assigned medical resident. Data recorded included patient demographics, patient’s level of education, type of medical insurance, data on the use of screening colonoscopy (SC), fecal occult blood testing (FOBT),

FS, and other preventative health measures such as influenza vaccination, screening mammography and Pap smear. For the purposes of this study, only the data relevant to CRC screening was analyzed. A patient’s CRC screening was considered “up to date” if it met any of the following criteria: (1) the patient has had a SC within the last 10 years;(2) the patient has had a screening FS within the last 5 years; and (3) a FOBT within the last 12 mo. These screening modalities are readily available at our institution and generally accepted as appropriate screening tools^[3]. FS, though a well-accepted screening modality, was not included in our survey as the procedure is not offered at our institution. Finally, the data was also then stratified between the resident’s level of training (PGY1, PGY2, and PGY3). This study received IRB approval; IRB reference No. 518027.

Statistical analysis

Data was analyzed using the binomial test and the χ^2 distribution test. The binomial statistical test was used to compare the medical resident’s screening rate to the New York state’s 2010 CDC average of 70.1% and to determine if insurance status, patient’s level of education, race, age or sex influenced the results. The χ^2 distribution test was used to determine if there were any statistical differences between the post graduate year level of training, age groups, sex, educational level, insurance status, or race. Statistical significance was defined as $P = 0.05$.

RESULTS

Four hundred and eighty three patients were considered appropriate for inclusion into the study. Table 1 depicts our patient characteristics. The study population consisted of 138 men with a mean age of 63.5 years (range, 50-88 years) and 345 women with a mean age of 64.17 years (range, 50-92 years). Thirty five patients were white (7.40%), one hundred and seventy four were black (39.79%) and two hundred and sixty four were Hispanic (55.81%). Two hundred and twenty nine (47.41%) responded that they had a high school education or above, ninety one (18.84%) responded that their educational level was below high school level and one hundred and sixty three (33.75%) did not provide their educational level. Table 2 depicts our statistical findings. The overall CRC screening rate at our hospital was 72%. We did not observe statistical difference between the CRC screening rates of our hospital compared to the 2010 United States or New York state screening rates as provided by the CDC^[1] ($P = 0.05$). There was no observed statistical difference between the screening rates of PGY-1’s, PGY-2’s, and PGY-3’s ($P = 0.096$), sex, insurance status or educational level. There was a statistically significant higher rate of CRC screening amongst Hispanics of 76% ($P = 0.034$) and in people within the ages of 70-79 years of 82% ($P = 0.015$).

Table 2 Statistical analysis comparing our colorectal cancer screening rates to the 2010 New York State screening rates as determined by the Center for Disease Control

Variable	Screening rate	P value	P value of the χ^2 distribution test comparing variability within groups
PGY-level			
PGY-1	0.66	0.3	
PGY-2	0.72	0.735	0.096
PGY-3	0.77	0.061	
Age of patient (yr)			
50-59	0.64	0.07	
60-69	0.77	0.58	
70-79	0.82	0.015 ¹	0.006 ¹
80-89	0.61	0.255	
90-99	0.67	1	
Sex			
Female	0.7	0.953	0.33
Male	0.75	0.26	
Race			
Black	0.68	0.508	
Hispanic	0.76	0.034 ¹	0.023 ¹
Other	0.8	0.733	
White	0.54	0.063	
Highest educational level			
College	0.72	0.869	
Elementary	0.75	0.682	
High School	0.74	0.336	0.888
Middle School	0.72	0.888	
Undisclosed	0.69	0.73	
Insurance type			
Medicare/Medicaid	0.73	0.245	
Private insurance	0.72	1	0.514
Undisclosed	0.68	0.607	
Overall screening rate	0.72	0.48	

¹Statistical significance is defined as $P = 0.05$. New York State screening rate was standardized to a base rate of 0.701 for comparison. Data was analyzed by binomial statistical analysis. PGY: Post graduate year.

DISCUSSION

Our study did not support the assumption that CRC screening would be offered more frequently at an institution with a residency training program when compared to the state and national average screening rates which include non-teaching outpatient practices. There was a numerical difference between the screening rates of PGY-1 compared to PGY-3 (11%) however statistical significance, possibly due to function of power, was not achieved. Willett *et al*^[5] had similar findings in 2005 when they compared PGY-1 and PGY-2 residents in their adherence rates to national guidelines for outpatient preventive health services and found no difference between the two groups for breast and colon cancer screening amongst others.

Despite didactics, emphasis on practicing evidence based medicine, and importance of implementing preventative measures with the use of well accepted screening measures CRC screening in our internal medicine residency training program was still found to be comparable to the national and state average CRC screening rates.

Prior studies have indeed shown poor CRC screening rates amongst internal medicine residents^[6]. Numerous studies have elucidated the deficiency in knowledge of and compliance with CRC screening recommendations amongst internal medicine residents^[6-9]. Our study however is unique in that we were able to compare the rates of CRC screening at an outpatient clinic of an urban teaching program to state and national rates which include non-teaching practices.

These results highlight the important fact that though we expect and anticipate that teaching programs ingrain the importance of screening and prevention in medicine, for reasons unknown, either fail to do this or just do not seem to reflect this in clinical training practice. If well accepted and proven screening techniques such as CRC screening are not offered more so by physicians in training who are assumed to be "up-to-date" with current screening guidelines and practices through their mandated hours of didactics, this raises the concern that perhaps there needs to be a change in the way both residents and their mentors are trained.

In the future, it is vital that efforts be made to improve education amongst physicians in training regarding CRC guidelines and the importance of CRC screening. A prior study by Gennarelli *et al*^[10] showed that knowledge of CRC screening guidelines amongst medical professions is low for both average and high risk patients. Internal medicine residents in our program like most others receive weekly didactics in the form of lectures by attending physicians, fellows, and visiting professors averaging approximately 7 h/wk however these lectures span a wide variety of topics and are not focused on primary prevention or screening. Perhaps physicians in training would benefit from a teaching series focused specifically on preventative measures and screening techniques. A retrospective chart review done by Borum showed that internal medicine residents who had increased exposure to and reinforcement of surveillance recommendations through lectures and required documentation as well as formal FS training adhered to guidelines far more than other resident physicians^[7].

Additionally, now that medical records are for the most part transitioning to electronic records across the country, clinical prompts incorporated into the standard outpatient note template may help as a reminder tool for physicians who have adequate knowledge of the topic but for the sake of time and other factors may not necessarily remember to ask their patients regarding their screening status. Seres *et al*^[11] showed that clinical prompts are superior to evidence based lectures when it comes to improving physician CRC screening rates.

Another aspect that must be considered is the patient's role in compliance with recommended screening. 1.5% of our patients had refused CRC screening when offered in the past and it is unknown if they were educated regarding the potential long term consequences of their decision. Residents in training

should learn early on the importance of patient education in both disease prevention and treatment. The realm of primary prevention and screening is one in which patient education regarding the importance of screening and potential dire outcomes of lack of screening become vital. Perhaps implementing use of patient educational tools such as easy-to-read brochures and pamphlets explaining current rates of CRC and screening modalities effect on prevention will help patient's make more educated decisions when it comes to screening. Rowe *et al*^[12] even implemented use of an educational video while patients were waiting to be seen by residents.

In assessing the need for further investigations and future direction we will review the limitations of our study. Generalizability of our study, which included only residents from our primarily categorical internal medicine residency program, and if our findings are representative of other residency programs especially those which include family medicine or primary care tracks is of concern. Another limitation of the study is that it was conducted over the span of 6 wk and may not be an adequate representation of overall practice. In addition, the patient population was not a good representation of the different races; with 54.66% of patients were Hispanic and 7.25% Whites, this may explain the perception of higher screening rates in Hispanics as compared to Whites.

COMMENTS

Background

Routine screening has been proven to be an effective tool at preventing colorectal cancer (CRC). Many efforts have been put forth to educate medical professionals on proper CRC screening. The authors investigate if current efforts on CRC screening education are producing improved CRC screening rates.

Research frontiers

The Center for Disease Control has been providing a big push in CRC prevention. Current studies center on methods of improving education towards not only patients but health care providers as well.

Innovations and breakthroughs

This is the only article comparing the screening rate of medical residents compared to the national average and one of the few manuscripts comparing the screening rates between post graduate years (PGY).

Applications

The study results demonstrate that there is no appreciable difference between PGY or compared to the national average. This exposes potential weaknesses in current educational strategies and opens up some proven ideas that may help increase CRC screening rates.

Peer-review

This is a well-designed observational study that was tailored to minimize selection bias. The results can be applied to family medicine and internal medicine training programs alike.

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Prospective Study

Tumor neoangiogenesis detection by confocal laser endomicroscopy and anti-CD105 antibody: Pilot study

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Abstract

AIM: To evaluate neoangiogenesis in patients with colon cancer by two fluorescently labeled antibodies on fresh biopsy samples imaged with confocal laser endomicroscopy (CLE).

METHODS: CLE is an imaging technique for gastrointestinal endoscopy providing *in vivo* microscopy at subcellular resolution. An important question in validating tumor angiogenesis is what proportion of the tumor vascular network is represented by pre-existing parent tissue vessels and newly formed vessels. CD105 (endoglin) represents a proliferation-associated endothelial cell adhesion molecule. In contrast to pan-endothelial markers, such as CD31, CD105 is preferentially expressed in activated endothelial cells that participate in neovascularization. Thus, we evaluated CD105 and CD31 expression from samples of ten patients with primary rectal adenocarcinoma, using a dedicated endomicroscopy system. A imaging software was used to obtain the Z projection of the confocal serial images from each biopsy sample previously combined into stacks. Vascular density and vessel diameters were measured within two 50 μm x 475 μm rectangular regions of interest centered in the middle of each image in the horizontal and vertical direction. The results were averaged over all the patients and were expressed as the mean \pm SE.

RESULTS: The use of an anti-CD105 antibody was found to be suitable for the detection of blood vessels in colon cancer. Whereas anti-CD31 antibodies stained blood vessels in both normal and pathologic colon equally, CD105 expression was observed primarily in malignant lesions, with little or no expression in the vessels of the normal mucosa (244.21 ± 130.7 vessels/ mm^3 in only four patients). The average diameter of anti-CD105 stained vessels was 10.97 ± 0.6 μm in tumor tissue, and the vessel density was 2787.40 ± 134.8 vessels/ mm^3 . When using the anti-CD31 antibody, the average diameter of vessels in the normal colon tissue was 7.67 ± 0.5 μm and the vessel density was 3191.60 ± 387.8 vessels/ mm^3 , while in the tumors we obtained an average diameter of 10.88 ± 0.8 μm and a vessel density of 4707.30 ± 448.85 vessels/ mm^3 . Thus, there were more vessels stained with CD31 than CD105 ($P < 0.05$). The average vessel diameter was similar for both CD31 and CD105 staining. A qualitative comparison between CLE *vs* immunohistochemistry lead to similar results.

CONCLUSION: Specific imaging and quantification of tumor microvessels are feasible in human rectal cancer using CLE examination and CD105 immunostaining of fresh tissue samples.

Key words: Rectal cancer; Neoangiogenesis; Confocal laser endomicroscopy; Panendothelial markers; Anti-CD105 antibody

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Core tip: We evaluated CD105 expression from fresh tissue samples of human rectal adenocarcinoma, using confocal laser endomicroscopy (CLE). While vessels marked with fluorescent CD31 were visible in both

normal and malignant tissue, CD105 was predominantly expressed in tumor lesions, having reduced affinity for normal rectal mucosa. Our data showed that CLE using CD105 antibody for tumor vascular network imaging is feasible and that CD105 represents a more specific marker for rectal cancer neoangiogenesis than panendothelial markers. To our knowledge, this is the first study to report the use of fluorescently-labeled CD105 antibody in conjunction with CLE in patients with rectal tumor.

Ciocâlțeu A, Săftoiu A, Pirici D, Georgescu CV, Cârțână T, Gheonea DI, Gruionu LG, Cristea CG, Gruionu G. Tumor neoangiogenesis detection by confocal laser endomicroscopy and anti-CD105 antibody: Pilot study. *World J Gastrointest Oncol* 2015; 7(11): 361-368 Available from: URL: <http://www.wjgnet.com/1948-5204/full/v7/i11/361.htm> DOI: <http://dx.doi.org/10.4251/wjgo.v7.i11.361>

INTRODUCTION

Tumor neoangiogenesis, defined as the neo-formation of blood vessels from pre-existing microvessels, represents an attractive target for both imaging and therapeutic strategies. It is thought that neovascularization is first activated by an "angiogenic switch" during premalignant phases of carcinogenesis, before tumors emerge (Folkman *et al*^[1]; Bolontrade *et al*^[2]; Huss *et al*^[3]). An important question in validating tumor neoangiogenesis is what proportion of tumor vascular network is represented by pre-existing *vs* newly formed vessels. In this respect, new imaging and diagnostic techniques which differentiate tumors vascularization at different stages are desired^[4].

Antihuman panendothelial cells antibodies are used to identify all types of blood vessels in a given tissue sample, irrespective of being mature or immature. Commonly used panendothelial markers such as CD31, CD34 or von Willebrand factor detect the parent vessels as well as the tumor vasculature, but they are not always expressed in all tumor blood vessels. Moreover, these antibodies seem to have a higher affinity for large than for microvessels^[5].

Endoglin (CD105) is a co-receptor for various TGF- β family members and therefore a target for tumor vasculature^[6]. The role of endoglin and the indispensable role for the TGF- β signaling pathway in developmental angiogenesis has been studied on genetically modified mice^[7-9]. Unlike all other markers, endoglin mediates direct pro-angiogenic effects of TGF- β on endothelial cells and is specifically overexpressed in tumor vessels, on proliferating endothelial cells, at sites of active angiogenesis. Its expression has also been associated with metastasis and patient survival^[6,10,11]. Recent reports suggest that elevated plasma levels of endoglin in patients with colorectal cancer correlate with poor prognosis (Li *et al*^[7]; Duff *et al*^[12]). As a result, endoglin

Table 1 Patient characteristics

Patient	Gender	Age	Tumor grading	Preoperative stage	RT	CTX
1	F	67	G1	T3N0M0	No	No
2	M	65	G2	T3N0M0	Neoadj	No
3	M	47	G2	T3N0M0	Neoadj	No
4	M	66	G2	T4N0M0	Adj	Adj
5	M	54	G2	T3N0M0	No	No
6	M	67	G1/G2	T3N1M0	Neoadj	Neoadj
7	F	80	G1 + Mucinous areas	T3N0M0	Neoadj	Neoadj
8	F	78	G2	T3N2M0	Neoadj	No
9	M	59	G1	T3N1M0	No	No
10	M	69	G1/G2	T3N0M0	Neoadj	No

RT: Radiotherapy; CTX: Chemotherapy; Neoadj: Neoadjuvant therapy; Adj: Adjuvant therapy; F: Female; M: Male.

could represent a valuable tool for the diagnosis, tumor vasculature visualization and targeted treatment of solid cancers^[4].

Since endoglin is highly and specifically expressed on tumor endothelial cells, in the present study we hypothesized that it could be used as an appropriate marker to assess the vascularization of a tumor.

Confocal laser endomicroscopy (CLE) gained an important role in the study and real-time histopathological diagnosis of various gastrointestinal diseases, such as celiac disease, Barrett esophagus, microscopic colitis, inflammatory bowel disease, and recently *Clostridium Difficile* associated colitis^[13]. Recent meta-analyses performed to determine the diagnostic accuracy of CLE in the detection of colorectal neoplasia showed high sensitivity and specificity of the method^[14,15].

Recently, we have used CLE to assess tumor vasculature by fluorescence labelled antibodies targeted against endothelial markers^[16,17]. In the present feasibility study, we used CLE to compare the selective expression of fluorescently labeled anti-CD105 antibodies in newly-formed vessels to fluorescently labeled anti-CD31 total vessel staining, and the gold standard of histopathology. More specifically, we aimed to answer the following questions: (1) Can the use of CLE in association with CD105 offer a more adequate quantitative and qualitative analysis of newly formed vessels than the commonly used panendothelial markers in human rectal cancer? and (2) Can this method be used *in vivo* for a rapid characterization of tumor microvascularization?

MATERIALS AND METHODS

Subjects

The current study was conducted according to the Code of Ethics of the World Medical Association (Declaration of Helsinki, 1964, as revised in 2004) and approved by the local Ethics Committee. All the patients included read and accepted the written informed consent prior to study entry.

Tissue specimens from ten patients 47-80 years old (mean age of 65.2 ± 9.9 years), with histologically diag-

nosed rectal cancer, were collected during colonoscopy before undergoing surgical resection or neoadjuvant therapy to avoid artifacts (*e.g.*, false positive resulted from fibrosis or inflammation increased in case of radio-chemotherapy). Fresh tissue samples from these patients were immediately processed for both CLE and immunohistochemistry assessment.

The ten patient population contained stage II - III (according to AJCC staging system) rectal adenocarcinomas without metastatic spread.

The main clinical signs the patients presented at admission in the hospital were alternating diarrhea and constipation, accelerated intestinal transit, recent constipation, unintended weight loss, rectal bleeding, abdominal pain or discomfort. Only three patients accused rectal bleeding as a single symptom, also confirmed by the physical examination (digital rectal examination). Seven patients had nonspecific findings for the laboratory tests such as moderate elevated hematological values of erythrocyte sedimentation rate (three patients), slightly elevated white blood cells count (two patients) and moderate anemia (two patients). Two patients presented slightly elevated values of both tumor markers CEA and CA19-9, while three of them had only slightly elevated CEA value. Computed tomography scan excluded the presence of metastases in all ten patients and described rectal wall thickening in four cases. Histological examination findings from endoscopic samples are summarized in Table 1.

CLE

The biopsy samples collected with a standard colonoscope (CFQ160ZL, Olympus, Tokyo, Japan) were processed following a standardized protocol. During the endoscopic procedure, for every patient, six biopsies were taken from tumor, avoiding the ulcerated areas (paired biopsies for CLE assessment, standard immunohistochemistry and histopathological examination, respectively), as well as four biopsies from macroscopically normal surrounding tissue samples (paired biopsies for both CLE processing and standard immunohistochemistry). The biopsies were immersed immediately in 10% neutral buffered formalin for histopathological analysis, as well as in saline solution

for the *ex vivo* immunohistochemical processing. Samples from saline solution were thoroughly washed and incubated for one hour in the dark, at 37 °C, with Alexa-Fluor 488-labeled anti-CD31 (PECAM) antibody (mouse anti-human IgG1, Exbio, Prague, Czech Republic) or respectively FITC-labeled anti-CD105/Endoglin antibody (mouse anti-human IgG2a, Exbio), diluted as 1:15 and 1:5 in saline with 1% bovine serum albumin (BSA, Sigma-Aldrich, Munich, Germany). Afterwards, the excess antibodies were washed away in saline and the samples were immediately visualized in CLE imaging to assess the microvascularization *ex vivo* up to a maximum depth of 250 μm. CLE images were acquired using Pentax EC-3870 CIFK, Tokyo, Japan, a dedicated endomicroscopy system with an excitation wavelength of 488 nm and with a maximum laser power output of ≤ 1 mW at the surface of the tissue^[16,17].

To assess both endothelial markers more accurately, we used the color overlay function in the ImageJ image processing software (National Institutes of Health, United States). This software was used to obtain the Z projection of the confocal serial image stacks from each biopsy sample (60-250 images per biopsy sample). The vascular density and the vessel diameters were measured from the Z projections within two 50 μm × 475 μm rectangular regions of interest (ROI) centered in the middle of each image in the horizontal and vertical direction as before^[17].

Statistical analysis

The results were averaged over all the patients and were expressed as the mean ± SE. We used unpaired two-tailed Student's *t*-test, with the level of significance set at $P \leq 0.05$ to evaluate the variation of CD105 expression vs CD31 expression in microvessels from the normal mucosa tissue and from the rectal tumors.

Immunohistochemistry

To confirm the role of CD105 vs CD31 in tumor neo-angiogenesis, adjacent samples from the same patient were processed for immunohistochemistry, for normal and tumor samples as described previously^[16,17]. Briefly, after formaldehyde fixation and paraffin embedding, 4 μm tissue sections were sliced from these blocks, deparaffinized, re-hydrated and processed for antigen retrieval by microwaving for 20 min in citrate buffer pH 6. Endogenous peroxidase was next blocked utilizing 1% H₂O₂ for 30 min, and the false antigenic sites were further blocked by incubating the slides in 5% skimmed milk (Bio-rad, München, Germany). Paraffin-certified antibodies were next incubated alternatively on the slides overnight at 4 °C (rabbit anti-human CD105 polyclonal antibody diluted as 1:50, LabVision, Fremont, CA, United States; and mouse anti-human CD31, IgG1, clone JC70A, Dako, Glostrup, Denmark). Next day the sections were washed in saline, signal amplified with a multi-species polymeric HRP system (EnVision, Dako),

and finally vessels were visualized by adding the 3-3' diaminobenzidine substrate (DAB, Dako). Afterwards, the sections were counterstained with Hematoxylin and 3-4 hotspot high vessel density areas were captured using a Nikon Eclipse 55i microscope equipped with a 5 Megapixel CCD color camera (Nikon, Tokyo, Japan). There were selected images from the regions with the highest vascular density ("hot-spots"- according to Weidner *et al.*^[18]). Under constant illumination conditions, images were obtained using the 40 × objective, and saved as uncompressed TIF files using the Image ProPlus AMS 6 software (Media Cybernetics Inc., Bethesda, Maryland, United States). The contour for each microvessel was drawn separately with a dedicated hand tool in Adobe Photoshop software, and these ROI were filled with black RGB color and saved as layers. Images were brought back in Image ProPlus and after distance-to-pixel calibration, they were utilized for automated measurements. Total vascular area, and total vessel count were normalized to 1 mm² and automatically measured, considering a total area of the field of 36527.48 μm². Inflammatory plasma cells or tumor cells picking up the signal have been excluded from this interpretation by two pathologists (DP and CG).

RESULTS

Targeted anti-CD31 antibodies expression on the confocal laser images

To analyze CD31 expression in rectal cancer, we evaluated tumor rectal cancer tissue and normal rectal mucosa for the vascular morphometric assessment. The CD31 antibody stained blood vessels in both normal and tumor rectal mucosa. In normal mucosa, the average diameter of vessels was of 7.67 ± 0.5 μm and the vessel density was 3191.6 ± 387.8 vessels/mm³. In the tumor sample, we obtained an average diameter of 10.88 ± 0.8 μm and a vessel density of 4707.3 ± 448.8 vessels/mm³ (Figure 1A and B).

Targeted anti-CD105 antibodies for CLE imaging of normal colorectal tissue and tumor microvasculature

In the CLE samples that were fluorescently labeled with both CD31 and CD105 antibodies, the typical tumor vasculature pattern was observed, with tortuous, dilated and branched vessels, but the expression of CD105 in tumor tissue was generally lower compared to CD31 vessel staining (Figure 1C and D).

Staining for CD105 was low or absent in normal mucosa (244.21 ± 130.7 vessels/mm³ in only four patients), whereas the microvascular network was visualized using CD31 as a control on samples from the same patients. The average diameter of anti-CD105 antibody stained vessels was 10.97 ± 0.6 μm in tumor tissue, and average density was 2787.4 ± 134.8 vessels/mm³.

Next we analyzed the relationship between the vascular expression with CD31 and CD105 in colorectal

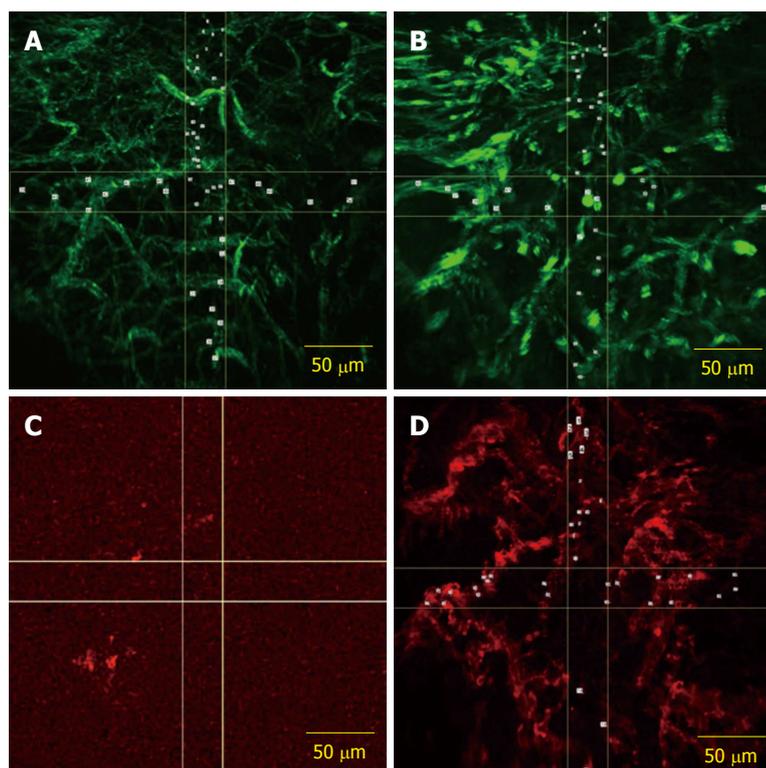


Figure 1 Confocal laser endomicroscopy. A: CLE images with AF488 anti-CD31 antibodies expression on vascular network from both normal; B: Tumor rectal mucosa; C: CLE image showing low expression of the fluorescently labeled anti-CD105 antibodies in normal rectal mucosa; D: Image from the same patient showing microvessels in rectal adenocarcinoma visualized by using CD105 staining as a specific endothelial marker. CLE: Confocal laser endomicroscopy.

Table 2 Quantitative results of vascular parameters from confocal laser endomicroscopy images

		CD31	CD105	P-value
Vascular Diameter (μm)	Normal Tissue	7.67 ± 0.5	3.46 ± 1.5	0.01
	Tumor	10.88 ± 0.8	10.97 ± 0.6	0.9
Vascular Density (vessels/mm ³)	Normal Tissue	3191.6 ± 387.8	244.21 ± 130.7	< 0.001
	Tumor	4707.3 ± 448.8	2787.4 ± 133.8	0.001

tumors. There were more vessels stained with CD31 than CD105 ($P = 0.0006$ for vascular density) in tumor. The average vessel diameter was similar for both CD31 and CD105 staining ($P = 0.018$ in normal samples, and $P = 0.932$ in malignant tissue).

The vascular density and the average diameter in tumor samples were significantly higher than the control in the 3D confocal reconstruction and in immunohistochemistry images. This fact was demonstrated by using both markers. In contrast, CD105 expression in colorectal tissues from the same patients was strongly enhanced in tumor vessels suggesting detection of the endoglin is an indication of angiogenesis particularly in malignant disease (Table 2).

Immunohistochemistry results

The CD105 and CD31 vascular expressions were studied in normal rectal mucosa and rectal cancer specimens.

The immunohistochemical analysis revealed that the samples from normal tissue showed low detectable CD105 expression. CD105 was rarely expressed in normal mucosa, while in tumor specimens, CD105-positive vascular endothelial cells were clearly identified (Figure 2).

In normal tissue images CD31-stained we measured an average of 202.9 ± 91.8 vessels/mm², with a significantly lower density of 56.5 ± 35.1 vessels/mm² for the vascular network stained with CD105 ($P = 0.00017$). The intratumoral MVD average was about 298.04 ± 132.6 vessels/mm² on CD31 stained images and on CD105 images - 205.7 ± 100.06 vessels/mm² ($P = 0.048$) (Figure 3).

The values for the vascular area when using the panendothelial marker CD31 were $3.4\% \pm 1.3\%$ in normal rectum and $9.4\% \pm 3.3\%$ in tumors ($P < 0.001$). On CD105 stained sections, the total vascular area was $1.3\% \pm 1.4\%$ in healthy tissue and $6.9\% \pm 3.1\%$ in malignant tissue ($P < 0.001$).

DISCUSSION

Rectal cancer is one of the cancers which can benefit from antiangiogenic therapy with high chances of curability when the treatment is applied at an early stage. To date, no appropriate tissue biomarkers exist for staging, prediction or monitoring of the clinical response to a therapeutic intervention (*e.g.*, antiangiogenic therapy).

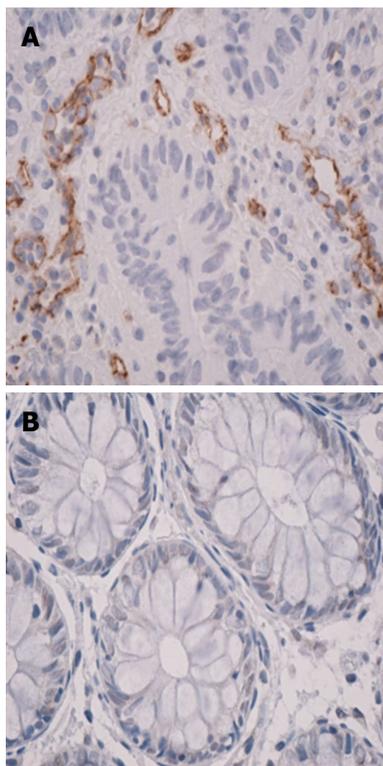


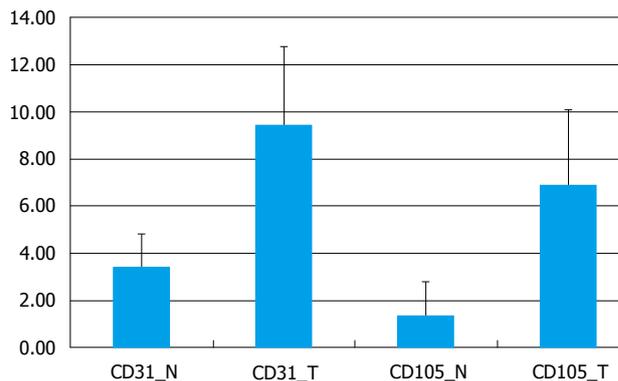
Figure 2 Immunohistochemistry on CD105 stained sequential sections from rectal cancer tissue samples (magnification 40 ×), CD105-positive vascular endothelial cells were clearly identified by their brown staining (A) and normal rectal mucosa displays the absence of endoglin expression (B).

Beyond its already presumed roles (higher affinity for microvascularization, prognostic role), recent *in vitro* studies suggested that endoglin targeting could improve treatment and could reverse resistance to bevacizumab in some refractory cancer patients^[19].

We hypothesized that the use of fluorescently-labeled CD105 antibodies will be suitable for identifying microvessels specific to tumor tissue. Indeed, while vessels marked with fluorescent CD31 were visible in both normal and malignant tissue, CD105 was predominantly expressed in tumor lesions, having reduced affinity for normal rectal mucosa. Thus, specific imaging and quantification of tumor microvessels were feasible using CLE examination and CD105 immunostaining of samples.

Our study proves that fluorescently labeled endoglin antibodies stained intensively intratumoral vessels, whereas vessels in non-neoplastic tissue did not or weakly expressed CD105. These results are consistent with previous observations that endoglin reacts specifically with angiogenic endothelial cells from the malignant tissues^[5]. Though, the endoglin expression on macroscopically normal mucosa in four of the patients could be explained by either the existent inflammation, or the tumor spread to normal surrounding tissue.

Endoglin, as a specific marker for activated endothelium, mainly reacts with fresh or frozen tissue, while its activity in paraffin-embedded specimens is



CD31_N- MVD in normal mucosa stained with anti-CD31 antibodies
 CD31_T- MVD in tumor mucosa stained with anti-CD31 antibodies
 CD105_N- MVD in normal mucosa stained with anti-CD105 antibodies
 CD105_T- MVD in tumor mucosa stained with anti-CD105 antibodies

Figure 3 Graphic representation of vascular density (microvessel density) obtained from CD31-immunostained images and CD105-immunostained images of normal mucosa in comparison with tumor mucosa (vessels/mm²). MVD: Microvessel density.

dependent on fixation^[17]. In the present study, a qualitative comparison between the two methods (CLE vs IHC) lead to similar results. The major advantage of the CLE method is time efficacy and less artifacts in comparison to common IHC regarding the processing techniques^[20].

Due to CD105 specific overexpression in malignant vessels, the endoglin antibodies for tumor imaging have the potential of becoming an optimal target for anticancer treatment, to improve rectal cancer diagnosis and to monitor the therapy^[4]. As there are already studies regarding tumor aggressiveness and the prognostic value of vascular density on IHC when using anti-CD105 antibodies, CLE opens the possibility of applying CD105 targeted therapy, which until now was only tested *in vitro* and on animal models, to *in vivo* human subjects. Its luminal distribution on newly formed vessels makes CD105 readily accessible for the antibodies and, consequently, an interesting candidate for CLE *in vivo*^[11].

CLE monitoring of the relationship between endothelial presence of CD105 and survival of patients would be of great interest. In our group of patients, we observed an inter-patients variation in MVD endoglin expression in tumor tissue. On one hand, this could be related to the tumor grading or staging, as an increase in MVD was demonstrated by using CD105 during progressive stages of colorectal carcinogenesis^[21]. On the other hand, reduced endoglin expression could also be caused by a decreased tumor vascularization in endoglin haploinsufficiency cases^[22]. There are also differences in reactivity to endothelial cells depending on tumor localization^[22-24]. However, in colorectal cancer, other studies showed that, with cancer progression, endoglin signaling was lost in most of the epithelial cancer cells which became refractory to the TGF-β growth inhibiting properties^[25-29]. All these factors could lead to differences in diagnostic, prognostic and therapeutic efficacy.

To our knowledge, no other studies using fluorescently-labeled CD105 with CLE imaging in patients with rectal cancer have been reported prior to this study. A larger number of patients is needed to study the correlation between MVD and tumor differentiation grade and stage, with great potential for CD105 staining combined with CLE analysis to provide a more reliable evaluation of the angiogenetic status of patients with colorectal cancer. Other studies are needed to investigate if the same CLE method could be applied to other tumor types.

In conclusion, our data showed that CLE using CD105 targeted antibodies for tumor vascular network imaging is feasible and, moreover, that this proangiogenic molecule represents a more specific marker for rectal cancer neoangiogenesis than commonly used panendothelial markers.

COMMENTS

Case characteristics

The main clinical signs the patients showed were alternating diarrhea and constipation, accelerated intestinal transit, recent constipation, unintended weight loss, rectal bleeding, abdominal pain or discomfort.

Clinical diagnosis

Only three patients accused rectal bleeding as a single symptom, also confirmed by the physical examination (digital rectal examination).

Differential diagnosis

Other common digestive diseases such as hemorrhoidal disease, inflammatory bowel disease or irritable bowel syndrome were excluded.

Laboratory diagnosis

Seven patients presented nonspecific laboratory tests findings such as moderate elevated hematological values of erythrocyte sedimentation rate (three patients), slightly elevated white blood cells count (two patients) and moderate anemia (two patients); two patients presented slightly elevated values of both tumor markers CEA and CA19-9, while three of them had only slightly elevated CEA values.

Imaging diagnosis

Computed tomography scan excluded the presence of metastases in all ten patients and described rectal wall thickening in four cases.

Pathological diagnosis

Histological examination of endoscopic samples revealed moderately differentiated adenocarcinoma (G2) in five cases, well differentiated adenocarcinoma in two cases (G1), mixed subtypes in three cases (G1/G2- two cases, G1 with mucinous areas - one case).

Treatment

Tissue samples from patients with histological diagnosis of rectal cancer were collected during colonoscopy before undergoing surgical resection or neoadjuvant therapy.

Term explanation

Immunofluorescence: Targeting markers of angiogenesis in association with confocal laser endomicroscopy (CLE) examination; Panendothelial markers: Present equal staining intensity in both small and large vessels and comparable reactivity in both frozen and paraffin sections, with obvious disadvantages regarding antigen specificity and sensitivity. They can identify all types of blood vessels in a given tissue sample, irrespective of being mature or immature.

Experiences and lessons

Specific imaging and quantification of tumor microvessels are feasible in human rectal cancer using CLE examination and CD105 immunostaining of fresh tissue samples. A larger number of patients is needed to study the correlation between MVD and tumor differentiation grade and staging, with great potential for CD105 staining combined with CLE analysis to provide a more reliable evaluation of the angiogenetic status of patients with colorectal cancer. CLE monitoring of the relationship between endothelial presence of CD105 and survival of patients would be of great interest.

Peer-review

The manuscript has original results. This is an interesting study on "Tumor neoangiogenesis detection by confocal laser endomicroscopy and anti-CD105 antibody: Pilot study". The research is limited to a small number of patients and, for this reason, this study should be considered pilot.

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Does St. John's Wort cause regression in gastrointestinal system adenocarcinomas?

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Abstract

St. John's Wort (SJW) is an old herb which has long been consumed widely for its anti-inflammatory, antiviral, and anti-depressive properties. Here we present a detailed clinical evaluation of three cases (two colon and one duodenal adenocarcinoma) with remarkable and intensive lymphoplasmocytic host reaction, at the basal part of tumor, intensive fibrosis, giant cells, plasma cell increase in lymph nodes and few giant cells in germinal centers in resection specimens. The observation of similar host reaction in those tumors having otherwise usual appearance was interesting. None of the cases received neoadjuvant chemoradiotherapy or additional treatment before surgery but only SJW. These cases are presented to increase the awareness about such cases. Further research is needed to reveal the possible effect of SJW, which has long been consumed for different treatment purposes, on human tumors.

Key words: St. John's Wort; Adenocarcinoma; Giant cell

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Core tip: St. John's Wort (SJW) is a well known herb that was used in treatment of many diseases during centuries. In this article we offer a perspective about the anti-tumoral effect of SJW with possible mechanisms and pathological data in three gastrointestinal cancer cases, where usage of SJW was identified in history questioning because of tumor regression and intensive inflammatory host reaction following pathological examination.

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INTRODUCTION

St. John's Wort (SJW) is a substance widely used for its anti-inflammatory, antiviral, antidepressant and anticancer effects^[1-3]. It contains two active compounds: Firstly, hyperforin is responsible for anti-depressant activity and has been reported to be also a good inhibitor of leukocyte elastase, exerting forceful inhibition of *in vitro* tumor cell chemoinvasion and reduction of neovascularization and metastasis formation *in vivo*^[4]. Secondly, hypericin is responsible for photocytotoxic effects *in vivo* and *in vitro*. The *in vivo* and *in vitro* photodynamic activities of hypericin as a photosensitizer mainly to induce a very potent anti-tumoral effect^[5]. Also, the anti-retroviral feature of hypericin has been demonstrated *in vitro* and in animal models^[6].

CASE REPORT

Case 1

A fifty-nine years old male patient has undergone colonoscopy for anemia evaluation, which revealed a tumoral mass in the cecum. The histological diagnosis of the biopsy was adenocarcinoma and no distant metastasis was detected in further clinic radiological investigation. Right hemicolectomy was performed and a pathological examination of surgical material revealed a cecal ulcero-vegetative mass which was 7 cm × 6 cm × 5 cm in size. The tumor invaded through muscularis propria to subserosal fat tissue and was consistent with a moderately differentiated adenocarcinoma. Notably, it showed fibrosis and inflammatory cell infiltration in the transitional zone between deep intestinal layers and normal mucosa, which was easily detectable even under low magnification (Figure 1A). Under higher magnifications, inflammatory cell infiltration was rich in plasma cells and lymphocytes, scattered eosinophils, polymorphonuclear leucocytes and few giant cells were also noted focally (Figure 1B). The inflammatory reaction and fibrosis were surrounding the tumor, as if they were trying to prevent the penetration of the tumor into deep tissue. Most of these lymphocytes were T lymphocytes and showed cytotoxic T cell (CD8⁺) phenotype on immunohistochemical examination (Figure 1C). CD20 and CD4 stains were almost negative. Plasma cells were stained positive with CD138 and polytypic with kappa/lambda. Two of 18 lymph nodes dissected from mesentery showed few tumor cells located in sub-capsular sinuses while no gross metastasis was detected. Notably, germinal centers of some lymph nodes had giant cells and increased number of plasma cells in inter-follicular areas (Figure 2A and B). Giant cells were CD68 positive on immunohistochemical examination (Figure 2C). These features were suggestive of changes

developed secondary to neoadjuvant chemotherapy/radiotherapy, but the patient's past medical history did not reveal such treatment. His detailed medical history was taken and when he was also asked for the usage of some alternative treatments, he mentioned usage of SJW for other complaints such as diabetes, dyspepsia. He has been consuming SJW tea in the morning for five years, then he had used SJW oil regularly (one teaspoon in the morning) for two years and he has been using it regularly (one teaspoon in the morning and evening) for the last three years. Medical records of the patient revealed that he had chemotherapy for six months after surgery (FOLFOX-4 protocol once every 14 d) and no recurrence or metastasis were detected during two years of follow up.

Case 2

A fifty-eight years old female patient has undergone colonoscopy for anemia evaluation, which revealed a tumoral mass in the transverse colon. No distant metastasis was detected and the patient had undergone colectomy. On macroscopic examination of colectomy specimen, an ulcerovegetative tumor infiltrating all layers of intestinal wall was detected, measuring 3.5 cm × 2.5 cm × 2 cm in size. Microscopic examination revealed moderately differentiated adenocarcinoma with mixed inflammatory cell infiltration rich in lymphoplasmacytes on the background (Figure 3). Eosinophils were also prominent with a few giant cells. Fourteen lymph nodes, dissected from mesentery, were reactive. However, one of the lymph nodes had an increased number of plasma cells and giant cells in germinal center of the follicle. Immunohistochemical characteristics were similar to that of the first case. Based on the experience of the morphology of the first case, the patient was also asked for usage of alternative treatments. To our surprise she has also mentioned usage of SJW oil (one teaspoon in the morning on an empty stomach) for 1.5 mo. Her medical records revealed that she has refused chemotherapy and followed-up without treatment. No recurrence or metastases were detected during the first six months of follow-up period.

Case 3

A duodenal mass was detected in a 73 years old male patient with the complaints of abdominal pain and weight loss. The biopsy was reported as adenocarcinoma. Since there was no distant metastasis, surgery was recommended. Although, he initially refused surgery he agreed to an operation three months later. On his second admission to hospital it was seen that the tumor size had somewhat reduced during this three months period. When a detailed medical history was taken, it was also revealed there was daily use of SJW oil of one teaspoon for the last three months. On macroscopic examination, an ulcero-vegetative ampullary tumor was observed measuring 3.8 cm × 2.5 cm × 2.5 cm in size, involving all layers of duodenum and infiltrating the pancreas.

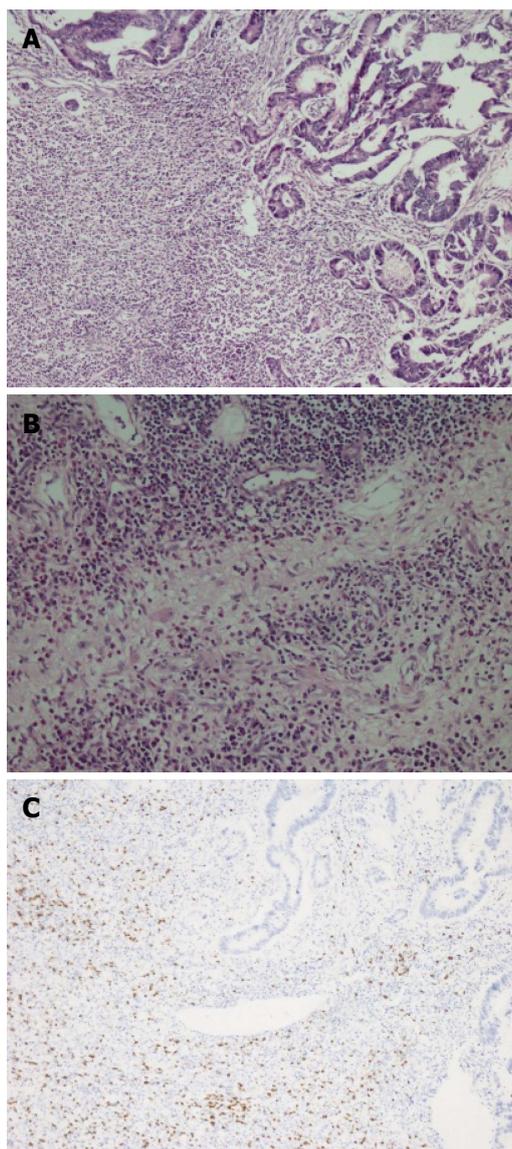


Figure 1 Adenocarcinoma. A: Adenocarcinoma showing fibrosis and inflammatory cell infiltration in the tumor base (HE \times 10); B: Inflammatory cell infiltration consisting of plasma cells, lymphocytes, eosinophils and PNLs was seen in these areas (HE \times 20); C: Inflammatory cell infiltration observed in the basis of tumors was rich in CD8 positive T lymphocytes (anti-CD8, \times 5).

Areas showing the characteristics of moderately differentiated adenocarcinoma and mixed inflammatory cell infiltration rich in PNLs were observed. Similar to the previous two cases, eosinophils were also present and most prominent in the basilar parts of these areas (Figure 4A). The most common lymphocytic component was again CD8 positive T cells immunohistochemically (Figure 4B). Giant cells were seen in all layers, being more prominent in the areas in the vicinity of serosal surfaces (Figure 5A and B). These cells were stained with CD68 immunohistochemically (Figure 5C). Additionally, extensive perineural infiltration and intra-lymphatic tumoral thrombi were present. Four of 12 lymph nodes dissected from surrounding adipose tissue showed metastasis. The patient died due to anastomosis leakage and bleeding complications after surgery.

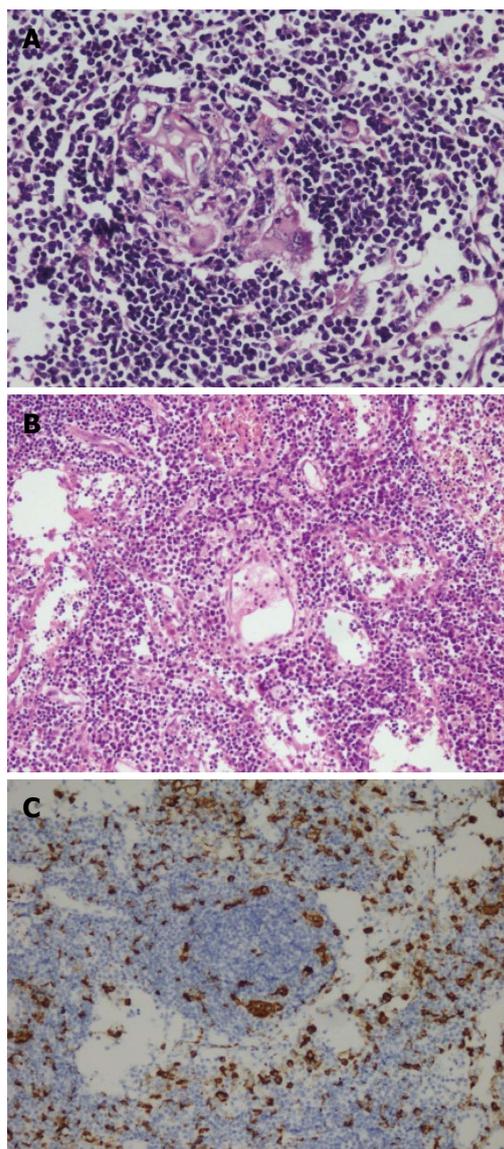


Figure 2 Germinal centers of some lymphoid follicles had giant cells and increased number of plasma cells in inter-follicular areas. A: Giant cells were detected in germinal centers of some lymph nodes (HE \times 20); B: Interfollicular areas of some lymph nodes had increased number of plasma cells (HE \times 10); C: Giant cells were stained with CD68 immunohistochemically (anti-CD68 \times 10).

DISCUSSION

Hypericum perforatum, known as SJW, is a plant of the genus *Hypericum* and a herb with antidepressant feature and effective anti-inflammatory characteristics as an arachidonic acid/5-lipoxygenase inhibitor and COX-1 inhibitor^[7]. In many countries, its drug form is available and sold out as an over the counter drug without prescription. It is most commonly used for the treatment of depression. Hyperforin is responsible for anti-depressant activity. The hyperforin constituent of SJW is TRPC6 receptor agonist and therefore, it causes noncompetitive reuptake inhibition of monoamines (especially, dopamine, norepinephrine, and serotonin), gamma-aminobutyric acid and glutamate^[8]. Hyperforin

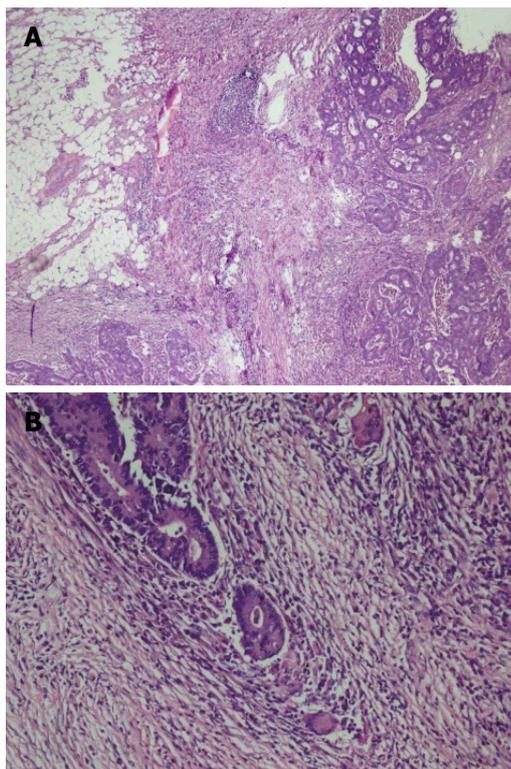


Figure 3 Moderately differentiated adenocarcinoma with mixed inflammatory cell infiltration rich of lymphoplasmacytes, eosinophils and few giant cells (A and B) (HE × 5, HE × 20).

inhibits reuptake of these neurotransmitters by increasing intra-cellular sodium ion amounts. Furthermore, SJW is known to downregulate the β_1 adrenoceptor and upregulate postsynaptic 5-HT_{1A} and 5-HT_{2A} receptors which are serotonin receptor^[9]. A 2008 Cochrane review of 29 clinical trials inferred that it was superior to placebo in cases with major depression^[10]. With respect to the National Center for Complementary and Integrative Health of the National Institutes of Health, it "may help some types of depression, though the evidence is not definitive"^[11]. Hyperforin is also an anti-inflammatory complex with anti-angiogenic, antibiotic, and neurotrophic estates^[12]. Moreover, it prevents neutrophil activation of matrix metalloproteinase-9 (MMP9) mobility and recruitment. Anti-proliferative and anti-metastatic feature has also been associated to down-regulation of NF- κ B and its regulated molecules for example survivin and MMP9^[13].

Hypericin is a photosensitive compound synthesized by SJW, and possesses properties suitable for photodynamic therapy (PDT). PDT is a carcinoma treatment methodology abusing non-toxic photosensitizer specifically localized in tumor tissue and its targeted activation with light. Thus, it leads to reactive oxygen kinds production and causes photochemically caused cell death^[14]. The response to PDT depends on the photosensitizer's features, the illumination circumstances and the oxygenation conditions of the tissue^[15]. It was also observed that hypericin blocks cell cycle at G2/M control point in colon cancer cell culture^[16] Another

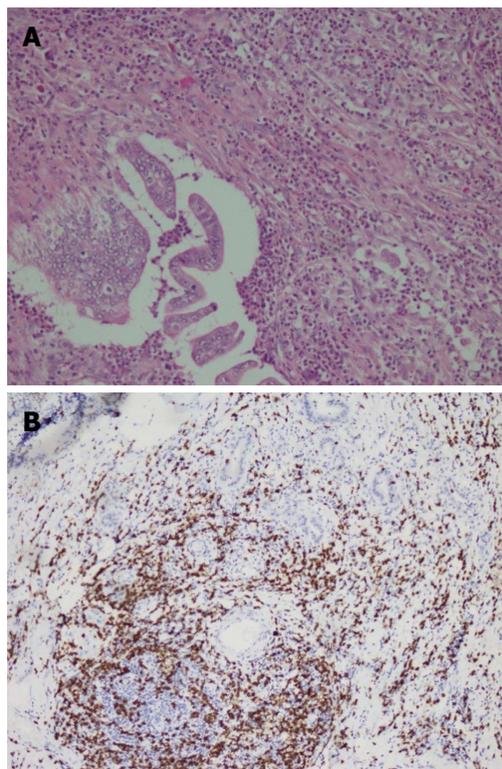


Figure 4 Adenocarcinoma showing mixed inflammatory cell infiltration rich in eosinophils and T - lymphocytes. A: Moderately differentiated adenocarcinoma showing mixed inflammatory cell infiltration rich in eosinophils and T - lymphocytes (HE × 20); B: The most prominent cellular component on immunohistochemical examination was CD8 positive T - lymphocytes (CD8 × 10).

colon cancer cell culture study showed re-localisation of apoptosis-inducing factor on the nucleus after hypericin treatment. Thus the anti-tumor effect of hypericins likely resulted from its apoptosis stimulating effect and its anti-proliferative effect by decreasing Ras protein^[17].

Besides its many benefits there are also some studies in the literature showing its undesired adverse effects. Development of hepatotoxicity, cirrhosis and alteration of dosage properties and bioavailability of some drugs are some of its important adverse effects^[18]. SJW has been displayed to cause a lot of drug interactions. Its effects are due to cytochrom P4503A enzyme activation and P-glycoprotein. This drug metabolizing enzyme induction effects in the raised metabolism of some drugs, such as indinavir, cyclosporine and oral contraceptives leading to reduced plasma density and possible clinical impact^[19]. The main constituent thought to be responsible is hyperforin. In an other study it has been shown that the amount of intestinal and hepatic cytochrome P4503A and intestinal P-glycoprotein are increased by the short term usage of SJW in humans and rats^[20]. Bone marrow necrosis, orofacial dystonia and radiation recall dermatitis are reported as less often adverse effects^[21-23].

In an experimental study by Martarelli *et al*^[24], on hormone independent human prostate cancer cells, it was shown that Hypericum perforatum extract decreased tumor cell proliferation by inhibiting serotonin

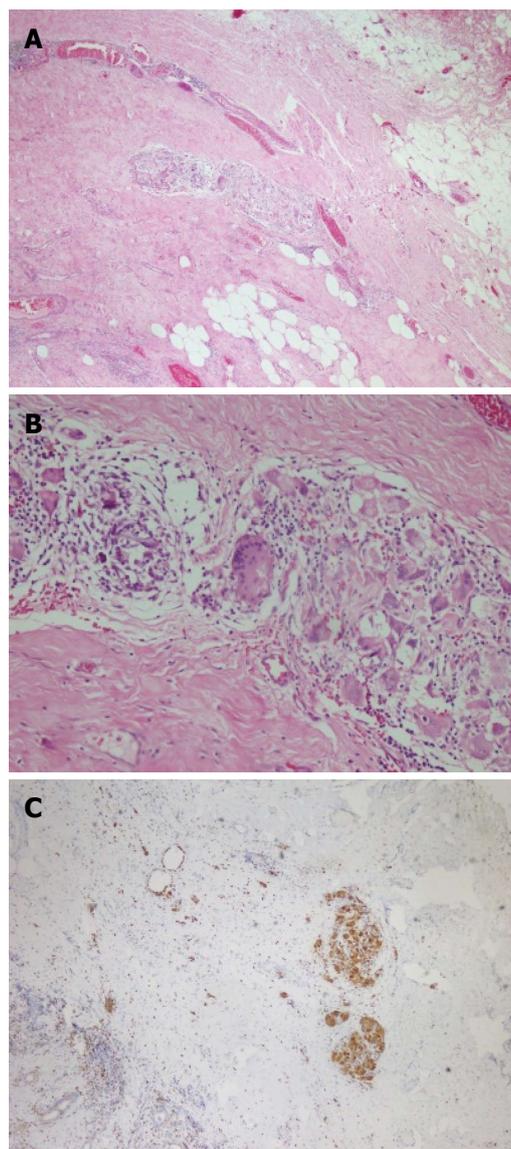


Figure 5 Giant cells in the areas beneath serosal surface and stained with CD68 immunohistochemically. A, B: Giant cells were seen in the areas beneath serosal surface (HE $\times 5$, HE $\times 20$); C: CD68 positivity in giant cells (anti-CD68 $\times 10$).

reuptake and showed cytotoxic effects. In addition, it decreased frequency of local lymph node metastasis when compared to the control group^[24]. There are experimental studies on the effects of SJW on colon, bladder and prostate carcinomas. In an experimental study by Dongre *et al.*^[25], the effect of Hypericum hookerianum on carcinomas was evaluated and it was found that serum neutrophil, lymphocyte, eosinophil, hemoglobin and erythrocyte values were closer to normal range when compared to control group^[25]. In our cases, neutrophils and histiocytes-giant cells were more prominent early in the course (2nd and 3rd cases), while plasma cells, histiocytes and lymphocytes (cytotoxic CD8+) took over during chronic usage (1st case). Similar to the study by Dongre *et al.*^[25], morphological properties of our 2nd and 3rd cases may be due to acute effects (15 d) of Hypericum. In our case with long term SJW use,

extensive host reaction and tendency to form barrier against tumor were remarkable and we interpreted it as a morphological sign of its anti-tumor response. Although the exact mechanism of these events is unknown, it may be a result of a chain of events triggered immunologically.

The aim of this presentation is not recommending SJW as a substitute for cancer treatment. The observations presented herein reflect the histological findings of only three cases and not enough to make a precise conclusion on its effects. We don't know yet either whether all cases using SJW present similar morphology or whether any other substances also induce a similar tumor-host reaction. We present these cases only to share our observations and draw attention to its possible effects on human tumor-host interaction. Further dedicated research is needed to unveil these questions.

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COMMENTS

Case characteristics

The authors present a detailed clinical evaluation of three intestinal adenocarcinoma cases which used St. John's Wort (SJW).

Clinical diagnosis

Patients have undergone colonoscopy for anemia, abdominal pain and weight loss evaluation, which revealed a tumoral mass in the colon and duodenum.

Pathological diagnosis

Biopsy and resection materials of all three cases were evaluated morphologically and immunohistochemically. Inflammatory cell population was rich in plasma cells and lymphocytes. In patients that used SJW in early stages polymorphonuclear leucocytes were significant. In patient those who used SWJ for long periods fibrosis and lymphoplasmositic cell infiltration was remarkable. Lymphocytes stained predominantly CD8 positive phenotype immunohistochemically. Plasma cells were found to be kappa/lambda polytypic nature.

Treatment

Case revealed that he had chemotherapy for six months after surgery (FOLFOX-4 1 protocole once every 14 d).

Experiences and lessons

The aim in this study is not about to recommend usage of SJW. The authors only want to indicate their awareness of SJW usage after pathologic examination. The authors thing that these pathologic features might flash the benefits of SJW that had been discussed for ages.

Peer-review

This manuscript reports the clinico-pathological findings of three adenocarcinoma cases treated with SJW.

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