

# World Journal of *Gastrointestinal Oncology*

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2016-2019

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*WJGO* covers topics concerning carcinogenesis, tumorigenesis, metastasis, diagnosis, prevention, prognosis, clinical manifestations, nutritional support, molecular mechanisms, and therapy of benign and malignant tumors of the digestive tract. The current columns of *WJGO* include editorial, frontier, diagnostic advances, therapeutics advances, field of vision, mini-reviews, review, topic highlight, medical ethics, original articles, case report, clinical case conference (Clinicopathological conference), and autobiography. Priority publication will be given to articles concerning diagnosis and treatment of gastrointestinal oncology diseases. The following aspects are covered: Clinical diagnosis, laboratory diagnosis, differential diagnosis, imaging tests, pathological diagnosis, molecular biological diagnosis, immunological diagnosis, genetic diagnosis, functional diagnostics, and physical diagnosis; and comprehensive therapy, drug therapy, surgical therapy, interventional treatment, minimally invasive therapy, and robot-assisted therapy.

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2016 Colorectal Cancer: Global view

## Clinical efficacy and drug resistance of anti-epidermal growth factor receptor therapy in colorectal cancer

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### Abstract

Colorectal cancer (CRC) ranked third in cancer related death and its incidence has been increasing worldwide. In recent decades important therapeutic advances have

been developed in treatment of metastatic CRC (mCRC), such as monoclonal antibodies against epidermal growth factor receptor (anti-EGFR), which provided additional clinical benefits in mCRC. However, anti-EGFR therapies have limited usage due to approximately 95% of patients with *KRAS* mutated mCRC do not response to anti-EGFR treatment. Thus, *KRAS* mutation is predictive of nonresponse to anti-EGFR therapies but it alone is not a sufficient basis to decide who should not be received such therapies because; approximately fifty percent (40%-60%) of CRC patients with wild-type *KRAS* mutation also have poor response to anti-EGFR based treatment. This fact leads us to suspect that there must be other molecular determinants of response to anti-EGFR therapies which have not been identified yet. Current article summarizes the clinical efficacy of anti-EGFR therapies and also evaluates its resistance mechanisms.

**Key words:** Colorectal cancer; Epidermal growth factor receptor; *KRAS* mutation; Anti-epidermal growth factor receptor antibody; Drug resistance

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**Core tip:** Molecular targeting agents, such as monoclonal antibodies against epidermal growth factor receptor (anti-EGFR), provide additional clinical benefits in metastatic colorectal cancer (CRC). However, anti-EGFR therapies have limited usage due to approximately 95% of patients with *KRAS* mutated metastatic CRC do not response to anti-EGFR treatment. Thus, *KRAS* mutation is predictive of nonresponse to anti-EGFR therapies but it alone is not a sufficient basis to decide who should not be received such therapies because approximately fifty percent (40%-60%) of CRC patients with wild-type *KRAS* mutation also have poor response to anti-EGFR based treatment. This fact leads us to suspect that there must be other molecular determinants of response to anti-EGFR therapies which have not been identified yet. Current article summarizes the clinical efficacy of

anti-EGFR therapies and also evaluates its resistance mechanisms.

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## INTRODUCTION

Colorectal cancer (CRC) is one of the most commonly diagnosed cancers in both genders (second in females and third in males)<sup>[1]</sup>; and it is also ranked third in cancer related death in both genders with approximately 15.1 deaths per 100000<sup>[2,3]</sup>. While the mortality rate of CRC has been decreasing in Western countries, its incidence has been increasing worldwide, except United States<sup>[4]</sup>. Despite of decreasing death rates, approximately fifty percent of patients with CRC are diagnosed with metastatic disease in their initial assessments<sup>[5]</sup>.

Several chemotherapeutic agents [*e.g.*, pyrimidine analogs (*e.g.*, 5-fluorouracil), platinum-based antineoplastic agents, and topoisomerase inhibitors] have become available in the past and thus survival rate of CRC patients significantly increased. Also, recently developed molecular targeting agents, such as monoclonal antibodies against epidermal growth factor receptor (EGFR) (*e.g.*, cetuximab and panitumumab)<sup>[6,7]</sup>, provided additional clinical benefits in metastatic CRC (mCRC)<sup>[8-10]</sup>.

In several types of cancer, including CRC, EGFR is overexpressed or amplified. Monoclonal antibodies keep EGFR in an inactive state by binding to and occluding the ligand-binding site of EGFR when the ligand is unbound (acting as competitive antagonists). This leads an inhibition of intracellular signaling pathways of EGFR (RAS/RAF/MAPK and PI3K/PTEN/AKT) that involved in several cellular activities including cell proliferation, motility, invasion, and survival<sup>[11]</sup>.

*KRAS*, a signal transduction molecule, transduces the signal from ligand-bound EGFR to the nucleus. Prospective randomized trials elucidated that presence of mutation in *KRAS* gene leads to non-response to anti-EGFR based treatment<sup>[6-10,12-14]</sup>. Therefore, it is highly recommended that *KRAS* mutation status should be known before initiating anti-EGFR based treatment in mCRC patients. Thus, *KRAS* mutation is predictive of nonresponse to anti-EGFR therapies but it alone is not a sufficient basis to decide who should not be received such therapies because almost 60% of CRC patients with wild-type (WT) *KRAS* mutation also have poor response to anti-EGFR based treatment<sup>[15]</sup>. This fact leads us to suspect that there must be other molecular determinants of response to anti-EGFR therapies which have not been identified yet. Current article summarizes

the clinical efficacy of anti-EGFR therapies and also evaluates its resistance mechanisms.

## CLINICAL EFFICACY OF ANTI-EGFR ANTIBODY IN MCRC

Both Cetuximab, an IgG1 type chimeric monoclonal antibody, and panitumumab, an IgG2 type fully human monoclonal antibody, induce apoptosis by inhibiting downstream signaling pathways of EGFR (RAS/RAF/MAPK and PI3K/PTEN/AKT). Also, these molecules, especially cetuximab, activate antibody-dependent cellular cytotoxicity which consequently improves their cytotoxic actions and therapeutic effectiveness<sup>[16]</sup>.

The recent published randomized non-inferiority phase III study showed median overall survival (OS) was similar in patients with mCRC who treated with panitumumab alone and with cetuximab alone<sup>[17]</sup>. The incidences of any grade and grade 3-4 adverse events were similar in both treatment groups, however, the incidence of grade 3-4 infusion reaction was lower and grade 3-4 hypomagnesaemia was higher in panitumumab group than in cetuximab group<sup>[18]</sup>. In some studies, cetuximab and panitumumab have been investigated in combination with FOLFIRI (folinic acid, fluorouracil, and irinotecan) and FOLFOX (folinic acid, fluorouracil, and oxaliplatin) as initial therapy option for treatment of mCRC. And a meta-analysis of these 14 randomized studies concluded that there is a clear benefit to the use EGFR inhibitors in patients with WT *KRAS* mCRC<sup>[18]</sup>. An updated analysis (CRYSTAL trial) demonstrated that adding cetuximab to FOLFIRI as first-line therapy improves survival in patients with WT *KRAS* mCRC<sup>[19]</sup>. Also another randomized phase III study showed that the combination of panitumumab and FOLFIRI significantly improves progression-free survival (PFS), but not OS, in mCRC patients with WT *KRAS*<sup>[9]</sup>. Three other trials have evaluated the addition of cetuximab to FOLFOX in first line treatment of patients WT *KRAS* mCRC. In randomized phase II OPUS study, combination of FOLFOX and cetuximab was associated with increased response rate and PFS. However, this treatment had no benefit in median OS<sup>[12]</sup>. In the Medical Research Council (MRC) COIN study, adding cetuximab to oxaliplatin-based chemotherapy in patients with WT *KRAS* mCRC increased response rate with no benefit in PFS or OS<sup>[20]</sup>. Similarly, another phase III study (NORDIC-VII) showed that cetuximab did not add significant benefit when combined with FOLFOX in treatment of patients with WT *KRAS* mCRC<sup>[21]</sup>. In contrast to earlier studies, the recent published randomized phase III CALGB/SWOG 80405 trial demonstrated that addition of cetuximab to FOLFOX or FOLFIRI chemotherapy was significantly increased PFS and OS in treatment of patients with all RAS-WT mCRC<sup>[22]</sup>. In the study by Douillard *et al.*<sup>[23]</sup> (the PRIME study), which compared panitumumab plus FOLFOX and FOLFOX alone in mCRC patients with WT *KRAS*/NRAS,

panitumumab plus FOLFOX group showed a statistically significant improvement in PFS and OS.

Based on this knowledge, all patients with newly diagnosed mCRC should be tested for *KRAS* mutation. Also screening of *KRAS* mutations seems essential in mCRC patients to initiate anti-EGFR based treatment. But *KRAS* mutation alone is not a sufficient basis to decide who should not be received such therapies because almost 60% of CRC patients with WT *KRAS* mutation also have poor response to anti-EGFR based treatment<sup>[15]</sup>. Also 5%-9% of CRC patients have a specific mutation in *BRAF* gene (V600E)<sup>[24,25]</sup>. But the use of *BRAF* as a predictive marker for response to anti-EGFR based treatment is unclear. This fact leads us to suspect that there must be other molecular determinants of response to anti-EGFR therapies which have not been identified yet.

## MECHANISMS OF RESISTANCE TO ANTI-EGFR TREATMENT

### *KRAS/NRAS/BRAF mutations*

Approximately 40% of CRC patients have mutation in exon 2 of the coding of the *KRAS* gene<sup>[26,27]</sup>. Prospective randomized studies showed that *KRAS* mutations are predictive of non-response to anti-EGFR based treatment<sup>[6-10,12-14]</sup>. These studies showed that tumors with a mutation in codon 12 or 13 of exon 2 of the *KRAS* gene are essentially unresponsive to anti-EGFR based treatment. Recent studies demonstrated that mutation in *KRAS* outside of exon 2 and mutation in *NRAS* are also predictive for unresponsiveness to anti-EGFR treatment<sup>[23,28]</sup>. Recently, a study assessed the superiority of FOLFOX plus panitumumab to FOLFOX alone according to *RAS* (*KRAS* or *NRAS*) or *BRAF* (B-type Raf kinase) mutation status. In that study, 17% of patients with non-mutated *KRAS* exon 2 had other *RAS* mutation which has been shown to be associated with inferior survival with panitumumab plus FOLFOX treatment<sup>[23]</sup>. Cetuximab or panitumumab treatments seem to be eligible for selected patients with WT *KRAS* tumors who also have *BRAF*-WT mutations<sup>[29]</sup>.

*BRAF* oncogene encodes *BRAF* protein which is a member of *RAS/RAF/MAPK* (mitogen-activated protein kinase) pathway<sup>[27]</sup>. Mutations in *BRAF* and *KRAS* genes are mutually exclusive<sup>[30]</sup>. Approximately 9% (5%-9%) of patients with CRC have a mutation in *BRAF* gene (V600E)<sup>[24,25]</sup>. CRYSTAL and PETACC-3 studies demonstrated that patients with *BRAF* mutation have a worse prognosis than those with the WT tumors<sup>[19,31]</sup>. However, the use of *BRAF* as a predictive marker is unclear. CRYSTAL study elucidated that *BRAF* mutation does not seem to be strong predictive biomarker for the addition cetuximab to FOLFIRI in the first line treatment of WT mCRC<sup>[19]</sup>. Also, subset analysis of the PRIME study found that *BRAF* mutation indicates poor prognosis but it may not be predictive of the benefit of adding panitumumab to FOLFOX in the first line treatment of

mCRC<sup>[8]</sup>. Tol *et al*<sup>[25]</sup> demonstrated that *BRAF* mutation is a negative indicator for prognosis in mCRC patients and in contrast to *KRAS* mutation, this feature is not restricted to the outcome of the cetuximab. In subsequent lines of therapy elucidated that *BRAF* mutation is a marker of resistance to anti-EGFR treatment in the non-first line setting of mCRC<sup>[29,32,33]</sup>.

Vemurafenib is orally administered selective inhibitor of *BRAF* V600 kinase but using it alone in *BRAF*-mutated CRC patients results insufficient activity<sup>[34]</sup>. Studies suggested that feedback activation of EGFR signaling might be responsible of the resistance to Vemurafenib in CRC<sup>[35,36]</sup>. In a cohort study by Hyman *et al*<sup>[37]</sup>, median PFS and OS did not change with vemurafenib monotherapy or vemurafenib and cetuximab combination therapy in patients with CRC (Table 1).

## HYPERACTIVATION OF PI3K-PTEN AXIS

Interestingly, 41% of patients do not have *KRAS* or *BRAF* mutation, and they do not respond to anti-EGFR treatment<sup>[29]</sup>. Some studies suggested that anti-EGFR downstream pathways other than *RAS/RAF/MAPK* [e.g., phosphoinositide 3-kinase/phosphatase and tensin homolog pathway (*PI3K/PTEN*)], might be responsible for the resistance to anti-EGFR based therapy. It was shown that mutation in *PI3KCA* (phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha) or loss of *PTEN* is associated with resistance to anti-EGFR based treatment<sup>[38-40]</sup>. Tural *et al*<sup>[41]</sup> investigated the effect of oncogenic activation of the members of EGFR downstream pathways (e.g., *PI3K*, *PTEN* and *BRAF*) on response to anti-EGFR therapy. They have showed that *PI3K* expression and *PTEN* loss might be used as predictive to the response to anti-EGFR treatment in mCRC patients with WT *KRAS*. According to this study, *BRAF* negative, *PTEN* expressing and *PI3K* non-expressing CRCs have higher response rate and longer PFS and OS than all others. Most studies evaluated *PI3K* mutation in response to cetuximab based treatments in CRC patients<sup>[38,42-45]</sup>. In these studies, *PI3K* mutation has been suggested as predictive of resistance to anti-EGFR-based therapies. On the other hand, the role of *PI3K* mutation in response is conflict. Perrone *et al*<sup>[38]</sup> has investigated *PI3KCA* gene mutations in CRC patients and they suggested that mutation in *PI3KCA* causes resistance to anti-EGFR therapies. Also Prenen *et al*<sup>[45]</sup> analyzed *PI3KCA* and *KRAS* mutations status in chemo-refractory mCRC patients who treated with anti-EGFR based treatment and they did not determine any correlation between *PI3KCA* mutation and response to anti-EGFR treatment. Nevertheless, most of studies have suggested that *PTEN* inactivation is a negative predictor of response to anti-EGFR therapy<sup>[38-40]</sup>. Bardellie *et al*<sup>[46]</sup> stated that *PI3K* expression and *PTEN* loss are correlated with decreased survival and are predictors of poor response to anti-EGFR therapy. Based on these studies, it is well known that activating mutation in *PI3KCA* or inactivation of *PTEN* phosphates

**Table 1 Clinical trials of targeted agents in combination with chemotherapy as first-line treatments for metastatic colorectal cancer**

Ref.	Year	Population	Patient number	Regimen	Median PFS (mo)	P <sup>1</sup>	Median OS (mo)	P <sup>1</sup>	Response rate (%)	P <sup>1</sup>
CRYSTAL <sup>[19]</sup>	2009	All	599	FOLFIRI	8.0	0.048	18.6	0.31	38.7	0.0038
			599	FOLFIRI + Cetuximab	8.9		19.9		46.9	
		KRAS WT	350	FOLFIRI	8.4	0.0012	20	0.0093	39.7	< 0.001
		subgroup	316	FOLFIRI + Cetuximab	9.9		23.5		57.3	
		KRAS MT	183	FOLFIRI	7.7	0.26	16.7	0.75	36.1	0.35
OPUS <sup>[12]</sup>	2009	subgroup	214	FOLFIRI + Cetuximab	7.4		16.2		31.3	
		All	168	FOLFOX4	7.2	0.62	18	0.91	36	0.064
			169	FOLFOX4 + Cetuximab	7.2		18.3		46	
		KRAS WT	97	FOLFOX4	7.2	0.0064	18.5	0.39	34	0.0027
		subgroup	82	FOLFOX4 + Cetuximab	8.3		22.8		57	
COIN <sup>[20]</sup>	2011	KRAS MT	59	FOLFOX4	8.6	0.0153	17.5	0.2	53	0.029
		subgroup	77	FOLFOX4 + Cetuximab	5.5		13.4		34	
		KRAS WT	367	FOLFOX/XELOX	8.6	0.60	17.9	0.68	57	0.049
		group	362	FOLFOX/XELOX + Cetuximab	8.6		17		64	
		KRAS WT	127	FOLFOX	9.2	0.056	-	-	-	-
NORDIC-VII <sup>[21]</sup>	2012	group	117	FOLFOX + Cetuximab	9.0		-		-	
		KRAS WT	240	XELOX	8.0	0.56	-	-	-	-
		group	245	XELOX + Cetuximab	8.4		-		-	
		KRAS MT	268	FOLFOX/XELOX	-	-	14.8	0.8	-	-
		group	297	FOLFOX/XELOX + Cetuximab	-		13.6		-	
CALGB/SWOG <sup>[22]</sup>	2014	All	185	Nordic FLOX (control group)	7.9	-	20.4	-	41	-
			194	FLOX + Cetuximab	8.3	0.31	19.7	0.67	49	0.15
			187	intermittent FLOX + Cetuximab	7.3	NA	20.3	0.79	47	NA
		KRAS WT	97	Nordic FLOX (control group)	8.7	-	22	-	47	-
		subgroup	97	FLOX + Cetuximab	7.9	0.66	20.1	0.48	46	0.89
PRIME <sup>[8]</sup>	2010		109	intermittent FLOX + Cetuximab	7.5	NA	21.4	0.66	51	NA
		KRAS MT	58	Nordic FLOX (control group)	7.8	-	20.4	-	40	-
		subgroup	72	FLOX + Cetuximab	9.2	0.07	21.1	0.89	49	0.31
			65	intermittent FLOX + Cetuximab	7.2	NA	20.5	0.84	42	NA
		KRAS WT	578	FOLFIRI or mFOLFOX6 + Cetuximab	10.45	NA	29.93	0.34	-	-
Hyman <i>et al</i> <sup>[37]</sup>	2015	group	559	FOLFIRI or mFOLFOX6 + Bevacizumab	10.84		29.04		-	
		KRAS WT	331	FOLFOX4	8.0	0.02	19.7	0.072	48	0.068
		group	325	FOLFOX4 + Panitumumab	9.6		23.9		55	
		KRAS MT	219	FOLFOX4	8.8	0.02	19.3	0.068	40	-
		group	221	FOLFOX4 + Panitumumab	7.3		15.5		40	
Reidy <i>et al</i> <sup>[51]</sup>	2010	BRAF V600	10	Vemurafenib	4.5	-	9.3	-	0	-
		group	27	Vemurafenib + Cetuximab	3.7		7.1		4	
		All	23	IMC-A12 (anti-IGF-1R antibody)	5.9	-	5.2	-	0	-
			21	IMC-A12 (anti-IGF-1R antibody) + Cetuximab	6.1		4.5		5	
		KRAS WT	20	IMC-A12 (anti-IGF-1R antibody) + Cetuximab	9.4		10.9		0	

<sup>1</sup>95% CI. PFS: Progression-free survival; OS: Overall survival; All: All patients group; WT: Wild type; MT: Mutant type; NA: Not available; KRAS: KRAS exon 2, codons 12 and 13; FOLFIRI: Irinotecan, fluorouracil, and leucovorin; FOLFOX: Fluorouracil, leucovorin, and oxaliplatin; XELOX: Capecitabine and oxaliplatin; FLOX: Fluorouracil, leucovorin, and oxaliplatin.

can deregulate PI3K signaling pathway<sup>[46]</sup>. Two studies demonstrated that PI3KCA mutation and PTEN loss which cause PI3K pathway activation are significant predictors of response to anti-EGFR treatment<sup>[38,42]</sup>. Also, Tural *et al*<sup>[41]</sup> indicated that PI3K expression and PTEN loss together are correlated with significantly worse outcome.

## HYPEREXPRESSION OR HYPERACTIVATION OF TYPE 1 INSULIN LIKE GROWTH FACTOR RECEPTOR

The type 1 insulin like growth factor receptor (IGF-

1R) belongs to the class of tyrosine kinase receptors. IGF-1R functions by activating downstream signaling pathways which include MAPK and PI3K/AKT. Previous studies showed that IGF-1R overexpression results neoplastic transformation of cultured cells<sup>[47]</sup>. Also IGF-1R overexpression was seen in several types of human tumors<sup>[48]</sup> and its downregulation has been shown to be able to inhibit the growth of these cells<sup>[49]</sup>. These findings make IGF-1R an attractive candidate as therapeutic target in anti-tumor therapies. A previous study showed that combination therapy of antibodies against to IGF-1R and anti-EGFR results in further inhibition of CRC cell line growth<sup>[50]</sup>. A phase II study evaluated the safety and the efficacy of human anti-IGF-1R monoclonal antibody

(either alone or in combination with cetuximab) in mCRC patients, and both treatment modalities was reported as insufficient in chemorefractory mCRC patients<sup>[51]</sup> (Table 1).

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2016 Gastric Cancer: Global view

## Robot-assisted surgery for gastric cancer

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### Abstract

Minimally invasive surgery for gastric cancer is a relatively new research field, with convincing results mostly stemming from Asian countries. The use of the robotic surgery platform, thus far assessed as a safe procedure, which is also easier to learn, sets the background for a wider spread of minimally invasive technique in the treatment of gastric cancer. This review will cover the literature published so far, analyzing the pros and cons of robotic surgery and highlighting the remaining study questions.

**Key words:** Gastric cancer survival; Robotic surgery; Gastric cancer surgery; Lymphadenectomy; Minimally invasive surgery

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**Core tip:** An important problem remains regarding the selection of the appropriate technique for a given gastric cancer case. Encouraging results are being published using the robotic technique, but the lack of homogenous study groups in terms of staging, comorbidities and adjuvant and neoadjuvant therapies makes it hard to establish a clear indication for the robotic gastrectomy in gastric cancer. Carefully weighing the treatment options is especially important since there are more and more groups publishing acceptable results with the robotic technique.

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## INTRODUCTION

Surgery is unanimously considered the mainstay curative treatment in gastric cancer. Technically, the possibilities range from open surgery to minimally invasive methods like laparoscopy or robotic surgery. However, the newer laparoscopic techniques have only proven their effectiveness in early gastric cancer<sup>[1]</sup>. The current challenge for robotic surgery in gastric cancer is to prove its benefit as a treatment option, ideally in the form of a survival advantage. Up until now studies only proved its non-inferiority compared with existent techniques.

Technologic progress has clearly had an impact in medicine and surgery, in particular. However the newest developments in the field of technology are not always the best ones and examples can easily be found in the last decades. Rejecting a new technique altogether is, however, not an option in the field of surgery. It would possibly mean closing the roads to a new development that could allow for patients to benefit from procedures which are not easily or not at all undertaken at the moment.

## MINIMALLY INVASIVE SURGERY FOR GASTRIC CANCER

The existence of so many treatment options for gastric cancer suggests that currently there is no consensus regarding the adequate therapeutic conduct. Thus far, the following objectives for gastric cancer surgery have been made clear and should be pursued in any case: (1) If surgery can be performed, it must proceed, usually as a part of multimodal cancer treatment<sup>[1]</sup>. The surgical approach is based on the Virchow-Halsted theory of centrifugal dissemination of carcinomas. This mechanistic theory dating from the end of the 19<sup>th</sup> century is based on the fact that cancer was believed to begin in the target organ and then spread in an orderly fashion through lymphatic drainage routes invading lymph nodes along the way<sup>[2,3]</sup>; (2) The tumor must be resected according to oncological safety limits<sup>[1]</sup>; and (3) An adequate lymphadenectomy must be performed. Its extent varies depending on the location and stage of the tumor<sup>[1]</sup>. Reaching these objectives correlates with a higher survival rate and a lower rate of recurrence<sup>[4,5]</sup>.

Modern day gastric cancer treatment was definitely impacted by technological progress. The laparoscopy revolution was quickly introduced in this field, with the first laparoscopic gastrectomy performed by Kitano *et al.*<sup>[6]</sup>. Experience accumulated with bariatric surgery must not be neglected either, as it led to an improvement

in the technique required to perform intracorporeal anastomoses. The consequence was a rapid development of laparoscopic surgery for gastric cancer beginning, of course, with the early stages. On the other hand, the treatment options for gastric cancer were also enriched by the development of endoscopy, which limited the indications for video-assisted surgery.

Nonetheless, minimally invasive surgery failed to disseminate with great speed worldwide owing mostly to the fact that it is a technically demanding procedure. It is currently particularly favored in Asian countries<sup>[7,8]</sup> where it is gaining terrain as a treatment for early gastric cancer, but it is interesting to note that laparoscopic surgery for gastric cancer is still an investigational procedure even in countries like Japan<sup>[1]</sup>. To advance this type of surgery into the category of standard procedures, results of large randomized controlled studies like KLASS-01<sup>[9]</sup>, KLASS-02<sup>[10]</sup> and JCOG 0912<sup>[11]</sup> comparing the results of open and laparoscopic surgery are still awaited.

At the moment, the benefits of laparoscopy are still being debated, despite all the published studies which seemingly accrue "pro" arguments at a constant rate. In our opinion, the main objection is that these studies presenting good postoperative as well as oncological outcomes, mostly come from highly experienced large-volume surgical centers, which offer a standard of care that is not easily reproducible everywhere in the world.

## ROBOTIC SURGERY

The robotic technologies were brought about to circumvent some of the difficulties of laparoscopic surgery. The laparoscopic procedures for gastric cancer have indeed been associated with improved postoperative outcomes and oncological results<sup>[12-15]</sup>, but the platform itself imposes a series of technical shortcomings. The two-dimensional views coupled with the fulcrum effect and the inherent tremor reduce the surgical range of motion and prolong the learning curve especially for large scale procedures such as gastrectomy. The robotic system comes with a three-dimensional view enabling depth perception, the EndoWrist<sup>®</sup> technology which allows for seven degrees of freedom and tremor filtration. Additionally, images can be enlarged enabling the performance of delicate steps such as lymph node dissection along great vessels which are essential in achieving a D2 dissection, suturing or knotting. These features could enable the performance of relatively complicated procedures such as function-preserving gastrectomy or extended resections for advanced gastric cancer using a minimally invasive method. Nonetheless this technique also has its disadvantages: Costs, duration of the procedures, the necessary trainings.

The use of the robotic platforms in general surgery did not enjoy the same success as it did in urologic surgery, and the field of gastric cancer is no exception. There are a series of shortcomings of the robotic platform explaining this situation. First of all the lack of robotic staplers and robotic seal and cut devices like

LigaSure™ is a considerable inconvenience. Second, due to the costs, the robotic platform cannot be used to cover the whole spectrum of procedures normally performed by a general surgeon<sup>[12]</sup>.

### **Current status of robotic surgery in early gastric cancer**

Studies evaluating robotic surgery for early gastric cancer alone are scarce and stem mostly from Asian countries. The higher incidence of gastric cancer in these countries, together with the wide extent and increased efficacy of the national gastric cancer screening programs fueled the search for minimally invasive treatment modalities for the early stages of the disease. This led not only to the development of endoscopic resection, but also to a large pool of surgeons well versed in minimally invasive gastrectomies. The encouraging results published in small non-randomized comparative studies of laparoscopic vs open surgery for early gastric cancer<sup>[13-15]</sup> were followed by the increased use of laparoscopy in clinical practice. Japan reports that at least 20% of the gastrectomies for early gastric cancer in its hospitals are now being performed laparoscopically<sup>[1]</sup>. The need for better statistical evidence supporting the minimally invasive treatment of early gastric cancer was answered by starting two major randomized controlled trials which are now underway in Japan and South Korea comparing laparoscopy and open surgery<sup>[9,11]</sup>.

Following the foot-steps of laparoscopic surgery, robotics was first introduced in the treatment of early stage patients by the same surgeons who had acquired experience in the field of laparoscopic gastrectomies. After the first robotic gastrectomy reported in 2003 by Hashizume *et al*<sup>[16]</sup>, a series of encouraging reports on robotic surgery for gastric carcinomas began to appear in literature (Table 1).

In keeping with the trends of gastric cancer incidence in the eastern and western continents, Asian studies focus on mixed cohorts of gastric cancer patients with a high prevalence of the early stages or on early gastric cancer patients alone (Table 1). The largest cohort of early-stage gastric cancer to date was published by Woo *et al*<sup>[17]</sup>. A total of 827 patients were included in this nonrandomized comparative study of robotic (236 patients) and laparoscopic surgery (591 patients) for stage Ia and Ib gastric carcinomas. The total operative time was significantly increased for the robotic procedures compared with laparoscopy (219.5 min vs 170.7 min,  $P < 0.001$ ), but the robotic group also showed a lower estimated blood loss (91.6 mL vs 147.8 mL,  $P = 0.02$ ). The length of hospital stay was slightly in favor of the laparoscopic group (7 d vs 7.7 d,  $P = 0.004$ ) and there were no differences regarding morbidity and mortality. In terms of oncological principles, the number of retrieved lymph nodes was not different and all the patients in the robotic group had negative resection margins<sup>[17]</sup>.

Other studies comparing robotic surgery to laparoscopy in the treatment of gastric cancer show the same operative outcomes. The operative times are always

significantly longer for the robotic group (Table 2). This has been attributed to longer docking times necessary for the robot. However, a learning curve effect can be derived from the two studies separating the laparoscopic surgery group into an initial and a recent subgroup<sup>[18,19]</sup>. The operating times reported for the initial laparoscopic technique subgroup are even longer than those of the robotic subgroup. That is no longer the case for the recent laparoscopy subgroup which yields the shortest operating time between the three subgroups (Table 2). In the study of Song *et al*<sup>[19]</sup> the difference between these mean operative times were 289.5, 230 and 134 min, respectively with a statistically significant difference. The decrease of the mean operative times between the initial and the latter robotic cases (231 min vs 208 min) in the large cohort published by Woo *et al*<sup>[17]</sup> indicates that shortening the operating times is also a matter of exercise, as was the case when the laparoscopic gastrectomies were introduced.

Regarding the estimated blood loss and the number of retrieved lymph nodes, there are conflicting results stemming from most of the cohorts comparing laparoscopy to robotic surgery (Table 2). A meta-analysis performed by Shen *et al*<sup>[20]</sup> including the studies which also appear in our retrospective tables (Tables 1-3) comparing robotics and laparoscopy also found no statistically significant difference on the number of retrieved lymph nodes. However, a significantly lower blood loss was found in favor of the robotic group.

### **Current status of robotic surgery in advanced gastric cancer**

Papers stemming from Europe, on the other hand, have a large prevalence of advanced gastric cancer cases in their study groups. In the largest study up to date (5839 patients) comparing robotic (436 patients), laparoscopic (861 patients) and open surgery (4542 patients) performed for stage I, II and III gastric cancer by Kim KM *et al*<sup>[47]</sup>, overall safety of these three types of surgery was the main focus. The overall complication rate was the same between the three groups (OG 10.7% LG 9.4% and RG 10.1%,  $P = 0.494$ ) and so was their severity ( $P = 0.424$ ). However, robotic surgery was prone to complications related to leaks ( $P = 0.017$ ), whereas ileus and abscesses were more prevalent in open surgery ( $P = 0.001$ ,  $P = 0.013$  respectively). The authors explain that stapling lines were not reinforced with sutures in minimally invasive surgery, as opposed to open surgery and that the patients included in the open surgery group were mainly patients with more advanced disease for whom the complexity of the resections was higher. The robotic group showed a faster recovery with a shorter time to starting the soft diet and a shorter postoperative stay ( $P < 0.001$  for both parameters) (Table 3). This study also showed an increased duration of the procedure compared to laparoscopic and open surgery (224 min vs 176 min vs 158 min,  $P < 0.001$ ) combined with a lower estimated blood loss for the robotic group ( $P < 0.001$ ). The

**Table 1** Summary of studies reporting use of robotic surgery for gastric cancer

Ref.	Year	Type of study	Type of surgery	Stage <sup>1</sup>	Type of resection	No. of patients			
						Total	R	L	O
Patriti <i>et al</i> <sup>[21]</sup>	2008	CS	R	6 patients I , 6 patients II , 1 patient III	8 DG, 4 TG, 1 PG	13	13		
Lee <i>et al</i> <sup>[22]</sup>	2011	CS	R	I	DG	12	12		
D'Annibale <i>et al</i> <sup>[23]</sup>	2011	CS	R	17 patients I , 6 patients II , 1 patient III	11 TG, 13 DG	24	24		
Isogaki <i>et al</i> <sup>[24]</sup>	2011	CS	R	N/A	46 DG, 14 TG, 1 PG	61	61		
Kim <i>et al</i> <sup>[25]</sup>	2013	CS	R	11 patients I , 1 patient III	N/A	12	12		
Liu <i>et al</i> <sup>[26]</sup>	2013	CS	R	26 patients I , 32 patients II , 46 patients III	38 DG, 54 TG, 12 PG	104	104		
Park <i>et al</i> <sup>[27]</sup>	2013	CS	R	178 patients I , 22 patients II or more advanced	154 STG, 46 TG	200	200		
Tokunaga <i>et al</i> <sup>[28]</sup>	2014	CS	R	I A	18 DG	18	18		
Anderson <i>et al</i> <sup>[29]</sup>	2007	CS	R	Early GC	7 STG	7	7		
Song <i>et al</i> <sup>[30]</sup>	2009	CS	R	Early GC	67 STG, 33 TG	100	100		
Hur <i>et al</i> <sup>[31]</sup>	2010	CS	R	N/A	5 STG, 2 TG	7	7		
Uyama <i>et al</i> <sup>[32]</sup>	2012	CS	R	18 patients I A, 7 patients II A to III C	25 DG	25	25		
Yu <i>et al</i> <sup>[33]</sup>	2012	CS	R	N/A	29 DG, 12 TG	41	41		
Jiang <i>et al</i> <sup>[34]</sup>	2012	CS	R	24 patients I , 28 patients II , 68 patients III <sup>2</sup>	62 DG, 35 TG, 23 PG	120	120		
Hyung <i>et al</i> <sup>[18]</sup>	2007	NC	R vs L	N/A	N/A	30	10	20	
Song <i>et al</i> <sup>[19]</sup>	2009	NC	R vs L	R: 20 patients I , L: 37 patients I , 3 patients II	R: 20 DG, L: 40 DG	60	20	40	
Pugliese <i>et al</i> <sup>[35]</sup>	2010	NC	R vs L	37 patients early GC, 33 patients advanced GC	64 STG	64	16	48	
Woo <i>et al</i> <sup>[17]</sup>	2011	NC	R vs L	827 patients I a or I b	R: 172 DG, 62, 2 CT; L: 481 DG, 108 TG, 2 CT	827	236	591	
Eom <i>et al</i> <sup>[36]</sup>	2012	NC	R vs L	R: 25 patients I , 3 patients II , 2 patients III, L: 56 patients I , 6 patients II	DG both groups	92	30	62	
Park <i>et al</i> <sup>[37]</sup>	2012	NC	R vs L	R: 27 patients I , 3 patients II ; L: 108 patients I , 11 patients II , 1 patient III	DG both groups	150	30	120	
Yoon <i>et al</i> <sup>[38]</sup>	2012	NC	R vs L	R: 29 patients I , 7 patients II , L: 55 patients I , 7 patients II , 3 patients III	TG both groups	101	36	65	
Kang <i>et al</i> <sup>[39]</sup>	2012	NC	R vs L	R: 82 patients I , 11 patients II , 7 patients III	R: 84 STG, 16 TG	382	100	282	
Hyun <i>et al</i> <sup>[40]</sup>	2013	NC	R vs L	R: 30 patients I , 5 patients II , 3 patients III; L: 67 patients I , 9 patients II , 7 patients III	R: 29 DG, 9 TG; L: 65 DG, 18 TG	121	38	83	
Noshiro <i>et al</i> <sup>[41]</sup>	2014	NC	R vs L	R: 18 patients I , 3 patients II -IV, L: 113 patients I , 47 patients II -IV	DG both groups	181	21	160	
Han <i>et al</i> <sup>[42]</sup>	2014	NC	R vs L	R: 59 patients I , 8 patients II , 1 patient III, L: 66 patients I , 2 patients II	PPG both groups	136	68	68	
Junfeng <i>et al</i> <sup>[43]</sup>	2014	NC	R vs L	R: 29 patients I , 36 patients II , 55 patients III, L: 115 patients I , 98 patients II , 181 patients III	R: 92 DG, 26 TG, 2 PG; L: 261 DG, 118 TG, 15 PG	510	120	394	
Kim <i>et al</i> <sup>[44]</sup>	2014	NC	R vs L	R: 145 patients I , 27 patients II and III; L: 422 patients I , 59 patients II and III	N/A	653	172	481	
Kim <i>et al</i> <sup>[45]</sup>	2010	NC	R vs L vs O	Lower than cT2N1M0	STG all groups	39	16	11	12
Huang <i>et al</i> <sup>[46]</sup>	2012	NC	R vs L vs O	R: 29 patients I , 7 patients II , 3 patients III; L: 55 patients I , 9 patients II , O: 198 patients I , 106 patients II , 282 patients III	R: 32 STG, 7 TG; L: 57 STG, 7 TG; O: 407 STG, 179 TG	689	39	64	586
Kim <i>et al</i> <sup>[47]</sup>	2012	NC	R vs L vs O	R: 3 patients O, 350 patients I , 51 patients II , 32 patients III; L: 8 patients O, 714 patients I , 96 patients II , 43 patients III, O: 28 patients O, 2376 patients I , 823 patients II , 1313 patients III	R: 327 DG, 109 TG, L: 703 DG, 158 TG; O: 3309 DG, 1232 TG	5839	436	861	4542
Pernazza <i>et al</i> <sup>[48]</sup>	2006	NC	R vs O	R: 2 patients O, 20 patients I , 12 patients II , 5 patients III, 6 patients IV	R: 21 DG, 24 TG	90	45	0	45
Caruso <i>et al</i> <sup>[49]</sup>	2011	NC	R vs O	R: 13 patients I , 9 patients II , 4 patients III, 3 patients IV, O: 57 patients I , 18 patients II , 33 patients III, 12 patients IV	R: 16 DG, 12 TG, 1 PG; O: 83 DG, 37 TG	149	29	0	120
Procopiuc <i>et al</i> <sup>[50]</sup>	2015	NC	R vs O	R: 9 patients II , 9 patients III, O: 15 patients II , 14 patients III	R: 7 DG, 10 TG, 1 PG; O: 6 DG, 23 TG	47	18		29

<sup>1</sup>Data as reported by the authors from preoperative evaluation; <sup>2</sup>Postoperatively obtained staging. CS: Clinical series; NC: Nonrandomized comparative study; R: Robotic surgery; L: Laparoscopic surgery; O: Open surgery; TG: Total gastrectomy; STG: Subtotal gastrectomy; DG: Distal gastrectomy; PG: Proximal gastrectomy; CT: Completion total gastrectomy; PPG: Pylorus-preserving gastrectomy; GC: Gastric cancer.

**Table 2** Main operative outcomes in studies reporting use of robotic surgery for gastric cancer

Ref.	OP time (min)	Estimated blood loss (mL)	No. of harvested lymph nodes	Conversions
Patriti <i>et al</i> <sup>[21]</sup>	286	103	28.1	0
Lee <i>et al</i> <sup>[14]</sup>	253	135	46	0
D'Annibale <i>et al</i> <sup>[23]</sup>	267.5	30	28	0
Isogaki <i>et al</i> <sup>[24]</sup>	TG > DG 520 > 388	TG > DG 150 > 61.8	TG approximately equal DG 43 approximately equal 42	0
Kim <i>et al</i> <sup>[25]</sup>	234.7	46.4	42.4	
Liu <i>et al</i> <sup>[26]</sup>	272.52	80.78	23.1	1.8
Park <i>et al</i> <sup>[27]</sup>	248.8	146.1	37.9	3.5
Tokunaga <i>et al</i> <sup>[28]</sup>	331.5	32.5	40	0
Anderson <i>et al</i> <sup>[29]</sup>	420	300	24	0
Song <i>et al</i> <sup>[30]</sup>	231.3	128.2	36.7	0
Hur <i>et al</i> <sup>[31]</sup>	205			
Uyama <i>et al</i> <sup>[32]</sup>	361	51.8	44.3	0
Yu <i>et al</i> <sup>[33]</sup>	TG > DG 285 > 225	TG > DG 180 > 150	34.2	4.8
Jiang <i>et al</i> <sup>[34]</sup>	245	70	22.5	
Hyung <i>et al</i> <sup>[18]</sup>	Initial L > R > Recent L 337 > 253 > 164	-	Recent L > R > Initial L 37.8 > 34 > 29.2	0
Song <i>et al</i> <sup>[19]</sup>	Initial L > R > Recent L 289.5 > 230 > 134 ss	R > Recent L 94.8 > 39.5	Recent L > R > Initial L 42.7 > 35.3 > 31.5	0
Pugliese <i>et al</i> <sup>[35]</sup>	R > L 344 > 235 ss	L > R 148 > 90 ss	L > R 31 > 25	L > R 3 > 2
Woo <i>et al</i> <sup>[17]</sup>	R > L 219.5 > 170.7 ss	L > R 147.9 > 91.6 ss	R > L 39 > 37.4	0 = 0
Eom <i>et al</i> <sup>[36]</sup>	R > L 229.1 > 189.4 ss	R > L 152.8 > 88.3	L > R 33.4 > 30.2	
Park <i>et al</i> <sup>[37]</sup>	R > L 218 > 140 ss	R > L 75 > 60	R approximately equal L 34 approximately equal 35	0
Yoon <i>et al</i> <sup>[38]</sup>	R > L 305.8 > 210.2 ss		R > L 42.8 > 39.4	
Kang <i>et al</i> <sup>[39]</sup>	R > L 202 > 173 ss	L > R 173.4 > 93.2 ss		
Hyun <i>et al</i> <sup>[40]</sup>	R > L 234.4 > 220	R approximately equal L 131.3 approximately equal 130.4	R approximately equal L 32.8 approximately equal 32.6	0 = 0
Noshiro <i>et al</i> <sup>[41]</sup>	R > L 439 > 315 ss	L > R 115 > 96	R > L 44 > 40	R = L 0 = 0
Han <i>et al</i> <sup>[42]</sup>	R > L 258 > 193 ss		L > R 36.5 > 33.4	0
Junfeng <i>et al</i> <sup>[43]</sup>	R > L 234.8 > 221.3 ss	L > R 137.6 > 118.3 ss	R > L 34.6 > 32.7 ss	
Kim <i>et al</i> <sup>[44]</sup>	R > L 206.4 > 167.1 ss	L > R 134.9 > 59.8 ss	R approximately equal L 37.3 approximately equal 36.8	R = L 0 = 0
Kim <i>et al</i> <sup>[45]</sup>	R > L > O 259.2 > 203.9 > 126.7 ss	O > L > R 78.8 > 44.7 > 30.3 ss	O > R > L 43.3 > 41.1 > 37.4	0 = 0
Huang <i>et al</i> <sup>[46]</sup>	R > L > O 430 > 350 > 320	O > L > R 400 > 100 > 50 ss	O > R > L 34 > 32 > 26	
Kim <i>et al</i> <sup>[47]</sup>	R > L > O 226 > 176 > 158 ss	O > L > R 182 > 112 > 85	O > R > L 40.5 > 40.2 > 37.6 ss	
Pernazza <i>et al</i> <sup>[48]</sup>	R > O 293.8 > 224.6		R 34.2	
Caruso <i>et al</i> <sup>[49]</sup>	R > O 290 > 222	O > R 386.1 > 197.6	O > R 31.7 > 28	
Procopiuc <i>et al</i> <sup>[50]</sup>	R > O 320.83 > 243.36 ss	O > R 564.62 > 208.26 ss	O > R 25 > 22	0

R: Robotic surgery; L: Laparoscopic surgery; O: Open surgery; TG: Total gastrectomy; DG: Distal gastrectomy; ss: Statistically significant.

number of harvested lymph nodes was no different between open and robotic surgery.

In the experience of our group, the robotic platform is a versatile tool in the surgical approach of advanced gastric cancer. Our study<sup>[50]</sup> enrolled 47 patients who were exclusively advanced gastric cancer patients and went on to receive either open ( $n = 29$ ) or robotic ( $n = 18$ ) surgery. Significantly longer mean operating times (320.83 min vs 243.36 min), but significantly lower blood loss (208.26 mL vs 546.62 mL) and shorter hospital stay (11.04 d vs 8.1 d) were obtained for the robotic group (Table 3). We found no difference in the number of retrieved lymph nodes or the rate of complications. After a mean follow up time of 31.66 mo for the open surgery group and a 24.72 for the robotic surgery group, the Kaplan-Meier analysis of the survival data revealed no statistically significant difference between the two cohorts ( $P = 0.177$ ).

The authors consider that special emphasis needs to be placed on the long-term results of robotic surgery in advanced gastric cancer. The MAGIC trial<sup>[51]</sup> published

in 2006 showed a survival benefit for gastric cancer patients receiving epirubicin, cisplatin and fluorouracil perioperatively when compared with patients treated with surgery alone. But the study also reported that 34% of the patients enrolled in the perioperative chemotherapy group, were unable to receive the regimen after surgery owing, among others, to postoperative complications. This creates a need for less invasive surgery like robotic surgery even in the treatment of the advanced gastric cancer patients. Patients would be thus enabled to receive the complete chemotherapy regimen, which would positively impact their survival prognosis<sup>[51]</sup>.

Another reason to investigate robotic surgery in the treatment of advanced gastric cancer would be the imperfect staging systems currently available. Studies report a considerable amount of patients staged as EGC perioperatively who turn out intraoperatively to suffer from advanced gastric cancer<sup>[52,53]</sup>. Given these numbers Pugliese *et al*<sup>[35]</sup> even proposed that all gastrectomies be performed including a D2 lymphadenectomy regardless

**Table 3** Main postoperative outcomes in studies reporting use of robotic surgery for gastric cancer

Ref.	Time to first flatus (d)	Time to oral feeding (d)	Postoperative hospital stay (d)	Morbidity (%)	Mortality (%)	Follow up time (mo)
Patriti <i>et al</i> <sup>[21]</sup>			11.2	41.4	0	12.2
Lee <i>et al</i> <sup>[22]</sup>	2.4	4.6	6.6	8.3	0	
D'Annibale <i>et al</i> <sup>[23]</sup>		5	6	2	0	48
Isogaki <i>et al</i> <sup>[24]</sup>				4	1	
Kim <i>et al</i> <sup>[25]</sup>			6	0	0	
Liu <i>et al</i> <sup>[26]</sup>	2.5	4.1	6.2	11.8	0	
Park <i>et al</i> <sup>[27]</sup>			8	19	1	
Tokunaga <i>et al</i> <sup>[28]</sup>			8	22.22		
Anderson <i>et al</i> <sup>[29]</sup>		4 (2-8)	4 (3-9)	14.3		
Song <i>et al</i> <sup>[30]</sup>	2.9 ± 0.5	4.2	7.8	13	0	
Hur <i>et al</i> <sup>[31]</sup>						
Uyama <i>et al</i> <sup>[32]</sup>		3.56	12.1	8	0	11
Yu <i>et al</i> <sup>[33]</sup>	3.1	3.7		4.8	0	11
Jiang <i>et al</i> <sup>[34]</sup>			6.3	5	0	
Hyung <i>et al</i> <sup>[18]</sup>	Recent L > Initial L > R 3.3 > 3.1 > 2.9	Initial L > Recent L > R 4.8 > 4.3 > 4	Initial L > R = Recent L 6.9 > 6 = 6			
Song <i>et al</i> <sup>[19]</sup>	Recent L > Initial L = R 3.25 > 3 = 3	Initial L > Recent L > R 4.95 > 4.1 > 4	Initial L > Recent L > R 7.7 > 6.2 > 5.7	Recent L > Initial L = R 10 > 5 = 5		
Pugliese <i>et al</i> <sup>[35]</sup>			R = L 10 = 10 R > L 7.7 > 7 ss	L > R 12.5 > 6.2 L > R 13.7 > 11	R > L 6.2 > 2 R approximately equal L 0.3 approximately equal 0.4	53
Woo <i>et al</i> <sup>[17]</sup>						
Eom <i>et al</i> <sup>[36]</sup>	R = L 3.4 = 3.4		R approximately equal L 7.9 approximately equal 7.8	R > L 13 > 6		
Park <i>et al</i> <sup>[37]</sup>				R > L 17 > 7.5	R = L 0 = 0	
Yoon <i>et al</i> <sup>[38]</sup>	L > R 4.9 > 4.2		L > R 10.3 > 8.8 R > L 9.8 > 8.1 ss	R > L 16.7 > 15.4 R > L 14 > 10.3	R = L 0 = 0 R = L 0 = 0	
Kang <i>et al</i> <sup>[39]</sup>			L > R 11.9 > 10.5	R > L 47.3 > 38.5	R = L 0 = 0	
Hyun <i>et al</i> <sup>[40]</sup>			L > R 13 > 8 ss	L > R 10 > 9.5	0	
Noshiro <i>et al</i> <sup>[41]</sup>		L > R 5 > 4.4	L > R 9.1 > 8.6	L > R 22.1 > 19.1	R = L 0 = 0	R > L 22.7 > 19.3
Han <i>et al</i> <sup>[42]</sup>						
Junfeng <i>et al</i> <sup>[43]</sup>	L > R 3.3 > 3.1	L > R 4.1 > 3.9	L approximately equal R 7.9 approximately equal 7.8 R > L 7.1 > 6.7	R > L 5.8 > 4.3	R > L 32.2 > 30.1	L > R 19 > 15
Kim <i>et al</i> <sup>[44]</sup>			O > L > R 6.7 > 6.5 > 5.1 ss	R > L 5.2 > 4.2	L > R 0.6 > 0 R = L 0 = 0	
Kim <i>et al</i> <sup>[45]</sup>	L > O > R 3.6 > 3.4 > 3.2					
Huang <i>et al</i> <sup>[46]</sup>				L > R > O 15.6 > 15.4 > 14.7		
Kim <i>et al</i> <sup>[47]</sup>		O > L > R 5.7 > 4.7 > 4.4 ss	O > L > R 10.2 > 7.8 > 7.5 ss	O > R > L 10.7 > 10.1 > 9.34	0.4 ND	
Pernazza <i>et al</i> <sup>[48]</sup>				R > O 24.5 > 13.3	O > R 8.9 > 4.4	R = O 26 = 26
Caruso <i>et al</i> <sup>[49]</sup>			O > R 13.4 > 9.6	O > R 42.5 > 41.4	O > R 3.3 > 0	O > R 44 > 25
Procopiuc <i>et al</i> <sup>[50]</sup>			O > R 11.04 > 8.1 ss	O > R 27.58 > 22.22	O = R 0 = 0	O > R 31.6 > 24.7

R: Robotic surgery; L: Laparoscopic surgery; O: Open surgery; TG: Total gastrectomy; DG: Distal gastrectomy; ss: Statistically significant; ND: No statistical difference.

of the initial tumoral staging.

## TECHNICAL ASPECTS

### Combined resections

There has been a lack of studies specifically focused on the possible benefits of robotic multivisceral resections for advanced gastric cancer. Previous research by surgeons experienced in minimally invasive surgery suggests that the precision offered by the robotic platform might be of more use in large, technically-challenging procedures like multivisceral resections, rather than in cases requiring less complex surgery<sup>[54,55]</sup>.

### Lymphadenectomy

To put forth robotic surgery as a viable surgical tech-

nique in gastric cancer treatment, its contribution to performing an extended lymphadenectomy needs to be made clear.

In laparoscopy, one of the major sources of intraoperative bleeding was shown to be lymph node dissection, especially when occurring around the large vessels<sup>[56,57]</sup>. In our experience with the robotic platform owing to the elimination of physiologic tremor, the 3D steady view, and the 7 degrees of freedom of the EndoWrist® instruments lymph node dissection along the celiac trunk, the left gastric artery and the hepatic pedicle which are usually associated with increased bleeding, are now performed in a more precise and safe environment<sup>[50]</sup>.

The cohorts of Hyung<sup>[18]</sup> and Song *et al*<sup>[30]</sup> both included an initial and a recent laparoscopy group thus

allowing the assessment of the evolution of surgery parameters along the learning curve for this type of surgery and their comparison to the initial experience in robotic surgery. Although not statistically significant, recent laparoscopy showed the highest number of retrieved lymph nodes, with initial robotic cases coming second, in front of the initial laparoscopic cases. This comes to support the view that laparoscopy has a steeper learning curve than robotic surgery and that even inexperienced surgeons may obtain easily reproducible, high quality results faster with the robotic platform. This difference between the two techniques may not be important in the east, where experienced laparoscopic surgeons show no difficulties in quickly adjusting to the robotic platform, but it could bring a significant advantage to the western surgeons who simply cannot benefit from the same training in laparoscopy for gastric cancer due to the particular epidemiology of this disease.

The majority of the studies listed in Tables 1-3 show a higher number of retrieved lymph nodes for robotic procedures, which is an encouraging result given the extent of the preoperative under staging reported until now and the probable need to perform D2 lymphadenectomies for all patients until a reliable method for precise preoperative staging is introduced.

### **Digestive tract reconstruction**

Key moments for the anastomosis are as follows: (1) closure of the duodenal stump; (2) closure of the stomach stump in subtotal gastrectomy or that of the esophageal stump in total gastrectomy; and (3) preparing the jejunum for the gastro-jejuno anastomosis or the eso-jejunoanastomosis. We generally opt for a Roux-en-Y anastomosis<sup>[58]</sup>.

The reconstruction solutions after total or subtotal gastrectomy can be grouped into two large categories. First, the extracorporeal anastomoses by the robot-assisted surgery require the performance of a minilaparotomy (smaller than 6 cm) through which the ends that need to be anastomosed are brought out and continuity of the digestive tract is reestablished, usually using circular stapler. This technique is not suitable for obese patients for whom the incision may need to be larger than 6 cm to perform the proximal resection and the purse-string suture on the esophageal stump.

To fully take advantage of the minimal invasiveness provided by the robotic platform, several techniques for intracorporeal anastomoses have been developed. They avoid the laparotomy and imply sectioning the esophagus under video control and then performing the anastomosis with a specific technique not requiring an abdominal incision. One option is using the OrVil™ device (Covidien, Mansfield, MA, United States). This consists of a foldable stapler anvil forming a 170° angle with the adjoining PVC tube. The OrVil™ device is introduced through the mouth and into the esophageal stump at which point the anvil is unfolded and connected to the circular stapler introduced abdominally. For this technique our team uses a 21 mm anvil followed by

a Roux-en-Y reconstruction with good postoperative results<sup>[58]</sup>. Similar to this is the technique described by Hiki *et al.*<sup>[59]</sup> in which the anvil of a circular stapler is attached to a nasogastric tube using sutures and then introduced trans-orally. Another technique was described by Inaba *et al.*<sup>[60]</sup> and involves the creation of a side-to-side anastomosis using a linear stapler. Yet another option would be the manual sewing of the anastomosis, which we do not recommend, since it would prolong operating times unnecessarily, given the fact that the available mechanical devices are reliable alternatives.

### **The role of the assistant surgeon**

In a study published by our team<sup>[61]</sup>, we assessed the role of the patient-side surgeon in robotic surgery. We found obvious benefits for the team when highly-trained assistants were involved in the procedure. Remarkable improvements were seen in handling the robot (docking and undocking times), the speed and precision in manipulating laparoscopic devices like the LigaSure or clip applier devices. Our data show that maintaining the same members of the team throughout more procedures and including assistants who undertook a structured, formal training program are more likely to warrant for fast and safe interventions.

## **OPEN QUESTIONS OF RESEARCH**

An important problem remains regarding the selection of the appropriate technique for a given gastric cancer case. Thus far indications for robotic gastrectomy were: (1) a diagnosis of early gastric cancer without evidence of lymph node involvement; (2) T1 cancer with perigastric lymph node involvement; and (3) serosa-negative gastric cancer without lymph node metastasis. However, many of the patients were understaged preoperatively. This raises the need to study the outcomes of robotic surgery on large patient cohorts in randomized prospective studies not only for early gastric cancer, but also for tumors possibly requiring the D2 lymphadenectomy.

A recently published study surveying gastric cancer surgery techniques in United States academic medical centers<sup>[62]</sup> shows that the number of robotic gastrectomies for gastric cancer has remained constant in 2011, 2012 and 2013. The study also mentioned that the robotic technique was utilized in the patients with the highest risk of mortality and severity of illness, in keeping with the fact that minimally invasive surgery has a lower impact on patient performance status and immune response mechanisms postoperatively<sup>[62-64]</sup>. Therefore, extending the indications of robotic surgery to advanced gastric cancer is also a valid study point, especially in the West.

The option between endoscopic, laparoscopic, robotic or open surgery must be made based on well-established diagnostic criteria. This is not easy and one must take into account the caveats of evidence based

medicine and randomized controlled trials. The case of the results published by Bonenkamp *et al.*<sup>[65]</sup> and Cuschieri *et al.*<sup>[66,67]</sup> regarding the survival benefit of the D2 lymphadenectomy and the controversies thereafter have marked a decade of debate regarding the strategies for gastric cancer treatment. Carefully weighing the treatment options is especially important since there are more and more groups publishing acceptable results with the robotic technique.

## CONCLUSION

Encouraging results are being published using the robotic technique, but the lack of homogenous study groups in terms of staging, comorbidities and adjuvant and neo-adjuvant therapies makes it hard to establish a clear indication for the robotic gastrectomy in gastric cancer.

Robotic surgery has proven to be safe and feasible thus far, but more convincing large volume prospective studies are needed to put it on the treatment list of early and advanced gastric cancer.

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## 2016 Pancreatic Cancer: Global view

# MicroRNA in pancreatic ductal adenocarcinoma and its precursor lesions

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## Abstract

Pancreatic ductal adenocarcinoma (PDAC) is the 4<sup>th</sup>

deadliest cancer in the United States, due to its aggressive nature, late detection, and resistance to chemotherapy. The majority of PDAC develops from 3 precursor lesions, pancreatic intraepithelial lesions (PanIN), intraductal papillary mucinous neoplasm (IPMN), and mucinous cystic neoplasm. Early detection and surgical resection can increase PDAC 5-year survival rate from 6% for Stage IV to 50% for Stage I. To date, there are no reliable biomarkers that can detect PDAC. MicroRNAs (miRNA) are small noncoding RNAs (18-25 nucleotides) that regulate gene expression by affecting translation of messenger RNA (mRNA). A large body of evidence suggests that miRNAs are dysregulated in various types of cancers. MiRNA has been profiled as a potential biomarker in pancreatic tumor tissue, blood, cyst fluid, stool, and saliva. Four miRNA biomarkers (miR-21, miR-155, miR-196, and miR-210) have been consistently dysregulated in PDAC. MiR-21, miR-155, and miR-196 have also been dysregulated in IPMN and PanIN lesions suggesting their use as early biomarkers of this disease. In this review, we explore current knowledge of miRNA sampling, miRNA dysregulation in PDAC and its precursor lesions, and advances that have been made in using miRNA as a biomarker for PDAC and its precursor lesions.

**Key words:** Pancreatic cancer; MicroRNA; Biomarkers; Pancreatic intraepithelial lesions; Intraductal papillary mucinous neoplasm

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**Core tip:** Reliable biomarkers are needed to detect pancreatic ductal adenocarcinoma (PDAC) early in order to decrease mortality. In this review, we discuss what the current knowledge is on microRNA (miRNA) in PDAC and its precursor lesions. MiR-21, miR-155, miR-196, miR-210 are dysregulated in tissue, serum, cyst fluid, and stool of PDAC patients. MiR-21, miR-155, and miR-196 are dysregulated in intraductal papillary

mucinous neoplasm and pancreatic intraepithelial lesions demonstrating that these miRNAs may serve as potential biomarkers for early stage lesions and cancer.

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## INTRODUCTION

Pancreatic ductal adenocarcinoma (PDAC) is the 4<sup>th</sup> deadliest cancer in the United States, due to its aggressive nature, late detection, and resistance to chemotherapy<sup>[1,2]</sup>. The majority of PDAC develops from 3 precursor lesions, pancreatic intraepithelial lesions (PanIN), intraductal papillary mucinous neoplasm (IPMN), and mucinous cystic neoplasm (MCN)<sup>[3]</sup>. The cystic precursor lesions of the pancreas are detectable by certain imaging modalities such as Endoscopic ultrasound (EUS)<sup>[4-6]</sup>, Magnetic Resonance Imaging of the Abdomen with Cholangiopancreatography<sup>[7]</sup>, and computerized tomography scan<sup>[8,9]</sup>. To date, there is no modality that clearly detects PanIN lesions, although studies have suggested a correlation between multifocal PanIN and lobular atrophy of the pancreas on EUS<sup>[10]</sup>.

Early detection and surgical resection can increase PDAC 5-year survival rate from 6% for Stage IV to 50% for Stage I<sup>[11,12]</sup>. Detection and surgical removal of precursor lesions has the potential to be curative. Because of this, there has been much research focused on identification of individuals at high-risk of PDAC, detection of early stage lesions, and on the discovery of reliable biomarkers of this deadly disease. Carbohydrate antigen (CA) 19-9 is a poor biomarker of PDAC, as it is elevated in 30%-40% of benign diseases of the pancreas<sup>[13,14]</sup> with a sensitivity of 79% (70%-90%) and specificity of 82% (68%-91%)<sup>[15]</sup> for PDAC.

MicroRNA (miRNA) expression has been studied in tumor detection, cancer development and progression, and prognosis<sup>[16]</sup>. MiRNAs are small noncoding RNAs (18-25 nucleotides) that regulate gene expression by affecting translation of messenger RNA (mRNA)<sup>[16-18]</sup>. MiRNA function to stabilize mRNA transcripts *via* post-transcriptional gene silencing *via* inhibition of the translation process or cleavage of their target mRNAs<sup>[16,19]</sup>. Over the last decade, the role of miRNA in cancer development and detection has evolved. MiRNA is very stable in tissue, plasma, stool, and other fluids and can be quantified in very small sample sizes, making it an excellent potential biomarker for the detection of PDAC. Current priorities include: (1) identification of miRNAs that are reliably dysregulated in PDAC; (2) determining which sample source(s) are easily accessible and have the highest yield for detecting these biomarkers; and (3) development of novel ways in which to use this

information to detect early onset PDAC and precursor lesions. Array-based analysis is used to evaluate the expression levels of thousands of miRNAs in various tissue types. Subsequent trials have validated these findings by performing quantitative real time PCR (QRT-PCR) and performed receiver operating characteristics (ROC) analysis to determine the sensitivity and specificity of these miRNAs as potential biomarkers for early or advanced disease. Some miRNAs, such as miR-21, miR-155, miR-196a, and miR-210 have stood out as potential biomarkers of this highly fatal disease<sup>[20-24]</sup>. Our review is aimed at exploring current knowledge of miRNA sampling, miRNA dysregulation in PDAC and its precursor lesions, and advances that have been made in using miRNA as a biomarker for PDAC and its precursor lesions.

## ROLE OF MIRNA IN PDAC DETECTION: SAMPLES FROM TISSUE, SERUM, PANCREATIC JUICE, STOOL AND SALIVA

Attention has been paid to circulating serological signatures, autoantibodies, epigenetic markers, circulating tumor cells (TCs), and miRNAs in order to detect PDAC at an earlier stage of disease<sup>[25,26]</sup>. The use of miRNA for diagnosis and screening is still an evolving field; in the right patient population, an ideal miRNA test would be highly sensitive and specific, minimally-invasive and cost-effective. MiRNA expression in PDAC was first examined in PDAC tissue cells<sup>[27]</sup>. Now miRNA has been found in serum, blood, whole plasma, stool, saliva, and cyst fluid (Table 1). Current knowledge is described below.

### MiRNA in whole pancreas tissue or PDAC biopsies

Szafranska *et al.*<sup>[27]</sup> performed the first analysis comparing miRNA expression in normal pancreas tissue, chronic pancreatitis (CP) tissue and PDAC tissue. On imaging, it can be challenging to distinguish CP from PDAC given the thick stroma and inflammation that may be found in both of these conditions. Furthermore, it is unclear if the aberrant expression of particular miRNAs is secondary to the desmoplastic reaction in CP and PDAC, and not related to tumorigenesis itself. They and others have found that miRNA-216 and miRNA-217 are significantly down-regulated in PDAC and miRNA-143, miR-145, miR-146a, miR-148a, miR-150, miR-155, miR-196a, miR-196b, miR-210, miR-222, miR-223, miR-31 are up-regulated in PDAC<sup>[24,27-29]</sup>. However, this study also demonstrated that dysregulation of miRNA-196a, miR-196b, miR-203, miR-210, miR-222, miR-217, and miR-375 were found only in PDAC, whereas miRNA-29c, miR-96, miR-143, miR-145, miR-148b, and miR-150 were abnormally expressed in both CP and PDAC. This may suggest that the latter are responsible for causing the desmoplastic reaction as opposed to tumorigenesis.

**Table 1** MiRNA in pancreatic ductal adenocarcinoma

MiRNA	Whole pancreas	Serum and plasma	Saliva	Stool	Pancreatic juice
miR-10b		↑[54]			
miR-16		↑[52]			
miR-18a		↑[29,56,57]			
miR-20a		↑[55,134]			↓[62]
miR-21	↑[22,24,27,32,34,38,55,71]	↑[55,71]		↑[63]↔[71]	↑[61,62,71]
miR-24		↑[55]			
miR-27a-3p		↑[134]			↑[62]
miR-29c	↓[27]				
miR-30a-3p	↓[27]				
miR-30c		↓[37]			
miR-31	↑[27]				
miR-34a		↑[37]			
miR-96	↓[27,135]				↓[62]
miR-99a		↑[52]			
miR-101	↑[32]				
miR-106b		↑[54]			
miR-130b	↓[27]				
miR-135b	↑[31]				
miR-139-3p		↓[37,58]			
miR-141	↓[27]				
miR-143	↑[27,71]			↓[71]	
miR-145	↑[27]				
miR-146a	↑[27]				↑[62]
miR-148a	↓[27,29]				
miR-148b	↓[27-29]				
miR-150	↑[27]				
miR-155	↑[22-24,27,32,66,71]	↑[22,54]		↑[63]↓[71]	↑[61,71]
miR-181a,b,d	↑[24]			↑[72]	
miR-185		↑[52,55,134]			
miR-191		↑[55]			
miR-192		↑[37,58]			
miR-194		↑[37]			
miR-196a	↑[22,23,27,49,52,71]	↑[21,22,52,71]		↑[72]↓[71]	↑[62,71]
miR-196b	↑[27]				↑[60]
miR-200a		↑[136]			↑[62]
miR-200b		↑[136]			
miR-205					
miR-210	↑[27,71,137,138]	↑[137]		↑[72], ↔ [71]	↑[60,71]
miR-212	↑[38]	↑[37]			
miR-216	↓[27,38]			↓[63]↓[71]	
miR-217	↓[27]				↓[62]
miR-222	↑[24,27,38]				
miR-223	↑[27]				
miR-375	↓[27,71]			↔[71]	
miR-492		↓[59]			↑[60]
miR-494	↓[27,74]				
miR-508-5p		↓[37]			
miR-513a-5p		↓[37]			
miR-602		↑[37]			
miR-630		↓[37]			
miR-663a		↓[59]			
miR-801		↑[37]			
miR-887		↓[37]			
miR-923		↓[37]			
miR-940			↑[74]	↑[74]	
miR-1290	↑[30]				
miR-1427					↑[60]
miR-3679-5p			↓[74]	↓[72,74]	

miR: MicroRNA; ↑: Up-regulated; ↓: Down-regulated; ↔: Unchanged.

MiR-1290 is elevated in early stage PDAC compared to normal controls<sup>[30]</sup>. Additionally, miR-135b has been shown to be an effective biomarker for distinguishing PDAC from CP with high sensitivity and specificity<sup>[31]</sup>.

MiR-21, MiR-155, and miR-196 have been demonstrated by multiple groups to differentiate PDAC from non-cancerous lesions of the pancreas<sup>[20-24,27,32]</sup>. Special attention has been placed on the role of miR-21 in

PDAC, as it has been implicated in tumorigenesis, TC invasion, the desmoplastic reaction, and metastasis of TC<sup>[33-36]</sup>. Further studies did not demonstrate that miR-21 expression in stromal cells correlated with tumor stage.

MiR-192 has also been found to be present in pancreatic TC, but is seldom seen in stromal cells and not found in adjacent normal pancreas tissue<sup>[37]</sup>. In this same study, miR-194 expression was detected in PDAC tissue, but not found in the surrounding normal pancreatic tissue. Unfortunately, despite these findings, no significant difference was found between the serum levels of miR-194 in patients with PDAC and healthy controls.

One proposed mechanism for PDAC development includes signaling between the molecular markers of the desmoplastic reaction and TCs<sup>[38-41]</sup>. Liffers *et al.*<sup>[29]</sup> demonstrated that miR-148a is down-regulated in microdissected PDAC tissue and when over-expressed prevents tumor growth. This suggests that miR-148a may have a crucial role in the molecular signaling by which tumorigenesis occurs. While it is important to find biomarkers that are deregulated in PDAC, it is also important to understand which miRNAs are involved in these aberrant signaling pathways.

#### **MiRNA in serum and plasma of PDAC patients**

MiRNAs are known to have organ-specific expression in many human cancers<sup>[42,43]</sup>. Less than a decade ago, studies found that miRNA could reliably be detected in the serum in both animal models and humans<sup>[44,45]</sup>, and since that time, there has been much research dedicated to identifying which miRNAs have differential expression and the implications of these findings in the detection, staging, treatment, and prognosis of cancers<sup>[46-50]</sup>.

Attempts to use miRNA biomarkers in conjunction with CA19-9 have yielded mixed results. A study examining 847 different miRNAs in patients with PDAC found increased expression of miR-375 in PDAC as opposed to controls. MiR-375 did not improve detection nor predict prognosis in patients with PDAC when compared to CA19-9 alone<sup>[51]</sup>. Liu *et al.*<sup>[52]</sup> found that using serum miR-16 and miR-196a in combination with CA19-9 increased detection of PDAC and Stage I lesions when compared to either modality alone, which suggests that miR-16 and miR-196a may be deregulated early in PDAC. These biomarkers were also up-regulated in studies performed on pancreas tissue, demonstrating that miR-16 and miR-196a can be used as peripheral biomarkers of PDAC. Gao, *et al.*<sup>[53]</sup> also demonstrated that miR-16, when combined with CA19-9, served as a potential biomarker for detection of PDAC when compared to patients with CP.

One limitation of CA19-9 as a biomarker is that it is elevated in a large portion of patients with benign pancreatic diseases. Because of this limitation, studies have evaluated the miRNA expression of patients with PDAC compared to those with benign diseases such as CP or choledocolithiasis. They found that miR-10b,

miR-155, and miR-106b were consistently elevated in the serum of patients with PDAC but not in those with benign pancreatic disease<sup>[54]</sup>. Liu *et al.*<sup>[55]</sup> have demonstrated that up-regulation of miR-20a, miR-21, miR-24, miR-25, miR-99a, miR-185, and miR-191 can be used to distinguish PDAC from healthy controls and CP. Additionally, miR-135b has been shown to be an effective biomarker for distinguishing PDAC from CP with high sensitivity and specificity<sup>[31]</sup>. MiR-18a levels have also been shown to have increased expression in patients with PDAC and interestingly decrease after surgical resection suggesting that miR-18a levels may be a good marker to not only detect disease but also to monitor disease recurrence<sup>[29,56,57]</sup>. Zhang *et al.*<sup>[37]</sup> also demonstrated that miR-194, miR-192, miR-602, miR-801, miR-212, miR-34a are up-regulated in PDAC, while miR-923, miR-139-3p, miR-513a-5p, miR-630, miR-30c-1, miR-887, miR-508-5p, and miR-139a-5p were down-regulated in PDAC specimens<sup>[37,58]</sup>. From these data, they demonstrated that miR-192 is neither present in the stromal cells of the pancreas nor the serum, but it is up-regulated in PDAC TCs and is involved in cell proliferation of PANC-1 TC lines *in vitro*<sup>[58]</sup>. Lin *et al.*<sup>[59]</sup> performed microarray on 1711 serum miRNAs and found that 23 were down-regulated and 22 were up-regulated in the serum of PDAC patients when compared to normal controls. Of these, miR-492 and miR-663a were found to have decreased expression that was statistically significant in PDAC; however, only miR-663a was found to have a positive correlation with stage of disease<sup>[59]</sup>. Further studies are needed to determine which miRNAs will be clinically relevant.

#### **Pancreatic juice miRNA**

Pancreatic juice sampling requires an invasive endoscopic procedure, but studying the miRNA concentrations of patients with PDAC, benign pancreatic lesions, and healthy controls can shed light on potential biomarkers for detecting disease as they are found in high concentration in cyst fluid. As EUS and endoscopic retrograde cholangiopancreatogram (ERCP) are two methods by which pancreatic masses are frequently detected and sampled, these specimens could be sent for miRNA analysis in order to determine the malignant potential of these lesions. Wang *et al.*<sup>[60]</sup> performed microarray of 49 miRNAs on secretin-stimulated pancreatic juice of a group of patients with PDAC, CP, and normal controls. They demonstrated that miR-205, miR-210, miR-492, and miR-1427 are all significantly elevated in PDAC when compared to controls; however, this statistical significance does not exist when compared to patients with CP<sup>[60]</sup>. Additionally, by using ROC curves, they determined that combining these 4 miRNAs with serum CA19-9 the sensitivity and specificity of PDAC detection is 91% and 100% respectively, though this analysis was limited by a sample size of 6. Other groups have evaluated the pancreatic juice of patients with PDAC pre-operatively *via* ERCP and from post-operative specimens<sup>[61,62]</sup>. Sadakari *et al.*<sup>[61]</sup> analyzed the expression

of miR-155 and miR-21 in pancreatic juice sampled *via* ERCP and found that these miRNAs were significantly elevated when compared to patients with CP and healthy controls, though the levels did not correlate with pancreatic juice cytology<sup>[61]</sup>. Again these findings are consistent with those from pancreatic tissue and serum. Hong *et al.*<sup>[62]</sup> evaluated 158 miRNAs in post-operative fine needle aspiration specimens and found by qRT-PCR that miR-21, miR-27a, miR-146a, and miR-186a were significantly over-expressed in PDAC tissue and miR-217, miR-20a, and miR-96 were significantly down-regulated in PDAC tissue when compared to normal controls<sup>[62]</sup>. These two studies have demonstrated the feasibility of detecting miRNA from pancreatic juice, thus indicating the potential for using pancreatic juice biomarkers to detect early lesions given the higher concentration of miRNA in this fluid sample.

### miRNA in stool specimens

Frozen stool specimens may serve as potential non-invasive biomarker samples for PDAC. Over-expressed miRNAs from gastrointestinal cancers are shed from the exfoliative cells of the gastrointestinal tract. Intraluminal release of pancreatic juice also allows for detection of miRNAs in the stool<sup>[63-69]</sup>. Previous studies have largely focused on genetic markers of tumorigenesis and not miRNA<sup>[70]</sup>. Yang *et al.*<sup>[63]</sup> performed a feasibility study of using stool miRNAs as a potential screening tool for detection of PDAC. They evaluated expression of 5 miRNAs that had been previously shown to be over-expressed in PDAC and found that miRNA-21 and miR-155 were over-expressed and miR-216 was under-expressed in all PDAC stool specimens when compared to normal controls and CP patients. These findings are consistent with what has been found in whole pancreas, pancreatic cyst fluid, and serum specimens. Additionally, with ROC analysis they demonstrated that combining miR-21 and miR-155 in stool samples there was a sensitivity of 93.33% and specificity of 66.67%. When they combined all 3 miRNAs (miR-21, miR-155, and miR-216), the sensitivity and specificity were 83.33% each. Link *et al.*<sup>[71]</sup> selected 7 miRNAs (miR-21, miR-210, miR-143, miR-155, miR-196a, miR-216a, miR-375) and determined that like Yang's group miR-216a was found in lower concentrations in the stool of patients with PDAC. However, unlike Yang's group, they found that miR-155 was down-regulated in this population and miR-21 was unchanged in the stool of controls compared to CP or PDAC<sup>[71]</sup>.

Ren *et al.*<sup>[72]</sup> also evaluated the expression of miR-21, miR-155, miR-181a, miR-196a, and miR-210 and found that miR-181b, miR-196a, and miR-210 were significantly over-expressed in PDAC patients when compared to controls, but only miR-181b and miR-210 were elevated in CP patients, though these elevations were not significant. Ren *et al.*<sup>[72]</sup> established a positive correlation between miR-196a levels and tumor size, which had not been previously described in studies of

the serum or stool. Overall, while studies of fecal miRNA have demonstrated feasibility, conflicting data have emerged on which miRNAs are differentially expressed in the stool of PDAC, benign pancreatic disease, and normal controls.

### Salivary miRNA

The field of salivonomics has been developing since blood molecules have been found in saliva<sup>[73]</sup>. As with stool miRNA, salivary miRNA may serve as a non-invasive biomarker for PDAC. Xie *et al.*<sup>[74]</sup> is the only group to have evaluated salivary miRNA in PDAC. They conducted a microarray of 2006 miRNAs and noted that 10, including miR-4433-5p, miR-4665-3p, miR-940, miR-1273g-3p, miR-3676-5p, miR-3679-5p, miR-3940-5p, miR-4327, miR-4442, and miR-5100, were up-regulated or down-regulated in salivary samples. Of these, only miR-940 was significantly up-regulated and miR-3679-5p was significantly down-regulated in the PDAC specimens during the validation phase of the study. Until now, neither has been implicated in PDAC in the serum, stool, whole pancreas, or pancreatic juice. More studies are needed in this area.

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## ROLE OF MIRNA IN DETECTION OF PRECURSOR LESIONS

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The absence of symptoms in early disease makes PDAC a cancer that is detected at very late stages when mortality approaches 100%. Much research has been dedicated to detecting miRNA in patients with PDAC as a novel biomarker for the presence of disease. Given the aggressive nature of PDAC, detection of precursor lesions with malignant potential would be critical to increasing the survival of these patients. PanIN lesions are microscopic PDAC precursor lesions that are graded 1-3 and are categorized based on the level of architectural and cytological atypia that is present<sup>[75,76]</sup>. Grade 1a is early intraepithelial proliferative lesions that have flat architecture, while grade 1b lesions have papillary architecture. PanIN-2 lesions have moderate abnormalities and PanIN-3 lesions have severe abnormalities, though none of these lesions invade the basement membrane<sup>[75,76]</sup>. IPMN lesions are mucin-producing cystic tumors, which arise from the epithelium of the pancreatic ducts and have the potential for malignant transformation<sup>[77,78]</sup>. They are categorized by main duct type (MD) or branch duct type (BD) and histologically are classified as having low-, intermediate-, and high-grade dysplasia<sup>[3]</sup>. Their malignant potential differs based on their location within the pancreatic ducts, and MD-IPMN carry a 44%-48% risk compared to BD-IPMNs, which only carry a 11%-17% risk of malignant transformation<sup>[79-82]</sup>. MCN are also mucin-producing epithelial neoplasms with ovarian-type stroma occur primarily in middle-aged females and are located in the body and tail of the pancreas and carry a 12% chance of tumor progression<sup>[83-86]</sup>. Cystic fluid is analyzed

**Table 2** MiRNA in precursor lesions

MiRNA	IPMN	PanIN-1	PanIN-2	PanIN-3
miR-10b			↑[101]	↑[101]
miR-21	↑[23,32,87,88]	↑[100,101]	↑[98,99]	↑[98,99]
miR-92a	↑[93]			
miR-99a	↓[91,93]			
miR-99b	↓[91]			
miR-100	↓[91,93]			
miR-101	↓[32]			
miR-125b	↑[93]			
miR-126	↓[91]			
miR-130a	↓[91]			
miR-145	↑[93]			
miR-148			↓[101]	↓[101]
miR-155	↑[23,32]	↑[101]	↑[98]	↑[98]
miR-182		↑[101]		
miR-196a	↑[90]		↑[97]	↑[97]
miR-196b			↑[97]	↑[97]
miR-200a		↑[101]		
miR-200b		↑[101]		
miR-212	↓[93]			
miR-217			↓[101]	↓[101]
miR-221	↑[87]			
miR-296-5p		↑[101]		
miR-342-3p	↓[91]			
miR-483-3p	↑[88,93]			

miR: MicroRNA; ↑: Up-regulated; ↓: Down-regulated; PanIN: Pancreatic intraepithelial lesions; IPMN: Intraductal papillary mucinous neoplasm.

for CEA and amylase as other tumor markers have not demonstrated reliability in detecting malignant lesions.

As cystic neoplasms of the pancreas carry the risk of malignant transformation, determining a way to accurately predict which will progress to invasive carcinomas may guide surgical management and treatment decisions. MiRNA has been examined in PanIN lesions and IPMN as a potential candidate for early detection and the likelihood of progression to cancer. Understanding which miRNAs become deregulated early in the disease process may lead to advances for treatment decisions (Table 2).

### MiRNA in IPMN lesions

Given the increased use of abdominal imaging, more pancreatic cystic lesions are being detected. There are guidelines in place to help guide management based on cystic characteristics that are consistent with malignancy<sup>[77]</sup>. The first study looking at miRNA expression levels in precursor lesions of the pancreas was performed by Habbe *et al.*<sup>[23]</sup> who determined that miR-155 and miR-21 were over-expressed in the IPMN neoplastic epithelium, specifically those with carcinoma-in-situ<sup>[23,87]</sup>. MiR-155 was also significantly elevated in the pancreatic juice of these patients. While the levels of up-regulation of miRNA-21 and miR-155 correlated with the degree of cellular atypia found in the IPMN lesions, the study lacked long-term outcome data, highlighting the need for large and more longitudinal studies. Caponi *et al.*<sup>[32]</sup> established a relationship between expression of miR-21 in invasive IPMNs and

clinical outcome and observed that higher levels of miR-21 were correlated with worse overall and disease-free survival. Furthermore, they demonstrated that miR-155 and miR-21 had higher expression levels in invasive IPMN lesions when compared to non-invasive lesions, suggesting that these miRNAs may serve as early markers of malignant transformation<sup>[32,88]</sup>. MiR-101 has been shown to be down-regulated in invasive IPMNs when compared to non-invasive IPMNs and normal tissue. This deregulation of MiR-101 has not been described in PDAC samples, which may indicate that miR-101 plays a role in tumor invasion<sup>[32,89]</sup>. As with studies of miRNA in the serum and tissue of PDAC patients, miR-196a was found to be up-regulated in the pancreatic juice of intestinal-type IPMN<sup>[90]</sup>. In a recent study miR-100, miR-99b, miR-99a, miR-342-3p, miR-126, miR-130a were found to be down-regulated were up-regulated in high-risk vs low-risk IPMN lesions<sup>[91]</sup>. Furthermore, low miR-99b in IPMN fluid was associated with MD involvement, which is associated with a greater risk for transformation into a malignant neoplasm. Abue *et al.*<sup>[88]</sup> found that miR-483-3p was up-regulated in PDAC cells and plasma when compared to IPMN lesions and may also serve as a useful biomarker in differentiating IPMN lesions with malignant potential from normal tissue and PDAC. The down-regulated miRNAs correlated with high-risk IPMNs and may be involved in cyst invasion and progression. Lee *et al.*<sup>[92]</sup> found that miRNA expression varied amongst pancreatic cystic neoplasm. Specifically, miR-31-5p, miR-4830-5p, miR-99a-5p, and miR-375 were characteristic of serous cyst adenomas (SCA), whereas miR-10-5p, miR-202-3p, miR-210, and miR-375 differentiated MCN from SCA, IPMN, and PDAC<sup>[92]</sup>. It is unclear why this overlap in miR-375 occurs<sup>[92]</sup>. Henry *et al.*<sup>[93]</sup> found that miR-92a, miR-99a, miR-100, miR-125b, miR-145, miR-212 and miR-483 were differentially expressed between benign and pre-malignant and malignant lesions of the pancreas and they suggested that a high amount of RNA present in the cystic fluid may suggest the presence of malignant transformation<sup>[93]</sup>. As previously described miR-21, miR-155, miR-196a have been implicated in both PDAC and IPMN and given these widely replicated results, studies aimed at detecting these biomarkers in serum, saliva, and stool could help to determine, in a non-invasive way, if they are increased in pre-malignant lesions.

### MiRNA in panin lesions

Currently, PanIN lesions are found in the neighboring pancreatic tissue of patients with PDAC; however, there is no consistent way to detect the presence of these lesions<sup>[10,94-96]</sup>. Identifying a biomarker to detect PanIN lesions may be critical in early detection of PDAC. Slater *et al.*<sup>[97]</sup> demonstrated that miRNA-196a and miR-196b were elevated in PDAC and PanIN-2/3 lesions in both animal models of PDAC and humans with PDAC. Ryu *et al.*<sup>[98]</sup> demonstrated that miR-155

is up-regulated in PanIN-2 and PanIN-3 lesions when compared to neighboring healthy pancreatic tissue, but not in PanIN-1 lesions. Furthermore, miR-21 has been shown to be over-expressed in PanIN-2<sup>[98,99]</sup> and PanIN-3<sup>[98,99]</sup>, but not PanIN-1 lesions suggesting that this is a marker for later disease. These are significant findings as miR-155 and miR-21 have been shown to be up-regulated in IPMN lesions and PDAC suggesting that they are early markers for cells with malignant potential. Yu *et al.*<sup>[100]</sup> found that miR-196b was up-regulated in PanIN-3 lesions, which correlates with previous studies that have found that miR-196b is up-regulated in PDAC lesions<sup>[100,101]</sup>. Importantly, miR-21, miR-155, miR200a, miR-200b, miR-182, and miR-296-5p were deregulated as early as PanIN-1 lesions and remained deregulated until progression to PDAC, with the exception of miR-200c that normalized in PanIN-3 lesions. A recent publication describing miRNA expression in PanIN lesions found that miRNA-148a and miR-217 were down-regulated while miR-10b was up-regulated in PanIN-2 and PanIN-3 lesions<sup>[101]</sup>. While miR-21 has been shown repeatedly to be over-expressed in PDAC, there are conflicting studies on its deregulation in early PanIN lesions suggesting that it may represent a later and more aggressive dysregulation in the progression to PDAC. A non-invasive method to detect advanced PanIN lesions would represent a significant advance in the field.

## DISCUSSION

While PDAC is the fourth most common cause of cancer-related deaths, there is still no reliable way to detect early disease and patients present with late-stage disease with a nearly 100% mortality. Research in the field of biomarkers shows a great deal of promise as current research aims to understand the molecular mechanisms and stromal microenvironment of this deadly tumor. MiRNA are small nucleotides that control the genetic expression in all cells and importantly in an organ-specific manner. Abberant miRNA expression has been identified in various cancers<sup>[102-106]</sup>, and factors such as transcriptional deregulation, epigenetic alterations, mutations, DNA copy number abnormalities, and defects in the miRNA biogenesis pathway may account for these differences in expression<sup>[107,108]</sup>. C-myc and p53 are two transcriptional factors that have been associated transcriptional deregulation of miRNA<sup>[109-111]</sup>. Epigenetic regulation of miRNAs by DNA methylation and histone tail modification play a role in miRNA expression through chromatin remodeling<sup>[105,112-114]</sup>. Both germ-line and somatic mutations are responsible for miRNA expression levels in various types of cancers<sup>[115-117]</sup>. It has been described by Calin *et al.*<sup>[118]</sup>, that miRNAs are located a fragile sites on the chromosome, minimal regions of loss of heterozygosity, minimal regions of amplifications, and common breakpoints, thus increasing the risk for DNA copy abnormalities. DNA copy abnormalities have been found in melanoma, breast cancer, ovarian cancer,

leukemia, colorectal cancer<sup>[119-122]</sup>. Lastly, defects in miRNA biogenesis pathway may contribute to varying expression levels and cancer phenotype as miRNA undergoes complex processing intracellularly prior to reaching its mature form<sup>[123-127]</sup>. In addition to the aforementioned mechanisms, dietary components, such as folate, retinoids, curcumin, and Vitamin D have been implicated in the modulation of miRNA expression<sup>[128-130]</sup>. Some miRNAs have been shown to increase muscle loss in cancer cachexia and specifically, increased miR-21 levels have been shown to increase muscle breakdown in pancreatic cancer<sup>[131,132]</sup>. Deeper understanding of the regulatory mechanisms of miRNA expression will hopefully give new insight to the factors responsible for miRNA deregulation and lead to miRNA-based diagnostic testing and miRNA-directed therapy for PDAC.

Some limitations that exist with the current miRNA research at this time include standardization of extraction, reproducibility of testing, diagnostic yield in the various sample methods, and small sample sizes. Additionally, despite finding biomarkers for this disease, there is limited evidence that miRNA will impact PDAC-related mortality. Dysregulation of miRNA affects the cell cycle, proliferation, apoptosis, epigenetics, oncogenesis, tumor differentiation, tumor invasion, tumor metastasis and migration, prognosis, and chemoresistance in numerous cancers<sup>[133]</sup>. Increased efforts to understand the biological function of miRNA expression and its effects on cancer development are needed.

Despite these limitations, great advances have been made in this field and now miRNA expression is being analyzed not just in pancreatic tissue and cystic fluid, but also in stool, saliva, and serum; which would lead to non-invasive ways by which to analyze the expression levels of miRNA in patients at high risk. There have been great efforts to identify which of the greater than 2000 miRNAs are deregulated in PDAC and its precursor lesions and miRNA-21, miR-155, and miR-196b seem to be dysregulated in both early lesions and advanced cancer and show promise as potential screening tools in the future.

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## Antitumor effects of the benzophenanthridine alkaloid sanguinarine: Evidence and perspectives

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### Abstract

Historically, natural products have represented a significant source of anticancer agents, with plant-derived drugs becoming increasingly explored. In particular, sanguinarine is a benzophenanthridine alkaloid obtained

from the root of *Sanguinaria canadensis*, and from other poppy *Fumaria* species, with recognized anti-microbial, anti-oxidant and anti-inflammatory properties. Recently, increasing evidence that sanguinarine exhibits anticancer potential through its capability of inducing apoptosis and/or antiproliferative effects on tumor cells, has been proved. Moreover, its antitumor seems to be due not only to its pro-apoptotic and inhibitory effects on tumor growth, but also to its antiangiogenic and anti-invasive properties. Although the precise mechanisms underlying the antitumor activity of this compound remain not fully understood, in this review we will focus on the most recent findings about the cellular and molecular pathways affected by sanguinarine, together with the rationale of its potential application in clinic. The complex of data currently available suggest the potential application of sanguinarine as an adjuvant in the therapy of cancer, but further pre-clinical studies are needed before such an antitumor strategy can be effectively translated in the clinical practice.

**Key words:** Sanguinarine; Cancer; Apoptosis; Cell-cycle; Chemotherapy

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**Core tip:** Sanguinarine is a benzophenanthridine alkaloid isolated from the root of *Sanguinaria canadensis*, and other poppy *Fumaria* species, which exhibits a clear-cut anticancer potential by inducing apoptosis and/or antiproliferative effects on tumor cells. Sanguinarine also shows antiangiogenic and anti-invasive properties, as demonstrated *in vitro* and *in vivo*. In consideration of the multiple biological effects of sanguinarine, which suggest its possible use in cancer therapy, further detailed pharmacokinetic and toxicologic studies are required to assess both the efficacy and safety of the compound before proposing a possible translation into the clinic.

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## INTRODUCTION

Tumor initiation is the result of multiple genetic and epigenetic events. Transformed cells are characterized by indefinite proliferation, apoptosis-resistance and the capability to metastasize and support angiogenesis<sup>[1]</sup>.

Chemotherapy, irradiation and/or immunotherapy represent the gold standard approach for the treatment of cancer worldwide. The increased frequency of tumor relapse and the toxicity of the anticancer drugs, however, often reduce the therapeutical effectiveness of several antitumor therapy protocols. Therefore, the identification of more effective therapeutic protocols is needed and, in this direction, phytochemicals may represent an attractive alternative because of their low toxicity and low cost<sup>[2]</sup>. In this scenario, sanguinarine (Figure 1) and chelerythrine are the principal members of quaternary benzo[*c*]phenanthridine alkaloids (QBAs)<sup>[3]</sup> obtained from *Sanguinaria canadensis*, *Chelidonium majus*, and *Macleaya cordata*. Alkaloids include a large group of secondary metabolites (SMs) that differ in relation to structure, function and biodistribution<sup>[4]</sup>. In the past, QBAs have attracted the attention of many pharmacologists because of their own low toxicity<sup>[5,6]</sup> and their multiple biological activities, such as the antitumor<sup>[7]</sup>, antimicrobial<sup>[8,9]</sup>, anti-inflammatory<sup>[10]</sup>, anti-HIV<sup>[11]</sup>, anti-platelet<sup>[12]</sup>, anti-angiogenesis<sup>[13]</sup>, and antiparasitic activities<sup>[14-16]</sup>. The influence of QBAs on the activity of various important biological enzymatic pathways has been also demonstrated<sup>[7]</sup>. For long times, sanguinarine-containing herbs were believed to possess anticancer activity but only recently evidence that sanguinarine possesses a strong anti-neoplastic activity, which is mediated mainly by the induction of tumor cell apoptosis has been proved.

This review summarizes the most recent findings on the molecular mechanisms underlying the antitumor activity of sanguinarine both *in vitro*, in a variety of human tumor cells, and *in vivo* in selected experimental tumor models, together with the rationale of its potential application in clinical practice.

## SANGUINARINE INDUCES APOPTOSIS IN TUMOR CELLS

Physiologically, the human body controls homeostasis by eliminating damaged and aged cells by means of a genetically programmed process named apoptosis<sup>[17,18]</sup>. Tumor cells evade apoptosis and grow indefinitely. Several proteins, among which are caspases, pro-

apoptotic Bax and anti-apoptotic B cell lymphoma (Bcl)-2, cytochrome c, and apoptotic protease activating factor -1, carry out the apoptotic programme either by intrinsic or extrinsic pathways. The first one is dependent on mitochondria, whereas the second one is initiated by the so-called death receptors (DRs). Selected anti-apoptotic proteins, among which Bcl-2, have been found over-expressed in different types of cancers. The down-regulation of anti-apoptotic proteins in cancer cells represents a promising therapeutic strategy of intervention in cancer therapy.

A number of plant-derived agents, have been shown to be capable of hampering disease progression by inducing cell apoptosis in multiple types of human and experimental cancers. Recently QBAs, and particularly sanguinarine, have been indicated as potential anti-cancer compounds. In detail, it has been reported that micromolar concentrations of sanguinarine are capable of inhibiting tumor cell growth, and this inhibitory effect is associated with cell cycle arrest and induction of apoptosis<sup>[19-22]</sup>. The anti-proliferative and/or pro-apoptotic activities of sanguinarine have been demonstrated in *in vitro* studies on several cancer cell types including epidermal<sup>[23]</sup>, keratinocyte<sup>[24,25]</sup>, prostate<sup>[26-28]</sup>, cervical<sup>[29]</sup>, breast<sup>[20,30-33]</sup>, leukaemia<sup>[34,35]</sup>, lymphoma<sup>[36]</sup>, melanoma<sup>[37-39]</sup>, colon<sup>[40,41]</sup>, colorectal<sup>[21]</sup>, gastric<sup>[42]</sup>, pancreatic<sup>[19]</sup>, lung<sup>[22]</sup>, neuroendocrine<sup>[43]</sup>, osteosarcoma<sup>[44]</sup>, and human neuroblastoma cells<sup>[45]</sup>. By contrast, there are few studies on the *in vivo* effectiveness of sanguinarine administration *per os*<sup>[46,47]</sup> in animal tumor models<sup>[33,48]</sup>.

It has been reported that sanguinarine exerts an antiproliferative activity on murine melanoma cells both *in vitro* and *in vivo* (B16 melanoma 4AS in the syngeneic host C57BL/mice), as well as in A375 human melanoma xenografts in athymic nude mice<sup>[48]</sup>. We also have conducted a study aimed at evaluating the anti-tumor effect of sanguinarine both *in vitro* and *in vivo* in a rat colorectal cancer model (DHD/K12/TRb cell line)<sup>[49]</sup>. We found that the *in vitro* addition of sanguinarine has a dose-dependent inhibitory effect on the proliferation of DHD/K12/TRb cells and induces tumor cell apoptosis. Sanguinarine also showed a clear-cut *in vivo* anti-tumor activity, leading to an inhibition of tumor growth higher than 70%<sup>[49]</sup>. The sanguinarine-induced inhibition of tumor growth was associated with its pro-apoptotic effect on tumor cells, as confirmed by the *ex-vivo* histopathological examinations performed on experimental tumor sections and by TUNEL assay<sup>[49]</sup>.

It is known that sanguinarine-induced apoptosis occurs through multiple pathways, including the activation of nuclear factor- $\kappa$ B (NF- $\kappa$ B)<sup>[50]</sup>, the mitochondrial damage resulting in activation of the caspase machinery<sup>[24]</sup> and the cell cycle arrest<sup>[27]</sup>. In detail, the sanguinarine-induced apoptosis occur either *via* a mitochondrial pathway dependent on caspase-9 or by the DR pathways, with the activation of caspase 8. The activation of caspase 3, which represents a key factor for apoptosis execution in both pathways, and the following

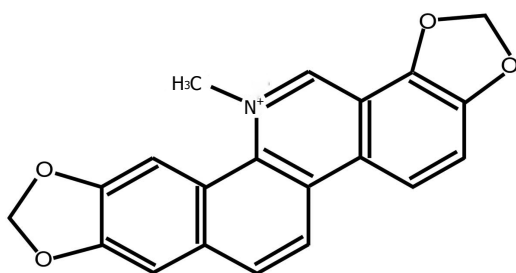


Figure 1 Chemical structure of sanguinarine.

cleavage of PARP together with the down-regulation of Bcl-2 and c-FLIP, may play a very important role in the apoptosis induced by sanguinarine<sup>[26,51,52]</sup>. Studies performed in human neuroblastoma cells SH-SY5Y have shown that sanguinarine reduces the expression of anti-apoptotic genes, particularly of NOL3, BCL2, and HRK genes<sup>[45]</sup>. A down-regulation of pro-caspase 3, Bcl-2, cIAP2, XIAP, and c-FLIPs<sup>[20,52]</sup> has been also observed in basal cell-like MDA-MB-231 human breast carcinoma cells treated with sanguinarine. The effect of sanguinarine treatment has been evaluated also on the expression levels of Bax and Bcl-2 proteins in immortalized human keratinocytes (HaCaT)<sup>[24,25]</sup>, human leukaemia JM1 and K562 cells<sup>[35]</sup> and in HeLa and SiHa human cervical tumor cells<sup>[53]</sup>. These findings indicate that sanguinarine, depending on the dose employed, down-regulates the expression levels of Bcl-2 protein while increasing those of Bax protein, which is a key regulator of mitochondrial damage. Notably, Bax expression has been associated with an increased sensitivity of cancer cells to chemotherapy<sup>[54]</sup>, whereas an increase of Bcl-2 has been associated with the occurrence of drug-resistance phenomena<sup>[55]</sup>.

It has been proved that sanguinarine is capable of inducing DNA damage, acting as an intercalating agent<sup>[56,57]</sup>, and also a very rapid cell apoptosis which does not seem to be mediated by a p53-dependent DNA damage signalling in human colon cancer<sup>[41]</sup> and in malignant melanoma cells<sup>[38]</sup>.

The concentration of sanguinarine plays a key role in the induction of cell death. Consistently, both apoptotic and non-apoptotic cell death pathways have been observed in response to sanguinarine. Thus, a sanguinarine-related and bimodal cell death effect, which consists of two different types of cell death, *i.e.*, by apoptosis (induced by low SA concentration; characterized by caspase 3 and PARP positivity) and oncosis (induced by high SA concentration; characterized by caspase 3 and PARP negativity), has been demonstrated in various cancer cells types<sup>[52]</sup>.

## SANGUINARINE INDUCES ALTERATIONS IN CELL CYCLE

Tumor cells are characterized by deregulated proliferation. Conversely, normal cells proliferation is the

results of the action of selected growth signals [cyclins and cyclin-dependent kinases (CDKs)] and anti-growth signals (p21 and p27 proteins). Cyclins and CDKs cooperate in G1 for the initiation of the S phase and in G2 for inducing mitosis, whereas p21 and p27 selectively block the catalytic activity of CDK. Following addition of anti-mitogenic compounds or DNA injury, p21 and p27 bind to cyclin-CDK complex blocking their catalytic activity and consequently the cell cycle progression.

Actually a number of inhibitors and/or regulators of the cell cycle, among which sanguinarine, are suggested as potential antitumor agents. Sanguinarine treatment (0.2-2 mol/L for 24 h) blocks cell cycle by enhancing the expression of CDK inhibitors and by reducing not only cyclin D1, D2 and E, but also CDK2, 4 and 6 in human prostate cancer cells<sup>[27]</sup>. This alkaloid also up-regulates p27 and down-regulates cyclin D1, while inhibiting the activation of STAT3, as demonstrated *in vitro* in basal cell-like MDA-MB-231 human breast cancer cells and *in vivo* in a murine breast cancer model<sup>[33]</sup>. Holy *et al.*<sup>[31]</sup> studied the effects of sanguinarine (5-10  $\mu$ mol/L) on the cell cycle regulatory molecules, by immunocytochemistry, that visualized the cyclin D1 and topoisomerase II in MCF-7 breast cancer cells. They reported that sanguinarine-mediated cellular events induce cell cycle arrest in G0/G1 and inhibit cell proliferation, which is associated with a striking re-localization of cyclin D1 and topoisomerase II from the nucleus to the cytoplasm.

## SANGUINARINE-INDUCED APOPTOSIS THROUGH THE GENERATION OF REACTIVE OXYGEN SPECIES

Apoptosis induced by sanguinarine has been associated also with the production of reactive oxygen species (ROS)<sup>[20,36,52,58]</sup>. ROS are a group of highly reactive molecules, among which are superoxide anion radical, hydrogen peroxide, singlet oxygen, and hydroxyl radical. ROS are the products of the oxygen metabolism within the cell. ROS are known as key regulators of normal cell proliferation and differentiation, however, high levels of ROS have also been associated with damage of DNA and proteins and thus with the occurrence of apoptosis<sup>[59,60]</sup>. Moreover, an overdone oxidative stress has been shown capable of inducing a reduction of the normal mitochondrial membrane potential, which in turn leads to apoptosis<sup>[21,61-63]</sup>. It has been shown that ROS generation, is crucial for the apoptosis induced by sanguinarine in human breast cancer<sup>[52]</sup>, SK-Mel-2 human melanoma<sup>[37]</sup>, human prostate cancer<sup>[25]</sup> and in both HCT-116<sup>[21]</sup> and HT-29 human colon cancer cells<sup>[40]</sup>. Consistently, pre-treatment of tumor cells with antioxidants such as *N-acetylcysteine* or glutathione counteracts the apoptosis induced by sanguinarine<sup>[21,32,37,52]</sup>. Moreover, the over-expression of cyclooxygenase-2 (COX-2) also rescues prostate cancer cells from sanguinarine-induced apoptosis by

inhibiting the activity of NO synthase, thus suggesting the possibility to use a combination of COX-2 inhibitors and sanguinarine in the treatment of human prostate cancer<sup>[28]</sup>.

## SANGUINARINE-MEDIATED INHIBITION OF NF- $\kappa$ B

The molecular pathways associated with carcinogenesis are linked also with chronic inflammation, which emerges as an important co-factor in tumor development. The NF- $\kappa$ B controls the inflammatory gene expression and recently it has been suspected to be involved also in the control of tumor development<sup>[64]</sup>. Resting NF- $\kappa$ B localizes within the cell cytoplasm in the form of a heterodimer composed by p50, p65, and the inhibitory subunit I $\kappa$ B $\alpha$ <sup>[65]</sup>. Following activation, the I $\kappa$ B $\alpha$  protein is phosphorylated, ubiquitinated and finally degraded. Then, the p50 and p65 reach the nucleus of cell, where they interact with selected DNA sequences localized in the promoter region of various genes, leading to their transcription. Consistently, the NF- $\kappa$ B signalling pathway has been indicated as a key-target for the development of new chemotherapeutic approaches in cancer.

Sanguinarine has been suggested as a potential actor in the control of NF- $\kappa$ B-dependent pathological responses by blocking phosphorylation and degradation of I $\kappa$ B $\alpha$ . Studies by Chaturvedi *et al.*<sup>[50]</sup> showed that in human myeloid ML-1a cells, the treatment with sanguinarine is capable of abrogating, dose- and time-dependently, the activation of NF- $\kappa$ B induced by tumor necrosis factor.

## INHIBITION OF TUMOR ANGIOGENESIS BY SANGUINARINE

Many reports indicate that sanguinarine exerts antitumor activity not only by inhibiting tumor cells migration and/or invasion, but also by repressing angiogenesis<sup>[22,66]</sup>. Since solid tumors require active angiogenesis, the inhibition of endothelial cell proliferation result in the inhibition of tumor growth and progression. The best known angiogenic growth factor is represented by VEGF. Several studies have explored the relationship existing among sanguinarine, angiogenesis and metastatization. In particular, Eun and Koh<sup>[13]</sup> showed that sanguinarine inhibits the VEGF-induced endothelial cell migration, sprouting and survival *in vitro*, and blocks blood vessel formation *in vivo* in different experimental models. Furthermore, Basini *et al.*<sup>[67]</sup> showed that sanguinarine is capable of blocking the VEGF-induced blood vessel growth. Depending on the concentration used, sanguinarine also inhibits VEGF secretion in human microvascular endothelial cells HMVEC as well as in A549 lung cancer cells<sup>[68]</sup>. This inhibitory effect has been associated with the suppression of the phosphorylation of Akt, p38 and VE-cadherin, which are well known modulators of the VEGF signal transduction pathway<sup>[67,69]</sup>. Moreover,

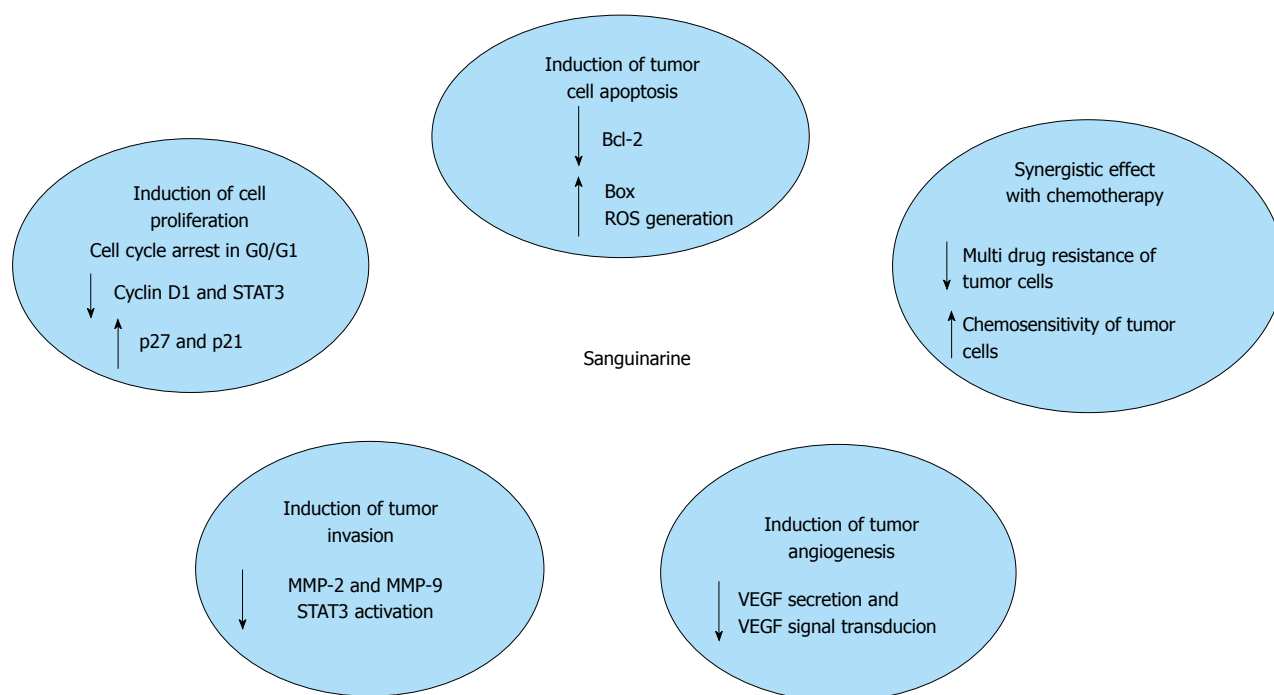
sanguinarine enhances apoptosis in human mammary adenocarcinoma MCF-7 through the inhibition of VEGF release, induced by generation of ROS<sup>[32]</sup>. Sanguinarine also inhibits angiogenesis in preclinical experimental tumor models, such as mouse melanoma<sup>[48]</sup> and rat colorectal cancer, as we reported previously<sup>[49]</sup>. In both the experimental studies, the therapeutic efficacy of sanguinarine could not be attributed only to a direct anti-proliferative activity but also to the inhibition of tumor angiogenesis induced by this alkaloid.

The rationale of using VEGF-targeted therapies in the treatment of cancer lies in the possibility they offer to counteract the over-expression of VEGF provoked by chemotherapeutic drugs and radiation<sup>[70]</sup>. Consistently, dacarbazine, which is used in the therapy of human melanoma, induces increased VEGF-A production<sup>[71]</sup>, and dacarbazine-resistant melanoma cells show an increased *in vivo* growth together with an increased microvessel density<sup>[72]</sup>. These studies suggest the potential application of sanguinarine, alone or in association with other VEGF inhibitors, in the control of both angiogenesis and metastatization of solid tumors.

## INHIBITION OF TUMOR CELL INVASION BY SANGUINARINE

In solid tumors, neoplastic cells can penetrate the basement membrane by proteolysis and initiate metastatization, which accounts for the majority of cancer deaths. Metastatization is the result of the cooperation between cancer cells and a sort of "inflamed" micro-environment<sup>[73]</sup>. Consistently, inflammatory cells are an important source of proteases capable of causing a degradation of extracellular matrix, which represents a crucial event in the initiation of cancer cell invasion. Matrix metalloproteinases (MMPs) are an example of agents capable to degrade the extracellular matrix<sup>[74,75]</sup> and an over-production of these enzymes has been detected in various metastatic cancers<sup>[76-78]</sup>. Indeed, there is a strong evidence that increased expression and activation of MMP-2 and MMP-9 is present in tumor tissues but not in normal tissues in patients with breast cancer<sup>[79]</sup> and that MMP-2 induces cancer cell migration by means of its interaction with collagen<sup>[80]</sup>.

Recent findings show that sanguinarine inhibits the tetradecanoylphorbolmyristate acetate (TPA)-induced breast cancer cell migration and invasion while inhibiting the expression of MMP-9, NF- $\kappa$ B and AP-1 signaling pathways<sup>[81]</sup>. Moreover, previous studies by Sun *et al.*<sup>[66]</sup> have showed that sanguinarine reduces prostate cancer cell growth and invasion by the inhibition of STAT3 activation. STAT3 is constitutively active in human prostate cancer metastases and has a key role in the phenomena of tumor cell migration and invasion in different types of cancer<sup>[82-84]</sup>. Since the invasivity and/or metastatic potential of a tumor parallel its malignancy, the above findings indicate that sanguinarine may play a crucial role as a therapeutic agent in anticancer therapy



**Figure 2** Cellular and molecular mechanisms underlying the antitumor activity of sanguinarine, as assessed by means of *in vitro* and *in vivo* experimental studies. ROS: Reactive oxygen species; Bcl: B cell lymphoma; VEGF: Vascular endothelial growth factor; MMP: Matrix metalloproteinase; STAT: Signal transducer and activator of transcription.

not only for its ability to induce apoptosis but also for its own “anti-invasive” properties.

## SYNERGISTIC INTERACTION OF SANGUINARINE WITH CHEMOTHERAPEUTIC AGENTS

Several plant SMs are capable of influencing effectively the multidrug resistance phenomenon in tumor cells and are able also to “chemo-sensitize” them<sup>[85-89]</sup>. Some clinical studies have explored the possible advantage of combining natural products with classical chemotherapeutic regimens<sup>[90-92]</sup>. Phytotherapy, which employs plants extracts, is still used worldwide for the treatment of various human diseases. However, evidence has been proved that combinations of individual SM in an extract may exert synergistic effects. As an example, a recent study demonstrates that the combined use of non-toxic concentrations of sanguinarine and digitonin with doxorubicin, synergistically sensitizes Caco-2 (human colorectal adenocarcinoma) and CEM/ADR5000 adriamycin-resistant leukemia cells and increases the cytotoxicity of the chemotherapeutic agent doxorubicin<sup>[93]</sup>. In this regard, it is worth mentioning that the main advantage of combination therapies is represented by the possibility of reducing the doses and thus the toxicity of chemotherapy, while retaining its own efficacy. Thus, because of its potential synergistic interaction with chemotherapeutic agents, the therapeutic use of sanguinarine as an adjuvant, in association with chemotherapy, might be considered as a theoretical option in cancer therapy.

## CONCLUSION

A successful resolution to the design of antitumor drugs relies, at least in part, on the possibility to overcome the intrinsic resistance to undergo apoptosis detected in many transformed cells. Findings from the studies above mentioned show that sanguinarine is capable of inhibiting tumor growth through different molecular pathways (Figure 2). A summary of the results is shown in Table 1. In conclusion, despite sanguinarine has been extensively studied, the precise mechanisms responsible for its antitumor effects still have not been completely elucidated and are strictly dependent on the cell type studied. According to the results obtained so far, it can be said that the anti-tumor action of this alkaloid is the result of a combined effect both on proliferation and invasiveness of tumor cells, that on regulation of the complex phenomena of tumor angiogenesis. In particular, owing to its pro-apoptotic potential, sanguinarine is a good candidate for the development of new anticancer therapies either when used alone or in combination with other chemotherapeutic regimens. More extensive investigation and greater caution are needed, however, to clarify the following important issues. First of all, most of the studies above mentioned have been performed *in vitro* using cancer cell lines, whereas there are only a few *in vivo* studies validating the efficacy and safety of sanguinarine administration in animal tumor models. The results of our *in vivo* studies confirm the effectiveness and safety of using oral sanguinarine administration to control tumor growth in rats<sup>[49]</sup>. Similar results had been previously reported in a murine melanoma model<sup>[48]</sup>. In that study, and

**Table 1** The antitumor activity of sanguinarine

Sanguinarine induces apoptosis in tumor cells through multiple pathways, including the activation of NF- $\kappa$ B, the mitochondrial damage and cell cycle arrest
Sanguinarine-induced apoptosis is associated with the decrease of Bcl-2 and the increase of Bax proteins and the generation of reactive oxygen species
Sanguinarine causes cell cycle arrest by increasing the expression of p27 and decreasing cyclin D1, D2 and E, and CDK2, 4 and 6
Sanguinarine inhibits tumor progression associated with chronic inflammation <i>via</i> the inhibition of NF- $\kappa$ B
Sanguinarine inhibits tumor angiogenesis through the inhibition of VEGF secretion and VEGF signal transduction (Akt, p38 and VE-cadherin)
Sanguinarine has an inhibitory effect on tumor cell migration by the inhibition of MMP-9 and STAT3 activation
Sanguinarine exerts a synergistic effect with chemotherapeutic agents and enhances the chemosensitivity of Caco 2 and CEM/ADR5000 adriamycin-resistant leukemia cells

NF- $\kappa$ B: Nuclear factor- $\kappa$ B; CDK: Cyclin-dependent kinase; Bcl: B cell lymphoma; VEGF: Vascular endothelial growth factor; STAT: Signal transducer and activator of transcription.

in agreement with our findings, the anti-proliferative and anti-angiogenic effects of the oral sanguinarine administration were observed at a dosage, *i.e.*, 5 mg/kg, devoid of apparent toxicity. On the other hand, an increase of serum levels of transaminases and LDH, hepatic vacuolization, lipid accumulation and peroxidation in the liver and a reduction of triglycerides, were observed in mice treated with high-dose sanguinarine (10 mg/kg), suggesting liver injury<sup>[94]</sup>. Previous studies showed that sanguinarine can cause physiological dysfunction in skeletal, smooth and cardiac muscles<sup>[95-97]</sup>. More recent studies clearly indicate that sanguinarine acts as a pro-apoptotic factor and alters mouse normal embryonic development at a physiological dosage, *i.e.*, 0.5-2  $\mu$ mol/L, which are obtained *via* dietary intake<sup>[98]</sup>. These experimental results need further confirmation in view of the possible administration of the compound in pregnancy, although at present no teratogenic effects have been reported in humans.

Most of the studies actually known have reported that sanguinarine exerts cytotoxic activity selectively on cancer cells. Consistently, sanguinarine is a negative regulator of human epidermoid carcinoma cells (A431) but not of normal epidermal keratinocytes<sup>[23]</sup>. Evidence of this differential activity have been reported recently, showing that mouse lymphocytic leukemic cells are more sensitive to sanguinarine than normal splenocytes<sup>[99]</sup>.

It is a matter of fact, however, that sanguinarine has been listed as responsible for the toxicity of *Argemone mexicana* seed oil<sup>[100-102]</sup>. Das *et al.*<sup>[103]</sup> reported that topical use of argemone oil (0.15-0.3 mL) or sanguinarine (4.5-18  $\mu$ mol/L) followed by application of TPA induces tumor development in a murine experimental model. Ansari *et al.*<sup>[104]</sup> also reported that intraperitoneal administration of sanguinarine induces DNA damage in Swiss albino mice. Sanguinarine in argemone oil, is suspected to cause glaucoma<sup>[101,102]</sup>. Argemone oil increases incidence of bladder cancer in animal models<sup>[103]</sup> and of gall bladder cancer in humans<sup>[104]</sup>. Furthermore, sanguinarine extract from bloodroot (*Sanguinaria canadensis*), previously used in oral hygiene products, was discontinued until a link between product administration and occurrence of leukoplakia was established<sup>[105,106]</sup>. Hepatic microsomes transform sanguinarine in a mutagenic epoxide and the same sanguinarine is capable of activating polycyclic aromatic

hydrocarbon signaling<sup>[107]</sup>. However, related to this topic, the results available in literature are not univocal<sup>[3]</sup>. So that is still not clear if sanguinarine may act as a carcinogenic without the cooperation of other risk factors or it is capable of acting in concert with various co-carcinogens. In light of the above facts, the possibility of obtaining beneficial effects in humans by using sanguinarine remains largely unpredictable.

Finally, since at present there is increasing interest in nanotechnology application in cancer therapy and in order to prevent the potential toxic and/or side effects induced by sanguinarine administration, *in vivo* studies might be performed in experimental tumor models by encapsulating the alkaloid in tumor-targeted nanoparticles<sup>[108]</sup>, which accumulate preferentially in tumors recognizing single cancer cells for diagnosis and treatment. Actually, the administration of sanguinarine (10 mg/kg) *per os* and encapsulated by lipid nanoparticles (SG-SLNs), has been shown to induce an anti-inflammatory effect in an LPS-induced endotoxin shock murine model, and the pharmacokinetic studies have proved that the AUC<sub>0-24</sub> and C<sub>max</sub> of SG-SLNs were significantly increased when compared to those of sanguinarine alone<sup>[109]</sup>.

In conclusion, several studies indicate the potential application of sanguinarine as an adjuvant in the therapy of cancer, but further detailed pharmacokinetic and toxicology studies, which have to be conducted in appropriate experimental tumor models, are absolutely required to assess the efficacy and safety of this compound before such an antitumor strategy can be translated in clinical trials.

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## ***Helicobacter pylori* infection and gastric carcinoma: Not all the strains and patients are alike**

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### **Abstract**

Gastric carcinoma (GC) develops in only 1%-3% of *Helicobacter pylori* (*H. pylori*) infected people. The role in GC formation of the bacterial genotypes, gene polymorphisms and host's factors may therefore be important. The risk of GC is enhanced when individuals are infected by strains expressing the oncoprotein CagA, in particular if CagA has a high number of repeats containing the EPIYA sequence in its C'-terminal variable region or particular amino acid sequences flank the EPIYA motifs. *H. pylori* infection triggers an inflammatory response characterised by an increased secretion of some chemokines by immunocytes and colonised gastric epithelial cells; these molecules are especially constituted by proteins composing the interleukin-1beta (IL-1 $\beta$ ) group and tumour necrosis factor-alpha (TNF- $\alpha$ ). Polymorphisms in the promoter regions of genes encoding these molecules, could account for high concentrations of IL-1 $\beta$  and TNF- $\alpha$  in the gastric mucosa, which may cause hypochlorhydria and eventually GC. Inconsistent results have been attained with other haplotypes of inflammatory and anti-inflammatory cytokines. Genomic mechanisms of GC development are mainly based on chromosomal or microsatellite instability (MSI) and deregulation of signalling transduction pathways. *H. pylori* infection may induce DNA instability and breaks of double-strand DNA in gastric mucocytes. Different *H. pylori* strains seem to differently increase the risk of cancer development run by the host. Certain *H. pylori* genotypes (such as the *cagA* positive) induce high degrees of chronic inflammation and determine an increase of mutagenesis rate, oxidative-stress, mismatch repair mechanisms, down-regulation of base excision and genetic instability, as well as generation of reactive oxygen species that modulate apoptosis; these phenomena may end to trigger or concur to GC development.

**Key words:** *Helicobacter pylori* infection; CagA; CagA gene polymorphism; Haplotype; Human gene mutation;

Gene methylation; Gastric carcinoma; Inflammatory cytokine

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**Core tip:** CagA and the *cagA* types may play different roles in the intestinal and diffuse histotypes of gastric carcinoma (GC); The current criteria of *Helicobacter pylori* (*H. pylori*) strain classification based on their carcinogenic potential gave rise to confusion and should be unified. The possible role of inflammatory cytokine haplotypes in GC development should be reassessed taking into account some host's factors, the most important being different ethnic origin. Infection by the *cagA* positive *H. pylori* genotype may determine an increased inflammatory response and a consequent enhancement of mutagenesis rate, oxidative-stress, reactive oxygen species generation, dysfunction of DNA repair mechanisms, genetic instability and resultant high risk of GC development.

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## INTRODUCTION

Gastric carcinoma (GC) is the second most frequent cause of death from cancer worldwide and the most common example of a neoplasia developing on a ground of a chronically inflamed mucosa. GC has also another record: It is the only known malignant tumour that can develop as a consequence of a chronic bacterial infection<sup>[1]</sup>. In 1994, the International Agency for Research on Cancer classified the organism responsible for the infection, *Helicobacter pylori* (*H. pylori*) - a Gram negative, microaerophilic and spiral-shaped species that finds its *habitat* in human stomachs - as a definite carcinogen to humans (Group 1): The connection of *H. pylori* with gastric cancer was considered similar to that existing between the cigarette smoke and lung cancer<sup>[2]</sup>.

### **The bacterium *H. pylori*: Not all the strains are alike**

It soon became clear, however, that such comparison was reductive and too simplistic, especially because the ability of these bacteria to trigger a neoplasm is not limited to the inflammatory and immune response to the infection that they cause, but it also resides in a series of bacterial factors capable of prompting and modulating the carcinogenic process<sup>[3]</sup>.

As is the case for all diseases, also GC develops from the concomitance of three factors: The etiological agent, the host and the environment. Of course, many other factors may occur; for example, the cancer histological

variant, the degree of differentiation of the neoplasia *etc.*<sup>[4]</sup>. Regarding the etiological agent, *H. pylori*, there are many indications that not all strains are equivalent in their carcinogenic potential and that those expressing an immunodominant peptide determinant called CagA (cytotoxin associated gene A), are endowed with an increased inflammatory and carcinogenic potential<sup>[5-9]</sup>. A first point has therefore been established: Strain genomic diversity corresponds to different ability to promote cancer. The possibility that a bacterial factor (CagA) could trigger or concur to the development of GC is one of the most important scientific achievements following the isolation of *H. pylori*.

### **The importance of being called CagA positive**

It is worthwhile mentioning the steps that paved the way to the discovery of CagA. At the end of the 80ies, Leunk *et al.*<sup>[10]</sup> first proposed that *H. pylori* should not be considered a clonal pathogen, as a relevant proportion of isolates produce a vacuolating toxin, which could account in part for the gastric mucosa damage observed in infected individuals. Afterward, our group suggested that infection by cytotoxic strains increased the risk of developing peptic ulceration<sup>[11]</sup> and that virtually all cytotoxic isolates also secreted a 120 kDa highly immunogenic protein, later called CagA<sup>[12]</sup>. In 1992, Crabtree *et al.*<sup>[13]</sup> demonstrated, through *ex vivo* experiments, that such a protein was produced either by the bacteria isolated in culture and also by the organisms colonizing the gastric epithelium: Gastric antral explants of patients with GC and other pathologies were cultured *in vitro* for a few days; the bacteria that colonized the mucosa kept on secreting this peptide, which could lastly be detected in the culture medium by using immunological methods<sup>[13]</sup>. In 1993, the same team established, for the first time, the existence of a relationship between infection by strains expressing the 120 kDa protein and GC development<sup>[14]</sup>. Their observations were important also because these researchers found anti-120 kDa protein mucosal IgA antibodies even in the absence of systemic IgG to this protein and, in some patients, also in cases with urease negative biopsies (false negatives). In the same year (1993), the gene encoding for the 120 kDa protein was cloned, sequenced and called *cagA* due to the strict association of protein expression with cytotoxin production<sup>[5]</sup>. As a result of these findings, the number of studies dealing with the characterisation of CagA and its potential carcinogenicity increased exponentially and results lead to the common conclusion that such peptide is a major factor in gastric carcinogenesis.

CagA is the product of the homonymous gene placed at the end of the so-called pathogenicity island (PAI) *cag*, a fragment of DNA encompassing an approximately 40 kb cluster of genes involved in virulence. In the field of bacteriology there are numerous examples of PAIs harboured by diverse bacterial species or their virulent variants, whether they are human (*Bordetella*

*pertussis*, *Escherichia coli*, *Salmonella enterica*, etc.) or plant pathogens (*Agrobacterium tumefaciens*). In some species, PAI genes cooperate to translate effectors (mainly proteins) endowed with carcinogenic potential inside colonised cells. In *H. pylori*, such determinant is CagA. Similarly, *A. tumefaciens* exploits the Type IV secretion system *vir* to translate a single-stranded form of T-region (T-strand) coated by the ssDNA-binding protein VirE2 (T-Complex) into the host's vegetal cell nuclei. Once inside the nucleus, the T-strand can be converted in a double-stranded form (T-DNA), whose expression causes an uncontrolled host cell proliferation and tumour development<sup>[15]</sup>.

Epidemiological and genomic studies suggest that the development of GC is a possible consequence of infection by strains expressing CagA<sup>[1,8,9,14,16]</sup>. In effects, using Mongolian gerbils infected experimentally, it was shown that only CagA positive (CagA+) *H. pylori* strains were able to induce stomach tumours<sup>[17]</sup>. In addition, a study of our group revealed that, while virtually all patients with intestinal histotype of GC had serum antibodies to CagA, the prevalence of anti-CagA antibodies in patients with the diffuse GC variety was similar to that observed in infected controls without neoplasia<sup>[16]</sup>. These data were confirmed by the results of an epidemiological study: The overall GC risk in infected people lacking anti-CagA antibodies (CagA-) was increased, but in non-significant way; in any case, CagA- *H. pylori* infection was associated with the growth of the diffuse variety of GC (with an OR of 9.0)<sup>[8]</sup>.

It therefore seems that infections by CagA+ strains expose people to an increased risk of GC respect to infections by CagA- *H. pylori* strains, which can only be associated with the diffuse histotype. In effect, things work slightly differently. In a recent study, we examined for the presence of *cagA* up to 25 distinct, well separated colonies per patient with GC; even though only individuals with diffuse histotype GC harboured *cagA* negative (*cagA*-) organisms, in all cases patients were also infected by at least one *cagA* positive (*cagA*+) strain<sup>[18]</sup>. These observations do not corroborate the supposed propensity of strains lacking *cag* PAI to concur to diffuse GC development and suggest that, for a better comprehension of the role played by *cagA* in the histological variety of GC, many colonies per patient should be examined genomically.

### **CagA phosphorylation by mucocytes: Like shooting oneself in the foot**

*H. pylori* organisms expressing CagA differ in their carcinogenic potential. Let us have a look at the mechanisms that may influence the ability of such a protein to trigger and/or concur to GC formation. CagA, following colonisation, is translated into the gastric epithelial cells through a conjugative apparatus encoded by the *cag* PAI genes upstream *cagA*; then, a portion of intracellular CagA is phosphorylated by numerous kinases, members of the host cell Src family (such as Yes, Lyn, Fyn and

c-Src,) at the EPIYA C'-terminal site (Glu-Pro-Ile-Tyr-Ala) motif of tyrosine<sup>[19]</sup>. Phosphorylated CagA physically interacts with the oncogenic tyrosine phosphatase SHP-2 (Src homology phosphatase 2), modifying cellular functions and altering mammalian signal transduction machineries. SHP-2, in fact, is implicated in the regulation of cell adhesion, spreading and migration. In this manner, phosphorylated CagA causes deregulation of SHP-2 and induces abnormal proliferation, as well as movement of cells of the gastric epithelial layer, activates mitogenic signalling and disturbs host-signalling routes<sup>[20]</sup>. All these events may also predispose cells to accumulate multiple genetic and epigenetic alterations involved in gastric tumorigenesis<sup>[21]</sup>.

Unphosphorylated CagA, on the other hand, interacts with the tumour suppressor protein of p53 (ASPP2), which also exert an apoptosis-stimulating activity<sup>[22]</sup>. In normal conditions, following genotoxic and oncogenic stimuli, ASPP2 associates with tumour suppressor p53, activates it and induces apoptosis. After interaction with CagA, cytosolic p53 is recruited by ASPP2 and subsequently is degraded by an enzyme complex that control cell-cycle and apoptosis, the proteasome. As a consequence, the apoptotic response of host cells is inhibited. In other words, unphosphorylated CagA takes control of ASPP2 and subverts the tumour suppressor pathway of apoptosis-stimulating protein p53 with consequent promotion of cell survival and cell transformation<sup>[20-22]</sup>. The resultant abnormal proliferation of gastric epithelial cells may contribute to GC development.

### **Individual CagA proteins have different biological activity and tumorigenic potential: When size matters**

*H. pylori* strains secreting CagA protein endowed with increased biological activity can be considered more virulent and even more closely associated with gastric cancer. At the end of 90's, the group of Graham discovered the ability of distinct CagA proteins to perturb cellular functions might vary in different isolates<sup>[23]</sup>. The CagA C'-terminal region contains one or more repeats of the same amino acids in sequence (Glu-Pro-Ile-Tyr-Ala, or EPIYA)<sup>[5]</sup>; the teleonomic significance of such phenomenon reflects the bacterial strategy to generate antigenic diversity, which may protect the organisms from the immune response. The number of EPIYA motifs correlates with the size of the *cagA* variable region. Yamaoka *et al.*<sup>[23]</sup> basing of the amplicon sizes obtained with primers encompassing the entire *cagA* variable region, classified *H. pylori* isolates in *cagA* structural types A, B, C and D (amplicons characterising types B and D have the same size and can be differentiated by sequencing). Strains with the *cagA* structural type C have the highest number of EPIYA phosphorylation motifs and were isolated significantly more often from patients with GC<sup>[23]</sup>, confirming a previous observation that individuals with GC are infected by strains expressing CagA proteins with higher mass<sup>[24]</sup>. The incr-

eased carcinogenic potential of the *cagA* structural type C was also confirmed by another study of the same group, which showed that patients infected by *H. pylori* with this *cagA* genotype run a higher risk of developing gastric mucosa atrophy, a precancerous condition<sup>[25]</sup>.

Now, it should be highlighted that the primers used in these studies to amplify the *cagA* variable region were designed on oriental (Japanese) strains, which may differ from western strains in the nucleotide sequence encoding the C'-terminal variable region<sup>[26]</sup>. Probably for this reason not all surveys on the same subject have confirmed the Yamaoka *et al.*<sup>[23,25]</sup>'s findings. In an initial study of our group, in which we used the Yamaoka's primers to amplify the *cagA* variable region of Italian strains<sup>[27]</sup>, we sometime obtained amplicons shorter than the PCR product that characterises the *cagA* structural type A; strains producing such amplicons, which presented a deletion of about 100 bp respect to *cagA* type A, were named type A(I), with (I) standing for Italy, because, as far as we know, similar *cagA* structural variety had not previously been described. In a more recent investigation, we observed similar proportions of the various *cagA* structural types in Italian *H. pylori* organisms isolated from GC cases and from controls (patients without neoplasia, with chronic gastritis only)<sup>[28]</sup>. In addition, in the control subjects, we frequently detected strains with the *cagA* structural type A(I). The increased prevalence of such a *cagA* type in individuals without GC prompted us to hypothesise that the reduced dimensions of the encoded CagA may decrease the ability of these bacteria to trigger a neoplastic process. As a matter of fact, the capability of CagA of binding SHP-2, and therefore of disturbing the various cellular functions, is regulated by the amounts of tyrosine phosphorylation site sequences, *i.e.*, the CagA size<sup>[20]</sup>; therefore, the shorter the protein, the less numerous are the EPIYA repeats that undergo phosphorylation and the lower is the carcinogenic potential of strains.

The employment of primers proposed by Yamaoka *et al.*<sup>[23]</sup> to amplify the *cagA* variable region of western strains has sometimes led to results similar to those of the Japanese researchers: South African researchers, for instance, have confirmed that patients with GC have an increased prevalence of strains with type C CagA<sup>[29]</sup>. Investigations dealing with this important subject, however, are not numerous; in addition, sometimes they attained different conclusions and have even contributed to create confusion in this subject. Malaysian authors, for instance, using the primers designed by Yamaoka *et al.*<sup>[23]</sup>, determined the presence and distribution of *cagA* variants among different ethnic groups and various gastroduodenal diseases<sup>[30]</sup>. They obtained three types of amplicons and named the *cagA* subtypes with capital letters, A, B and C (like did Yamaoka *et al.*<sup>[23]</sup>), but, just to complicate this topic further, they used a different criterion (respect to that of the previous study) and called subtype C the strains with the smallest amplicon

size and subtype B those with the greatest one. Specific *cagA* subtype A strains (those yielding amplicons of intermediate size) were predominantly isolated from Chinese compared to Malays and Indians patients. Since Chinese patients have the highest risk of GC disease respect to the other ethnic groups, these investigators concluded that *cagA* subtyping could be used as a clinical biomarker for severe outcome of infection. Such statement, however, was based on indirect observations because they did not examine strains from GC cases<sup>[30]</sup>.

In 2002, Higashi *et al.*<sup>[20]</sup> observed that the ability of CagA secreted by different strains to disturb host-cell functions can be influenced by the strength of SHP-2 binding activity, which was increased in *H. pylori* strains obtained from patients living in East Asian areas (Japan, Chorea and China) respect to those isolated from patients of Western countries (Europe, America, and Australia). In addition to the number of EPIYA repeats, it was also found that polymorphism in the nucleotide sequence flanking the regions that encode EPIYA could affect the potential of different *H. pylori* strains to promote gastric carcinogenesis<sup>[31]</sup>. According to the geographic regions in which strains are isolated, it is possible to characterise the *cagA* variable region on the basis of the number and the type of sequences. The Western *H. pylori* CagA has two segments of 32 and 40 amino acids flanking EPIYA (EPIYA-A and EPIYA-B types) and one to three 34 amino acid EPIYA-C segments (A-B-C type CagA)<sup>[21]</sup>. Eastern CagA presents EPIYA-A and EPIYA-B segments, but none of the EPIYA-C fragment; it has instead one copy alone of a segment called EPIYA-D, which represents the main tyrosine phosphorylation site<sup>[20,21]</sup>. In western strains, the major site of tyrosine phosphorylation of CagA is EPIYA-C; the tyrosine residues that characterize EPIYA-A and EPIYA-B segments are phosphorylated only very weakly. Such a difference in phosphorylation degrees resides in the diverse consensus high-affinity binding sequence for the SH2 domains of SHP-2. Unlike what happens for EPIYA-D type, the western EPIYA-C type of CagA differs by a single amino acid from the consensus SHP-2 binding sequence<sup>[21]</sup>.

In conclusion, the carcinogenic potential of *H. pylori* varies according to the number and the *cagA* structural types of the EPIYA flanking regions. East Asian CagA has an increased virulence and a strong ability to trigger GC, while, among western isolates, more carcinogenic are the helicobacters with two or three CagA EPIYA-C sites. This was also demonstrated by a study in which it was observed that 83.3% of GC strains possessed multiple EPIYA-C sites, vs only 5.2% of strains isolated from patients with chronic gastritis only (controls)<sup>[32]</sup>.

Often, *cagA*+ strains are also isolated from patients with duodenal ulcer (NF personal observation). This finding may create confusion, because is common knowledge that patients with duodenal ulcer are like protected from GC development; however, the results of a recent study<sup>[33]</sup> showed that the increased virulence

of strains with CagA EPIYA-C type augmented the risk of gastric cancer and not peptic ulceration. Some studies diverge from these conclusions: Findings of an investigation carried out in Colombia suggest that polymorphic CagA proteins, based on sequences flanking the EPIYA motifs, are not clearly associated with the outcome of the infection<sup>[34]</sup>. The absence of association between the CagA polymorphisms and pathogenesis of gastroduodenal diseases could be due to geographic factors and/or the host's genetic features and environmental determinants.

In conclusion, the results of this kind of investigations are potentially useful, but the confusion existing in this field ought to be rectified and the different researchers should use the same criteria for classification. The various groups, however, have reached a common conclusion: Not all the strains are alike in their carcinogenic potential.

## NOT ALL PATIENTS ARE ALIKE: THE ROLE OF THE HOST'S INFLAMMATORY CYTOKINE HAPLOTYPES IN GC DEVELOPMENT

### Background

The hypothesis that human genetic polymorphisms may affect predisposition to GC has recently been explored. GC develops in only 1%-3% of *H. pylori* infected individuals, which suggests that the host background matters in this neoplasia. Several pro-inflammatory cytokines are produced by the immune system against *H. pylori*; among them, IL-1 $\beta$  is of paramount importance; a second one is tumor necrosis factor-alpha (TNF- $\alpha$ ); both of them are closely related to epithelial injury and gastric hypochlorhydria<sup>[35,36]</sup>. At low concentrations, TNF- $\alpha$  enhances the protective inflammatory response; at high concentrations, it can injure the gastric mucosa and cause severe pathology<sup>[37]</sup>. IL-1 $\beta$  increases the surface molecule expression on endothelial cells, causing leukocytes to adhere; IL-1 $\beta$  also induces the production of macrophage chemokines leading to neutrophil activation. Recent investigations have revealed that there is a genetic regulation of the host cytokine response to inflammatory stimuli. Genomic variants of *IL-1 $\beta$*  and *TNF- $\alpha$*  were shown to correlate with the clinical outcomes of tumors, including GC<sup>[38,39]</sup>. The *IL-1 $\beta$*  gene cluster is polymorphic, with some alleles present at relatively high frequencies. Particular *IL-1 $\beta$*  haplotypes enhance the risk of GC because they induce an over expression of its product in the stomach, causing chronic hypochlorhydria, which in turn may produce gastric atrophy and, eventually and in the presence of other risk factors, GC<sup>[40]</sup>. In addition, patients with a particular haplotype of the gene that encodes IL-1RA (receptor antagonist) have an elevated risk of developing GC. IL-1RA is an anti-inflammatory cytokine, which is a competitor for IL-1 $\beta$  receptors, thus regulating the possible

harmful effects of IL-1 $\beta$  receptors.

The role of the host in GC development could be important because the inflammatory response to infections varies from patient to patient due to the gene polymorphism of inflammatory and anti-inflammatory cytokines. Many studies have been performed in the last 15 years, with the scope of identifying a genetic marker that can determine whether or not people carrying the infection might be at risk of developing GC in *H. pylori* infected patients<sup>[41-59]</sup>. Such a marker is still lacking, and we shall try to explain some of the reasons underlying this problem.

The association between chronic inflammation and cancer has been known since Virchow, in 1864, wrote that cancer would arise from sites of inflammation: "Chronic irritation which is manifested by a chronic inflammation is a key promoter of cancer" (Quoted by Balkwill and Mantovani<sup>[60]</sup>). Individual cytokines were specifically examined, in particular the proinflammatory ones. The most well known cytokine is IL-1, along with its receptor (IL-1R) and the antagonist of this receptor (IL-1RA); all of them share the chromosomal location of the *IL-1* gene family (namely 2q13-14). IL-1 $\beta$  has thus been established as an important regulator of carcinogenesis, characteristic of interactions between the host and environment<sup>[54]</sup>.

### IL-1 $\beta$ haplotypes

The *IL-1 $\beta$*  gene displays considerable polymorphism<sup>[54]</sup>; the presence of C to T transition was frequently found either in the promoter region at positions -511 (CT; dbSNP: rs16944), at position -31 (TC; dbSNP: rs1143627) or in the coding region at position +3954 (CT; dbSNP: rs1143634) base pairs from the origin of transcription. The two single nucleotide polymorphisms (SNPs) within promoter region are in linkage disequilibrium. The *IL-1 $\beta$*  -31 TC substitution disrupts a TATA-box motif; this leads to several transcription factors having altered binding affinities, resulting in modified IL-1 $\beta$  transcription. The *IL-1 $\beta$*  +3954 CT substitution is a synonymous SNP. It was demonstrated *in vitro* that the C to T transition at positions -511 and +3954 correlated with elevated IL-1 $\beta$  levels as a result of lipopolysaccharide (LPS)-stimulated IL-1 $\beta$  protein secretion<sup>[54]</sup>.

The paradigm of all subsequent studies regarding GC with respect to different haplotypes in cytokines was the focus of the paper by El-Omar *et al.*<sup>[38]</sup>, who noted for the first time that the presence of two polymorphisms (rs16944 and rs1143627) in the promoter region of the *IL-1 $\beta$*  gene, identified an increased risk of hypochlorhydria, as a result of *H. pylori* infection and GC<sup>[38]</sup>. These polymorphisms determine an increased secretion of IL-1 $\beta$ <sup>[61]</sup>, a conclusion confirmed and generalized by later reports<sup>[62]</sup>. The discrepancy of results reached in different papers was clarified only after several years, once taking into account the origin of the population and the type of GC. Overall, more than 90 publications dealt with this issue, over half of them from Asia, and a single one

from North America, a clear indication of the perceived relevance of this neoplasia in the different populations.

Since the single studies are extremely inconsistent and, if taken alone, contribute little to the general overview, we opted for reporting from selected meta-analyses in this paper. Meta-analyses accrued from time to time in a number of studies originating from different countries, which is one of the main causes of contradictory results, as well as from different histological variety of stomach malignancies, another cause of strong difference in results<sup>[41-59]</sup>.

The overall findings from the large amount of efforts can be summarized as follows:

(1) *IL-1 $\beta$  receptor antagonist (IL-1 $\beta$  RA)* polymorphism: The most credible and consistent association of peculiar genetic variation with GC was found for *IL-1 $\beta$  RA* haplotypes. Four alleles, numbered 1 to 4, are widely present in the general populations. People carrying the homozygous allele 2/2 (*IL-1 $\beta$  RN2*) were found to be at higher risk of developing cancer among non-Asian populations. Moreover, the analysis of GC patients altogether, without stratifying according to histological type, anatomic site or country of origin, showed that patients carrying homozygous allele 2, or *IL-1 RN2* had an increased risk of developing cancer, which was statistically significant. The risk was found both in cardia and non-cardia types of neoplasia. A possible explanation for the risk stems from the high *IL-1 $\beta$*  levels circulating among *IL-RA* allele 2/2 carriers<sup>[63]</sup>.

(2) *IL-1 $\beta$  -31 CT* polymorphism: A second plausible association was the decreased risk of GC in Asians carrying the haplotypes in the *IL-1 $\beta$  -31 CC* promoter region. A decreased risk of GC among *IL-1 $\beta$  -31C* carriers was confirmed, but solely for Asian patients.

(3) *IL-1 $\beta$  -511 CT* polymorphism in populations of different ethnic origin: Sub-analysis of various populations revealed a statistically significant association of stomach cancer with the *IL-1 $\beta$*  polymorphism at promoter region -511 CT in case-control studies based on populations (OR = 1.20, 95%CI: 1.00-1.43)<sup>[54]</sup>. The association is more consistent if only Caucasian populations are analyzed. Nevertheless, if taken together, the studies failed to show the association when stratified by ethnicities; *IL-1 $\beta$  -511 CT* polymorphism according to tumor site: A significant association of *IL-1 $\beta$  -511 CT* promoter region polymorphism was observed for stomach cancers when the tumor site (cardia vs non-cardia) was taken into account, as well as for histology subtypes (intestinal or diffuse/mixed). The association was present both in the case of non-cardia GC (OR = 1.57, 95%CI: 1.06-2.31) as well as intestinal GC (respectively OR = 1.57, 95%CI: 1.06-2.31 and OR = 1.24, 95%CI: 1.04-1.49)<sup>[54]</sup>; *IL-1 $\beta$  +3954 CT* polymorphism: Recently, Xu *et al*<sup>[54]</sup> performed a meta-analysis that was confirmed by that one by Xue *et al*<sup>[49]</sup>: There is a lack of association between *IL-1 $\beta$  +3954 CT* and GC risk.

(4) *IL-10* haplotypes: *IL-10* - regarded as the ma-

jor anti-inflammatory cytokine - will bind in form of homodimer its complex receptor, comprising four *IL-10* receptor molecules, namely 2 *IL-10 R1* and 2 *IL-10 R2*. The binding induces *STAT3* signaling *via* the phosphorylation of the cytoplasmic tails of *IL-10* receptor 1. *IL-10* can inhibit the synthesis of pro-inflammatory cytokines; moreover it can block the function of nuclear factor-kappa B (*NF- $\kappa$ B*), and has other regulatory properties, *e.g.*, *JAK-STAT* signaling<sup>[64]</sup>. The *IL-10* gene is known to possess several SNPs, some in the distal region upstream of the coding gene (-1082 A/G, -819 T/C) and a proximal one (the -592 A/C). Again, the complex signaling and polymorphism of *IL-10* can explain the contradictory results of the investigations.

(5) *IL-10 -1082 AG* polymorphism: A clear and curious dichotomy is evident, that is, when the studies were stratified according to Asian and non-Asian populations the observations reached opposite results. The Asian populations had greater risk of GC among *IL-10 -1082 G* carriers; conversely, there was a decreased risk among the non-Asian populations. Meta-analysis specific for *IL-10* confirmed for Asian population the increased risk for intestinal type of gastric neoplasia in *IL-10 -1082 GG* or *GA* haplotypes<sup>[53]</sup>; *IL-10 -592 AC* polymorphism: The -592 AC polymorphism failed to show any association, as the odd ratios for GC were 0.93 and 0.94 for homozygous and heterozygous population<sup>[55,65]</sup>; *IL-10 -819 TC* polymorphism: Little data is available for this polymorphism, confirming a protective effect in Asian populations. Nevertheless, it was not found to be associated with the reduced susceptibility to GC in individuals infected with *H. pylori* compared to uninfected controls. The *IL-10 -819 TT* genotype was found to be inversely correlated with the risk of the diffuse subtype, but not the intestinal subtype GC<sup>[51]</sup>.

(6) *IL-8 - 251* polymorphisms: Continuous expression of human *IL-8* in transgenic mice (whereby *IL-8* is under the control of its own regulatory elements) increased tumorigenesis. Therefore, *IL-8* may play an important role in gastrointestinal cancers. Elevated *IL-8* levels could be linked to a poor prognosis of neoplasia, henceforth its levels may be indicative of more aggressive GCs.

Early data seemed to provide a possible association in GC as well<sup>[66]</sup>. A recent meta-analysis showed that the *IL-8 -251 AA* genotype in the Han population correlates with augmented risk of developing GC and *AA* genotype carriers appear to be more likely to develop GC in Asian populations. In addition, the *IL-8 -251 AA* genotype tended to be related to intestinal GC, but not with *H. pylori* infectious status<sup>[52]</sup>. There was no link between *IL-8* polymorphisms and *H. pylori*-related gastric malignancies in non-Asian populations in all the meta-analyses examined<sup>[48,67]</sup>.

(7) *TNF- $\alpha$*  polymorphism: Experimental studies have implicated *TNF- $\alpha$*  in processes that are involved in cancer progression, including promotion of metastatic behaviour and cancer associated cachexia<sup>[68,69]</sup>. The lack of *TNF- $\alpha$*

in mice makes them resistant to carcinogenesis<sup>[70]</sup>. Clearly, such observation highlighted the link between genetic haplotypes for *TNF-α* and GC.

***TNF-α* -308 AG polymorphism:** It was surprising to find a lack of association of this polymorphism with increased risk of GC, with only one exception: Non-Asian patients with distal cancer and homozygous for -308 AA alleles; the association, moreover, appeared to exist for cancer of diffuse type only. However, this association was not confirmed when only good quality studies were taken into account, according to Persson *et al.*<sup>[48]</sup>. Opposite conclusions were obtained by Zhu *et al.*<sup>[59]</sup>; they recently analyzed all studies and concluded that, in the Caucasian populations, *TNF-α* rs1800629 (-308 AG) polymorphism indeed posed increased risk of GC. They used several genetic comparison models, *i.e.*, A vs G, AA vs GG and AA vs GG/GA that gave OR respectively of 1.32, 1.76 and 1.62, all highly significant (A vs G: OR = 1.32, 95%CI: 1.12-1.56, *P* = 0.001; AA vs GG: OR = 1.76, 95%CI: 1.37-2.26, *P* < 0.001; AA vs GG/GA: OR = 1.62, 95%CI: 1.27-2.07, *P* < 0.001)<sup>[59]</sup>.

***TNF-α* -238 polymorphism** did not correlate with an increased cancer risk<sup>[48,58]</sup>.

***TNF-α* 857 CT polymorphism:** Reports on this topic are quite controversial. Cen *et al.*<sup>[57]</sup> recently published his analysis of nine studies (all the reported ones); overall, they confirm that the *TNF-α* 857 CT polymorphism posed an elevated risk of GC solely among Asians; all four genetic models considered T vs C, TT vs CC, CT vs CC and TT vs CT gave consistent data, respectively with OR of 1.19, 1.44, 1.19 and 1.21 (their statistical significance being *P* = 0.002, *P* = 0.032, *P* = 0.008, *P* = 0.003 respectively).

***TNF-β* 252 AG polymorphism:** A weak association with stomach malignancy was present in Asian populations, according to Xu *et al.*<sup>[71]</sup>. Analysis by ethnicity revealed that the *TNF-β* 252 AG polymorphism correlated with a minor risk of GC (G vs A: OR = 1.10, 95%CI: 1.02-1.19, *P* = 0.015) exclusively in Asians, not in Caucasians.

Dutch patients were analyzed for their polymorphism of IL-1β; they were found to carry lower risk of GC when heterozygous for either the IL-1B -511 and for the IL1β -31 TATA-box (genotype T/C)<sup>[72]</sup>. The EBV status of the patients did not affect this correlation and there could therefore be an early shared molecular mechanism in the progression of EBV-positive and negative GCs<sup>[72]</sup>.

IL-6 polymorphism was not studied in relation to GC.

IL-6 knockout mice develop cancer less frequently<sup>[73]</sup>. It is therefore plausible that high IL-6 levels will promote tumorigenesis. Today, IL-6 is considered to be a relevant tumor-promoting factor also in humans. Indeed, it was correlated with glioma, lymphoma and melanoma at first, then with solid cancers such as breast and colorectal neoplasia (also ovarian and pancreatic), prostate, renal and colorectal cancers.

IL-6 is a critical factor during chronic inflammation, since it is required for the induction of effector Th17

cells and inhibits the differentiation of regulatory T cells.

Stomach cells, however, lack IL-6 receptors; hence it cannot dimerize with the second receptor (gp 130) and the "classic signaling" is restricted to cells bearing both mIL-6R and gp130 on their surface. The latter is widely expressed, whilst mIL-6R expression is limited to some leukocytes, hepatocytes and cancer cells. It is therefore quite understandable that, as recently reported, a large meta-analysis on 105000 people established the lack of association of cancer risk with *IL-6* polymorphism in Caucasians<sup>[74]</sup>, despite the association which holds true for Africans.

### Other cytokines

Gene polymorphism concerning cytokine different from those we have dealt with was recently considered in relation to the risk of developing GC. The studies are not sufficiently large so far; however it is worth reporting that a haplotypes of *IL-17*, *IL-17F* rs763780 TC, was significantly associated with GC development in Asian population<sup>[75]</sup>.

IL-11 was taken into consideration in a single study<sup>[76]</sup>. A reduced risk for developing cancer at the gastric site was found for a polymorphism in the *IL-4* -590 CT gene in Caucasian but not in Asian populations. *H. pylori* status was not taken into consideration in these studies<sup>[77]</sup>.

### Different results in different studies: The origin of the problem

IL-1β, *TNF-α* and the remaining dozens of cytokines are not the final executor of immune signaling or the resulting consequences in cancer promotion and spread. IL-1, *TNF-α*, together with bacterial antigens, LPS and several other signaling molecules bind their respective receptors on the cell membrane; a cascade of signals ensues upon receptor activation, which depends on the levels of Mg-ATP availability (in turn on Mg<sup>2+</sup> concentration in cells). Numerous different proteins are involved and regulate the signaling pathway, which finally results in the activation of a large family of DNA-binding proteins, the NF-κB family<sup>[78]</sup>, which is a complex that regulates DNA transcription. NF-κB dimers are formed upon activation, stimulating the transcription of genes that encode cytokines, growth factors, chemokines, and anti-apoptotic factors<sup>[79]</sup>. However, some NF-κB dimers act by repressing, whilst others activate specific genes.

### Cytokine polymorphism and Epstein-Barr virus-associated GC

Worldwide, it was noted that Epstein-Barr virus (EBV) is present in a relevant proportion of malignant tumors of the stomach, with an incidence that is inversely proportional to that of GC. In the USA 16% to 18% of all stomach tumors were found EBV-associated (EBVaGC), in Southern China only 4.3%<sup>[80]</sup>; a survey of 101 published papers reported that EBVaGC was evident in 7.08% of intestinal type GC, while diffuse type GC had

an incidence of 9.82%<sup>[80]</sup>. Western and Central Asian countries had significantly more EBV positive cases than South-Eastern countries; in Europe, the frequency of EBV infection ranged from 1.7% in the United Kingdom to 40% in Poland<sup>[80]</sup>.

An *in vitro* model of EBVaGC was used to demonstrate that gastric cells, following EBV infection, have a high IL-1 $\beta$  expression, compared to EBV-negative gastric tumour cells. EBV-positive clones rapidly proliferated and were shown to be anchorage-independent in colony-forming assays<sup>[81]</sup>.

Since EBV infection is highly prevalent in all populations, whilst EBVaGC is quite rare, there were attempts to identify people who run an increased risk of developing GC. Polymorphisms of proinflammatory, as well as anti-inflammatory cytokines were studied, in particular in the promoter regions of *IL-10* and *TNF- $\alpha$* . For the latter, the allele -308 A (linked to high levels of *TNF- $\alpha$* ) had significantly higher frequency among EBVaGC individuals (23.3%) when compared to control subjects (12.0%,  $P < 0.05$ ). The opposite was found in the case of the anti-inflammatory *IL-10*: The high-producer allele (-1082 G) was found to be less frequent in EBVaGC patients in comparison to controls (6.3% vs 3.0%,  $P < 0.05$ )<sup>[39,72]</sup>.

The extreme complexities of all these interactions can explain the great variability in data when investigating the possible correlation between cytokine haplotypes and GC.

#### **Gleanings on the usefulness of characterising *H. pylori* infected individuals for inflammatory haplotype**

In addition to the complexity of this subject, the expectations created by the assertion that the host's factors could contribute to the development of GC are disappointing, at least as far as the host's inflammatory response to *H. pylori* infection is concerned. Once we get into details, we realize that in fact, the only determinant that really matters is the infection. The examination of the scientific literature on the cytokine subject has led to contradictory results: For each cytokine, the observations made by studying Caucasian people cannot be applied tout course to Asians; in certain cases, we get opposite results. In the different surveys, one can find association of determined haplotypes of inflammatory cytokines with an increased risk of GC, the opposite, or nil. Even the results of meta-analyses do not agree one another, according to whether studies are carried out by Chines or researchers from other nations. What does it mean? Is it because cytokines are not the final effectors, as they principally work on the long and winding road paved by the broad NF- $\kappa$ B family, which leads to GC (which means that the final response to inflammatory stimuli is far from hitting its target)? And what about the observations that people suffering from diseases far more inflammatory than chronic gastritis, such as rheumatoid arthritis, are likely protected from developing GC<sup>[82]</sup>.

These observations may suggest that, if host factors are important in GC development, they probably have to be sought outside of the genes encoding the inflammatory cytokines.

## **NOT ALL PATIENTS ARE ALIKE:**

### **MOLECULAR BIOLOGY**

The recent advances of molecular biological techniques allowed researchers to reach important insights into the oncogenesis mechanisms in gastric cancer. Besides the well-known pathogenic factor, *H. pylori*, several oncogenes and tumour suppressor genes, including cell cycle regulation genes involved in the growth and signal transduction pathways, have been identified<sup>[83-85]</sup>. In particular, alterations of genes involved in signalling pathways deregulation, patterns of aberrant DNA methylation, and chromosomal imbalances have been evidenced<sup>[86,87]</sup>.

### **CHROMOSOMAL INSTABILITY**

Chromosomal instability (CIN) represents one of the main type of genomic instability observed in several neoplasms and it has been observed in a large cohort of patients with gastric cancer<sup>[88]</sup>. In particular, it is commonly detected in gastric malignant tumours and has been shown in up to 84% of gastrointestinal cancers<sup>[89]</sup>.

CIN is characterized by chromosomal anomalies, including gain or loss of the complete chromosome (aneuploidy) and segments of chromosomes (loss of heterozygosity, amplifications and translocations)<sup>[90]</sup>. These abnormalities can impact on the oncogenes expression, tumour suppressor genes and other genes, as well as those involved in digestion, DNA repair, growth regulation, and control of cell cycle checkpoint<sup>[91-93]</sup>. The genetic mechanisms leading to CIN are not entirely known; *H. pylori* infection, smoking habit and some chemical substances such as nitrates and nitrites probably have an effect on inducing CIN; anyway their influence is actually uncertain<sup>[94]</sup>. On the other side, defects of chromosome segregation (CS), imperfect DNA damage response (DDR), anomalies in cell cycle regulators and telomere dysfunction have been identified as factors leading to numerical and structural chromosome alterations<sup>[95,96]</sup>. These carcinogens may alter chromosomes and the cytoskeleton promoting malignant modification<sup>[97]</sup>.

#### **CS alterations**

CS represents an important cellular process inducing the gastric epithelial cells division. Alterations of CS regulating mechanisms can cause DNA alterations or mitotic failures, leading to unfixable mutations as well as chromosomal number alterations<sup>[98]</sup>. In particular, the three recently proposed ways producing CIN are: Altered expression, polymorphisms and/or mutations of mitotic genes implicated in CS and the carcinogen activity upon

susceptible genetic background of individuals<sup>[99,100]</sup>. Many authors showed an aberrant expression of mitotic genes in CS. Moreover, the altered expression of BUB1 protein (involved in controlling the spindle assembly checkpoint), was significantly increased in patients with diffuse type gastric adenocarcinoma, but not related to DNA ploidy<sup>[89]</sup>. Furthermore, in another study, BubR1 and AURKB (proteins involved in the mitotic spindle assembly) expression resulted in association with a low risk of GC progression<sup>[101-103]</sup>. Aurora kinase A (AURKA/STK15), a cell-cycle-regulated kinase with important role in microtubule formation and stabilization during CS, is often overexpressed in adenocarcinomas of the stomach, showing a suggestive new oncogenic pathway in GC<sup>[104]</sup>.

### Defective DDR

The mucosa of the stomach is continually subject to several environmental and intracellular mutagens, like ROS, *H. pylori* infection, nitrates, sodium, nitrites, and other water and food contaminants, able to induce DNA damage through different mechanisms<sup>[105,106]</sup>. Failure of the most important mechanisms of repair [nucleotide excision repair, base excision repair, mismatch repair (MMR) and recombination and/or DDR] may conduce to CIN and genetic aberrations, favouring carcinogenic process<sup>[107,108]</sup>. Several studies revealed differential mRNA expression of genes implicated in DNA repair process: *ATM* and *HMGB1* (implicated in base excision repair), *RAD23B* (involved in nucleotide excision repair), *UBE2V2*, *MUS81* [involved in resolving Holliday junctions (a branched DNA structure that contains four double-stranded arms joined together, considered the central intermediate in homologous recombination)], *REV3L* (involved in replication post-DNA damage), *TP53*, *hHR23A* and *DDB1* (implicated in nucleotide excision repair), and *XRCC1* (implicated in single-strand breaks repair) and *MUTYH* (implicated in base excision repair)<sup>[109-113]</sup>.

### *H. pylori*

*H. pylori* has been shown to be able to induce DDR and double-strand breaks in gastric cancer with a mechanism of adhesion of bacteria that takes place between Lewis epitopes of the host and BabA adhesin<sup>[114]</sup>. Anyway, gastric mucosa cells can repair the DNA lesions induced by short-term infections. On the other side, prolonged infections induce saturation of repair mechanisms with a consequent ineffective DNA repair and malignant process begin. Moreover, continued infections lead to chronic inflammation, with resulting increase of mutagenesis rate, oxidative-stress, down-regulation of MMR mechanisms, instability of genes and modulation of apoptosis by means of ROS formation<sup>[115-119]</sup>. Gastric inflammation represents an important host response able to induce *H. pylori*-related carcinogenesis<sup>[120]</sup>. In fact, in infected patients with *IL-1 $\beta$* , *TNF- $\alpha$* , *IL-10* and *IL-8* polymorphisms, has been observed an in-

creased risk of distal gastric cancer progression<sup>[120,121]</sup>. Furthermore, different *H. pylori* strains seem to differently increase cancer risk by means of host genotypes<sup>[122]</sup> as these bacteria are able to communicate with their hosts. The equilibrium is determined both by host and bacterial features and may explain the reason why some *H. pylori* strains augment the carcinogenesis risk. For example, CagA positive strains promote severe gastritis and increase the pro-inflammatory cytokines' level. This may lead to an environment favourable to the growth of other bacteria that can support inflammation and continually induce oxidative stress, increasing the risk for GC<sup>[1]</sup>.

## MICROSATELLITE INSTABILITY

Microsatellite instability (MSI) represents a genomic instability commonly detected in almost half of patients with GC. It is often observed in the Lynch syndrome (hereditary non-polyposis colorectal cancer) and in several sporadic cancers<sup>[123]</sup>. MSI phenotype is characterized by a high replication mistake rate leading to insertions and/or deletions of nucleotides within microsatellite repeats in neoplastic areas<sup>[123]</sup>. The MMR proteins are able to detect and repair these alterations, causing the dysfunction in MMR genes (*MLH1* and *MSH2*) a MSI phenotype's establishment, with a consequently power off of cancer suppressor genes' and loss of heterozygosity<sup>[124,125]</sup>. To this address, genes that are frequently modified induce cell cycle regulation and apoptosis (*TGF $\beta$  RII*, *RIZ*, *IGFIR*, *TCF4*, *BAX*, *FAS*, *CASPASE5*, *BCL10* and *APAF1*) or are involved in the maintenance of genomic integrity (*MSH6*, *MED1*, *MSH3*, *BLM*, *RAD50*, *ATR*, and *MRE11*)<sup>[126]</sup>.

## DEREGULATION OF SIGNALLING TRASDUCTION PATHWAYS

The effects of genomic destabilization consist of aneuploidy and gain or loss of the chromosome tracts involved in mRNA transcription. Genomic alterations can modify the normal cellular biology with a consequent neoplastic switch<sup>[127]</sup>. The clearly explored pathways that probably are involved in gastric pathogenesis are Wnt/betacatenin, extracellular signal-regulated MAPK, Hedgehog, Notch, NF- $\kappa$ B, TGF- $\beta$ /BMP pathways, COX2/PGE<sub>2</sub>, and tyrosine kinase signalling<sup>[128-143]</sup>.

Finally, several studies evidenced that pathway deregulation involved in systemic inflammatory response, such as IL-11/STAT1/gp130/STAT3, can induce a carcinogenic transformation too<sup>[144,145]</sup>.

## CONCLUSION

GC is a multifactorial disease. The main determinant, *H. pylori* infection, can be considered a *sine qua non* for GC development; however, despite almost all individuals who get GC are currently, or have been infected, it

is neither a necessary nor a sufficient condition. The intricacy of this topic resides in the proportion of infected people that will never get GC: 97% to 99%, according to the ethnic groups and geographic areas. Other remarks are unraveling the tangle: Almost all *H. pylori* strains from Japan and East Asia, the areas with the highest incidence of GC, are *cagA*+ and can be considered highly carcinogenic; in addition, the infection by certain *cagA* genotypes in western countries increases by far the risk of GC.

At this point, one may wonder why these strains keep on infecting people. Following along with the evolution, only the characteristics that provide a selective advantage continue to be transmitted; this is a basic rule in eukaryotic and prokaryotic worlds. What is the benefit of being infected by carcinogenic strains? Why do they not disappear? People infected by strains that multiply the risk of GC by many times over, cannot be considered advantaged. Possible answers could reside in the following observations: (1) 97% to 99% of people never acquire GC; (2) the development of the sequence gastritis-metaplasia-dysplasia-cancer takes 40 years, or more, after the infection; which means that all women, as well as men, are fertile before the age at which GC occurs (many men also in old age, but they are less important, statistically speaking); hence, fertility is not affected by cancer development; and (3) women, who develop GC far less frequently than men, are the necessary genetic traits holders. Could these answers satisfy the laws of evolution (or distract them)? And how can the occurrence of GC in younger and younger ages be explained?

Apart from the complexity of this subject, the prospect created by the assertion that the host's factors, such as the way the host reacts to infectious stimuli, may be important in the development of GC is discouraging. Despite cytokines involved in the inflammatory response to infection, there are more than 30, just over half a dozen that have been examined in the relationship of *H. pylori* infection with GC and only haplotypes of *IL-1* and *TNF- $\alpha$*  genes were found to possibly increase the GC risk, but only if the ethnicity of patients is not considered. Pursuing this line of inquiry makes us run the risk of sounding racist.

The hypothesis that the dissection of oncogenes and tumour suppressing genes could provide us with an answer to the question whether host factors are important in GC development has only been partly proved. However, the conclusions have led us to a starting point, that is, they ended to indirectly confirm the pathogenic role of strains expressing CagA. The local and systemic levels of substances endowed with an increased mutagenic potential, ROS, generated by immunocytes, and the consequent DNA damage are far higher when the infecting organisms harbour the *cag* PAI.

In conclusion, as regards the development of GC, not all the *H. pylori* strains and patients are alike and not all share the same responsibility, but the only deter-

minant that really matters is the infection.

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## State of the art biological therapies in pancreatic cancer

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### Abstract

Pancreatic ductal adenocarcinoma (PDAC) is one of the most lethal malignancies with a five-year survival rate of approximately 5%. Several target agents have been tested in PDAC, but almost all have failed to demonstrate efficacy in late phase clinical trials, despite the better understanding of PDAC molecular biology generated by large cancer sequencing initiatives in the past decade. Erlotinib (a small-molecule tyrosine-kinase inhibitor of epidermal growth factor receptor) plus gemcitabine is the only schedule with a biological agent approved for advanced pancreatic cancer, but it has resulted in a very modest survival benefit in unselected patients. In our work, we report a summary of the main clinical trials (closed and ongoing) that refer to biological therapy evaluation in pancreatic cancer treatment.

**Key words:** Pancreatic cancer; Molecular characterization; Targeted therapy; Epidermal growth factor receptor inhibitors; Embryonic pathway inhibitors; Antiangiogenic therapies

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**Core tip:** Our study aims to give an overview of the progress made in molecular targeted therapy for pancreatic cancer in recent years and the current status of clinical trials in the field. Pancreatic ductal adenocarcinoma (PDAC) is one of the most lethal malignancies with a five-year survival rate of approximately 5%. Several target agents have been tested in PDAC but almost all have failed to demonstrate efficacy in late phase clinical trials, even with a better understanding of PDAC molecular biology generated by large cancer sequencing initiatives in the past decade. Erlotinib (small-molecule tyrosine-kinase inhibitor of epidermal growth factor receptor) plus gemcitabine is actually the only schedule

with a biological agent approved for advanced pancreatic cancer, but it resulted in a very modest survival benefit in unselected patients. In our work, we reported a summary of the main clinical trials (close and ongoing) that refer to biological therapy evaluation in pancreatic cancer treatment.

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## INTRODUCTION

Pancreatic ductal adenocarcinoma (PDAC) is one of the most lethal malignancies, representing the fourth leading cause of cancer death. The five-year survival rate is approximately 5%, and surgery remains the most effective treatment<sup>[1]</sup>.

Unfortunately, only 20% of patients are suitable for radical resection, and recurrence of disease occurs in 80% of patients who undergo resection<sup>[2]</sup>.

The most important improvement concerns the conventional chemotherapy, represented by FOLFIRINOX and gemcitabine plus nab-paclitaxel regimens, but it results in a modest outcome advantage<sup>[3,4]</sup>.

No significant progress has been made in the field of targeted therapy. Erlotinib [a small-molecule tyrosine-kinase inhibitor of epidermal growth factor receptor (EGFR)] plus gemcitabine is actually the only schedule with a biological agent approved for pancreatic cancer, but it results in a very modest survival benefit in unselected patients<sup>[5]</sup>.

In recent decades, several combinations of classic chemotherapy and novel biological agents have been studied, but they have not improved overall survival, and furthermore, those trials did not use biomarkers to select responder patients<sup>[6]</sup>.

Our study aims to give an overview of the progress made in molecularly targeted therapy for pancreatic cancer in recent years and the current status of clinical trials in the field, as summarized in Tables 1-3.

## MOLECULAR CHARACTERIZATION OF PDAC: HAS A BETTER UNDERSTANDING OF THE TUMOUR'S MOLECULAR BIOLOGY REALLY IMPROVED TARGETED THERAPY APPLICATIONS?

Large cancer sequencing initiatives generated a large quantity of data in the past decades. Those findings showed a complex genomic landscape characterized particularly by inter-tumoural and intra-tumoural hetero-

geneity involving genomic aberration<sup>[7]</sup>.

With the exception of the well-known KRAS, TP53, CDKN2A and SMAD4 alterations occurring at respective frequencies of 71%, 49%, 22% and 20%, a large number of genomic rearrangements with mutational frequencies less than 2% were found<sup>[8,9]</sup>.

The majority of single gene mutations in pancreatic cancer can be grouped into common cellular pathways. Jones *et al.*<sup>[10]</sup> identified 69 mutated gene sets in most of the 24 samples analysed in their pioneering sequencing study, of which 31 could be grouped into 12 core signalling pathways. These pathways included KRAS signalling, the transforming growth factor  $\beta$  (TGF- $\beta$ ) pathway, DNA damage control, apoptosis, regulation of G1/S cell cycle transition, Hedgehog signalling, the homophilic cell adhesion pathway, integrin signalling, TGF- $\beta$  signalling, Wnt/Notch signalling, and the invasion pathway<sup>[10]</sup>.

Genomic heterogeneity, a characteristic of PDAC, implies genomic instability, which is due to the acquisition of telomere dysfunction and abnormal cell-cycle control occurring predominantly in early cancer stages, but it persists after cancer dissemination, resulting in parallel evolution among different metastases. Cell clones arranging metastasis may require other driver mutations compared with primary tumour cells implementing genetic variation in pancreatic cancer<sup>[11,12]</sup>.

Given this molecular complexity, it is very difficult to separate passenger from driver mutations, to identify molecular mutations with a crucial role in pancreatic carcinogenesis that can be developed into actionable molecular targets of novel biological agents or to identify patients potentially responsive to existing agents already approved for human use in other cancers (Figure 1), and currently no predictive or prognostic biological factors are employed in clinical practice.

## TARGETED THERAPY IN PDAC

### EGFR pathway inhibitors

EGFR is a transmembrane receptor member of the ErbB family with a tyrosine kinase domain that is activated by many ligands including epidermal growth factor (EGF), TGF- $\alpha$ , heparin-binding EGF, amphiregulin, epiregulin, betacellulin and neuregulin (an epidermal growth factor). EGFR is involved in cell cycle regulation, cell survival, adhesion and differentiation through activation of the Ras/MAP kinase, phosphatidylinositol 3'-kinase (PI3K)/Akt, Janus kinase/Stat and phospholipase C/protein kinase C pathways. Several trials showed that EGFR is overexpressed in up to 90% of pancreatic cancer samples. Therefore, inhibitors targeting EGFR have been considered a promising therapeutic agent<sup>[13]</sup>.

Erlotinib is a tyrosine kinase inhibitor (TKI) molecule that competes with ATP for binding to the kinase domain, thereby blocking downstream signal transduction. A possible therapeutic role was evaluated in a large phase III trial, enrolling 569 chemotherapy naïve patients with locally advanced or metastatic pancreatic

**Table 1 Principal phase III clinical trials involving targeted therapy in pancreatic cancer**

Agent	Target pathway	Treatment	Setting	n	mOS (mo)	PFS (mo)	FDA approval	Ref.
Erlotinib	EGFR signaling	GEM plus erlotinib vs GEM plus P	M/LA	569	6.24 vs 5.91 ( <i>P</i> = 0.038)	3.75 vs 3.55 ( <i>P</i> = 0.004)	Yes	[5]
Cetuximab	EGFR signaling	GEM plus cetuximab vs GEM	M/LA	766	6.5 vs 6 ( <i>P</i> = 0.14)	3.5 vs 3 ( <i>P</i> = 0.058)	No	[17]
Tipifarnib	KRAS pathway	GEM plus tipifarnib vs GEM	M/LA	688	6.3 vs 6 ( <i>P</i> = 0.75)	3.7 vs 3.6 ( <i>P</i> = 0.72)	No	[30]
Ganitumab	IGFR pathway	GEM plus ganitumab (12 mg/kg or 20 mg/kg) vs GEM plus P	M	800	12 mg/kg arm 7.0 vs 7.2 ( <i>P</i> = 0.494) 60 mg/kg arm 7.1 vs 7.2 ( <i>P</i> = 0.397)	12 mg/kg arm 3.7 vs 3.6 ( <i>P</i> = 0.520) 60 mg/kg arm 3.7 vs 3.7 ( <i>P</i> = 0.403)	No	[35]
Bevacizumab	Angiogenesis	GEM plus bevacizumab vs GEM plus P	M/LA	602	5.7 vs 6.0 ( <i>P</i> = 0.40)	4.8 vs 4.3 ( <i>P</i> = 0.99)	No	[36]
Aflibercept	Angiogenesis	GEM plus aflibercept vs GEM plus P	M/LA	546	6.5 vs 7.8 ( <i>P</i> = 0.203)	3.7 vs 3.7 ( <i>P</i> = 0.864)	No	[38]
Axitinib	Angiogenesis	GEM plus axitinib vs GEM plus P	M/LA	632	8.5 vs 8.2 ( <i>P</i> = 0.543)	4.4 vs 4.4 ( <i>P</i> = 0.520)	No	[41]
Marimastat	Tumor stroma	GEM plus marimastat vs GEM	M/LA	239	5.4 vs 5.4 (NA)	3 vs 3.1 (NA)	No	[75]

GEM: Gemcitabine; P: Placebo; mOS: Median overall survival; PFS: Progression free survival; n: Number of patients enrolled; LA: Locally advanced cancer; M: Metastatic cancer; NA: Not available.

**Table 2 Principal phase II clinical trials involving targeted therapy in pancreatic cancer**

Agent	Target pathway	Treatment	Setting	n	Ref.
Cetuximab	EGFR signaling	GEM plus cisplatin plus cetuximab vs GEM plus cisplatin	M/LA	84	[16]
Gefitinib	EGFR signaling	GEM plus gefitinib (single arm)	M/LA	57	[18]
Trastuzumab	EGFR signaling	GEM plus trastuzumab (single arm)	M/LA	34	[20]
Trastuzumab	EGFR signaling	Capecitabine plus trastuzumab (single arm)	M/LA 2+/3+ HER-2 expression 3+ HER-2 expression or gene amplification	17 (212 screened)	[21]
Nimotuzumab	EGFR signaling	GEM plus nimotuzumab (single arm)	M/LA	18	[23]
Nimotuzumab	EGFR signaling	Nimotuzumab monotherapy (single arm)	Refractory to first line standard chemotherapy M/LA	56	[24]
Selumetinib	KRAS/MEK pathway	Capecitabine plus selumetinib vs Capecitabine	Refractory to first line standard chemotherapy M/LA	70	[31]
Trametinib	KRAS/MEK pathway	GEM plus trametinib vs GEM plus P	M/LA	160	[32]
Sorafenib	Angiogenesis	GEM plus sorafenib (single arm)	M/LA	70	[40]
RO4929097	Hedgehog signaling	RO4929097 monotherapy (single arm)	Refractory to first line standard chemotherapy M	18	[57]
Everolimus	mTOR pathway	Everolimus plus capecitabine (single arm)	M/LA	31	[67]

GEM: Gemcitabine; P: Placebo; n: Number of patients enrolled; LA: Locally advanced cancer; M: Metastatic cancer.

adenocarcinoma randomized to receive gemcitabine plus placebo or gemcitabine plus erlotinib 100-150 mg daily. The median overall survival (mOS) and progression free survival (PFS) were modestly, but statistically significantly, improved in the combination arm, 6.24 mo vs 5.91 mo (*P* = 0.038) and 3.75 mo vs 3.55 mo (*P* = 0.004), respectively<sup>[5]</sup>.

Neither EGFR status nor KRAS status analysed in the

subgroup of patients treated with erlotinib was shown to be predictive of a survival benefit in patients receiving the combination schedule<sup>[14]</sup>.

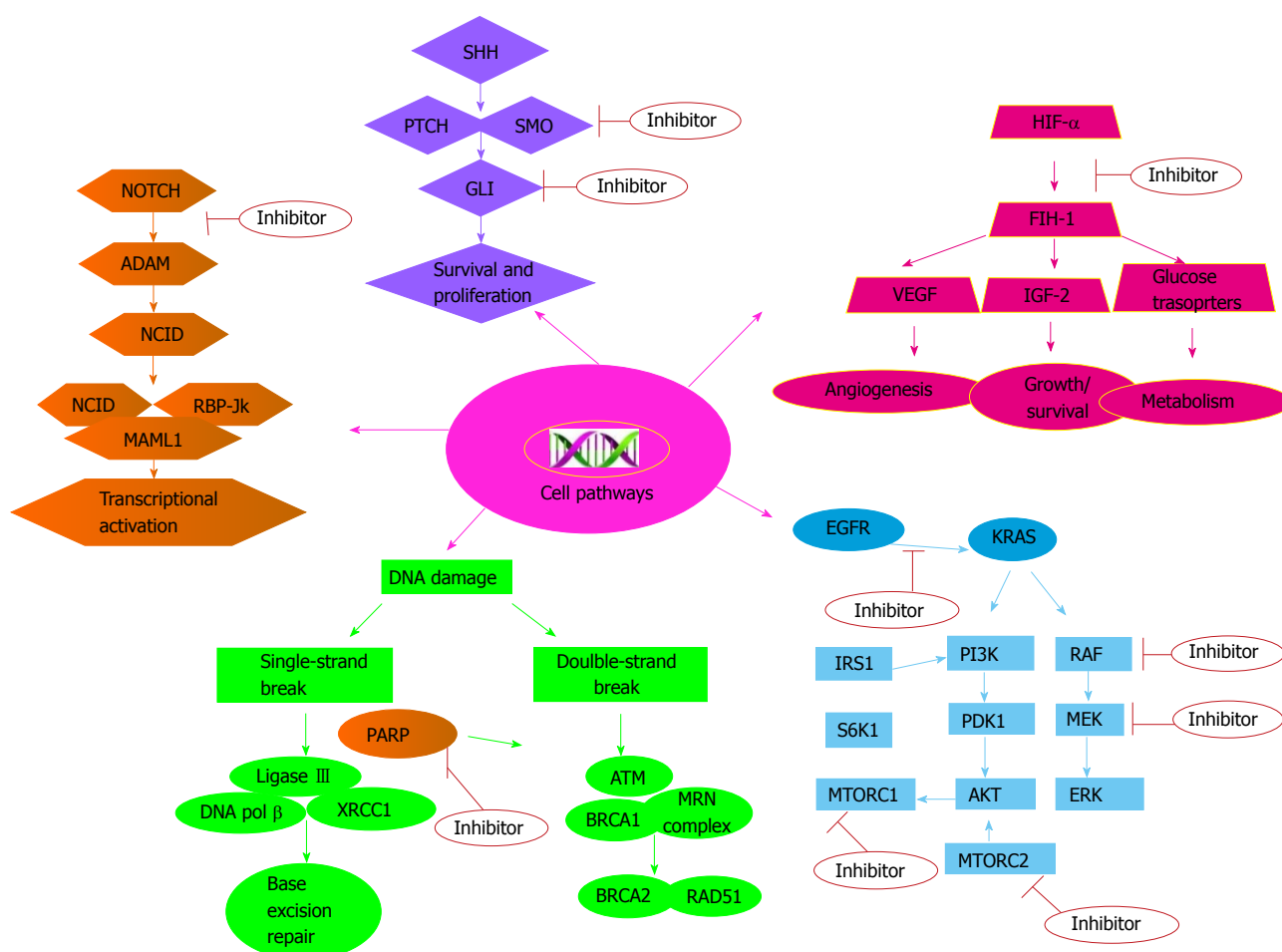
Erlotinib has been approved by the FDA in combination with gemcitabine as a first-line treatment for advanced pancreatic adenocarcinoma.

Cetuximab is a monoclonal antibody binding the extracellular domain of EGFR. After encouraging results

**Table 3** Principal ongoing trials involving targeted therapy in pancreatic cancer

ClinicalTrials.gov identifier	Agent	Target	Status
NCT01728818	Afatinib	EGFR signaling	Recruiting
NCT01659502	TL-118	Angiogenesis	Not yet recruiting
NCT01621243	Necuparab	Angiogenesis	Recruiting
NCT01088815	Vismodegib	Hedgehog signaling	Recruiting
NCT01096732	Vismodegib	Hedgehog signaling	Terminated
NCT01431794	LDE-225	Hedgehog signaling	Recruiting
NCT00515866	KU-0059436	PARP inhibitor	Completed
NCT01585805	Veliparib	PARP inhibitor	Recruiting
NCT01571024	BKM120	mTOR and PI3K/ Akt pathway	Recruiting
NCT01028495	RX-0201	mTOR and PI3K/ Akt pathway	Completed
NCT01337765	BEZ235 + MEK162	mTOR and PI3K/ Akt pathway	Completed
NCT00560963	Everolimus	mTOR pathway	Completed
NCT00075647	Temsirolimus	mTOR pathway	Completed
NCT01839487	PEGPH20	Tumor stroma	Recruiting

EGFR: Epidermal growth factor receptor; mTOR: Mammalian target of rapamycin.



**Figure 1** Principal cell signaling pathways involved in pancreatic ductal adenocarcinoma carcinogenesis and actionable molecular targets. SHH: Sonic hedgehog; PARP: Poly ADP-ribose polymerase; VEGF: Vascular endothelial growth factor; IGF: Insulin like growth factor; EGFR: Epidermal growth factor receptor; PI3K: Phosphatidylinositol 3'-kinase.

in a phase I trial, subsequent studies in association with gemcitabine-based chemotherapy have failed to demonstrate any survival benefit<sup>[15,16]</sup>.

A phase II study has evaluated the possible therapeutic role of gefitinib, a competitive inhibitor of ATP binding to the intracellular kinase domain of EGFR, in

combination with gemcitabine in inoperable or metastatic pancreatic cancer patients. The combination demonstrated promising activity with a mOS and PFS in the combination arm of 7.3 and 4.1 mo, respectively, but other evidence supporting a role of gefitinib in PDAC treatment is lacking<sup>[17]</sup>.

Another ErbB family of transmembrane tyrosine kinase receptors is HER-2, which is overexpressed in 11% of pancreatic adenocarcinoma cases. HER2-positive status has also been correlated with shorter survival<sup>[18]</sup>.

Trastuzumab plus gemcitabine was tested in 34 metastatic pancreatic cancer patients with HER-2 overexpression as determined by immunohistochemistry, and partial responses were observed in 6% of cases<sup>[19]</sup>. Harder *et al.*<sup>[20]</sup> in a multicentre phase II study, investigated the efficacy and toxicity of the HER2 antibody, trastuzumab, plus capecitabine in patients with pancreatic cancer and HER2 overexpression, but this treatment did not perform favourably with respect to either PFS or OS compared with standard chemotherapy.

After FDA approval of lapatinib, clinical trials have been initiated to test the effect of this HER-2 inhibitor combined with chemotherapy in pancreatic carcinoma. In particular, lapatinib was tested in combination with capecitabine as a second-line treatment in advanced pancreatic cancer with promising preliminary results. Further studies are needed to evaluate the real effectiveness and role of this molecule in the treatment of PADC<sup>[21]</sup>.

Nimotuzumab, another anti-EGFR monoclonal antibody, showed promising results<sup>[22]</sup>. In a phase II trial where advanced pancreatic cancer patients were randomized to receive second-line monotherapy with nimotuzumab, Strumberg *et al.*<sup>[23]</sup> showed PFS after 1 year of 10.3% and median overall survival of 18.1 wk with a tolerable toxicity profile.

Based on preclinical evidence, afatinib, an inhibitor of EGFR, HER2 and HER4, is under evaluation in an ongoing phase II trial<sup>[24,25]</sup>.

### **The KRAS pathway and downstream signalling cascade inhibitors**

KRAS activating mutations are present in 70% to 90% of cases of pancreatic cancer. K-Ras is a GTPase protein belonging to the Ras protein family, which has oncogenic activity, and gain-of-function mutations resulting in constitutive activation promote proliferation and inhibit apoptosis through the RAF/MEK/ERK and PIK3/AKT pathways. K-Ras is very difficult to target, and no inhibitors are actually available to use in clinical practice<sup>[26]</sup>.

Preclinical study has shown that farnesylation is an important post-translational modification required for Ras activation, allowing the protein to be attached to the plasma membrane for signal transduction<sup>[27]</sup>.

After promising results in terms of anti-proliferative activity in pancreatic tumour cell lines, farnesyl-transferase inhibitors, particularly tipifarnib, failed to improve overall survival either as a single agent or in combination with gemcitabine in a phase III trial<sup>[28,29]</sup>.

Due to the difficulty of targeting Ras directly, a possible solution could be to block targets downstream of KRAS, such as the protein kinase MEK. Selumetinib is an oral small molecule that inhibits MEK1/2. In a phase II trial, patients were randomized to receive single-agent

capecitabine or selumetinib as a second-line treatment for advanced pancreatic cancer. The selumetinib arm showed a median overall survival of 5.4 mo vs 5.0 mo in the capecitabine arm, but this result was not statistically significant<sup>[30]</sup>.

Another MEK1/2 inhibitor, trametinib, was tested in pancreatic cancer in combination with gemcitabine against a regimen of gemcitabine plus placebo in a phase II randomized multicentre study. Nevertheless, no significant advantages were demonstrated in terms of overall survival or PFS<sup>[31]</sup>.

Rigosertib, a first-in-class Ras mimetic and small molecule inhibitor of multiple signalling pathways, including polo-like kinase 1 and phosphoinositide 3-kinase (PI3K), was assessed in combination with gemcitabine in patients with treatment-naïve metastatic pancreatic adenocarcinoma in a phase II/III randomized study, but the combination regimen did not improve survival or response, as recently presented at the 2015 ASCO Annual Meeting<sup>[32]</sup>.

Research in this field is in development, but the available trials have failed to show any survival benefit.

### **IGFR pathway inhibitors**

Another possible target in ductal pancreatic cancer is represented by insulin like growth factor 1 receptor, which is highly expressed in pancreatic cells, and upon ligand binding activates several pathways involved in cell proliferation and cell survival such as the PIK3/AKT pathway<sup>[33]</sup>.

Monoclonal antibodies against IGFR (cixutumumab, ganitumab) were evaluated in PDAC treatment, but unfortunately, they failed to show a statically significant survival benefit<sup>[34]</sup>.

In particular, the phase III trial assessing ganitumab in combination with gemcitabine was closed early based on a pre-planned futility analysis: The median overall survival was 7.1 mo in the maximum dose ganitumab arm vs 7.2 mo in the placebo arm (HR, 0.97, *P* = 0.397)<sup>[35]</sup>.

### **Angiogenesis pathway inhibitors**

Neoangiogenesis is essential for tumour progression and metastatization mechanisms. Vascular endothelial growth factor (VEGF) stimulates the proliferation of endothelial cells and is overexpressed in human pancreatic cancer. Nevertheless, neoangiogenesis inhibitors, particularly VEGF inhibitors, failed to improve overall survival in combination with gemcitabine in advanced pancreatic cancer. After encouraging results, phase III trials that tested the efficacy of bevacizumab in association with gemcitabine alone, or gemcitabine plus erlotinib, did not confirm previous findings<sup>[36,37]</sup>.

Aflibercept, a new recombinant fusion protein with extracellular portions of VEGFR-1 and VEGFR-2, which binds VEGF-A, VEGF-B and placental growth factors 1 and 2 thereby inhibiting VEGF-ligand-dependent signalling processes, suppresses tumour growth in pancreatic cell lines and xenografts. Nevertheless, a

phase III study aiming to investigate OS in metastatic pancreatic cancer patients receiving standard gemcitabine and either aflibercept or placebo demonstrated that adding aflibercept to gemcitabine did not improve OS in metastatic pancreatic cancer patients<sup>[38]</sup>.

Similarly sorafenib, an oral multikinase inhibitor of Raf-kinase, VEGF-R2/-R3 and PDGFR- $\beta$ , tested alone or in combination with gemcitabine in small phase I and II trials, and axitinib, an anti-angiogenesis agent assessed in combination with gemcitabine, showed no statistically significant efficacy in a phase III trial in advanced PDAC<sup>[39-41]</sup>.

Phase II studies combining chemotherapy with promising new anti-angiogenic molecular agents, such as TL-118, a nonsteroidal anti-inflammatory oral medication, or necuparanib, which is re-engineered from heparin with possible anti-tumour activity, are underway<sup>[42,43]</sup>.

### **Embryonic pathway inhibitors**

Hedgehog signalling has a critical role in cell proliferation and survival during embryonic development. Normal pancreatic cells silence this pathway, but pathological activation is observed in many solid tumours, particularly in PADC. Hedgehog binds to the extracellular receptor Patched, which, in the absence of Hedgehog, suppresses activation of the G-protein-coupled receptor Smoothened and upregulates glioma associated oncogene homolog1 transcriptional activity. Cancer cell lines show both Hedgehog ligand-dependent and -independent mechanisms of aberrant signalling<sup>[44]</sup>.

Bailey *et al.*<sup>[45]</sup> showed how Sonic hedgehog (SHH) and other proteins downstream of the Hedgehog pathway, detected in precursor lesions and in PDAC primary tumour samples, contribute to the formation of the desmoplastic reaction, an important characteristic of pancreatic cancer that limits the effective delivery of anticancer agents to pancreatic cancer cells. Genetically engineered mouse models demonstrated a depletion of tumour matrix from SHH pathway inhibition, which could be a promising strategy in pancreatic cancer therapy<sup>[46]</sup>.

Vismodegib (GDC-0449), an oral small-molecule inhibitor targeting Smoothened<sup>[47]</sup>, is under assessment in open phase II trials in combination with gemcitabine in advanced cancer, in combination with gemcitabine and nab-paclitaxel in metastatic settings with promising preliminary data<sup>[48]</sup>, and as a single agent in neoadjuvant settings followed by surgery<sup>[49-51]</sup>.

The Smoothened inhibitor saridegib (IPI-926) was tested in association with gemcitabine against gemcitabine plus placebo in a randomized, double-blind, placebo-controlled phase II trial enrolling patients with metastatic disease. Unfortunately, this study was closed ahead of time due to evidence of decreased patient survival in the saridegib arm<sup>[52]</sup>.

Hedgehog inhibitors are an active research field, and several clinical trials are ongoing<sup>[53]</sup>. Notch signalling is another embryonic pathway crucial for pancreatic organogenesis, but after pancreas development, it is

active only in a stem cell subgroup. This pathway is upregulated in PDAC and promotes tumourigenesis. Binding of Notch ligand to its receptor promotes a cascade of proteolytic cleavages, mediated by  $\gamma$ -secretase (presenilin). The activated form ICN (intra cellular notch) forms part of a transcription complex that, after translocating to the nucleus, regulates transcription of several genes involved in proliferation and differentiation of cells, interacting with other pathways such as Hedgehog, KRAS and NF- $\kappa$ B signalling<sup>[54,55]</sup>.

RO4929097 is a selective inhibitor of the  $\gamma$ -secretase enzyme with anti-tumour activity in preclinical studies<sup>[56]</sup>.

A recent phase II single-arm trial assessed the possible role of RO4929097, enrolling 18 previously treated advanced PDAC patients. The treatment was well tolerated; the median survival was 4.1 mo, and the median progression-free survival was 1.5 mo<sup>[57]</sup>.

Encouraging clinical results were observed testing demcizumab, an anti- Delta-like ligand 4 antibody, plus gemcitabine and nab-paclitaxel in advanced PDAC in a phase I b trial. Further evidence is needed to confirm these preliminary data<sup>[58]</sup>.

### **PARP inhibitors**

Mutations affecting BRCA pathway components, especially the tumour suppressor gene BRCA2, which is associated with hereditary predisposition to breast, ovarian and pancreatic cancer, promote deficiency in DNA damage repair mechanisms and genomic instability<sup>[11]</sup>.

Poly ADP-ribose polymerase (PARP) is a nuclear enzyme recruited to repair cell DNA damage, and as recent evidence showed, patients with defects in the homologous DNA recombination pathway may benefit from the use of PARP inhibitors as monotherapy or in combination with radiation or other chemotherapeutic agents. Clinical trials testing those new agents in selected patients are currently in the development phase<sup>[59-61]</sup>.

### **mTOR and PI3K/Akt pathway inhibitors**

After activation, Ras can phosphorylate PI3K, which activates Akt, a serine/threonine kinase. Signal transduction by activated PI3K/Akt plays a role in tumour cell proliferation, survival and metabolism, usually through several downstream targets, including the mammalian target of rapamycin (mTOR)<sup>[62]</sup>.

Several trials testing PI3K/AKT axis inhibitors are currently ongoing in advanced pancreatic cancer patients after encouraging preclinical model results<sup>[63]</sup>. These trials included the following PI3K/AKT axis inhibitors: BKM120, a PI3K inhibitor tested in combination with the mFOLFOX-6 schedule; RX-0201, an Akt antisense oligonucleotide tested in a phase II study plus gemcitabine; and BEZ235, a combined inhibitor of PI3K and mTOR assessed in a phase study in combination with the MEK inhibitor MEK162<sup>[64-66]</sup>.

Wolpin *et al.*<sup>[67]</sup> evaluated a possible role of everolimus, an oral mTOR inhibitor, as monotherapy in 33

gemcitabine-refractory pancreatic cancer patients. The PFS and OS were 1.8 and 4.5 mo, respectively.

Recently, the results of a single arm phase II study where everolimus was tested in combination with capecitabine were published. The median OS was 8.9 mo and PFS was 3.6 mo<sup>[68]</sup>.

The results of a phase I / II study testing everolimus in combination with gemcitabine in advanced settings and the results of a phase II trial testing temsirolimus, another mTOR inhibitor, in locally advanced or metastatic settings are anticipated<sup>[69,70]</sup>.

### **Tumour stroma inhibitors**

The stroma is a dynamic compartment of pancreatic tumours that is critically involved in tumour formation, progression and the metastasis process. Therefore, targeting stromal microenvironment elements could be an efficient therapeutic strategy in addition to previously described trials evaluating Hedgehog signalling inhibitors<sup>[71]</sup>.

After promising data derived from a preliminary clinical study on the possible role of PEGPH20, a pegylated formulation of recombinant hyaluronidase, a phase II trial is currently in the recruitment phase. The purpose of that study is to enrol untreated patients with metastatic disease to receive a combination of PEGPH20, nab-nab-paclitaxel and gemcitabine or a combination of nab-paclitaxel and gemcitabine<sup>[72,73]</sup>.

Additionally, inhibition of PDGFR, a receptor expressed in stromal cells with a critical role in recruiting pericytes and in interstitial fluid pressure in the tumour stroma, could be an interesting molecular target, as suggested by preclinical studies using an orthotopic pancreatic tumour mouse model<sup>[74]</sup>.

TKI258, a PDGFR inhibitor, is under evaluation in a phase I dose assessment for advanced pancreatic cancer patients<sup>[75]</sup>.

In the past, matrix metalloproteinase inhibitors such as marimastat were tested. Matrix metalloproteinases (MMPs) are a family of proteolytic enzymes responsible for the degradation of connective tissue proteins, and aberrant MMP expression is observed in PDAC. Nevertheless, the results of a phase III trial provided no evidence to support a combination of marimastat with gemcitabine in patients with advanced pancreatic cancer<sup>[76]</sup>.

## **CONCLUSION**

Knowledge of the molecular biology of PDAC has important potential clinical relevance, but current efforts to improve understanding of the mutational profile of this tumour have not provided any significant advantage in the use of targeted therapy. Several agents have been tested in PDAC, but almost all have failed to demonstrate efficacy in late phase clinical trials. Only erlotinib has been approved by the FDA for advanced pancreatic cancer treatment, but the improvement of overall survival is barely 2 wk compared with gemcit-

abine alone<sup>[5]</sup>.

There could be many reasons for those unsatisfying results. First of all, the extreme genomic heterogeneity of PDAC is an important block to identifying new candidate actionable molecular targets or to testing existing biological therapies already approved for human use for other cancers. In addition, no significant results have been observed by matching targeted agents with patients harbouring the cognate molecular abnormality, such as, for example, the use of trastuzumab in HER2 overexpression cases. Due to poor results derived from targeting a single molecule, new strategies using multitargeted agents or molecular agent combinations are in the development phase in order to block more than one driving genomic aberration and to prevent or evade resistance.

Additionally, the type of chemotherapy used in combination could be a failure factor. Indeed, the majority of trials have combined target agents with gemcitabine, but actually, the first-line schedules are represented by FOLFIRINOX or gemcitabine plus Nab-paclitaxel. Therefore, greater efficacy may be obtained from the combination of target agents with those chemotherapeutic drugs.

Furthermore, most studies in which molecular or chemotherapeutic agents in pancreatic cancer were tested enrolled an unselected population of patients to treat. In the last 3 years, approximately 116 trials specific for PDAC systemic therapy were registered of which only about 8% applied criteria to select a patient subset based upon molecular biomarkers<sup>[77]</sup>.

## **FUTURE CHALLENGES**

Most studies in which molecular or chemotherapeutic agents in pancreatic cancer were tested enrolled an unselected population of patients to treat. In the last 3 years, approximately 116 trials specific for PDAC systemic therapy were registered of which only about the 8% applied criteria to select a patient subset based upon molecular biomarkers<sup>[77]</sup>.

To stratify patients, the Australian Pancreatic Cancer Genome Initiative has started a pilot study to evaluate the feasibility of assessing a more stratified approach in the management of pancreatic cancer through predefined actionable molecular phenotypes. Patients are enrolled in this trial, called IMPaCT (Individualised Molecular Pancreatic Cancer Therapy), after a preliminary phenotype screening in order to compare the use of gemcitabine in an unselected population to a stratified approach. The aim of the study is to create a tailored approach to pancreatic cancer treatment, which seems to be one of the major challenges for the future<sup>[78]</sup>.

Finally, thanks to biotechnology advancement, biological agents can find application in cancer treatment by tumour-targeted delivery of cytotoxic drugs. Particularly, Ahn *et al.*<sup>[79]</sup> developed antibody fragment-installed polymeric micelles *via* maleimide-thiol conjugation

for selective delivery of platinum drugs to pancreatic tumours. This antibody-drug conjugate significantly suppressed the growth of pancreatic tumour xenografts. This technology, with potential activity *in vitro* and in a mouse model, could be a promising future strategy in pancreatic cancer therapy<sup>[79]</sup>.

In conclusion, the lack of efficacy of targeted therapy in PDAC represents a challenge for the future, and more efforts are needed in order to make pancreatic cancer a curable disease.

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## Multimodality treatment strategies have changed prognosis of peritoneal metastases

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### Abstract

For a long time, treatment of peritoneal metastases (PM) was mostly palliative and thus, this status was link with "terminal status/despair". The current multimodal treatment strategy, consisting of cytoreductive surgery (CRS) and hyperthermic intraperitoneal chemotherapy (HIPEC), has been strenuously achieved over time, but seems to be the best treatment option for PM patients. As we reviewed the literature data, we could emphasize some milestones and also, controversies in the history of proposed multimodal treatment and thus, outline the philosophy of this approach, which seems to be an unusual one indeed. Initially marked by nihilism and fear, but benefiting from a remarkable joint effort of human and material resources (multi-center and -institutional research), over a period of 30 years, CRS and HIPEC found their place in the treatment of PM. The next 4 years were dedicated to the refinement of the multimodal treatment, by launching research pathways. In selected patients, with requires training, it demonstrated a significant survival results (similar to the Hepatic Metastases treatment), with acceptable risks and costs. The main debates regarding CRS and HIPEC treatment were based on the oncologists' perspective and the small number of randomized clinical trials. It is important to statement the PM patient has the right to be informed of the existence of CRS and HIPEC, as a real treatment resource, the decision being made by multidisciplinary teams.

**Key words:** Hyperthermic intraperitoneal chemotherapy; Peritonectomy procedures; Systemic chemotherapy; Peritoneal metastases; Survival

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**Core tip:** The multimodal treatment of peritoneal metastases (PM), involving cytoreductive surgery and hyperthermic intraperitoneal chemotherapy, has been strenuously achieved over time, but seems to be the best treatment option, for selected cases. This paper addresses data about the multimodal treatment strategy, focused to patient's survival, the key indicator for assessing results, in the case of PM. Also, it were highlighted the treatment key aspects and the controversies, high in the 35 years of treatment implementing. By understanding the philosophy of multimodal treatment, physicians will be able to offer an alternative to the routine systemic chemotherapy.

Lungoci C, Mironiuc AI, Muntean V, Oniu T, Leebmann H, Mayr M, Piso P. Multimodality treatment strategies have changed prognosis of peritoneal metastases. *World J Gastrointest Oncol* 2016; 8(1): 67-82 Available from: URL: <http://www.wjgnet.com/1948-5204/full/v8/i1/67.htm> DOI: <http://dx.doi.org/10.4251/wjgo.v8.i1.67>

## INTRODUCTION

Peritoneal metastases (PM) were described by Sampson *et al.*<sup>[1]</sup> (1931) in an ovarian cancer patient. For a long time since then, treatment was mostly palliative and thus, PM was linked to "terminal status/despair". The current multimodal treatment consisting of cytoreductive surgery (CRS) and hyperthermic intraperitoneal chemotherapy (HIPEC) has been strenuously achieved over time, but seems to be the best treatment option for selected PM cases.

As we reviewed the literature data, we could emphasize some milestones and also, controversies in the history of PM treatment and thus, outline the philosophy of proposed multimodal radical treatment, which seems to be an unusual one indeed. To understand this radical treatment, we start with the natural evolution of PM and "conventional" systemic chemotherapy approach, in fact the treatment of choice for stage IV cancer, regardless of the dissemination type and location. Four periods must be considered in the evolution of "dedicated" PM treatment: Before 1980; 1980-2000; 2000-2010 and 2010-present. The first time period, before 1980, was a period of palliative intraperitoneal treatment of ascites. In 1980-2000 were proposed the methods and define the foundation laying for a new multimodal approach of PM by intraperitoneal chemotherapy and CRS. The next periods, until 2010, were those of the progressive development of dedicated multimodal treatment strategy, concluding with the actual CRS-HIPEC. From 2010, the studies were focused about new research pathways. The PM treatment approach related survival was the main issue considered in this review.

## NATURAL EVOLUTION OF PM

In the literature concerned with PM, the EVOCAPE I study<sup>[2]</sup> is classical and it reflected the natural evolution of patients with non-gynecological PM. The mean survival (mS) was 6 mo, significantly correlated with the PM stage (Figure 1), according Gilly system<sup>[3]</sup> (nodules/lumps < 5 mm: 9.8 mo; > 2 cm: 3.1 mo). PM of pancreatic origin had the lowest mS (2.9 mo), followed by PM of gastric origin (6.5 mo) and of colorectal origin (6.9 mo). The degree of differentiation had no influence on survival.

Several other "historical"<sup>[4-6]</sup> studies confirmed the unfavorable prognosis of PM. Ascites is a negative prognostic factor: In pancreatic cancer, median survival (MS) was < 1 mo, with an important negative impact on the quality of life. Surgery was aimed at palliating gastrointestinal complications, as it was contraindicated in patients with gastric, pancreatic tumors or ascites<sup>[4]</sup>. In colorectal cancer (marked by a favorable biological pattern), MS was significantly less for synchronous PM than that in metachronous (7 mo vs 28 mo,  $P < 0.001$ )<sup>[6]</sup>.

## "CONVENTIONAL" SYSTEMIC CHEMOTHERAPY OF PM

Recent studies on colorectal cancer compared patients having only PM, as a distant metastatic location, with patients having other systemic dissemination. Franko *et al.*<sup>[7]</sup> (2012) revealed a significantly lower ( $P < 0.001$ ) global MS (12.7 mo vs 17.6 mo) and disease-free survival (5.8 mo vs 7.2 mo) for patients with PM vs other metastatic locations. Also, the poor global MS of PM metastasis patient was unchanged by various chemotherapy regimens (Figure 2).

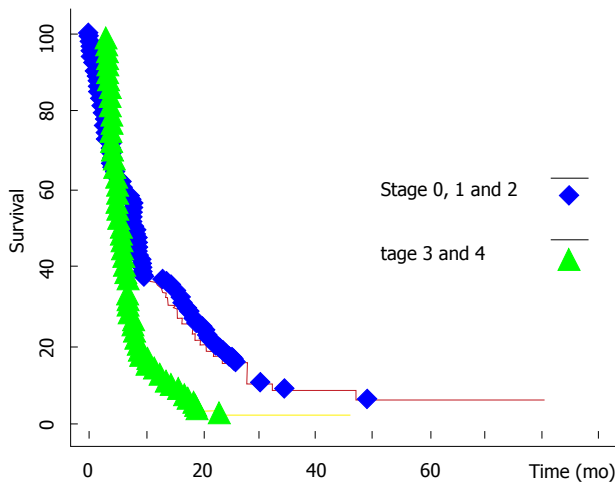
Systemic chemotherapy carried MS significant benefit ( $P = 0.026$ ) in colorectal PM patients only compared to those patients who did not receive chemotherapy (Figure 3): Increasing from 5 mo without chemotherapy (95%CI: 3-7 mo) to 11 mo with the fluorouracil-leucovorin protocol (95%CI: 6-9 mo), and to 12 mo with the oxaliplatin-irinotecan protocol (95%CI: 4-20 mo)<sup>[8]</sup>.

Despite the progressive development of systemic chemotherapy, in a population-based study, Lemmens *et al.*<sup>[9]</sup> confirmed the poor MS in PM patients (1995-2001: 7 mo; 2002-2008: 8 mo), unlike that of patients with liver metastases, which underwent improvement (1995-2001: 8 mo; 2002-2008: 12 mo).

## "DEDICATED" INTRAPERITONEAL TREATMENT OF PM

### Palliative treatment (< 1980)

The first attempts for a treatment approach of peritoneal malignancies began in 1950, with the sporadic use of intraperitoneal chemotherapy for malignant ascites. For this intraperitoneal treatment, hemisulphur mustard<sup>[10]</sup>,



**Figure 1** Kaplan-Meier survival curve of non-gynecological peritoneal carcinomatosis, stratified according to the Gilly staging system (Stage 0, 1 and 2 vs Stage 3 and 4)<sup>[2]</sup> (with permission). Kaplan-Meier survival curve according to PM staging<sup>[2]</sup>. Available from: URL: <http://click.info.copyright.com/?qs=e232cb87f594dcec17211f4d00b2929249713825e6b912c104538a1695c335dde91d3fd5f03fa97>. PM: Peritoneal metastases.

thiotepa<sup>[11]</sup>, nitrogen mustard<sup>[12]</sup>, quinacrine<sup>[13]</sup> and bleomycin<sup>[14]</sup> were used. Nitrogen mustard had a high digestive toxicity, so it was replaced by thiotepa (considered elective for ascites control in 1964), but even at that time it was foreseen that it would be replaced by 5-fluorouracil in digestive cancer palliation<sup>[15]</sup>. Nevertheless, nitrogen mustard was the basis for developing further drugs: Cyclophosphamide, chlorambucil, uramustine, ifosfamide, melphalan, and bendamustine.

#### **Multimodal treatment - methods and foundation-laying (1980-2000)**

In 1978-1980, the first documented data became available, at first referring to the clearance of intraperitoneal cytostatic drugs<sup>[16]</sup>, then to circulating intraperitoneal cytostatic solutions, all thanks to the contributions of Speyer *et al*<sup>[17]</sup> and Spratt *et al*<sup>[18]</sup>. They were “the fathers” of regional intraperitoneal chemotherapy. Spratt augmented the cytostatic effect by hyperthermia using a specially designed device (Thermal Infusion Filtration System). Thus, the foundation was laid for a multimodal treatment of PM by normothermic and HIPEC.

The mechanism by which hyperthermia cytotoxic effects associating with and increasing the cytostatic drug effect is due to certain particularities of these drugs; studies regarding this aspect are exhaustive<sup>[19-25]</sup>.

The key merit in developing and implementing this multimodal treatment strategy belongs to Sugarbaker, who outlined and detailed the premises substantiating it. The starting model was that of PM in appendiceal cancer<sup>[26]</sup>. The most important phase was the adjustment in the existing pathophysiological concept of PM, as a systemic disease and, consecutively, its treatment with systemic chemotherapy. In the new approach, the peritoneum was regarded as an organ (similar to the liver), the pathogeny of PM implying, first and foremost, peritoneal dissemination. Thus, it appears natural to use

a regional treatment in PM<sup>[27-31]</sup>. Sugarbaker’s research was regarded mistrustfully, and 25 years had to pass before the “European contributions to the Sugarbaker protocol”<sup>[32]</sup> appeared: One multicenter retrospective study<sup>[33]</sup>, two randomized prospective phase III studies<sup>[34,35]</sup> and the use of oxaliplatin and irinotecan as new cytostatic drugs in the protocols for intraperitoneal chemotherapy<sup>[36,37]</sup>.

Sugarbaker also has the merit of being the first to have described and implemented the surgical procedures associated with regional chemotherapy, generically named “Peritonectomy”<sup>[38]</sup>. So, the road lay open for the PM multimodal treatment by CRS and HIPEC.

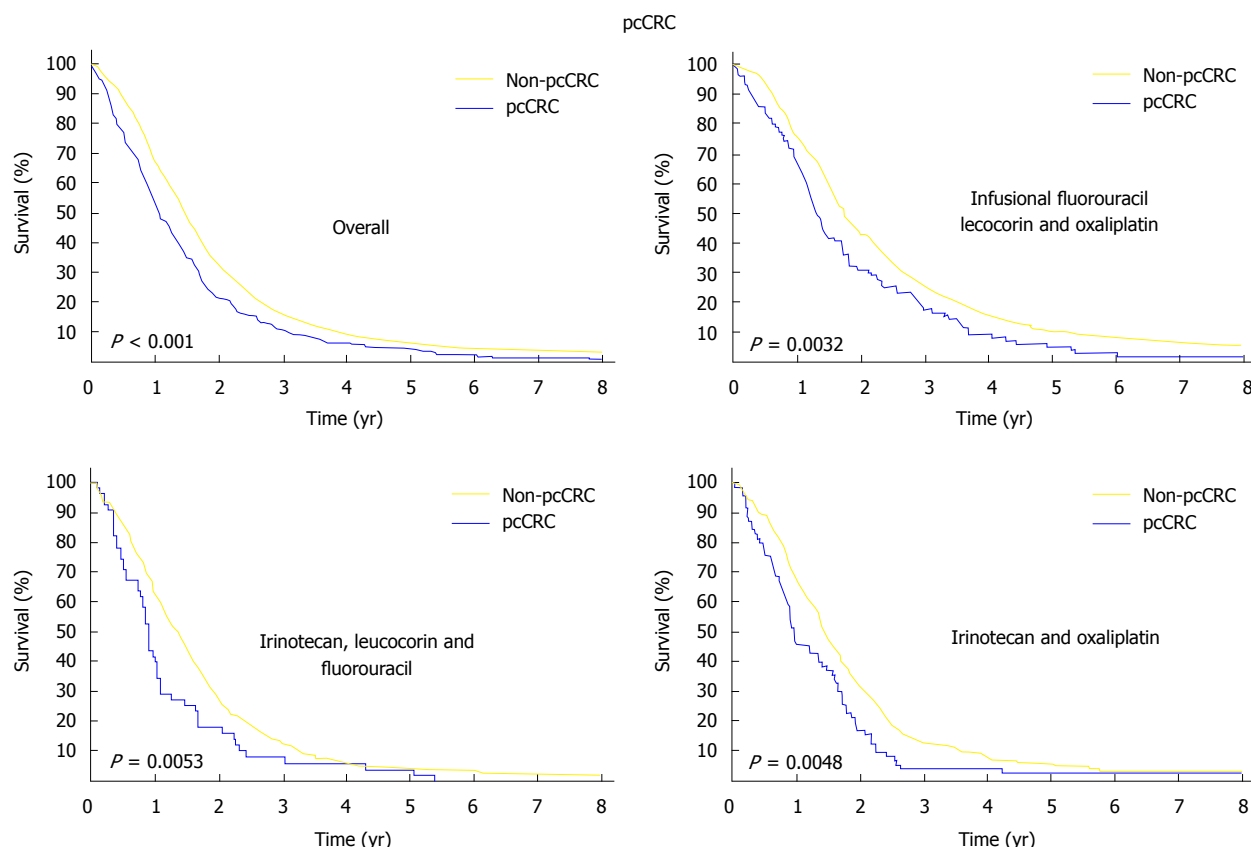
He then brought in other special aspects regarding the surgical technique of Peritonectomy procedures: Required electrocautery, circumferential skin traction, dissection of subpyloric space and falciform ligament<sup>[39-42]</sup>. He also described a method for staging PM and assessing the result of CRS, which were subsequently used in the majority of studies: The “Peritoneal Cancer Index” (PCI), based on the extension of peritoneal injury and the size of peritoneal deposits, respectively, the “Completeness of Cytoreduction Score” (CCRS), based on the size of the remaining peritoneal nodules/lumps<sup>[43]</sup>.

## **PM MULTIMODAL TREATMENT - CONFIRMATION, ASPECTS, PATIENT SELECTION, CONTROVERSIES (2000-2010)**

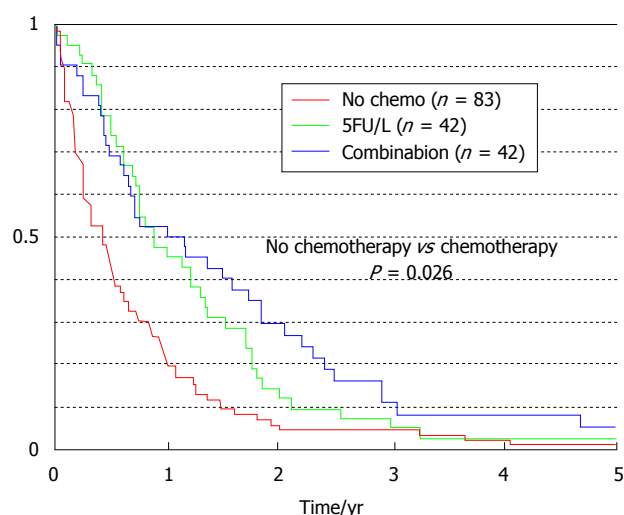
### **“Confirmation”**

Although the number of patients progressively and significantly increased and the so-called “long-term survivors” were identified, it took about 20 years before the “confirmations of a multimodal treatment option for PM” appeared. The initiator was Verwaal (2003)<sup>[35]</sup>, who carried out a randomized clinical trial for patients with colorectal PM. He showed that, during a mean follow-up of 21.6 mo, the MS of patients treated with CRS-HIPEC (22.3 mo) was significantly ( $P < 0.032$ ) improved compared to patients treated with palliative surgery and systemic chemotherapy with fluorouracil-leucovorin (12.6 mo) (Figure 4A).

Verwaal’s research was confirmed by two other reference-worthy studies, which had the merit of comparing CRS-HIPEC with modern systemic chemotherapy treatment, in colorectal PM. Elias *et al*<sup>[44]</sup> (2009) compared systemic irinotecan-oxaliplatin chemotherapy with CRS-HIPEC. Global survival in the CRS-HIPEC group (2 years: 81%, 5 years: 51%) was significantly ( $P < 0.05$ ) improved compared to the systemic chemotherapy (2 years: 65%, 5 years: 13%). Franko *et al*<sup>[45]</sup> (2010) analyzed systemic chemotherapy with irinotecan, oxaliplatin, bevacizumab, and cetuximab. MS in the CRS-HIPEC treatment group (34.7 mo) was significantly ( $P < 0.01$ ) longer than systemic chemotherapy (16.8 mo) (Figure 4B). It was emphasized that the best results



**Figure 2** Kaplan-Meier survival curve of metastatic colorectal cancer stratified according to the metastatic locations (peritoneal carcinomatosis vs non peritoneal carcinomatosis) and chemotherapy protocols (fluorouracil, leucovorin and oxaliplatin; fluorouracil, leucovorin and irinotecan; irinotecan and oxaliplatin)<sup>[7]</sup> (with permission). Kaplan-Meier survival curve of Metastatic Colorectal Cancer stratified by peritoneal metastatic status and chemotherapy protocols<sup>[7]</sup>. Available from: URL: <http://click.info.copyright.com/?qs=da4305023350a474912bb7bdbc04210a63a294c209e715b6497fdff613ea3697d486bdb9bffe0470>. pcCRC: Peritoneal carcinomatosis from colorectal cancer.



**Figure 3** Kaplan-Meier survival curve of colorectal peritoneal carcinomatosis stratified by chemotherapy protocols<sup>[8]</sup> (with permission). Kaplan-Meier survival curve of Colorectal PM stratified by chemotherapy protocols<sup>[8]</sup>. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (Available from: URL: <http://creativecommons.org/licenses/by/2.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. PM: Peritoneal metastases. 5FU: 5-fluorouracil.

systemic chemotherapy.

For gastric PM, studies also showed a benefit in terms of survival. The prospective randomized clinical trial GYMSSA<sup>[46]</sup> compared survival in patients treated with CRS-HIPEC and systemic chemotherapy vs systemic chemotherapy treatment alone. Within the limitation of a small number of patients, it showed a longer MS (11.3 mo vs 4.3 mo) for CRS-HIPEC treatment trial arm.

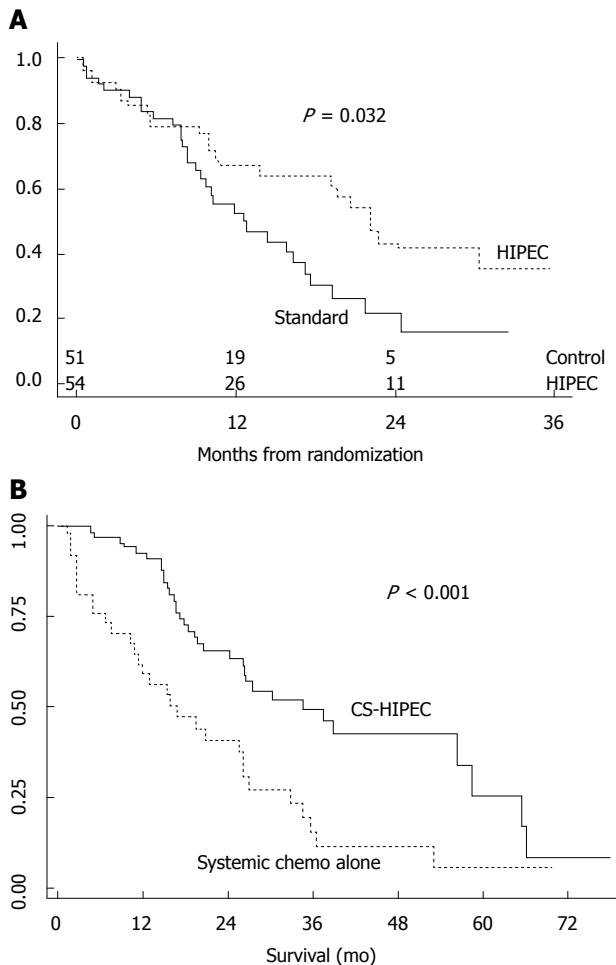
Likewise, Yang *et al.*<sup>[47]</sup> showed in a phase III randomized clinical trial the importance of connecting CRS with HIPEC, in the treatment of PM of gastric cancer origin. The CRS-HIPEC association vs CRS alone significantly ( $P = 0.046$ ) increased MS: 11 mo (95%CI: 10-11.9 mo) vs 6.5 mo (95%CI: 4.8-8.2 mo) (Figure 5).

A meta-analysis of randomized clinical trials performed by Yan *et al.*<sup>[48]</sup> showed that in advanced gastric cancer, HIPEC associated with surgery led to a significant increase in survival, compared with patients benefiting from surgery alone.

In addition to randomized clinical trials (the gold standard in the treatment implementation), there are a series of multi-center studies showing survival results for patients treated with CRS-HIPEC.

Thus, several multi-center studies, focused on pseudomyxoma peritonei, colorectal and ovarian cancers, were conducted in France (Figure 6). For the treatment of

were achieved by associating CRS-HIPEC treatment with

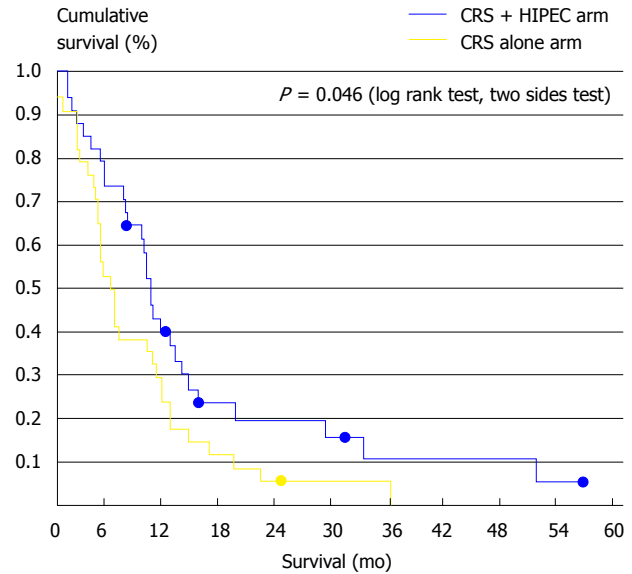


**Figure 4** Kaplan-Meier survival curve comparing hyperthermic intraperitoneal chemotherapy to standard treatment, for colorectal peritoneal carcinomatosis<sup>[35]</sup> (with permission) (A) and comparing cytoreductive surgery and hyperthermic intraperitoneal chemotherapy treatment to systemic chemotherapy alone, for colorectal peritoneal carcinomatosis<sup>[45]</sup> (with permission) (B). A: Kaplan-Meier survival curve comparing HIPEC to standard treatment, for Colorectal PM<sup>[35]</sup>. Available from: URL: <http://click.info.copyright.com/?qs=2b7046b10dd0c5471bbb88bac0096e00e895f442c0326423c4ec2ccdd7b4701b99fd4bd5b32f0283>; B: Kaplan-Meier survival curves comparing CRS-HIPEC treatment to systemic chemotherapy alone, for Colorectal PM<sup>[45]</sup>. Available from: URL: <http://click.info.copyright.com/?qs=2b7046b10dd0c5471bbb88bac0096e00e895f442c0326423c4ec2ccdd7b4701b99fd4bd5b32f0283>. CRS-HIPEC: Cytoreductive surgery and hyperthermic intraperitoneal chemotherapy; PM: Peritoneal metastases.

pseudomyxoma peritonei, CRS-HIPEC was designated the “gold standard” due to the yielded results (at 5 years: 73% global survival, 56% disease-free survival)<sup>[49]</sup>. Favorable results were shown for colorectal cancer (at 5 years: 27% global survival, 10% disease-free survival)<sup>[50]</sup>, and also for ovarian cancer (global survival: Advanced forms 35.4 mo, recurrent forms 45.7 mo)<sup>[51]</sup>.

The results were also confirmed by a long-term data analysis in the Netherlands, after the implementation of the CRS-HIPEC treatment: MS was 33 mo (95%CI: 28-38 mo) in colorectal cancer and 130 mo (95%CI: 98-162 mo) in pseudomyxoma peritonei (Figure 6)<sup>[52]</sup>.

The experience of a reference center for PM treatment (St. George's Hospital, Sydney) sustains the higher results obtained by the use of CRS-HIPEC treatment in



**Figure 5** Kaplan-Meier survival curves comparing cytoreductive surgery and hyperthermic intraperitoneal chemotherapy treatment to cytoreductive surgery alone, for gastric peritoneal carcinomatosis<sup>[47]</sup> (with permission). Kaplan-Meier survival curves comparing CRS-HIPEC treatment to CRS alone, for Gastric PM<sup>[47]</sup>. This is an open access article distributed under the terms of the Creative Commons Attribution Noncommercial License, which permits any noncommercial use, distribution, and reproduction in any medium, provided the original author(s) and source are credited. CRS-HIPEC: Cytoreductive surgery and hyperthermic intraperitoneal chemotherapy; PM: Peritoneal metastases.

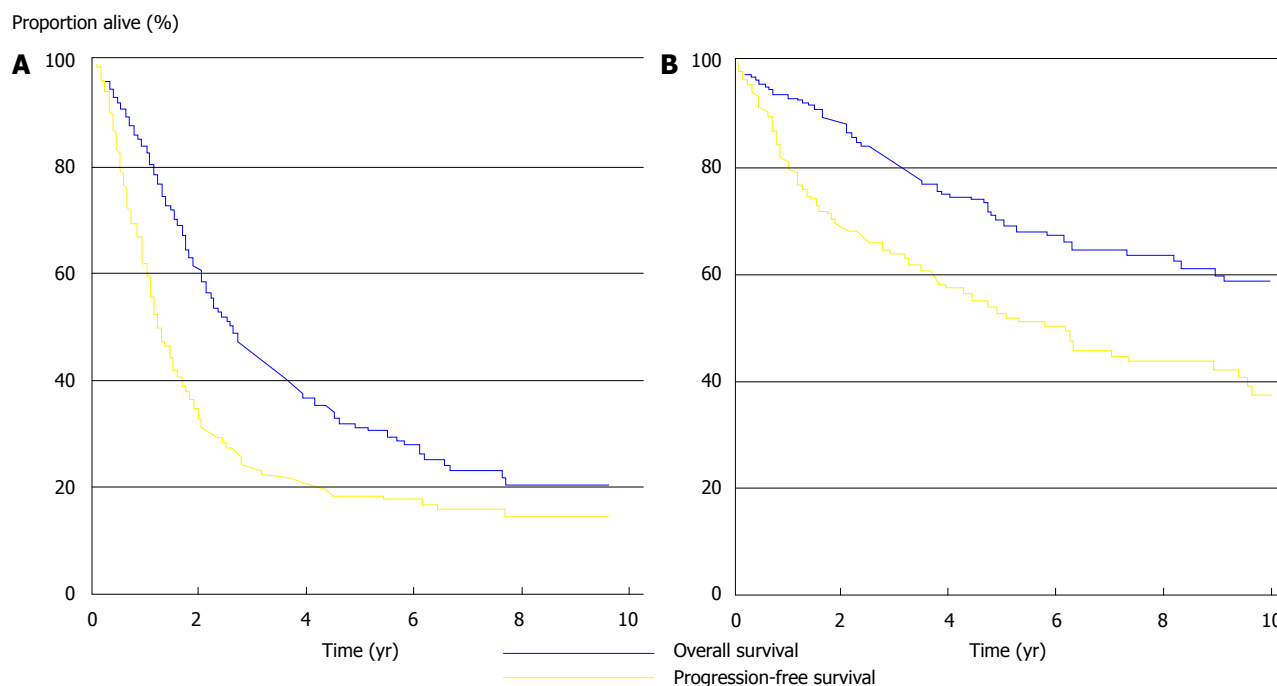
pseudomyxoma peritonei (MS 104 mo; 5-year survival 75%) and colorectal cancer (MS 33 mo; 3-year survival 46%)<sup>[53]</sup>.

A series of systematic reviews were conducted under the leadership of Sugarbaker, demonstrating a better survival for CRS-HIPEC treatment compared to conventional systemic chemotherapy. PMs of different origins were analyzed: Colorectal<sup>[54]</sup>, gastric<sup>[48]</sup>, ovarian<sup>[55]</sup> cancers, and malignant peritoneal mesothelioma<sup>[56]</sup>. Other systematic review studies also reported higher results for CRS-HIPEC in colorectal<sup>[57]</sup> and gastric<sup>[58]</sup> cancers.

All these studies (numerous and enrolling an increased number of patients) shows joint international efforts to identify the role of CRS-HIPEC in multimodal PM treatment. They have allowed the development of an important medical database which, by confirming the higher results in terms of survival and disease-free survival, upholds this treatment strategy. This is also confirmed by the evidence-based medicine approach studies<sup>[59]</sup>.

The MS, as a result of CRS-HIPEC treatment, related to the tumor entities and study type, were presented in Table 1.

As a recognition of the foundation-laying treatment of PM with CRS-HIPEC, this was included in the treatment guidelines in France<sup>[60]</sup>, Germany<sup>[61]</sup>, United Kingdom (<http://www.nice.org.uk/guidance/IPG331/PublicInfo>), the Netherlands<sup>[52,62]</sup>. There are a number of ongoing symposia focused on Peritoneal Surface Malignancies, under the patronage of the European Society of Surgical



**Figure 6 Overall survival compared with disease-free survival for pseudomyxoma peritonei (A) and colorectal peritoneal carcinomatosis (B), treated with cytoreductive surgery and hyperthermic intraperitoneal chemotherapy, from the Netherlands<sup>[52]</sup> (with permission).** Overall and disease-free survival of Pseudomyxoma Peritonei (A) and Colorectal PM (B), treated with CRS-HIPEC, from the Netherlands<sup>[52]</sup>. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. CRS-HIPEC: Cytoreductive surgery and hyperthermic intraperitoneal chemotherapy; PM: Peritoneal metastases.

**Table 1 Cytoreductive surgery and hyperthermic intraperitoneal chemotherapy median survival, related to the tumor entities and study type**

Primitive tumor origin	Study type	Median survival (mo)
Colorectal	Randomized clinical trials	22.3 <sup>[35]</sup>
	Single center experience	33 <sup>[33]</sup> , 34.7 <sup>[45]</sup>
	Systematic reviews	13-29 <sup>[34]</sup>
	Multi-institutional studies	33 <sup>[52]</sup>
Gastric	Randomized clinical trials	11.3 <sup>[46]</sup> , 11 <sup>[47]</sup>
	Systematic reviews	10.4 <sup>[53]</sup>
Pseudomyxoma peritonei	Single center experience	104 <sup>[53]</sup>
	Multi-institutional studies	130 <sup>[52]</sup>
Ovarian	Multi-institutional studies	35.4-45.7 <sup>[51]</sup>
	Systematic reviews	22-54 <sup>[55]</sup>
Malignant peritoneal mesothelioma	Systematic reviews	34-92 <sup>[56]</sup>

Oncology, as well as a world congress.

The view of those who consider that multimodal PM treatment is "more of an experimental kind, based on common-sense evidence rather than on solid data"<sup>[63,64]</sup> is already obsolete. Even so, the confirmation of CRS-HIPEC, as an effective treatment approach by medical studies, such as randomized clinical trials, is not mandatory<sup>[65]</sup>. And more than that, the life of patients could be endangered by denying them a treatment resource, since the validation process may take as long as 40 years<sup>[66]</sup>.

### Aspects

Unfortunately, there is no single perfect treatment

option, valid in any setting, so the problems raised were concerned with treatment risk (morbidity, mortality, medical team risk), costs and with the indication of CRS-HIPEC, in terms of prognostic factors.

In the beginning, morbidity and mortality were the key factors initiating distrust among patients and physicians<sup>[67]</sup>. The causes of morbidity and mortality may well be suspected to belong to either CRS (surgery proper), or HIPEC (thermal effects of circulating fluid and toxic cytostatic drug effects). In a systematic-review study, morbidity was 21.5% and mortality 4.8%<sup>[68]</sup>, but literature reports data within a large range: Morbidity 12%-67% and mortality 0%-9%. The main complications include digestive fistulae, postoperative bleeding, pleural-pulmonary complications, bone marrow suppression, hemodynamic instability and renal failure. Protective ileostomy, chest drain and postoperative thoracic imaging are routinely used.

However, it was shown that morbidity and mortality were not significantly increased, compared to extensive organ resection surgery (e.g., Whipple's operation)<sup>[69]</sup>. Treatment complications were significantly correlated with the number of Peritonectomy procedures, left diaphragmatic Peritonectomy, duration of surgery and the number of large bowel anastomoses<sup>[70]</sup>. The global incidence for the 1<sup>st</sup> to 4<sup>th</sup> degree of gastrointestinal toxicities (according to the Common Terminology Criteria for Adverse Events) was 17%, and for symptomatic surgical site infections incidence reached 35.85% (with a global morbidity of 45%)<sup>[71]</sup>.

The learning curve must be respected by any medi-

cal procedure, even more so when it implies new skills for the surgeon. The “breaking points” of the learning curve in achieving complete CRS, of a morbidity less than 3<sup>th</sup> degree and an absence of treatment-related mortality are evaluated to be 141, 158 and 144 cases, respectively (the Milan experience), or 126, 134 and 60 cases, respectively (the Bentivoglio experience)<sup>[72]</sup>.

As the Dutch model of CRS multimodal treatment implementation was analyzed, it was proven that, unlike in the initial stage (experience gathering), in the stage of treatment becoming standard, the percentage of radical surgeries increased significantly (66% vs 86%,  $P < 0.001$ ) and major morbidity (3<sup>th</sup>-5<sup>th</sup> degree) decreased significantly (64% vs 32%,  $P < 0.001$ )<sup>[73]</sup>.

If there existed accreditation centers and HIPEC registers, coursing through the learning curve could be faster<sup>[74]</sup>. Suggestions were made for training in CRS-HIPEC to begin during the residency programmer<sup>[75]</sup>.

As for the risks the medical team are exposed to during HIPEC, it was shown in several pharmacological studies that, in relation to the HIPEC method (closed/open), with required training, these risks may be reduced to a minimum<sup>[76-78]</sup>.

The costs implied by CRS-HIPEC treatment are definitely high, but financial calculations show that it is a better solution in terms of treatment results<sup>[53,79-81]</sup>. This is why in Germany, HIPEC is adopted, considered a surgical procedure and coded as such<sup>[61]</sup>.

### Patient selection

One of today's challenges in treating PM is patient selection. This is why literature studies are focused on factors/variables correlating with survival.

The randomized clinical trial performed by Verwaal *et al.*<sup>[35]</sup> showed that in colorectal cancer, the variables with the highest impact are extension of PM and the radical feature of CRS ( $P < 0.0001$ ) (Figure 7). The GYMSSA randomized clinical trial<sup>[46]</sup> also showed that essential conditions for a significant increase in survival in gastric cancer are complete CRS and a PCI  $\leq 15$ .

A single-center experience, the most comprehensive in terms of the number of patients (1000 patients), shows that the prognostic factors significantly correlated with survival ( $P < 0.001$ ) are: The performance index, the location of the primary tumor, the CCRS, and the center experience<sup>[82]</sup>. Another single-center experience (109 patients) correlated survival to the following factors: Histology of non-adenocarcinoma ( $P = 0.001$ ), appendiceal location ( $P = 0.001$ ), absence of liver metastases ( $P = 0.01$ ), and complete resection of all gross disease ( $P < 0.001$ )<sup>[83]</sup>.

A multi-center French study shows that in colorectal cancer, CCRS is the most important prognostic factor for MS: 32.4 mo for complete vs 8.4 mo for incomplete CCRS ( $P < 0.001$ ) (Figure 8)<sup>[33]</sup>. The multi-center SITILO study<sup>[84]</sup> also reveals in colorectal cancer the following independent prognostic variables correlated with survival: PCI, CCRS, and presence of hepatic metastases.

The consensus conference on PM treatment in

colon cancer statutes that the indication of CRS-HIPEC treatment should be based on complete CRS<sup>[85]</sup>.

All those prognostic factors are in dynamics, the trend being towards broadening the indication range, except for the radical feature of CRS: It is absolutely necessary that this should be complete, or at least optimal. Traditionally, the treatment approach in PM was reserved for colon or appendicular cancer, pseudomyxoma peritonei and peritoneal malignant mesothelioma, but now the range of indications includes rectal, gastric and ovarian cancers. The importance of PCI is not an absolute one, it must be correlated with primary tumor location (colonic PM origin vs gastric), histological grading (well and moderate differentiated vs poorly differentiated and undifferentiated), and the anatomical sites involved (Treitz ligament, porta hepatis and suprahepatic veins, coelic axis and mesenteric vessels). The presence of other systemic dissemination (abdominal or extra-abdominal) was a contraindication for the treatment approach in PM, but this is no longer (Figure 9) the case provided that complete CRS can be obtained<sup>[86-89]</sup>.

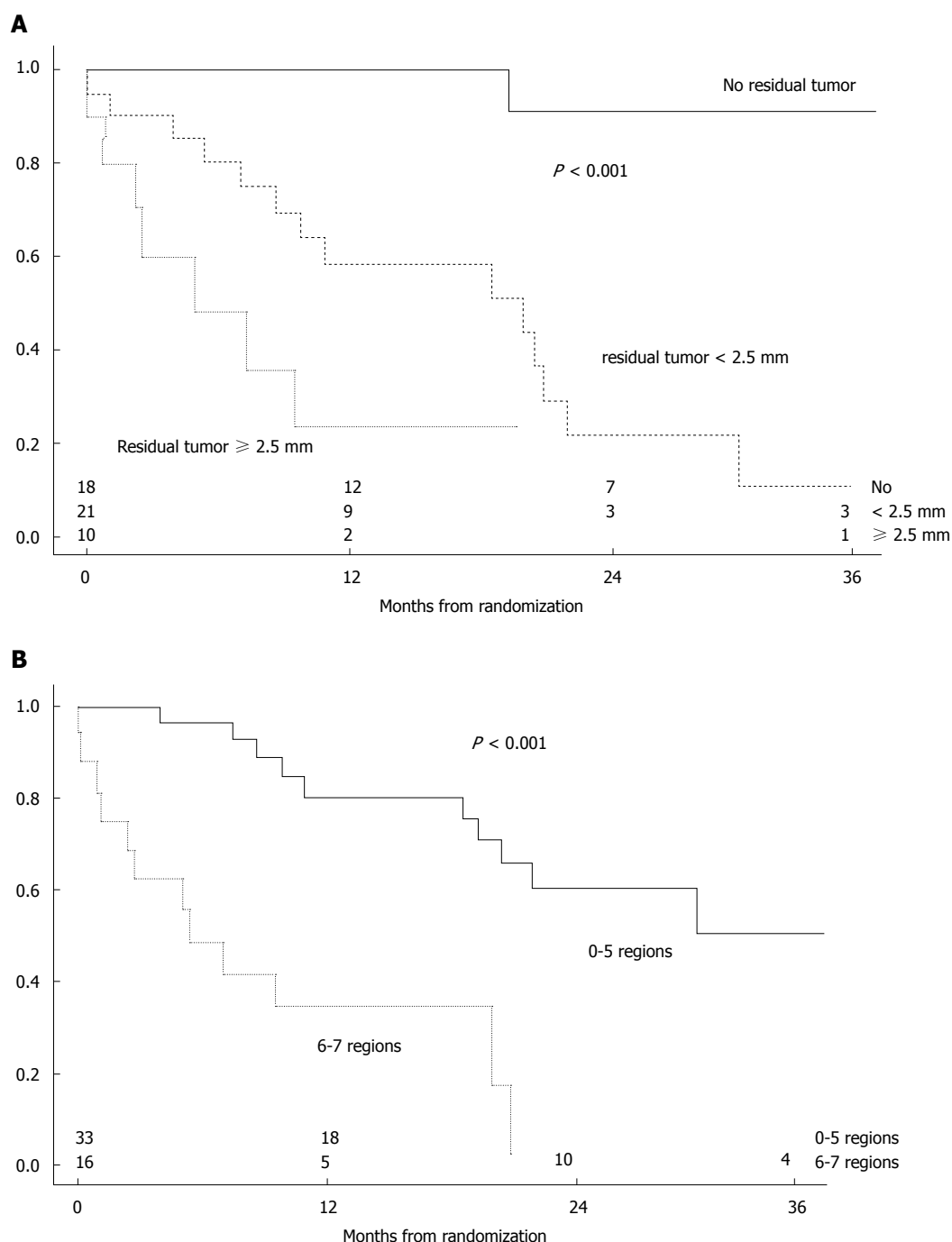
Except for the patient status (evaluated by the performance index), the main CRS-HIPEC treatment contraindication is small bowel involvement<sup>[90]</sup>, which is regarded as an independent prognostic factor<sup>[91-93]</sup>.

A series of studies have confirmed the prognostic value of tumor grading in colorectal cancer. The “signet-ring cell” vs other types of differentiation has a significantly poorer MS (14.1 mo vs 35.1 mo;  $P < 0.01$ ) and an increased relapse rate (68.8% vs 43.7%;  $P = 0.05$ )<sup>[94]</sup>. CRS-HIPEC treatment carries no survival benefit in colorectal PM with signet-ring cell histology, unless complete CRS is obtained<sup>[95]</sup>. Also, for the aggressive type of pseudomyxoma peritonei, systemic chemotherapy is indicated instead of CRS-HIPEC treatment<sup>[96]</sup>.

In some studies, the prognostic factors were grouped into scores. The Peritoneal Surface Disease Severity Score may be used to stratify patients in clinical trials<sup>[97]</sup>. Different scores used in PM of colorectal origin are: The Peritoneal Surface Disease Severity Score, the Prognostic Score, and the Colorectal Peritoneal Score. The Colorectal Peritoneal Score (value  $\geq 6$ ) identifies patients with an unfavorable prognosis in terms of survival, and it does so better than PCI (value  $> 20$ ) or the other two scoring systems<sup>[98]</sup>.

### Controversies

At the same time, there are also reserved attitudes regarding the CRS-HIPEC approach of PM. This is mainly the position of oncologists, who are refractory to this treatment option, using the argument of the risk/benefit ratio. The theoretical premise they use is based on the lack of difference (pathophysiology, evolution, and treatment) between PM and other systemic dissemination. The treatment is not adapted, so different protocols of systemic chemotherapy (from the classic de Gramont chemotherapy to oxaliplatin, irinotecan and biological molecular agents) are given in different clinical

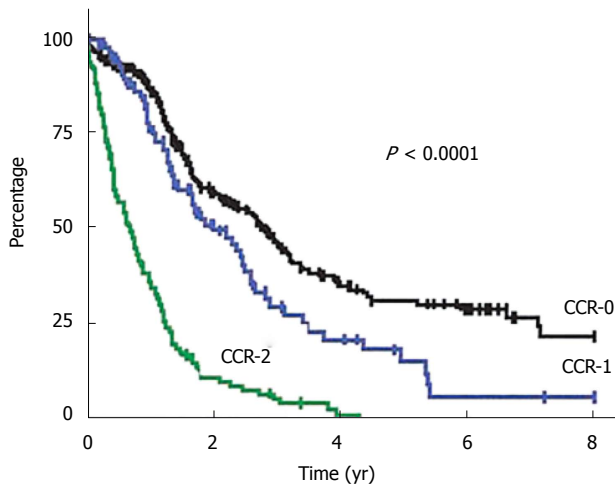


**Figure 7** Kaplan-Meier survival curve of colorectal peritoneal carcinomatosis treated by cytoreductive surgery and hyperthermic intraperitoneal chemotherapy, stratified according to the size of residual tumors (A) and the number of regions with residual tumors (B)<sup>[35]</sup> (with permission). Kaplan-Meier survival curve of CRS-HIPEC treatment, for Colorectal PM, stratified by the number of regions affected (A) and the number of regions with residual tumors (B)<sup>[35]</sup>: <http://click.info.copyright.com/?qs=2b7046b10dd0c5471b8bb8bac0096e00e895f442c0326423c4ec2ccdd7b4701b99fd4bd5b32f0283>. CRS-HIPEC: Cytoreductive surgery and hyperthermic intraperitoneal chemotherapy; PM: Peritoneal metastases.

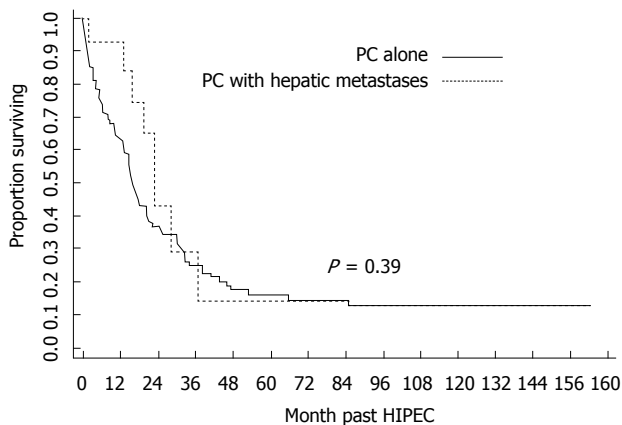
trials, without considering the variances between the specific dissemination biology<sup>[99-101]</sup>. The indispensable condition that oncologists require for inclusion in a clinical trial is the presence of measurable lesions. In the case of PM, this condition is almost impossible to meet. Imaging modalities have a low sensitivity in detecting the peritoneal dissemination, and this is true for computer tomography as well as for magnetic resonance imaging. The only parameters based on which the results of CRS-

HIPEC treatment may be assessed are disease-free survival and global survival.

Furthermore, concerning the oncologists' perspective, there is at least one more important argument supporting the dedicated multimodal treatment of PM: The studies matching hepatic metastases vs PM. These have shown that the pathway of dissemination are different and the treatment results are comparable (Figure 10), if treatment is potentially radical<sup>[102-104]</sup>.



**Figure 8** Kaplan-Meier survival curve of cytoreductive surgery and hyperthermic intraperitoneal chemotherapy treatment, for colorectal peritoneal carcinomatosis, stratified by completeness of cytoreduction score<sup>[33]</sup> (with permission). Kaplan-Meier survival curve of CRS-HIPEC treatment, for Colorectal PM, stratified by CCRS<sup>[33]</sup>. Available from: URL: <http://click.info.copyright.com/?qs=2b7046b10dd0c5471bbb8bac0096e00e895f442c0326423b795894c1892230b84270e7e00c4e014>. CCRS: Completeness of cytoreduction score; CRS-HIPEC: Cytoreductive surgery and hyperthermic intraperitoneal chemotherapy; PM: Peritoneal metastases.

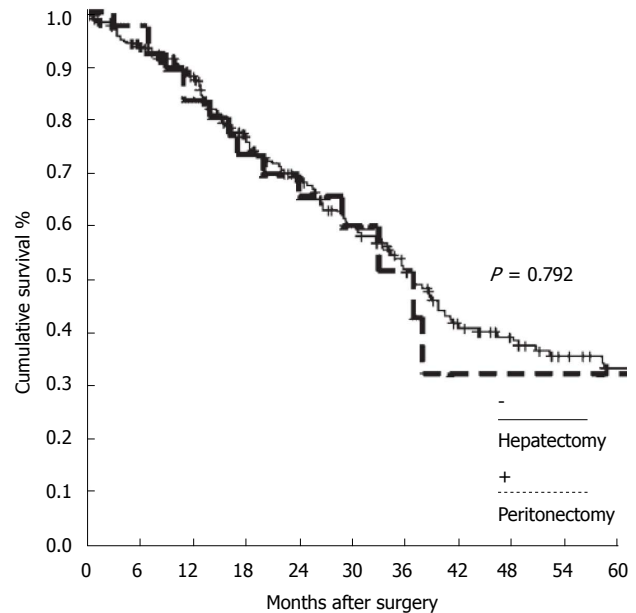


**Figure 9** Kaplan-Meier survival curve of colorectal peritoneal carcinomatosis stratified according to hepatic involvement (peritoneal carcinomatosis alone vs peritoneal carcinomatosis with hepatic metastases)<sup>[86]</sup> (with permission). Kaplan-Meier survival curve of Colorectal PM alone and PM with Hepatic Metastases<sup>[86]</sup>. Available from: URL: <http://click.info.copyright.com/?qs=2b7046b10dd0c5471bbb8bac0096e00e895f442c032642364879a25688a50cc82757e6f8509f6e1>. PM: Peritoneal metastases.

Nowadays, in colorectal cancer, by analogy with Hepatic Metastases, multimodal CRS-HIPEC treatment has been adopted and is the indicated approach for CP, in most institutions in the United States<sup>[31]</sup>.

## PM MULTIMODAL TREATMENT - RESEARCH PATHWAYS (2010-2014)

Currently, there is reason to talk about a higher level, where the problem of timing for CRS-HIPEC is raised. There are studies showing that PM prophylaxis is a valid approach.



**Figure 10** Kaplan-Meier survival curve for colorectal peritoneal metastases and colorectal hepatic metastases, who achieved optimal treatment<sup>[102]</sup> (with permission). Kaplan-Meier survival curve for Colorectal PM and Colorectal Hepatic Metastases, with optimal treatment<sup>[102]</sup>. Available from: URL: <http://click.info.copyright.com/?qs=751ae7c8f8e03ecb0a4741c79a3b341599b5318899e258b3d458148f31158885e37d98de5cb03229>. PM: Peritoneal metastases.

“Proactive management” defines a treatment concept, targeting patients with a high risk to develop PM, and prescribes surgery with HIPEC. In colorectal cancer, this has brought about a significant results ( $P < 0.03$ ), related to control group (only surgery), in terms of PM developed and local recurrence (4% vs 28%, over a 48-mo follow-up period). Patients had also significant longer MS (59.2 mo vs 52 mo;  $P < 0.04$ ) and disease-free survival ( $P < 0.05$ )<sup>[105]</sup>.

There was a hypothesis of second-look surgery at 1 year in patients at high risk for PM, after the first radical surgery for colorectal cancer. PM might be identified and treated at an earlier stage in about 55% of patients<sup>[106]</sup>. Such researches were also led for gastric cancer, with promising preliminary results<sup>[107,108]</sup>.

In the same context of colorectal PM prophylaxis, the HIPEC laparoscopic approach was described and indicated after a mean interval of 6 wk (3-9 wk). This approach showed its feasibility<sup>[109]</sup>.

The main issue is selecting high-risk patients for developing PM. The debated risk factors are: Invasion of or beyond the serosa (pT3, pT4), perforated tumors, positive peritoneal cytology (augmented by immunohistochemistry), occurrence of Krukenberg tumors and mucinous type of tumor<sup>[110]</sup>. Following a systematic review, three situations were identified to be associated with an increased frequency of metachronous PM development: Synchronous PM, ovarian metastases, and perforated tumor<sup>[111]</sup>.

Despite all human and material efforts dedicated to CRS-HIPEC treatment, there are patients in whom evolving disease occurs. The right question is whether

**Table 2** Key aspects and peritoneal metastases model in the evolution of multimodal treatment

Period	PM treatment	Key aspects	PM model
All the period	"Conventional" systemic chemotherapy	Significant lower survival for PM <i>vs</i> other type of metastases	Colo-rectal
1950-1980	"Dedicated" intraperitoneal treatment - Palliative treatment	The basis for developing further cytostatic drugs	Malignant ascites
1980-2000	"Dedicated" intraperitoneal treatment - Multimodal radical treatment	Regional intraperitoneal normothermic and hyperthermic chemotherapy Peritonectomy procedures Define PCI and CCRS	Appendicular
2000-2010	Multimodal radical treatment - confirmation, aspects, patient selection, controversies	Significant higher survival <i>vs</i> palliative surgery and diverse systemic chemotherapy regimes Acceptable morbidity and mortality, no significant risk for medical team Respect de learning curve High costs Define the prognostic factors Position of oncologists Comparison with hepatic metastases	Colo-rectal Appendicular Pseudomyxoma peritonei Malignant peritoneal mesothelioma Gastric Ovarian PM with hepatic metastases
2010-2014	Multimodal treatment - research pathways	PM prophylaxis Laparoscopic HIPEC Integration of chemotherapy with surgery Extension of CRS	High-risk patients for developing PM Recurrent PM

PM: Peritoneal metastases; CCRS: Completeness of cytoreduction score; CRS-HIPEC: Cytoreductive surgery and hyperthermic intraperitoneal chemotherapy; PCI: Peritoneal cancer index.

iterative treatment of PM might be a solution. There are at least three problems: Estimate the morbidity/mortality associated with the iterative treatment; documentation the prognostic factors; estimation the treatment results in terms of survival. The only few related studies define no clear attitude, supported by statistically significant data. Morbidity/mortality does not seem to differ significantly<sup>[112-114]</sup>, only one single study reporting increased values<sup>[115]</sup>.

HIPEC remains an important tool in the treatment of recurrent PM. Age ( $P = 0.049$ ), time lapse between surgeries ( $P = 0.08$ ), association of HIPEC ( $P = 0.005$ ), and small bowel resections ( $P < 0.001$ ) are statistically correlated with survival in PM appendiceal origin and malignant peritoneal mesothelioma<sup>[113]</sup>. The iterative approach of colorectal PM results in a MS of 22.6 mo, with the following survival percentages: 1 year - 94%; 2 years - 48%; 3 years - 12%<sup>[114]</sup>.

The iterative approach treatment of the patient with PM and Hepatic Metastases has also promising results<sup>[116]</sup>.

An important research pathway is the way by which chemotherapy might be integrated into various treatment approaches: Perioperative neoadjuvant; HIPEC; bidirectional intraoperative; early postoperative intraperitoneal. The multidisciplinary approach of PM is based on treatment with complete CRS. Unfortunately, this cannot be achieved in approximately 70% of patients<sup>[31]</sup>.

The place of systemic chemotherapy in PM mul-

timodal treatment is difficult to assess. There are definite reports regarding the results of perioperative neoadjuvant chemotherapy, demonstrated by histological response in colon cancer<sup>[117]</sup> and by increased survival in appendix cancer<sup>[118]</sup>. Likewise, in gastric cancer, survival benefits have been shown for perioperative neoadjuvant and early postoperative intraperitoneal chemotherapy<sup>[119]</sup>.

The complexity of multimodal treatment approach is also certified by the wide range of cytostatic drugs and the occurrence of new principles. It is possible that Mitomycin C, in colorectal PM, in the context of complete CRS, may yield superior survival results compared to oxaliplatin<sup>[120]</sup>. For gastric PM, catumaxomab seems to confirm positive results<sup>[119]</sup>, but in colorectal PM, bevacizumab leads to a double mortality rate after CRS-HIPEC treatment<sup>[121]</sup>.

Furthermore, as far as the array of CRS treatment is concerned, along with visceral resection and Peritonectomy procedures, surgery on the urinary tract was assessed. Partial cystectomy and ureter segmental resection were the most used. There was no further increase in the recorded morbidity or mortality and survival was comparable to that of patients with CRS-HIPEC without urinary tract surgery<sup>[122,123]</sup>. The same statute was dedicated to the hepatobiliary procedures<sup>[124]</sup>.

At present, there are over 50 clinical trials underway, aimed at assessing multimodal radical PM treatment (<http://clinicaltrialsfeeds.org/clinical-trials/results/?term=HIPEC>). Out of these, some were reported in the literature: GASTRICHIP (D2 gastric resection and HIPEC

for locally advanced gastric cancer)<sup>[125]</sup>, COMBATAC (multimodal treatment of PM of appendiceal and colorectal origin)<sup>[126]</sup>, NCT01095523 (second-look and CRS-HIPEC treatment for colorectal cancer at risk for PM)<sup>[127]</sup>.

Key aspects and PM model in the evolution of multimodal treatment strategies

We summarized the key aspects of the evolution of multimodal treatment strategies in Table 2.

## CONCLUSION

Initially marked by nihilism and fear, but benefiting from a remarkable joint effort of human and material resources (multi-center and -institutional research), over a period of 30 years, CRS-HIPEC found its place in the multimodal treatment of PM. The next 4 years were dedicated to the refinement of multimodal treatment, by launching research pathways. In selected patients, with requires training, it demonstrated a significant survival results (similar to the Hepatic Metastases treatment), with acceptable risks and costs. Also, CRS-HIPEC opens a lot of new opportunities with reference to the patients' selection and adopted methodology of this multimodal treatment.

The main debates regarding CRS-HIPEC were based on the oncologists' perspective and the small number of randomized clinical trials. It is hard to find a common view on different challenges, raised by CRS-HIPEC in the treatment of PM. Probably, Dr. Bernard Fisher met the same mistrust as he revolutionized breast cancer treatment and the same could be said about the surgical approach to metastatic melanoma. Indeed, there is a discrepancy between the great number of multi-center, -institutional studies and the small number of randomized clinical trials.

We may say that there are a series of determining factors, for the long-term assessment of multimodal PM treatment and the bias in medical studies type. Treatment complexity, results from the interaction between different therapeutic principles (surgery, chemotherapy, and hyperthermia), are an essential factor. Also, the peritoneal cavity is a complex anatomical space, and the pathogenesis of PM is indeed multifactorial conditioning (loco-regional and systemic dissemination). Not least, the multidisciplinary approach of PM implies the teamwork of specialists with different training, treatment concepts and results assessment, making it difficult to find a common view.

It is important to statement the patients with colorectal, appendicular, gastric, and ovarian peritoneal carcinomatosis, as well as patients with pseudomyxoma peritonei and peritoneal malignant mesothelioma must be informed about CRS-HIPEC as a valid treatment resource. The eligibility criteria for patients' selection will be assessed by multidisciplinary teams, in high level, dedicated treatment centers, according to the performance index, PCI, histological grading, the perspective to obtaining a complete CRS, and the availability of sustaining chemotherapy protocols.

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## Molecular approach to genetic and epigenetic pathogenesis of early-onset colorectal cancer

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### Abstract

Colorectal cancer (CRC) is the third most frequent cancer type and the incidence of this disease is increasing gradually per year in individuals younger than 50 years old. The current knowledge is that early-onset CRC (EOCRC) cases are heterogeneous population that

includes both hereditary and sporadic forms of the CRC. Although EOCRC cases have some distinguishing clinical and pathological features than elder age CRC, the molecular mechanism underlying the EOCRC is poorly clarified. Given the significance of CRC in the world of medicine, the present review will focus on the recent knowledge in the molecular basis of genetic and epigenetic mechanism of the hereditary forms of EOCRC, which includes Lynch syndrome, Familial CRC type X, Familial adenomatous polyposis, MutYH-associated polyposis, Juvenile polyposis syndrome, Peutz-Jeghers Syndrome and sporadic forms of EOCRC. Recent findings about molecular genetics and epigenetic basis of EOCRC gave rise to new alternative therapy protocols. Although exact diagnosis of these cases still remains complicated, the present review paves way for better predictions and contributes to more accurate diagnostic and therapeutic strategies into clinical approach.

**Key words:** Early-onset; Colorectal cancer; Epigenetic mechanism; Genetic mechanism; Clinical outcome

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**Core tip:** Early-onset colorectal cancer (EOCRC) cases are heterogeneous population that include both hereditary and sporadic forms of the colorectal cancer (CRC). EOCRC cases have some distinguishing clinical and pathological features than elder age CRC. Recent findings about molecular genetics and epigenetic basis of EOCRC gave rise to new alternative therapy protocols. We herein discuss the latest findings about genetic and epigenetic features of EOCRC.

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## INTRODUCTION

Colorectal cancer (CRC) is the third most frequent cancer type and despite improvements in diagnosis and treatment, this disease is the second leading cause of cancer death in developed countries<sup>[1]</sup>. The highest incidence of CRC is observed in Western Europe, North America and Australia in western populations. It is notable that although the rate of this disease is relatively lower in the communities of the sub-Saharan Africa, South America and Asia, the rate is gradually increasing depending on assimilating life-style and dietary habits of the western countries<sup>[2]</sup>. In more developed countries, screening programs for 50 years and elder people leads to early detection of CRC and opportunity for more satisfactory treatments; thus, death rates reduced approximately 2% per year<sup>[3-5]</sup>. However, CRC screening is not common for young adults (between 20-40 ages), the incidence of this disease is increasing gradually per year in individuals younger than 50 years<sup>[6]</sup>. The tumors of early-onset patients are more aggressive than elder cases<sup>[7,8]</sup>.

Because of the advances in our understanding concerning the molecular mechanism of elder age CRC, we can describe the presenting phenotype depending on the molecular characteristics of the tumor in majority of the cases<sup>[9]</sup>. This vital knowledge contributes to the available studies in the literature for individual-specific and targeted therapies for CRC patients related to their drug responses. However, the molecular mechanism underlying the early-onset CRC (EOCRC) is poorly clarified in the relevant literature. Recent studies have revealed that EOCRC might evolve in a different pathway and the molecular basis of these cases may be unique for individuals<sup>[10]</sup>. Therefore, determining identifiable markers of this disease for early diagnoses is required to develop unique treatment protocols and increase the survival of the patients. However, to date, little knowledge has been gained about the molecular basis of young age. Given this gap to be highlighted, the aim of our review is to synthesize and evaluate the current literature regarding the genetic and epigenetic pathogenesis of EOCRC at molecular level.

## MOLECULAR PATHOGENESIS OF EOCRC

In comparison to elder CRC, EOCRC cases have some distinguishing clinical and pathological features<sup>[11,12]</sup>. These tumors are pathologically recognized with low-grade tumor differentiation, mucinous component and high signet ring cells frequency<sup>[11,13]</sup>. Polyp development is contently observed during the follow-up period of EOCRC<sup>[10]</sup>. The majority of early-onset tumors occur in the distal colon and the rectum<sup>[14]</sup>. Previous studies underlined the significance of heritance as an indicator of EOCRC<sup>[11,12]</sup>. Supporting these views, early-onset and hereditary forms of CRC demonstrate similar well-known pathological features<sup>[11,13]</sup>. Nevertheless, the current knowledge is that EOCRC is a heterogeneous disease

with both familial and sporadic cases. The molecular basis of this heterogeneity has not yet been fully clarified in the literature, however, the severe histopathological properties and a possible genetic feature of the tumor may predispose to expedited tumor growth in young age patients as reported<sup>[15,16]</sup>.

## HEREDITARY FORMS OF EOCRC

In the hereditary forms of CRC, the disease can be observed in one or more first and/or second degree relatives of the patient. Thus, familial CRC counts approximately 20% of all CRC patients<sup>[17]</sup>. With almost 3% observation rate, the most frequently occurring familial CRC is Lynch syndrome (LS)<sup>[18]</sup>. On the other hand, polyposis syndromes, such as familial adenomatous polyposis (FAP), MUTYH-associated polyposis (MAP), Juvenile polyposis syndrome (JPS) and Peutz-Jeghers syndrome (PJS), are less often observed familial colorectal syndromes<sup>[17]</sup>.

### LS

LS is frequently right-sided, an autosomal dominant cancer predisposition. The majority of these tumors are synchronous and metachronous. Extracolonic sites of patients, such as brain, ovary, endometrium, renal pelvis, ureter, stomach, small intestine and skin, are also among a high cancer risk<sup>[18]</sup>. LS is caused by various germline DNA mismatch repair (MMR) gene mutations<sup>[19-21]</sup>. Approximately 90% of the identified LS mutations are observed in *MLH1* or *MSH2* genes and approximately 10% of the LS mutations were identified in *MSH6* and *PMS2* genes<sup>[17,22]</sup>. The prevalence and characteristics of these mutations vary widely among populations. In 2010, we defined two frame-shift mutations (*MLH1* c.1843dupC and *MLH1* c.1743delG) and three missense mutations (*MLH1* c.293G < C, *MLH1* c.954\_955delinsTA and *MSH2* c.2210G < A) uniquely in Turkish LS cases<sup>[23]</sup>. In a study of Italian LS families, c.643\_648 dupA, c.2156\_2157 dupT, c.684\_685 dupC and c.1701\_1704 delT frameshift mutations and c.2206 G < T, that cause a truncating protein were first time determined in *MLH1* gene. Other truncating protein causing mutations, c.1089 G < T and c.2634-2 A < G, that results with a splice defect was originally reported in *MSH2* gene<sup>[24]</sup>. In Malaysia population, two novel mutations, c.3341\_3342insC and c.3885\_3891delTAAAAGC were characterized in *MSH6* and c.2395C > T mutation was defined in *PMS2* gene<sup>[25]</sup>. Recently, an unidentified mutation of *MLH1*, c.2044\_2045del was linked to LS in a Caribbean Hispanic family<sup>[26]</sup>.

Deficient MMR function of LS cases usually promotes microsatellite instability (MSI)<sup>[27,28]</sup>. MSI is characterized by length alterations within simple repeated sequences that are called microsatellites<sup>[28]</sup>. MSI is essential for deregulation of cell growth, differentiation and death<sup>[29]</sup>. MSI also plays roles in modulating the response of patients to various chemotherapeutic agents<sup>[27]</sup>. Losing the expression of MMR proteins *via* inactivation of MMR-

**Table 1** MiRNA profile of lynch syndrome patients

MiRNA	Expression status	Function	Ref.
miR-155	Up	MMR deficiency	Valeri <i>et al</i> <sup>[46]</sup>
		MSI	Earle <i>et al</i> <sup>[48]</sup>
miR-26b	Down	MSS	Earle <i>et al</i> <sup>[48]</sup>
miR-31	Up	MSI	Earle <i>et al</i> <sup>[48]</sup>
miR-223	Up	MSI	Earle <i>et al</i> <sup>[48]</sup>
miR-486-5p	Down	MSI	Balaguer <i>et al</i> <sup>[47]</sup>
miR-622	Up	MSI	Balaguer <i>et al</i> <sup>[47]</sup>
miR-1238	Up	MSI	Balaguer <i>et al</i> <sup>[47]</sup>
miR-1362-5p	Down	MSI	Balaguer <i>et al</i> <sup>[47]</sup>
miR-132	Down	MMR deficiency	Kaur <i>et al</i> <sup>[49]</sup>
miR-345	Down	MMR deficiency	Kaur <i>et al</i> <sup>[49]</sup>

MSS: Microsatellite stable; MSI: Microsatellite instability; MMR: Mismatch repair.

deficient crypt foci genes causes an MSI phenotype<sup>[30]</sup>. In these patients, the mutation rates of *ACVR2*, *TAF1B* and *ASTE1*, microsatellite-bearing target genes are higher than 80%<sup>[29-33]</sup>. Recent studies indicated that in MSI cases, frameshift mutations of apoptotic genes, such as *APAF1*, *BAX* and *FLASH*, lead to intratumoral heterogeneity<sup>[28]</sup>. The study of Markowitz *et al*<sup>[34]</sup> demonstrated the relation with DNA repair defects with a specific pathway of CRC progression and three different mutation of *TGFBR2* gene in 1995<sup>[34]</sup>. However, the latest study of de Miranda *et al*<sup>[35]</sup> showed the transcription and translation of *TGFBR2* with a 1 nucleotide deletion at its microsatellite sequence still produced a functional *TGFBR2* protein. This protein is required for phosphorylation of *SMAD2*, which is phosphorylated in most of the MSI CRC tissues<sup>[35]</sup>.

The *MMR* gene modifications of LS occur by two hit usually point mutations or large rearrangements may give rise to the first hit. Accordingly, gene conversion or loss of the wild-type allele evokes the second hit<sup>[36]</sup>. However, recent observations demonstrated the high rate of promoter methylation occurrence as the second hit<sup>[37,38]</sup>. These findings emphasize the role of epigenetic events in formation of LS<sup>[37,38]</sup>. Indeed, depending on the studies, germ line hemiallelic methylation of *MLH1* and epimutations of *MSH2* lead to LS with insufficient *MLH1* or *MSH2* protein expression in mutation negative families<sup>[39-42]</sup>. Ligtenberg *et al*<sup>[43]</sup> state that germ line 3' end deletions of *EPCAM* gene that is located upstream of *MSH2*, correlate with MSI and a loss of *MSH2* protein even though there was no identifiable mutation in *MSH2* gene<sup>[44]</sup>. Kuiper *et al*<sup>[44]</sup> found *EPCAM* deletions in approximately 2.3% of *MSH2*-deficient families. This study affirms the epigenetic transgenerational inheritance and the possibility of aberrant promoter methylation occurrence in neighbouring tumor suppressor genes by loosing of polyadenylation signals<sup>[28]</sup>. In addition, current evidence in the empirical studies supports the role of miRNAs that is responsible for translational rearrangement of proteins, in regulation of MMR genes expressions<sup>[45]</sup>. In comparison to sporadic MSI tumors, LS patients have a typical miRNA profile. Valeri *et al*<sup>[46]</sup>

demonstrated the association of reduced expression of *MSH2*, *MLH1* and *MSH6* and induction of a mutator phenotype and MSI with over expression of miR-155 in LS. In another study, Balaguer *et al*<sup>[47]</sup> determined the up-regulation of miR-622 and miR-1238 in these patients. MSI status modulates the miRNA expression levels<sup>[48]</sup>. Earle *et al*<sup>[48]</sup> defined the increased expression of miR-155, miR-31, miR-223 and miR-26b in MSI tumors. In addition, Earle *et al*<sup>[48]</sup> linked over expression of miR-31 and miR-223 to LS. Not only miRNA regulates gene expression in an epigenetic way but also miRNA expressions may be regulated epigenetically. With containing a CpG island in the promoter region, most of the miRNAs are favorable for aberrant methylation which can give rise to dysregulation of miRNA<sup>[49,50]</sup>. Kaur *et al*<sup>[49]</sup> identified a correlation between miR-345 and miR-132 hypermethylation and MMR deficiency (Table 1).

### Familial CRC type X

MMR germline mutations are observed in approximately 60% of the families, fulfilling clinical criteria for LS<sup>[51]</sup>. Although familial colorectal cancer type X (FCCTX) accomplish the same clinical criteria with LS, the morphological features, such as right-sided tumor location, poor differentiation, expansive growth pattern, tumor-infiltrating lymphocytes, peritumorous lymphocytes, Crohn-like reactions and lack of dirty necrosis, are not common in FCCTX as LS<sup>[52]</sup>. In addition, despite these, families demonstrate clinical features in which CRCs with MSI, FCCTX is not related to germline MMR gene mutations<sup>[51,53]</sup>. The age onset of FCCTX is relatively older than LS cases and this disease differ from LS with the tumorigenic pathways<sup>[54,55]</sup>. Basically, two individual molecular pathways involve in these families. One of these pathways is loosing of tumor suppressor gene loci genes, such as *TP53*, *APC*, *SMAD4* and *DCC*, somatic mutations of *APC* and *KRAS* and *MGMT* promoter methylation. At the second partway, there is no loosing of tumor suppressor gene loci genes and rarely presenting promoter methylation<sup>[56]</sup>. Therikildsen *et al*<sup>[57]</sup> linked to FCCTX tumors with gain of genetic material in two separate regions encompassing, 20q12-13.12 and 20q13.2-13.32. This study revealed that gain of material on chromosome 20q and loss on chromosome 18 differentiate FCCTX from LS. Findings of Dominguez-Valentin *et al*<sup>[58]</sup> showed that gaining mutations of *GNAS* gene which is located in 20q13.32 and encodes for the Gα-subunit may cause FCCTX *via* activation of the Wnt and ERK1/2 MAPK signalling pathways. Moreover, other 20q located genes, *CDH26*, *SRC* and *ASIP* that play role in proliferation and migration may have a potential to cause FCCTX<sup>[58]</sup>. Dominguez-Valentin *et al*<sup>[58]</sup> defined the up-regulation of *PTGER1* in these tumors which can cause tumor growth through altered prostaglandin E2 function<sup>[59,60]</sup>. Recently, an *SEMA4A* gene variant c.232G > A was determined in Austrian kindred with FCCTX. This study revealed that *SEMA4A* (V78M) lead to activation of MAPK/Erk and PI3K/Akt signaling. Moreover, *SEMA4A* mutations, c.1451G > C and c.977C > T and the single-nucleotide polymorphism c.2044C

**Table 2** Molecular characterization of familial colorectal cancer type X patients

Molecular features		Ref.
Germline <i>MMR</i> gene mutations	-	Lindor <i>et al</i> <sup>[51]</sup> Klarskov <i>et al</i> <sup>[52]</sup> Sánchez-Tomé <i>et al</i> <sup>[53]</sup>
Tumor suppressor gene loci loss		
<i>APC</i> mutations	77%	Francisco <i>et al</i> <sup>[56]</sup>
<i>KRAS</i> mutations	46%	Francisco <i>et al</i> <sup>[56]</sup>
<i>MGMT</i> methylation	36%	Francisco <i>et al</i> <sup>[56]</sup>
Chromosome gains	20q, 19 and 17	Therkildsen <i>et al</i> <sup>[57]</sup>
Chromosome loss	8p, 15, 18	Therkildsen <i>et al</i> <sup>[57]</sup>
Signaling by G protein coupled receptor	up-regulated	Dominguez-Valentin <i>et al</i> <sup>[58]</sup>
(GNAS, F2R, F2RL2, EDN1, EDNRA, GRM8, GNA2, GNG11, GNG12, HCRT, PTGER1, P2RY2, RAMP2, MC1R, TUBB3, VIP) SEMA4A variants		Schulz <i>et al</i> <sup>[61]</sup>

> T were determined as associated with the FCCTX phenotype<sup>[61]</sup>. Recent knowledge about the molecular characterization of FCCTX is summarized in Table 2.

### FAP

FAP is an autosomal dominant cancer syndrome<sup>[62]</sup>. FAP is diagnosed with 100 or more adenomatous polyps in colon or rectum in patients with younger than 40 age<sup>[62]</sup>. Patients with FAP carry germline mutations of the adenomatous polyposis coli (*APC*) gene located on chromosome 5q21-q22<sup>[63]</sup>. *APC* protein is a large scaffolding protein which involves in Wnt signaling pathway. In this protein complex, *APC* leads to down regulation of b-catenin activity and play a central role in a destruction complex of Axin, GSK-3 $\beta$  and casein kinase 1. This complex directs a series of phosphorylation events on  $\beta$ -catenin that target it for ubiquitination and subsequent proteolysis<sup>[64]</sup>. In the absence of *APC* protein, b-catenin binds to several transcription factors of the TCF/LEF and initiates the altered expression of genes associated with proliferation, differentiation, migration and apoptosis. Moreover, the depletion of *APC* can lead to abnormal chromosome segregation and aberrant mitosis<sup>[65,66]</sup>. FAP occurs when there are mutations between codons 168-1580 and with severe disease between codons 1250-1464 of *APC* gene<sup>[67,68]</sup>. The majority of *APC* mutations are either frameshift or nonsense mutations resulting in a truncated protein<sup>[69]</sup>. The two most frequently described germline mutations are located at codon 1309 (c3927\_3931delAAAGA) and codon 1061 (c.3183\_87delACAAA)<sup>[70]</sup>. Although two-thirds of FAP patient disease is inherited, the rest of the cases have no family history and carry unique mutations. Almost all *APC* mutations results with a colonic phenotype but variable for extra-colonic manifestations, such as desmoid tumor, hepatoblastoma, thyroid carcinoma, medulloblastoma, a litany of benign lesions and brain tumors, particularly medulloblastomas<sup>[71-73]</sup>. Lamberti *et al*<sup>[74]</sup> found that *GSTT1* polymorphism showed an uncertain association

with extra-intestinal manifestations in a study of 411 FAP patients. Recent studies demonstrated the enrichment of pyloric gland adenomas of the stomach, in addition to fundic gland polyps and foveolar-type adenomas in patients with FAP<sup>[75,76]</sup>. Hashimoto *et al*<sup>[75]</sup> analyzed the genetic alterations in these FAP-associated gastric lesions and they demonstrated that, as well as *APC* mutations, these cases had *GNAS* and *KRAS* mutations.

*KRAS* mutations have been observed in the early development of approximately 40% of colon cancers. Simultaneous *APC* depletion and *KRAS* mutation results with an augmentation in adenomas<sup>[76]</sup> and induce the spread of stem cell marker carrying cells within the tumor epithelium<sup>[77]</sup>. Phelps *et al*<sup>[78]</sup> stated that in FAP adenomas, intestinal differentiation is required two consecutive steps. In the first step, after *APC* loss, CtBP1 contributes to adenoma initiation and in the following step, *KRAS* activation and  $\beta$ -catenin nuclear localization promote adenoma progression to carcinomas. On the other hand, Obrador-Hevia *et al*<sup>[79]</sup> analysed somatic *APC* and *KRAS* mutations, beta-catenin immunostaining, and qRT-PCR of *APC*, *MYC*, *AXIN2* and *SFRP1* genes in sixty adenomas from six FAP patients with known pathogenic *APC* mutations. Based on this study, the Wnt pathway was constitutively activated in all *APC*-FAP tumors, with alterations occurring both upstream and downstream of *APC*. Thus, Obrador-Hevia *et al*<sup>[79]</sup> suggest that for Wnt signalling activation in *APC*-associated FAP adenomas, oncogenic *KRAS* is not essential.

FAP may also pursue a different way to Wnt signalling pathway alterations through epigenetic mechanisms. Although epigenetic alterations of Wnt signalling are an effective factor for FAP formation, *APC* mutations exist in almost all FAP patients. Romero-Giménez *et al*<sup>[80]</sup> evaluated the possible role of germline hypermethylation of the *APC* promoter in FAP families that were negative for *APC* mutations in 21 FAP families and they did not identify signs of abnormal promoter methylation, indicating that this form of epigenetic silencing is not a common cause of FAP. However, Kámory *et al*<sup>[81]</sup> observed promoter hypermethylation that causes somatic inactivation of *APC* in 21 sporadic cases (30%). In the study of Zhang *et al*<sup>[82]</sup> within FAP families, although methylation was not present in normal tissues, hypermethylation was determined in tumor tissues of one proband and her son. In addition, loss of heterozygosity was observed in another patient from the same FAP family. Segditsas *et al*<sup>[83]</sup> declared similar findings with Zhang *et al*<sup>[82]</sup>. They detected *APC* promoter methylation in 27%-45% of colorectal tumors and cell lines but did not detect in normal colorectum. However, they substantially observed that methylation was independent of the *APC* mutations and was not associated with the CpG island methylator phenotype. Although methylation caused the loosing of 1A isoform mRNA and a reduction in total *APC* transcript levels, *APC* gene expression was retained from promoter 1B<sup>[83]</sup>. Moreover, a recent study of Pavicic demonstrated that promoter 1B deletions of *APC* are not very common<sup>[84]</sup>. Thus, all these studies imply that

**Table 3 Genetic and epigenetic alterations of familial adenomatous polyposis patients besides adenomatous polyposis coli**

Alteration		Ref.
Gene		
	GNAS	Mutation Hashimoto <i>et al</i> <sup>[75]</sup>
	MYC	Gene activation Obrador-Hevia <i>et al</i> <sup>[79]</sup>
	AXIN2	Gene activation Obrador-Hevia <i>et al</i> <sup>[79]</sup>
	SFRP1	Gene activation Obrador-Hevia <i>et al</i> <sup>[79]</sup>
	GSTT1	Polymorphism Lamberti <i>et al</i> <sup>[74]</sup>
	MGMT	Methylation Wynter <i>et al</i> <sup>[86]</sup>
	p14ARF	Methylation Wynter <i>et al</i> <sup>[86]</sup>
	p16INK4	Methylation Wynter <i>et al</i> <sup>[86]</sup>
	IGSF4	Methylation Berkhout <i>et al</i> <sup>[85]</sup>
	TIMP3	Methylation Berkhout <i>et al</i> <sup>[85]</sup>
	ESR1	Methylation Berkhout <i>et al</i> <sup>[85]</sup>
	CDH13	Methylation Berkhout <i>et al</i> <sup>[85]</sup>
miRNA		
	miR-143	Down regulation Kamatani <i>et al</i> <sup>[87]</sup>
	miR-145	Down regulation Kamatani <i>et al</i> <sup>[87]</sup>
	miR-126	Down regulation Yamaguchi <i>et al</i> <sup>[88]</sup>
	miR-20b	Down regulation Yamaguchi <i>et al</i> <sup>[88]</sup>

even though *APC* promoter methylation occurs in early during colon neoplasia progression, it does not result in complete gene inactivation or act as a "second hit"<sup>[84]</sup> and promoter-specific alterations of *APC* rarely leads to mutation-negative FAP<sup>[84]</sup>.

In addition to *APC*, hypermethylation of other genes are usually observed in both FAP-related and sporadic duodenal carcinomas<sup>[85]</sup>. Wynter *et al*<sup>[86]</sup> study showed that the methylation of *MGMT*, *p14ARF* and *p16INK4* genes promoter regions are frequently observed in both sporadic and familial adenomas. Berkhout *et al*<sup>[85]</sup> defined the high methylation rate of the *IGSF4*, *TIMP3*, *ESR1*, *APC* and *CDH13*, in both of these cases, however, in the same study, *PAX6* gene was determined as hypermethylated only in FAP-related carcinomas. Recently, the role of altered miRNA expression in Wnt signalling regulation and FAP development has also been evaluated. Lately, the studies indicated the decreased expression of miR-143, miR-145, miR-126 and miR-20b as an early event of colorectal carcinogenesis in FAP tumors<sup>[87,88]</sup>. Specifically, miR-126 and miR-20b play role in angiogenesis<sup>[88]</sup>. Thus, downregulation of these miRNAs is an important genetic event for the initiation step in colorectal tumor development<sup>[87]</sup>. Besides *APC* alterations, other genetic and epigenetic events determined in FAP patients were summarized in Table 3.

### MAP

MAP is an autosomal recessive polyposis syndrome. Approximately 0.3%-1% of all CRCs is associated with MAP<sup>[89,90]</sup>. Cases with MAP typically present multiple colon adenomas, thus at the first glance, these cases may be diagnosed as FAP. However, because they also can have *MMR* gene mutations, it can reverberate to phenotype as LS<sup>[91]</sup>. Although existing of multiple colon adenomas, there is not any alteration in *APC* gene of these cases, but further analyses identified mutations in

**Table 4 *MUTYH* mutations that vary with ethnicity**

<i>MUTYH</i> mutation	Ethnicity	Ref.
c.231 C > T	Japan	Miyaki <i>et al</i> <sup>[99]</sup>
c.934-2A > C	Japan	Miyaki <i>et al</i> <sup>[99]</sup>
c.1376C > A	Finland	Alhopuro <i>et al</i> <sup>[100]</sup>
c.933 + 3A > C	North-Eastern Italy, Germany	Pin <i>et al</i> <sup>[101]</sup>
c.536A > G	Caucasians	Yamaguchi <i>et al</i> <sup>[92]</sup>
c.1187 G > A	Caucasians	Yamaguchi <i>et al</i> <sup>[92]</sup>

*MUTYH* gene which is a component of a base excision repair system and involves in protecting DNA from oxidative damage<sup>[92]</sup>. Farrington *et al*<sup>[93]</sup> reported that mutations of both *MUTYH* gene alleles increase the risk of endometrial tumors. These cases are rare and well known *MUTYH* mutations are linked to this disease are c.494A > G and c.1145G > A<sup>[94-96]</sup>. However, *MUTYH* mutations can vary with ethnicity<sup>[97]</sup>. c.536A > G and c.1187G > A in Caucasians, c.231 C > T and c.934-2A > C in Japan, c.1227\_1228dup in Portugal, c.1376C > A in Finland were determined as the most frequent *MUTYH* mutations<sup>[98-100]</sup>. In the North-Eastern Italy, c.933+3A > C (IVS10 + 3A > C), accounts for nearly 1/5 of all *MUTYH* mutations<sup>[101]</sup>. In addition, because this mutation is also common in Germany, it is supposed to have a common origin in Western Europe<sup>[101]</sup>. *MUTYH* mutations that vary with ethnicity are summarized in Table 4.

Germline *MUTYH* mutations may also lead to the mutation of cancer-related genes, such as the *APC* and/or the *KRAS* genes, via G to T transversion<sup>[92]</sup>. In the study of Venesio *et al*<sup>[102]</sup>, mutated *MUTYH*-associated-polyposis adenomas exhibited only c.34G > T transversion in codon 12, or mutations in codon 13. They affirm that neither of these mutations was found in classical/attenuated familial polyposis adenomas.

### JPS

JPS is a rare autosomal dominant disorder. JPS is diagnosed with numerous colon and rectum polyps or polyps with family history or juvenile polyps inside and outside of the intestine<sup>[103]</sup>. 20%-50% of JPS demonstrates familial pattern and the average disease onset of cases are 16 to 18<sup>[103]</sup>. JPS may coexist with Osler-Weber-Rendu syndrome [hereditary hemorrhagic telangiectasia (HHT)]. The most frequently encountered symptoms of HHT are Skin telangiectasia, epistaxis, intracranial haemorrhage, development of pulmonary arteriovenous fistulas, brain cavernous angioma and haemangioma<sup>[104]</sup>. Almost 60% of JPS cases demonstrate mutations in *SMADH4* and *BMPRI1A* genes that are connected with TGF- $\beta$ /BMP signal pathway<sup>[105]</sup>.

To date, a number of mutations leading JPS and/or HHT have been described in *SMAD4* gene. These mutations include point mutations that are resulting with a stop codon or a change in the coded amino acid into another one, codons 361, 533 and 534 mutations, small deletions and insertions<sup>[103]</sup>. Specifically, Howe *et al*<sup>[106]</sup> determined the mutation, c.1244-1247delAGAC, in the hot spot of the *SMAD4* gene which leads to a

**Table 5 Pathogenic germline mutations of juvenile polyposis syndrome**

Mutation	Effect	Ref.
<i>SMAD4</i> c.1244-1247delAGAC	Hotspot mutation serious course of JPS with numerous cases of polyps, tumors located in the stomach and intestines	Howe <i>et al</i> <sup>[106]</sup>
<i>BMPRI1A</i> c.230+452_333+441dup 1995	Frameshift mutation producing a truncated protein (p.D112NfsX2)	Yamaguchi <i>et al</i> <sup>[107]</sup>

JPS: Juvenile polyposis syndrome.

serious course of JPS with numerous cases of polyps and tumors located in the stomach and intestines. In addition, a considerable proportion of mutations in the *BMPRI1A* gene are nucleotide changes generating a stop codon (nonsense) or leading to amino acid changes (missense). These mutations are distributed evenly in the entire gene sequence, intronic mutations (intron 1, 3, 4 and 5) and deletions between codon 224 and 359<sup>[103]</sup>. Yamaguchi *et al*<sup>[107]</sup> identified a *BMPRI1A* mutation, which involves a duplication of coding exon 3 (c.230p452\_333p441dup1995) that causes a frameshift mutation, producing a truncated protein (p.D112NfsX2) in a patient with JPS (Table 5).

In addition to mutations in *SMAD4* and *BMPRI1A* genes, Juvenile polyps also was observed in Cowden, Bannayan-Zonana, and Gorlin syndromes. Cowden and Bannayan-Zonana syndromes is occurred by *PTEN* mutations and Gorlin syndrome develops *via* germline *PTCH* mutations. *PTEN* and *PTCH* mutations have been excluded as the causative mutations in almost all JPS patients<sup>[108-110]</sup>.

To the best of our knowledge, there is a lack of knowledge about epigenetic regulation of JPS so far. However, recently, Ling *et al*<sup>[111]</sup> defined *SMAD4* as a miR-224 target as a metastasis factor, yet the relation of miR-224 and *SMAD4* expression in formation of juvenile polyps has not been clarified.

## PJS

PJS is a rare (approximately 1 in 200000 observation rate) autosomal dominant disease<sup>[112,113]</sup>. PJS is characterized by occurrence of benign hamartomatous, Peutz-Jeghers-type polyps in the gastrointestinal tract in association with mucocutaneous pigmentation on the lips and oral mucosa<sup>[114]</sup>. PJS is diagnosed with presence of a hamartoma associated with two of the following three signs: Family history of PJS, mucocutaneous lentiginosis or polyposis of the small-bowel<sup>[115]</sup>. PJS patients face with abdominal symptoms during the first 10 years of life, almost 50% of patients experience the symptoms before the age of 20 years and they have an increased risk of developing gastrointestinal and extradigestive cancers<sup>[115-117]</sup>. Cancer development localized in small intestine, stomach, pancreas and colon in most of the cases<sup>[116]</sup>. In 93% of the affected individuals, there is a

risk of developing complicating cancers between aged 15-64 years<sup>[116]</sup>.

Percent of eighty to 90% of patients with PJS have family history<sup>[118]</sup> and according to genetic analysis, 40%-60% of these cases have germline STK11 (also known as LKB1) mutations as the major cause of this disease<sup>[112]</sup>. Because the downstream signalling pathway of STK11 has not been fully clarified, the knowledge about the mechanism of hamartomatous polyp formation and mucocutaneous pigmentation also insufficient at present. Studies demonstrated that induced *COX-2* gene expression has also been involved in the promotion of tumor formation from PJS polyps<sup>[119,120]</sup>. On the other hand, PJS cases with wild-type STK11 demonstrates multiple causative loci such as chromosome1p, a pericentric inversion in chromosome 6, a second PJS locus at 19q13.4 and a heterozygous germline mutation in the MYH11 gene<sup>[121-125]</sup>. Lately, Wang *et al*<sup>[121]</sup> performed sequence analysing in three Chinese individuals with PJS and identified 2 variants, OR4C45 c.767-768insAG and ZAN c.5767insG, which occur in PJS cases independently of STK11.

More than 145 different STK11 germline mutations have been reported in the literature result in a truncated premature protein or in transcriptional splicing errors<sup>[121,126-129]</sup> (Table 6). On the other hand, transcriptional silencing of this tumor suppressor gene by promoter hypermethylation has been shown as an alternative inactivation mechanism<sup>[130-133]</sup>. In addition to germline mutations, and promoter methylation, Wang *et al*<sup>[121]</sup> discovered four mutations in pre-microRNAs, MI0003131, MI0003530, MI0014206, and MI0005525, of which the corresponding mature miRNA, hsa-mir-492, hsa-mir-487b, hsa-mir-323b, hsa-mir-300 respectively.

## SPORADIC FORMS OF EOCRC

The most well-defined hereditary form of CRC, LS, account for 2%-4% of total CRC and one-third of EOCRC cases<sup>[134,135]</sup>. FAP cases are observed in less than 1% frequency in total CRC cases. Thus, 70% of all CRC and the majority of EOCRC cases are introduced in sporadic form<sup>[136-138]</sup>. Sporadic EOCRCs are classified into two major groups. Chromosome unstable CRC (CIN) is characterized by gross chromosomal abnormalities and MSI<sup>[135]</sup>. Although MSI tumors behave less aggressively compared to CIN, CIN or MSI tumors do not always appear separately<sup>[139-141]</sup>.

Sporadic EOCRC are morphologically characterized with poor cell differentiation, colloid component and lymphocytic stromal reaction<sup>[8,12,142]</sup>. Therefore, these cases are likely to be confused with LS patients. However, while MMR defects are observed *via* MSI pathway in LS, in sporadic cases MSI is not frequent. Studies to date imply that colorectal tumors characterized by MSI may be distinct from microsatellite stabile (MSS) tumors in many molecular aspects, such as an association with the methylator phenotype, a higher frequency of *BRAF* mutations and a lower frequency of *KRAS*, *APC*, and *TP53* mutations. Thus, MSI and MSS colon tumors

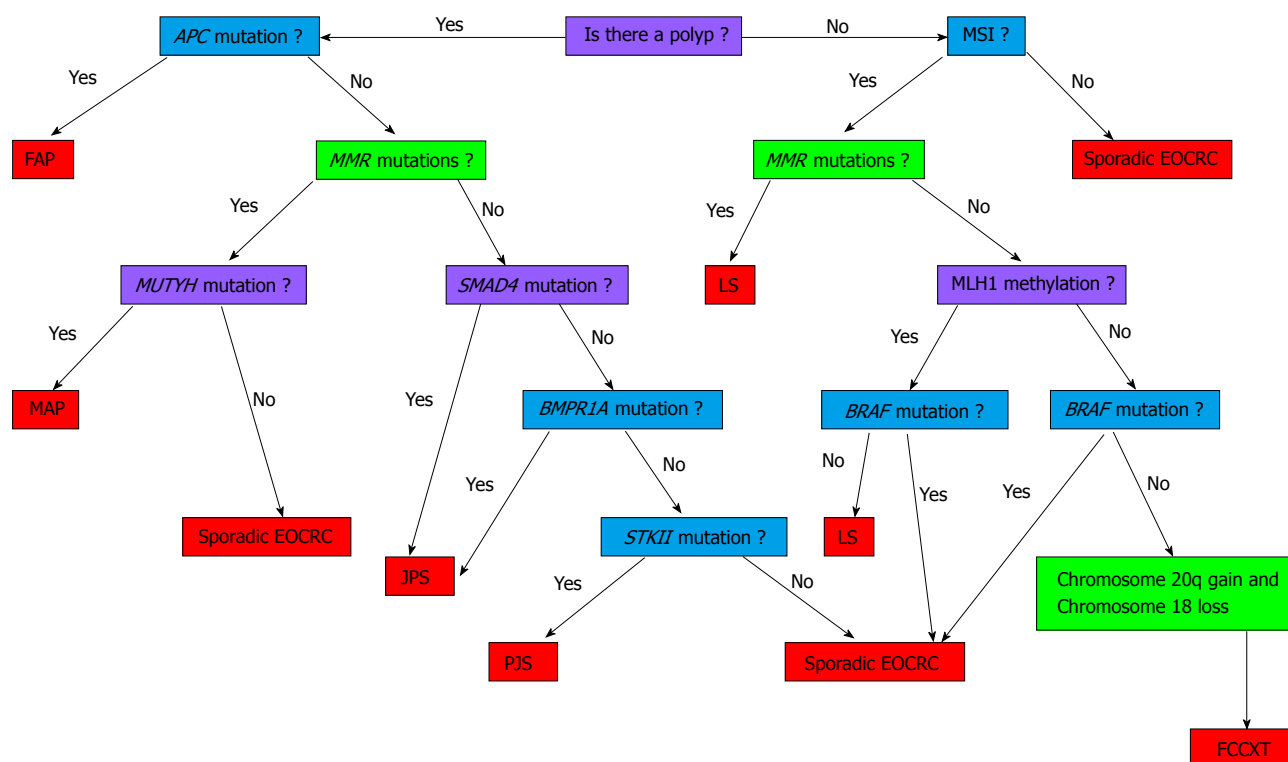
**Table 6** *STK11* mutations associated with colorectal cancer caused by peutz-jeghers syndrome

<i>STK11</i> mutation	Mutation type	Effect on protein	Ref.
c.511 G > A	Missense mutation	G171S	Dong <i>et al</i> <sup>[127]</sup>
c.595 G > A	Missense mutation	E199K	Dong <i>et al</i> <sup>[127]</sup>
c.622 G > A	Missense mutation	D208N	Dong <i>et al</i> <sup>[127]</sup>
c.644 G > A	Missense mutation	G215D	Dong <i>et al</i> <sup>[127]</sup>
c.941 C > A	Missense mutation	P314H	Resta <i>et al</i> <sup>[128]</sup>
c.1062 C > G	Missense mutation	F354L	Dong <i>et al</i> <sup>[127]</sup>
c.1100 C > T	Missense mutation	T367M	Dong <i>et al</i> <sup>[127]</sup>
c.842delC	Frameshift mutation	truncates	Dong <i>et al</i> <sup>[127]</sup> , Bartosova <i>et al</i> <sup>[129]</sup>
IVS2 + 1A > G	Intronic splice site mutation		Bartosova <i>et al</i> <sup>[129]</sup>
OR4C45 c.767-768insAG	Frameshift mutation	truncates	Wang <i>et al</i> <sup>[121]</sup>
ZAN c.5767insG	Frameshift mutation	truncates	Wang <i>et al</i> <sup>[121]</sup>

originate from different molecular backgrounds<sup>[143]</sup>. In sporadic cases, MMR deficiency occurs mainly through epigenetic inactivation of the *MLH1* gene through biallelic promoter methylation instead of MSI<sup>[136]</sup>. Both genetic and epigenetic inactivation of MMR genes result in a mutator phenotype, mutations in cancer related genes and CRC development<sup>[144]</sup>. Kirzin *et al*<sup>[137]</sup> identified *CTNWB1* as one of the most over-expressed genes in MSS-young patients compared to MSS-old patients and this leads to an over-activation of beta catenin in sporadic EOCRC. In addition, Fernandez-Rozadilla *et al*<sup>[145]</sup> determined a heterozygous deletion in the 10q22-q23 region involving *BMPRI1A* gene of EOCRC cases with MMR proficiency. According to Luo *et al*<sup>[146]</sup> CDC42, TEX11, QKI, CAV1 and FN1 proteins are representative elements of EOCRC specific networks. Moreover, we defined *REG1A*, *CK20* and *MAP3K8* gene expressions strongly upregulated (more than twofold) in early-onset MSS CRC compared with MSI CRC tumors<sup>[147]</sup>. *CK20* expression is observed in the majority of colorectal tumors<sup>[148,149]</sup>, however, a limited number of studies have evaluated the relationship between *CK20* expression levels and MSI status<sup>[147]</sup>. In one study, it was suggested that reduced or absent *CK20* expression in CRC is associated with both sporadic and hereditary MSI<sup>[150]</sup>. In another study associated with EOCRC, *CK20* expression levels were also identified as relatively reduced in MSI tumors<sup>[10]</sup>. It was determined that *CK20* expression levels are inversely correlated with numbers of aberrant microsatellite locus<sup>[150]</sup>. We determined the upregulation of *CK20* expression levels in MSS tumors compared with MSI-low (MSI-L) and MSI-high (MSI-H) tumors<sup>[150]</sup>. According to McGregor *et al*<sup>[150]</sup> regulation of *CK20* gene expression involves molecular pathways that are altered by MSI-H. We defined 3.98-fold high *CK20* gene expression levels in MSS tumors with lymph nodes metastases than in MSI tumors with lymph nodes metastases<sup>[147]</sup>. In addition, 17.5-fold upregulation was identified in *CK20* expression levels in low-grade MSS tumors of patients with recurrence and distant metastases<sup>[147]</sup>. These results indicate that upregulation of *CK20* expression, specifically, is related to poor prognosis in patients with MSS tumors. Therefore, the results of our study indicate that *CK20* expression in MSS tumors allows for the determination

of the biological characteristics of EOCRC tissues<sup>[147]</sup>. The encoded protein by *MAP3K8* gene is a member of the serine/threonine protein kinase family. In one of our study, *MAP3K8* expression in CRC was determined significantly elevated compared with normal mucosa<sup>[149]</sup>. In addition, we determined *MAP3K8* expression levels more than two fold upregulated in early-onset MSS CRC compared with MSI CRC tumors<sup>[147]</sup>. *MAP3K8* expression levels were significantly higher in the MSS tumors of patients with a short median survival. Thus, our observations revealed that upregulated *MAP3K8* expression was associated with a poor prognosis in patients with MSS tumors<sup>[147]</sup>. Human *REG1A* belongs to the superfamily of calcium-dependent lectins. In several previous studies, *REG1A* was found to be upregulated in CRC<sup>[151-153]</sup>. We also found that *REG1A* is upregulated in the tumors of early-onset sporadic CRC patients. Furthermore, 25.8-fold high *REG1A* gene expression levels were observed in MSS tumors with lymph nodes metastases. In addition, median survival and disease-free survival were significantly longer only for patients with MSI tumors with low *REG1A* expression compared with those with high expression of this gene. This result indicates that upregulated *REG1A* expression may be related to sporadic EOCRC tumor formation and characterization<sup>[147]</sup>. Additionally, a recent study from Sengupta *et al*<sup>[154]</sup> defined a relation with MSS CRC tumors and deletion in *RBFOX1* gene which encodes a highly conserved RNA-binding protein that regulates tissue-specific alternative splicing indicating important basic functions in development and differentiation in a British Bangladeshi MSS CRC population. This study showed that loss of *RBFOX1* activity may lead to aberrations in the splicing of genes associated with CRC<sup>[154]</sup>.

Different from MSS tumors, some sporadic EOCRC tumors belong to the MSI pathway<sup>[28]</sup>. Sporadic EOCRC with MSI is likely to arise from sessile serrated polyps through the serrated neoplastic pathway<sup>[155]</sup>. The *BRAF* gene, which plays an important role in the mitogen-activated protein kinase signalling pathway, is frequently mutated in these cases. *BRAF* V600E mutation is widely accepted as a prognostic factor of sporadic CRC with MSI and methylated *MLH1*<sup>[156]</sup>. Although the frequency of *BRAF* V600E mutation is high in MSI tumors, this mut-



**Figure 1 Genetic algorithm of early-onset colorectal cancer.** MMR: Mismatch repair; EOCRC: Early-onset colorectal cancer; MSI: Microsatellite instability; APC: Adenomatous polyposis coli; FAP: Familial adenomatous polyposis; MAP: MUTYH-associated polyposis; LS: Lynch syndrome; JPS: Juvenile polyposis syndrome; PJS: Peutz-jeghers syndrome.

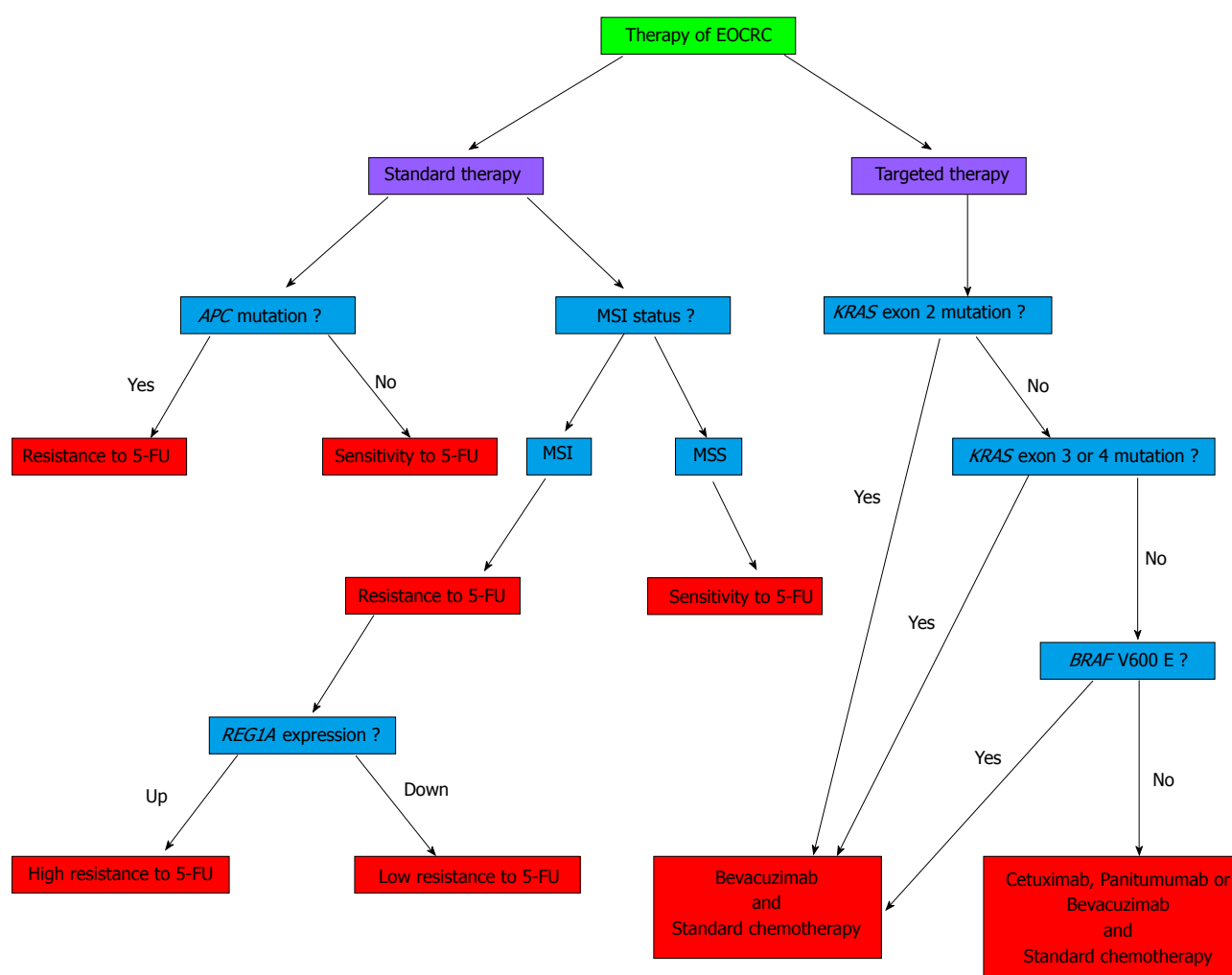
ation is not observed in LS cases, thus, this discrepancy between sporadic MSI cancer and LS might be used in a strategy for the detection of LS<sup>[156]</sup>.

The different attitude of sporadic and hereditary forms of EOCRC may also be caused by epigenetic modifications, such as miRNA expressions and their methylation patterns<sup>[47,157]</sup>. Balaguer *et al.*<sup>[47]</sup> demonstrated that miR-622, miR-362-5p and miR-486-5p could accurately classify the LS and sporadic MSI cases. The similarity of miRNA expression status of LS and sporadic MSI cases may be explained with occurrence of frameshift mutations in *TARBP2*, a miRNA processing gene, in both of these diseases<sup>[158]</sup>. Moreover, in one of our study, using miRNA polymerase chain reaction arrays, the expression profiles of 38 different miRNAs associated with CRC were evaluated in 40 sporadic Turkish EOCRC patients<sup>[157]</sup>. The expression of miR-106a was found to be upregulated, and miR-143 and miR-125b levels were found to be downregulated in sporadic EOCRC tissues compared with the normal tissues. In addition, 2.42-fold high expression level of miR-106a and 2.42-fold low expression level of miR-125b were observed in tumors with lymph node metastases compared with the normal colorectal mucosa samples<sup>[157]</sup>. On the other hand, epigenetic regulations of sporadic EOCRC tumors also differ between each other depend on MSI status. Earle *et al.*<sup>[48]</sup> described the different expression profile of miR-223, miR-155, and miR-92 between MSI and MSS CRCs. So far, Kaur *et al.*<sup>[49]</sup> have investigated the association of miR-132 methylation and sporadic MSI CRC tumors located in

the proximal colon in a comparative study of Finnish and Australian population. In addition, different from MSS tumors, hypermethylation of miR-345 had a significant association with sporadic MSI in Finnish CRCs<sup>[49]</sup>.

## CLINICAL OUTCOME OF GENETIC AND EPIGENETIC FEATURES OF EOCRC

A major challenge in CRC therapy is drug resistance. The current knowledge of CRC genetics has increased the sufficiency of applied conventional cytotoxic chemotherapy and targeted therapy. Genetic screening of EOCRC patients for hereditary cancer syndrome is determinative not only for the rate of cancer risk of relatives but also for appropriate treatment. A pyrimidine analogue, 5-fluorouracil (5-FU) which is widely used in CRC therapy, involves in induction of DNA replication stress response in cells through inhibiting thymidylate synthase. However, studies showed that *APC* mutations reduces the sensitivity to 5-FU<sup>[159]</sup>. On the other hand, performance of MSI test is advisable for patients with strongly suspected on the basis of a known family history of colorectal and extracolonic cancers in the case of LS (Figure 1). Studies revealed that while adjuvant chemotherapy with a fluoropyrimidine does not have a beneficial effect on MSI cases and may even worsen the clinical picture, combination of oxaliplatin and infusional 5-FU/leucovorin regarded as more beneficial for these cases<sup>[160,161]</sup>. According to Violette *et al.*<sup>[162]</sup> increased expression of Reg genes caused *in vitro* resistance to



**Figure 2** Therapy of early-onset colorectal cancer. EOCRC: Early-onset colorectal cancer; MSI: Microsatellite instability; MSS: Microsatellite stabile; 5-FU: 5-fluorouracil.

the 5-FU. Bishnupuri *et al*<sup>[163]</sup> observed a mitogenic effect of the Reg IV protein, with subsequent changes in the expression of genes associated with apoptosis and metastasis. The Reg proteins are previously unappreciated regulators of antiapoptotic proteins in early tumorigenesis and may contribute to increased resistance to apoptotic death during therapy<sup>[163]</sup>. As another mechanism of resistance to therapy, the result of our study of the poor prognosis of MSI tumors supports the hypothesis that high *REG1A* expression may contribute to increased resistance to apoptotic death during therapy in MSI tumors<sup>[147]</sup>. Because of the important role of *REG1A* in tumorigenesis and development of metastasis in MSI tumors, the use of *REG1A*-specific inhibitors in CRC patients have MSI that may represent a novel significant approach to the treatment of cancer. In addition, according to recent studies, alterations in epigenetic regulation of these genes may also lead to resistance to chemotherapeutic agents. For example, Deng *et al*<sup>[164]</sup> found out that reduced expression of miR-21 plays role in resistance to 5-FU therapy *via* targeting *MSH2*. However, miRNA studies have been performing in *in vitro* conditions and to prove the decisive importance of these markers further

advanced studies required.

Nowadays, the application of targeted therapy for CRC has been increasing. The goals of these therapies are interrupting the survival and proliferation of cancer cells<sup>[165]</sup>. To date, United States Food and Drug Administration has approved several targeted drugs, such as cetuximab and panitumumab, the anti-EGFR antibodies that suppress the tumor angiogenesis and bevacizumab, an anti-VEGF antibody. Recently, different from bevacizumab, aflibercept and regorafenib have been used as new antiangiogenic agents<sup>[166-168]</sup>. Although EGFR is overexpressed in most of the CRC cases, because of the down-stream modifications of EGFR signalling pathway, patients demonstrated different response to this therapy<sup>[169]</sup>. Particularly, *KRAS* activating mutations in exon 2 avoid the sufficient therapy with EGFR inhibitors<sup>[170,171]</sup>. A small number of patients with wild type *KRAS* exon 2 were demonstrated to have mutations exons 3 and 4 that are also caused *KRAS* activation<sup>[172]</sup>. Activating mutations in the other genes that play role in downstream pathway of EGFR signalling, *NRAS*, *BRAF*, *PIK3CA* and *PTEN* are able to lead to resistance to anti-EGFR therapies<sup>[173]</sup>. Thus, to predict the success of anti-EGFR monoclonal antibody

therapy, examination of downstream mutations of EGFR signalling pathway should be required before receiving an EGFR inhibitor<sup>[170]</sup> (Figure 2). Second targeted signal pathway for CRC therapy is angiogenesis pathway. Bevacizumab is a monoclonal antibody that binds to VEGF-A preventing its interaction with VEGFR-2<sup>[174]</sup>. Regorafenib demonstrated a multikinase inhibitor activity against VEGFR-2, VEGFR-3, TIE-2, PDGFR, FGFR, RET, c-Kit and RAF/MEK/ERK pathway<sup>[175]</sup>. Aflibercept is a recombinant fusion protein and play a role in the inhibition of interactions between VEGF-A, VEGFB proteins and their specific receptors by acting as a trap receptor binding to VEGF-A and VEGFB<sup>[176]</sup>. Thus, the blockage of the genes that encoded these proteins enhances the success of the therapy.

## CONCLUSION

Genetic predispositions have been identified in EOCRC clearly distinct from the other types of CRC. The current knowledge about the molecular and genetic basis of EOCRC provides information regarding prognosis of this disease and response to therapies. A proportion of EOCRCs are hereditary forms. Hence, cases should be evaluated for existing of a germline mutation in one of the several MMR genes for suspicion of LS, in the APC gene for suspicion of FAP, or in one of the genes associated with a more uncommon syndrome. Identification of a hereditary syndrome in individuals also provides predictive mutational testing for non-symptomatic relatives. They are found to be positive for the mutation can take precaution for reduction of the risk of cancer-associated morbidity and mortality in this way. In addition, a better understanding of the genetic mechanism of EOCRC is highly likely to lead to develop more beneficial targeted therapies. To date, specifically, studies on MSI CRC, such as LS, herald new diagnostic and therapeutic strategies into clinical approach. It is notable that further research remains to be conducted to more finely characterize the underlying mechanism of sporadic EOCRC, which could allow improved prevention, diagnosis, and treatment of these cases.

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## Novel therapeutic agents in the treatment of metastatic colorectal cancer

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### Abstract

Over the past couple of decades considerable prog-

ress has been made in the management of metastatic colorectal cancers (mCRC) leading to a significant improvement in five-year survival. Although part of this success has been rightly attributed to aggressive surgical management and advances in other adjunct treatments, our understanding of the pathogenesis of cancer and emergence of newer molecular targets for colon cancer has created a powerful impact. In this review article we will discuss various targeted therapies in the management of mCRC. Newer agents on the horizon soon to be incorporated in clinical practice will be briefly reviewed as well.

**Key words:** Metastatic colorectal cancer; Molecular targeted drugs; Anti-angiogenesis inhibitors; Epidermal growth factor receptor inhibitors; Novel therapeutic agents

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**Core tip:** This article reviews the novel agents in the management of metastatic colorectal cancer. The core principles and the evidence behind the use of these agents are discussed. Clinically relevant features are highlighted to help the health care provider involved in the care of metastatic colorectal cancer patients.

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### INTRODUCTION

In 2015, a total of 132700 new cases of colorectal cancer are expected to be diagnosed in the United States accounting for about 8% of all new cancer diagnoses. In this same year 49700 patients will die of metastatic colorectal cancers (mCRC), which will contribute to 8.4%

of all cancer related mortality<sup>[1]</sup>. With the widespread use of screening colonoscopy and newer modalities like Stool DNA based screening, we can expect early diagnosis and curative treatments in patients diagnosed with early disease and hence better survival. However up to > 25% of patients will present with metastatic disease, where systemic treatment options will be desired. Widespread use of genetic screening and sharing platforms like the cancer Genome Atlas has led to a better understanding of carcinogenesis and as a consequence newer molecular targets for colon cancer have been discovered<sup>[2]</sup>. In this review article we will discuss some of the well-known targetable pathways as well as shed light on some of the novel pathways where we can expect newer therapies to emerge.

## ANTI-ANGIOGENESIS AGENTS

Anti-angiogenesis was proposed as an anticancer therapy over four decades ago<sup>[3]</sup>. We know that angiogenesis is required for invasive tumor growth and metastasis and is an integral part of cancer progression<sup>[4]</sup>. Angiogenesis is mediated through vascular endothelial growth factor (VEGF), the altered regulation of which is associated with several diseases including malignancy. VEGF is a heparin-binding growth factor specific for vascular endothelial cells that is able to induce angiogenesis *in vivo*<sup>[5]</sup>. Three notable anti-VEGF agents have been approved by United States Food and Drug Administration (USFDA) for treating mCRC and will be reviewed here.

### Bevacizumab

Bevacizumab is a recombinant humanized IgG-1 antibody against soluble VEGF-A which has a high binding specificity with VEGF-A. Once bound, Bevacizumab prevents its interaction with receptors on vascular endothelial cells and thereby truncates the abnormal downstream signaling. After success in early phase trials, this agent was tested in phase 3 clinical trials<sup>[6]</sup>. In the pivotal trial which had 813 previously untreated patients with mCRC randomized to the two arms, the median duration of survival was 20.3 mo in the Irinotecan, 5-Fluorouracil and Leucovorin (IFL) plus Bevacizumab group, as compared with 15.6 mo in the IFL plus placebo group, corresponding to a hazard ratio for death of 0.66 ( $P < 0.001$ )<sup>[7]</sup>. An Eastern Cooperative Oncology Group Study (E3200) showed median duration of survival for the group treated with FOLFOX4 and Bevacizumab was 12.9 mo compared with 10.8 mo for the group treated with FOLFOX4 alone (corresponding hazard ratio for death 0.75,  $P < 0.001$ ), and 10.2 mo for those treated with Bevacizumab alone. Bevacizumab is approved by the USFDA in combination with either an Irinotecan or Oxaliplatin based regimen for the treatment of mCRC<sup>[8,9]</sup>.

Bevacizumab is generally well tolerated when administered in combination with chemotherapy for mCRC. Hypertension, proteinuria, epistaxis and thrombosis are

some of the common adverse events associated with its use<sup>[6]</sup>. No clear guidelines exist on the management of hypertension but in most patients it is usually possible to control hypertension with standard antihypertensive medications. On occasion, it may be necessary to temporarily or permanently discontinue Bevacizumab if hypertension is severe or persistent<sup>[10]</sup>.

Routine use of Bevacizumab as maintenance therapy is controversial. A recent study found no clear benefits of continuing Bevacizumab after 4-6 mo of standard first-line chemotherapy plus Bevacizumab and given the cost and lack of clear benefit, it was not recommended<sup>[11]</sup>. Whether a certain subgroup with high-risk disease such as high metastatic burden would benefit from this approach needs further investigation<sup>[12]</sup>.

### Ziv-Aflibercept

Ziv-Aflibercept is a fusion protein consisting of human VEGF receptor extracellular domains fused to the Fc portion of human immunoglobulin G1, and works by inhibiting VEGF receptor. Aflibercept was used in a large phase 3 trial in combination with 5-Fluorouracil, Irinotecan and Leucovorin (FOLFIRI) and was found to confer a statistically significant survival benefit over FOLFIRI combined with placebo in patients with mCRC previously treated with an Oxaliplatin based regimen<sup>[13]</sup>. Adding Aflibercept to FOLFIRI showed an improved overall survival relative to placebo plus FOLFIRI (HR = 0.817, 95%CI: 0.713-0.937,  $P = 0.0032$ ) with median survival times of 13.50 mo vs 12.06 mo, respectively. Efficacy was maintained across demographic and baseline characteristics and stratification factors at randomization, irrespective of prior treatment with Bevacizumab, with a similar safety profile<sup>[14]</sup>.

### Ramucirumab

Ramucirumab is a recombinant human monoclonal anti vascular endothelial growth factor-receptor 2 antibody which was recently approved by USFDA for use in combination with FOLFIRI for the treatment of patients with mCRC whose disease has progressed on first line Bevacizumab, Oxaliplatin- and Fluoropyrimidine-containing regimen. Approval was based on a study that enrolled 1072 patients (536 in each group) and patients were randomized either to receive Ramucirumab or placebo<sup>[15]</sup>. PFS was significantly improved in patients who received Ramucirumab in combination with FOLFIRI compared to placebo [Median PFS was 5.7 and 4.5 mo; HR = 0.79 (95%CI: 0.70-0.90,  $P < 0.001$ ). Median overall survival was 13.3 mo (95%CI: 12.4-14.5) for patients in the Ramucirumab group vs 11.7 mo (10.8-12.7) for the placebo group (HR = 0.844, 95%CI: 0.730-0.976, log-rank  $P = 0.0219$ ). Diarrhea, hypertension and fatigue were the common adverse events with the use of Ramucirumab, consistent with the previously known safety profile established in previously approved indications.

## EPIDERMAL GROWTH FACTOR RECEPTOR AND OTHER KINASES

The epidermal growth factor receptor (EGFR) autocrine pathway has been known to affect a number of processes important to carcinogenesis including cell proliferation, apoptosis and angiogenesis. This has been the rationale for developing EGFR inhibitors, both monoclonal antibodies to prevent ligand binding as well as small molecule inhibitors of the tyrosine kinase enzymatic activity to inhibit auto-phosphorylation and downstream intracellular signaling<sup>[16]</sup>. Although monoclonal antibodies like cetuximab were initially developed to treat head and neck cancer, traditionally known to highly express EGFR on immunohistochemistry, their use was extended to treating colorectal cancer.

**Cetuximab:** Cetuximab is a chimeric (mouse/human) monoclonal antibody used in the management of mCRC, which was initially approved by USFDA as a third line single agent in patients who have failed Oxaliplatin- or Irinotecan- based chemotherapy and who are intolerant to Irinotecan. In the pivotal trial which compared FOLFIRI plus Cetuximab vs FOLFIRI plus Bevacizumab as first-line treatment for patients with mCRC, 592 patients with KRAS exon 2 wild-type tumors were randomly assigned and received treatment. Median progression-free survival was 10.0 mo (95%CI: 8.8-10.8) in the Cetuximab group and 10.3 mo (95%CI: 9.8-11.3) in the Bevacizumab group (HR = 1.06, 95%CI: 0.88-1.26,  $P = 0.55$ ); however, median overall survival was 28.7 mo (95%CI: 24.0-36.6) in the Cetuximab group compared with 25.0 mo (22.7-27.6) in the Bevacizumab group (HR = 0.77, 95%CI: 0.62-0.96,  $P = 0.017$ ). Anti-EGFR monoclonal antibodies are well tolerated, the most important adverse event being cutaneous reaction including rash, pruritus, and nail changes. These adverse reactions can usually be medically managed and patients tend to continue on the drugs. Occasionally the drug may need to be discontinued due to intolerable side effects.

### **Panitumumab**

Panitumumab is a fully humanized monoclonal antibody specific to EGFR. The efficacy of Panitumumab was established in the PRIME study which showed that in the wild-type KRAS stratum, Panitumumab-FOLFOX4 significantly improved PFS compared with FOLFOX4 (median PFS, 9.6 mo vs 8.0 mo, respectively; HR = 0.80; 95%CI: 0.66-0.97,  $P = 0.02$ ). Also noted was a nonsignificant increase in OS for Panitumumab-FOLFOX4 vs FOLFOX4 (median OS, 23.9 mo vs 19.7 mo, respectively; HR = 0.83, 95%CI: 0.67-1.02,  $P = 0.072$ )<sup>[17]</sup>. In an open-label, phase 3 head-to-head study of Panitumumab vs Cetuximab which enrolled patients with chemotherapy-refractory mCRC Panitumumab was non-inferior to Cetuximab. Median overall survival was 10.4 mo (95%CI: 9.4-11.6) with Panitumumab and 10.0 mo (9.3-11.0) with Cetuximab (HR = 0.97,

95%CI: 0.84-1.11)<sup>[18]</sup>. Panitumumab has been shown to induce pathological near complete response or complete response when given along with neoadjuvant concurrent radiation therapy in patients with KRAS wild-type locally advanced rectal cancer<sup>[19]</sup>. Panitumumab is generally well tolerated and has a similar side effect profile as Cetuximab.

### **Ras testing and use of egfr antibodies**

EGFR expression as measured by immunohistochemistry on many occasions does not predict clinical benefit with the use of EGFR inhibitors<sup>[20,21]</sup>. It has also been shown that mutations in the KRAS exon 2 (codons 12 and 13), which was down stream to EGFR, dictated the response to EGFR antibodies. Additional mutations like KRAS exon 3 (at codons 59 and 61) and exon 4 (at codons 117 and 146), NRAS exon 2 (at codons 12 and 13), exon 3 (at codons 59 and 61), and exon 4 (at codons 117 and 146), have been demonstrated to be negative predictive biomarkers for EGFR antibody treatment. These additional mutations now account for approximately 17% of patients with wild-type KRAS exon 2 status who harbor a mutation in other RAS exons<sup>[22]</sup>. Testing for extended EGFR mutation is highly recommended and if truly wild type then use of EGFR antibodies is justified in those cases.

## TYROSINE KINASE INHIBITORS

Regorafenib (BAY 73-4506) is a novel oral diphenylurea based multikinase inhibitor, shown to be a potent inhibitor of a wide variety of Tyrosine kinases which include several angiogenic, stromal receptor and oncogenic tyrosine kinases as well as intracellular signaling kinases in preclinical studies<sup>[23]</sup>. A phase III trial in refractory mCRC, (CORRECT) randomized 760 patients between Regorafenib ( $n = 505$ ) and placebo ( $n = 255$ ). It showed a small but statistically significant improvement in OS (median 6.4 mo vs 5 mo, one-sided  $P$  value 0.005) and progression-free survival (median 1.9 mo vs 1.7 mo, one-sided  $P$  value < 0.000001) for Regorafenib<sup>[24]</sup>. The most common side effects of Regorafenib are fatigue, hand-foot skin reaction (palmar-plantar erythrodysesthesia), diarrhea, mucositis and weight loss for which the patients need to be monitored closely<sup>[25]</sup>. A novel germline mutation of PDGFR-beta might be associated with clinical response of colorectal cancer to Regorafenib<sup>[26]</sup>.

## EMERGING AGENTS

### **Targeting cancer stem cells**

Human cancers have been shown to harbor cancer stem cells which are thought to play an important role in cancer recurrence and metastasis. With the recent discoveries of small molecules that target highly conserved cell homeostasis pathways which have been implicated in the pathogenesis of colorectal cancer, gives us an

**Table 1** Ongoing clinical trials in Immunotherapy in colorectal cancer

Drug name	Class	Phase	ClinicalTrials.gov Identifier	Sponsor	Remarks
AMP-224	PD-1 inhibitor	1	NCT02298946	NCI	Combination with stereotactic body radiation therapy
MPDL3280A	Engineered anti-PDL1 antibody	1	NCT01375842	Genentech	Administered as single agent
Varlilumab and nivolumab	Monoclonal antibodies that binds to CD27 and PD-1	1/2	NCT02335918	Celldex therapeutics/bristol-myers squibb	Phase II to determine objective response rate
MPDL3280A and bevacizumab	Engineered anti-PDL1 antibody	1b	NCT01633970	Genentech	Assess the safety, pharmacology and preliminary efficacy of the combination
Avelumab	Antibody targeting PDL-1	1	NCT01772004	EMD serono	Open-label, dose-escalation trial
MEDI4736	Anti PDL-1	2	NCT02227667	Memorial sloan Kettering cancer center	Study to evaluate the efficacy of MEDI4736

Available from: URL: <http://www.clinicaltrials.gov>, accessed on 4/25/2015.

exciting avenue in treating mCRC. BBI608, an orally-administered first-in-class cancer stem cell inhibitor, has been tried in a Phase 1 study after excellent preclinical evidence. This has shown some promising anticancer activity in patients with CRC<sup>[27]</sup>. An open label, multi-center, Phase 2 study of BBI608 in combination with cetuximab, Panitumumab or Capecitabine in patients with advanced colorectal cancer is ongoing (ClinicalTrials.gov Identifier: NCT01776307). Another phase 1 dose escalation study with LGK974 is currently ongoing and recruiting patients with special emphasis on those with B-RAF mutant colorectal cancer with documented Wnt pathway alteration (ClinicalTrials.gov Identifier: NCT01351103).

### **BRAF**

BRAF mutations have been shown to be the cause of sporadic CRCs through altered mismatch repair pathway and occur mutually exclusive of *KRAS* mutations<sup>[28]</sup>. At this time *BRAF* mutation is known to confer a poor prognosis in mCRC, but is not a validated target for anti-cancer therapy<sup>[29,30]</sup>. Although this mutation is found in a relatively small proportion of CRC (5%-8%), targeting BRAF has been unsuccessful as feedback stimulation of EGFR pathway has been suggested as the reason for the treatment failure<sup>[31]</sup>. Current studies are focused on dual blockade of BRAF and EGFR or of the subsequent downstream pathway. Initial experience of combining BRAF inhibitor Vemurafenib with EGFR inhibitor Panitumumab has been safe, although the response has been modest<sup>[32]</sup>. Another Phase II Study of Irinotecan and Cetuximab with or without Vemurafenib in BRAF mCRC is still recruiting patients (ClinicalTrials.gov Identifier: NCT02164916). Another potential strategy is the use of ERK inhibitor that is thought to suppress MAPK activity, which is usually upregulated in patients on RAF inhibitors and may overcome resistance. ERK inhibitors are currently in early phase clinical trials<sup>[33]</sup>.

### **Immunotherapy**

The advent of immune check point blockade has been an exciting field in cancer immunotherapy. Already of considerable success in other types of cancers like melanoma and squamous cell lung cancer where Anti

PD-1 drugs are approved by USFDA, various groups are studying the efficacy in colorectal cancer. Mismatch-repair status has been useful in predicting clinical benefit of immune checkpoint blockade with Pembrolizumab, with higher response in Microsatellite Instability High (MSI-High) tumors<sup>[34]</sup>. The table summarizes the current ongoing trials mainly targeting PD-1 - PDL-1 immune checkpoint pathway (Table 1).

### **Targeting *kras* with reolysin**

Biological strategies like Reovirus Serotype 3 - Dearing Strain (Reolysin), a naturally occurring ubiquitous, non-enveloped human Reovirus, have been explored in mCRC for targeting *KRAS*. Reovirus has been shown to replicate selectively in RAS-transformed cells causing cell lysis. Activating mutations in RAS or mutations in oncogenes signaling through the RAS pathway may occur in as many as 80% of human tumors and can be targeted by this approach. A multicenter phase 1 study Reolysin in combination with FOLFIRI and Bevacizumab in FOLFIRI naive patients with *KRAS* mCRC is ongoing (ClinicalTrials.gov Identifier: NCT01274624).

### **TAS-102**

TAS-102 is a novel oral nucleoside and works as an antimetabolite. TAS-102 is a combination of trifluridine, a nucleoside analog, and tipiracil hydrochloride, a thymidine phosphorylase inhibitor. In a double-blind, randomized, placebo-controlled phase 2 trial, 112 patients were allocated to TAS-102 and 57 allocated to placebo. Median overall survival was 9.0 mo (95%CI: 7.3-11.3) in the TAS-102 group and 6.6 mo (4.9-8.0) in the placebo group (hazard ratio for death 0.56, 80%CI: 0.44-0.71, 95%CI: 0.39-0.81,  $P = 0.0011$ ) on a median follow up of 11.3 mo (interquartile range 10.7-14.0 mo). Hematological toxicities were the important side effects to consider in patients on TAS- 108 arm, 57 (50%) neutropenia of grade 3 or 4, 32 (28%) leucopenia and 19 (17%) experiencing anemia. Serious adverse events were reported in 21 (19%) patients in the TAS-102 group. Recent data from RECURSE study has shown that median overall survival improved from 5.3 mo with placebo to 7.1 mo with TAS-102. Hazard ratio for death

in the TAS-102 group vs the placebo group was 0.68 (95%CI: 0.58-0.81,  $P < 0.001$ ), and this data led to its FDA approval<sup>[35]</sup>.

## CONCLUSION

In conclusion, mCRC treatment is a rapidly evolving field with many novel agents under investigation. Although many targeted drugs have been approved and are already in clinical use, there is a clear need for further research and development of more effective treatments. Over the coming years, as understanding of the biology of the disease improves, newer treatment modalities will be investigated. The optimum use and sequencing of these agents, especially in combination with chemotherapy and other targeted agents will need to be better defined.

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## Long-term outcomes after stenting as a “bridge to surgery” for the management of acute obstruction secondary to colorectal cancer

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the time of initial diagnosis in cases of colorectal cancer. Emergency surgery has been classically considered the treatment of choice in these patients. However, in the majority of studies, emergency colorectal surgery is burdened with higher morbidity and mortality rates than elective surgery, and many patients require temporal colostomy which deteriorates their quality of life and becomes permanent in 10%-40% of cases. The aim of stenting by-pass to surgery is to transform emergency surgery into elective surgery in order to improve surgical results, obtain an accurate tumoral staging and detection of synchronous lesions, stabilization of comorbidities and performance of laparoscopic surgery. Immediate results were more favourable in patients who were stented concerning primary anastomosis, permanent stoma, wound infection and overall morbidity, having the higher surgical risk patients the greater benefit. However, some findings laid out the possible implication of stenting in long-term results of oncologic treatment. Perforation after stenting is related to tumoral recurrence. In studies with perforation rates above 8%, higher recurrences rates in young patients and lower disease free survival have been shown. On the other hand, after stenting the number of removed lymph nodes in the surgical specimen is larger, patients can receive adjuvant chemotherapy earlier and in a greater percentage and the number of patients who can be surgically treated with laparoscopic surgery is larger. Finally, there are no consistent studies able to demonstrate that one strategy is superior to the other in terms of oncologic benefits. At present, it would seem wise to assume a higher initial complication rate in young patients without relevant comorbidities and to accept the risk of local recurrence in old patients (> 70 years) or with high surgical risk (ASA III/IV).

**Key words:** Self-expanding metallic stent; Colorectal cancer; Obstructive colorectal cancer; Colorectal cancer chemotherapy; Colorectal cancer surgery

### Abstract

Obstructive symptoms are present in 8% of cases at

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**Core tip:** Self-expanding metal stents placement as a bridge to surgery in patients with obstructive left-colon cancer is controversial. Stent insertion is beneficial regarding perioperative morbidity, being patients with advanced age or with important comorbidity the ones who could obtain more benefit of transforming emergency surgery into elective surgery. But, on the other hand, an increase of local recurrence rate has been shown after stent placement when compared with emergency surgery, compromising oncologic outcome of these patients. Without definitive data, it seems cautious to consider emergency surgery and assume a higher initial complication rate in young patients without relevant co-morbidities avoiding the risk of local recurrence and stenting, accepting the risk of local recurrence but with a lesser perioperative complications rate, in old patients with high surgical risk.

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## INTRODUCTION

Colorectal cancer is one of the most frequently diagnosed cancer in developed countries<sup>[1]</sup>, with over 400000 new cases and more than 200000 cancer related deaths per year in Europe<sup>[2]</sup>. Some patients present colorectal obstruction at the time of diagnosis. Although in previous studies this situation was reported in up to 30% of patients<sup>[3]</sup>, recent papers conclude that obstructive symptoms are present in 8% of cases at the time of initial diagnosis in cases of metastatic tumors<sup>[4]</sup> and also independently of the tumoral stage<sup>[5]</sup>. Emergency surgery has been classically considered the treatment of choice in these patients, although patients operated on emergency basis have poorer prognosis than those undergoing elective surgery<sup>[6]</sup>. Ascanelli *et al*<sup>[7]</sup> found a 5-year survival rate of 59% in patients electively operated in contrast with 39% in patients surgically treated on emergency basis. For some authors, this worse prognosis correlates with a lower quality surgery due to the emergency situation<sup>[8,9]</sup>. However, other studies suggest that poorer long-term prognosis in patients undergoing emergency surgery is due to a more advanced tumoral stage<sup>[10]</sup>.

Some studies have been recently published supporting the possibility of performing colonic segmental resection with primary anastomosis in emergency surgery with a complication rate comparable to that of elective surgery. Zorcolo *et al*<sup>[11]</sup> analysed surgical outcomes in 323 patients and found that primary

anastomosis can be performed in emergency surgery with low morbidity and mortality rates in selected patients. However, in the majority of studies, emergency colorectal surgery is burdened with higher morbidity and mortality rates than elective surgery. In a series of 989 patients, Tekkis *et al*<sup>[12]</sup> proved, after multivariate analysis, that emergency surgery is significantly associated with a higher postoperative mortality (20% vs 12.8%) as well as ASA classification and patient age. In another recent study comparing 171 surgically treated patients with obstructive left colon cancer by means of resection and primary anastomosis after intraoperative lavage and 1053 patients operated on elective basis, emergency surgery patients were older and with a more advanced tumoral stage. Besides, both postoperative mortality (4.1% vs 0.9%:  $P = 0.001$ ) and morbidity (11.7% vs 7.6%:  $P = 0.07$ ) rates were higher in obstructed patients<sup>[13]</sup>.

In this clinical scenario, not all patients are candidates for surgery with primary anastomosis and so, many patients require temporal colostomy which deteriorates their quality of life and becomes permanent in 10%-40% of cases<sup>[3,14]</sup>.

## BENEFITS OF SELF-EXPANDABLE METAL STENTS

Self-expandable metal stents can restore large bowel transit achieving colonic decompression. Initially used in patients with non resectable malignant tumors, stents were then indicated in patients with resectable colorectal tumors and obstructive symptoms as a bridge to surgery procedure. The aim of stenting is to transform, in left colon cancer, emergency surgery into elective surgery in order to allow, with lower morbidity, mortality and stoma requirements, accurate tumoral staging and detection of synchronous lesions with CT-colonoscopy or conventional colonoscopy<sup>[15,16]</sup>, stabilization of comorbidities and improvement of the nutritional status before surgery and performance of laparoscopic surgery<sup>[17]</sup>. Tejero *et al*<sup>[18]</sup> reported the outcomes of the first two patients treated with this strategy in 1994.

Although the definition of clinical success can be different in published papers, the most commonly used is to consider clinical success as the resolution of obstructive symptoms within the first 72 h after stent placement. In a systematic review including 1785 patients and 1845 stents, Watt *et al*<sup>[19]</sup> reported a clinical success rate of 92% (46%-100%). Concerning technical success, defined as the passage of the guide wire and the stent across the stricture with further appropriate stent release and expansion, the same authors reported a 96.2% success rate. A multicenter European prospective study, including 182 stented patients under the bridge to surgery indication, reported similar results for both technical (98%) and clinical success (94%) rates<sup>[20]</sup>.

The advantages of stenting were confirmed in retrospective studies. Watt *et al*<sup>[19]</sup> found that the

rate of primary anastomosis performance in patients treated with elective surgery was two-fold higher than in patients operated on emergency basis. Patients electively operated presented lower stoma requirements, lower complication rate and shorter hospital stay. However, results were not so consistent in randomized control trials. Pirlet *et al*<sup>[21]</sup> randomized 60 patients with obstructive left colon cancer into two groups, emergency surgery vs stenting plus elective surgery. No differences were found concerning stoma performance (56% vs 43.3%;  $P = 0.30$ ), mortality, morbidity or hospital stay. However, stenting technical success rate was as low as 46.7% with a perforation rate of 6.7%.

In a Dutch study, 98 patients with obstructive left colon tumors were randomized for emergency surgery or emergency stenting. No differences were found regarding 30-d mortality, overall mortality, morbidity and permanent stoma at the end of follow-up. However, patients included in the emergency surgery arm, presented a higher rate of initial stoma confection (absolute risk difference: 0.23, 95%CI: 0.04-0.40,  $P = 0.016$ ) as well as a reduced rate of stoma related complications (between-group difference: -12.0, 95%CI: -23.7-0.2,  $P = 0.046$ ). Stenting technical success rate was 70.2% and perforation rate 12.8%<sup>[22]</sup>.

The low rates of technical success at the time of stenting in both studies and the high perforation rate of the Dutch publication are surprising, worrisome, and, to a certain extent, question the results of both studies considering that in most published papers reported technical success rates are higher than 85% and perforation rate does not exceed 5%. There is no comment in the French paper about the expertise of participant endoscopists concerning stenting, while the Dutch study mentions that colonic stenting was done by endoscopists who had placed at least 10 colonic stents. According to the recently published clinical guideline of the European Society of Gastrointestinal Endoscopy regarding stenting for obstructive colonic and extracolonic cancer, one of the recommendations is that colonic stent placement should be performed or directly supervised by an experienced operator who has performed at least 20 colonic stent placement procedures<sup>[23]</sup>. These data might have influenced the study results.

Nevertheless, perioperative results of SEMS insertion are actually better known. In a recent meta-analysis published by Huang *et al*<sup>[24]</sup> including 7 randomized control trials comparing emergency surgery and stenting plus further elective surgery (382 patients), results were more favourable in patients who were stented concerning primary anastomosis (OR = 0.28; 95%CI: 0.12-0.62;  $P = 0.002$ ), permanent stoma (OR = 2.01; 95%CI: 1.21-3.31;  $P = 0.007$ ), wound infection (OR = 0.31; 95%CI: 0.14-0.68;  $P = 0.004$ ) and overall morbidity (OR = 0.30; 95%CI: 0.11-0.86;  $P = 0.03$ ). No differences were found regarding mortality, anastomosis dehiscence and intra-abdominal infection.

Uncovered SEMS has lesser tendency to migrate

than covered SEMS but showed higher tumor in growth rates. Globally, both types are equally effective and safe. Surgery might be performed 5 to 10 d after stent placement<sup>[23]</sup>.

This benefit may not be the same in all groups of patients and, in old patients these benefits can be greater. Gorissen *et al*<sup>[25]</sup> demonstrated that in-hospital mortality of patients older than 75 was higher in patients undergoing emergency surgery than in those who received a stent as a bridge to surgery procedure (21% vs 8%;  $P = 0.228$ ). In a study published in 2007 and based on a decision model (Markov Chain Monte Carlo), authors conclude that stenting is cheaper and more effective than emergency surgery due to a lower mortality and lower permanent stoma requirements. A low perforation rate with stenting and a high surgical risk were determinant factors to obtain these beneficial results with stenting, having the higher risk patient the greater benefit<sup>[26]</sup>.

## STENTING AND LONG-TERM ONCOLOGIC OUTCOMES

Although initial studies were focused on short-term results of bridge to surgery stenting, some results laid out the possible implication of stenting in long-term results of oncologic treatment. Maruthachalam *et al*<sup>[27]</sup> could demonstrate that peripheral blood levels of a tumoral marker, CK20 mRNA, increased after stent placement while did not modify after performing a diagnostic colonoscopy in patients with colorectal cancer. The consequence of this finding on tumoral behaviour is unknown. In a recent prospective multicenter study including 519 patients with stage III colonic cancer and receiving adjuvant therapy with FOLFOX, the presence of circulating tumoral cells after surgery did not correlate with a poorer disease-free survival or overall survival<sup>[28]</sup>.

Another study reported an increased perineural tumoral invasion in patients with obstructive left colon cancer and treated with a stent under the bridge to surgery indication in comparison with patients surgically treated on emergency basis. In spite of this finding, no significant differences were found regarding overall survival or disease-free survival between the two groups of patients. Even more, perineural invasion did not correlate with tumoral recurrence or 5-year survival<sup>[29]</sup>. Anyhow, the finding of an increased perineural invasion and lymph node involvement after stenting has been confirmed by other authors<sup>[30]</sup>.

Kim *et al*<sup>[31]</sup> reported a shorter overall survival (38.4% vs 65.6%;  $P = 0.025$ ) and 5-year disease free survival (48.3% vs 75.5%;  $P = 0.024$ ) in patients with obstructive left colon cancer treated with a stent plus elective surgery than in patients with non-obstructive tumors surgically treated on elective basis. Very likely, this poor prognosis associated with stenting is not due to the stent but to the fact that stented patients presented with a large bowel obstruction.

**Table 1** Data of recurrence and survival in studies comparing self-expandable metallic stents by-pass to elective surgery and emergency operation for obstructive colorectal cancer

Ref.	Perforation rate	Recurrence SEMS vs EO	Survival SEMS vs EO
Ghazal <i>et al</i> <sup>[43]</sup> Saida <i>et al</i> <sup>[45]</sup>	0 -	RR: 17.2% vs 13.3%; $P = 0.228$ RR of Dukes B: 23% vs 14%; $P = 0.51$ )	3 yr-OS: 48% vs 50% 5 yr-OS: 40% vs 44%. Log-rank test: $P = 0.84$ DFS of Dukes B: Log-rank test: $P = 0.71$
Alcántara <i>et al</i> <sup>[46]</sup>	0	RR: 53.3% vs 15.3%; $P = 0.055$	DFS: 25.4 m vs 27 m; $P = 0.096$ OS: Log-rank test: $P = 0.843$
Tung <i>et al</i> <sup>[34]</sup>	0		5 yr-OS: 48% vs 27%; $P = 0.076$ 5 yr-DFS: 52% vs 48%; $P = 0.63$
Pessione <i>et al</i> <sup>[47]</sup> Gianotti <i>et al</i> <sup>[40]</sup>	0 1.2%		2 yr-OS: 66.6% vs 28.5% HR: 0.412 $P = 0.007$ OS: Log-rank test: $P = 0.004$
van den Berg <i>et al</i> <sup>[42]</sup>	1.7%	5 yr-RR of stage I - II: 33% vs 26%; $P = 0.81$ 5 yr-RR of stage III: 35% vs 51%; $P = 0.24$ 3 yr-RR of stage IV: 32% vs 58%; $P = 0.30$	5 yr-OS of stage I - II: Log-rank test: $P = 0.85$ 5 yr-OS of stage III: Log-rank test: $P = 0.48$ 5 yr-OS of stage IV: Log-rank test: $P = 0.08$
Kim <i>et al</i> <sup>[29]</sup>	3.3%	RR: 35% vs 35%; $P = 1.000$ LR: 0% vs 1.6%	5 yr-OSR: 67.2% vs 61.6%; $P = 0.386$ 5 yr-DFS: 61.2% vs 60%; $P = 0.932$ 5 yr-CRSR: 77% vs 65%; $P = 0.233$
Sabbagh <i>et al</i> <sup>[33]</sup>	4.2%	Patients with no perforation or metastases 34% vs 28 %	Patients with no perforation or metastases 5 yr-OSR: 30% vs 67%; $P = 0.001$ 5 yr-DFS: 27% vs 43%; $P = 0.16$ 5 yr-CSMR: 29% vs 22%; $P = 0.62$
Kavanagh <i>et al</i> <sup>[44]</sup>	4.3%	RR 17.3% vs 23%	OS: Log-rank test: $P = 0.13$ CSM: Log-rank test: $P = 0.21$ CSMR: 13% vs 15.3%
Dastur <i>et al</i> <sup>[48]</sup> Gorissen <i>et al</i> <sup>[25]</sup>	5.2% 8%	RR: 31.6 vs 28.2; $P = 0.824$ LRR: 23% vs 15%; $P = 0.443$ LRR in young patients: 32% vs 8%; Log-rank test: $P = 0.038$	3 yr-OS: 48% vs 46%; $P = 0.54$ CSMR: 24.1% vs 37.2%; $P = 0.180$
Sloothaak <i>et al</i> <sup>[32]</sup>	11.5%		4 yr-DFS: 30% vs 49%; Log-rank test: $P = 0.149$ 4 yr-DSS: 66% vs 87%; Log-rank test: $P = 0.061$ 4 yr-OS: 58% vs 67%; Log-rank test: $P = 0.468$ Stent-related perforation vs no perforation 4 yr-DFS: 0% vs 45%; Log-rank test: $P = 0.007$ 4 yr-DSS: 60% vs 69%; Log-rank test: $P = 0.099$ 4 yr-OS: 50% vs 62%; Log-rank test: $P = 0.478$ 5yOSR: 49% vs 40%; OR: 0.98; 95%CI 0.9-1.07
Erichsen <i>et al</i> <sup>[49]</sup>	Non-reported	5 yr-RR: 38% vs 29%; OR: 1.12; 95%CI: 0.99-1.28	
Choi <i>et al</i> <sup>[50]</sup>	Non-reported		5yOSR: 97.8% vs 94.3%; $P = 0.469$

RR: Recurrence rate; LRR: Local recurrence rate; OS: Overall survival; OSR: Overall survival rate; DFS: Disease-free survival; DFSR: Disease-free survival rate; CRSR: Cancer related survival rate; CSM: Cancer-specific mortality; CSMR: Cancer-specific mortality rate; DSS: Disease-specific survival; EO: Emergency operation; SEMS: Self-expandable metallic stents.

Going beyond these findings with unclear significance, more relevant data are available now.

### Perforation after stenting and tumoral recurrence

Results of stent-in 2 trial showed that, although no significant statistical differences were found regarding disease free survival, cancer related survival and overall survival when comparing patients treated with a stent and further elective surgery and patients who underwent emergency surgery, tumoral recurrence was significantly higher in patients who had been stented and presented a colonic perforation than in those also stented but without any secondary complication (4 year disease free survival: 0% vs 45%;  $P = 0.007$ ). However, this fact had no influence on overall survival (4 year overall survival: 50% vs 62%;  $P = 0.478$ )<sup>[32]</sup>. Gorissen *et al*<sup>[25]</sup> also reported a slightly higher recurrence rate in the

group of stented patients (31.6% vs 28.2%;  $P = 0.824$ ). This difference was due to an increased local recurrence in these patients (23% vs 15%;  $P = 0.443$ ). Patients younger than 75 years had a significantly higher local recurrence rate (32% vs 8%;  $P = 0.038$ ) and, after multivariate analysis, stenting almost reached statistical significance as a risk factor for local recurrence (OR = 12.45, 95%CI: 0.99-156.08;  $P = 0.051$ ). However, it is paramount to remark that the perforation rate in these two studies was 11.5% and 8% respectively (Table 1).

### Oncologic benefits of stenting and further elective surgery

In addition to colonic perforation, other factors can affect oncologic evolution of these patients. Quality of surgery could be better in previously stented patients. Sabbagh *et al*<sup>[33]</sup> reported a significant higher lymph node retrieval

**Table 2** Data of lymph node count, administration of adjuvant chemotherapy and laparoscopic surgery in studies comparing self-expandable metallic stents by-pass to elective surgery and emergency operation for obstructive colorectal cancer

Ref.	Lymph node count SEMS vs EO	Adjuvant chemotherapy SEMS vs EO	Laparoscopic surgery SEMS vs EO
Ghazal <i>et al</i> <sup>[43]</sup>		80% vs 76.7%	
Saida <i>et al</i> <sup>[45]</sup>		66% vs 53%; $P = 0.54$	
Alcántara <i>et al</i> <sup>[46]</sup>	17.7 vs 24.2; $P = 0.099$		
Tung <i>et al</i> <sup>[34]</sup>	23 vs 11; $P = 0.005$	75% vs 54%; $P = 0.2$	
Gianotti <i>et al</i> <sup>[40]</sup>	23 vs 18; $P = 0.08$	46.7% vs 34%; $P = 0.28$	38.7% vs 0%; $P = 0.000$
van den Berg <i>et al</i> <sup>[42]</sup>	Lymph node harvest > 12 62.7% vs 60.7%; $P = NS$	39 vs 39; $P = NS$	
Kim <i>et al</i> <sup>[29]</sup>	28.9 vs 24.4; $P = 0.25$	84% vs 65.7%; $P = 0.085$	
Sabbagh <i>et al</i> <sup>[33]</sup>	22 vs 15; $P = 0.002$	56.2% vs 43.6%; $P = 0.28$	
Kavanagh <i>et al</i> <sup>[44]</sup>	17 vs 17; $P = 0.29$	36% vs 46%; $P = 0.29$	27% vs 12%; $P = 0.1$
Gorissen <i>et al</i> <sup>[25]</sup>		41.6 vs 25.6%; $P = 0.13$	59.6% vs 23%; $P = 0.001$
Sloothaak <i>et al</i> <sup>[32]</sup>	15 vs 13; $P = 0.180$	13 vs 15; $P = 1.000$	

SEMS: Self-expandable metallic stents; EO: Emergency operation.

in the surgical specimen of patients electively operated after initial bridge to surgery stenting, reaching statistical significance in some published papers. In a French study, the number of removed lymph nodes was 22 in the stenting group and 15 in the emergency surgery group ( $P = 0.002$ ). Results were similar in an Asian publication (23 vs 11;  $P = 0.005$ )<sup>[34]</sup>. Significant differences were not reached in other reports (Table 2). In this sense, several studies have correlated the number of removed lymph nodes with survival<sup>[35,36]</sup>. Furthermore, Tung *et al*<sup>[34]</sup> reported a higher percentage of curative resection surgery in patients previously stented (91.6% vs 54.1%;  $P = 0.01$ ).

Moreover, stent placement is associated with a decreased postoperative complication rate, which is relevant regarding survival<sup>[24]</sup>. In a recent analysis including 12075 patients, it has been shown that post-operative complications are associated with shorter survival (HR = 1.24; 95%CI: 1.15-1.34;  $P = 0.001$ ). Analysing complications, infectious complications had a significant influence on long-term survival (HR = 1.31; 95%CI: 1.21-1.42;  $P = 0.001$ )<sup>[37]</sup>.

Another potential benefit could be the percentage of patients receiving adjuvant chemotherapy. A non-statistically significant higher percentage of patients received adjuvant chemotherapy after SEMS placement in seven of ten studies (Table 2).

Finally, the number of patients who can be surgically treated with laparoscopic surgery is larger in patients operated on elective basis after bridge to surgery stenting than in the group of patients undergoing emergency surgery. Laparoscopic surgery could have a beneficial effect on long-term survival. In a randomized study published by Lacy *et al*<sup>[38]</sup> including 219 patients with colonic cancer, laparoscopic surgery was significantly related to lower recurrence rate (HR = 0.47; 95%CI: 0.23-0.94,  $P = 0.03$ ), cancer-related mortality (HR = 0.44; 95%CI: 0.21-0.92;  $P = 0.03$ ) and overall mortality (HR = 0.59; 95%CI: 0.35-0.98;  $P = 0.04$ ) when compared with open surgery. A similar finding has been reported from COLOR II trial; in patients with

stage-III rectal cancer disease-free survival rate was 64.9% in the laparoscopic surgery group and 52% in the open surgery group (difference 12.9 percentage points, 95%CI: 2.2-23.6)<sup>[39]</sup>. In Gorissen *et al*<sup>[25]</sup> publication, 59.6% of stented patients and 23.2% of patients who underwent emergency surgery were operated by means of laparoscopic surgery ( $P < 0.001$ ). Gianotti *et al*<sup>[40]</sup> also found significant differences concerning laparoscopic surgery performance when comparing stented patients and emergency surgery patients (63.3% vs 0%;  $P = 0.001$ ) (Table 2).

### Stenting vs emergency surgery: Which strategy is more beneficial regarding oncologic outcomes?

At present, there are no consistent studies able to demonstrate that one strategy is superior to the other in terms of oncologic benefits.

In a multicenter French study, 5-year overall survival was lower in the group of stented patients than in the emergency surgery group after excluding patients with colonic perforation or metastases at the time of hospital admission (30% vs 67%;  $P = 0.001$ )<sup>[33]</sup>. However, the type of patient (more stage IV patients in one center) and the type of treatment (stenting only in one center) was different in each participating hospital, fact which was not taken into account in multivariate analysis. Moreover, it really attracts attention that with a similar 5-year cancer related mortality (29% vs 22%;  $P = 0.62$ ), overall survival differences are considered attributable to one therapeutic strategy.

In stent-in 2 trial, there was a non significant benefit in the emergency surgery group concerning 4-year disease free survival (Stenting: 30% vs Emergency Surgery: 49%;  $P = 0.149$ ) and 4-year overall survival (Stenting: 58% vs Emergency Surgery: 67%;  $P = 0.468$ ) in relation to colonic perforation after stenting<sup>[32]</sup> and, a higher rate of local recurrence in young patients was reported by Gorissen<sup>[25]</sup>.

However, these results have not been reproduced in other studies with lower stent-related perforation rates. Kim *et al*<sup>[29]</sup> reported a similar overall recurrence rate

in both groups of patients (Stenting: 35%; Emergency Surgery: 35%;  $P = 1$ ), with non-significant better results concerning 5-year disease free survival (66.7% vs 54.8%;  $P = 0.948$ ) and 5-years overall survival (100% vs 77.9%;  $P = 0.103$ ) in the stenting group. In this study no case of local recurrence was registered in the stenting group. Tung *et al.*<sup>[34]</sup> also reported an almost significant benefit in the stenting group regarding 5-year overall survival (48% vs 27%;  $P = 0.076$ ) and Gianotti *et al.*<sup>[40]</sup> demonstrated that stenting was the only parameter related to long-term survival (HR = 0.412; 95%CI: 0.217-0.785;  $P = 0.007$ ). Stent related perforation rate in these three studies was 3.3%, 0% and 1.2% respectively. In a recent meta-analysis including 8 clinical trials, four of them reporting long-term results, no significant differences were found regarding 1-year survival (HR = 1.07; 95%CI: 0.87-1.31;  $P = 0.51$ ), 2-year survival (HR = 1.14; 95%CI: 0.98-1.34;  $P = 0.10$ ) and 3-year survival (HR = 1.08; 95%CI: 0.90-1.31;  $P = 0.39$ ) although it was always better in the stenting group<sup>[41]</sup>. Other studies which evaluate long-term results comparing stenting plus elective surgery vs emergency surgery do not find statistical differences in favour of any of the two strategies. Table 1 includes data regarding stent-related perforation, recurrence and survival. Oncologic evolution seems to be better in stented patients while the perforation rate is lower than 8% (Table 1).

In summary, we can't assure that stenting has a deleterious or beneficial effect on oncologic prognosis unless in those cases in which the patient presents a stent-related perforation.

### Quality of life

The relevance of choosing one treatment strategy or the other concerning its influence on patient's quality of life has been seldom studied. In the Dutch study, quality of life was assessed with EORTC QLQ-C30 and QLQ-C38 questionnaires and no differences were found comparing stenting with emergency surgery, in spite of the more frequent stoma-related complications in the stenting group<sup>[22]</sup>.

Other studies have described different parameters directly related with quality of life. Permanent stoma performance is significantly higher in patients undergoing emergency surgery according to Tung *et al.*<sup>[34]</sup> (25% vs 0%;  $P = 0.03$ ) and Gianotti (26% vs 6.3%;  $P = 0.01$ )<sup>[40]</sup> publications. In another paper it was also described that stented patients presented milder abdominal pain (4 vs 5;  $P = 0.02$ ) and lower postoperative requirements of acetaminophen (8 tablets vs 16 tablets;  $P = 0.04$ ) or morphine (40 mg vs 60 mg;  $P = 0.001$ )<sup>[17]</sup>. On the other hand, other studies did not find differences regarding permanent stoma performance<sup>[22,42]</sup>.

Another interesting aspect to be assessed is the quality of bowel movements, as it is clearly related with the surgical technique. Ghazal *et al.*<sup>[43]</sup> showed that patients operated on emergency basis performing a subtotal colectomy had a significantly larger number

of bowel movements than patients treated with a stent and elective surgery (6 vs 2;  $P = 0.013$ ). In this sense, total colectomy was less common in surgically treated patients after bridge to surgery stenting in both Kavanagh *et al.*<sup>[44]</sup> (4.3% vs 23%;  $P = 0.027$ ) and Saida *et al.*<sup>[45]</sup> (2% vs 30%;  $P$  value is not reported) studies.

## CONCLUSION

Placement of a bridge to surgery self-expandable metal stent is beneficial for the surgical treatment of patients with an obstructive colorectal cancer. This benefit is not identical for every patient, being those patients with an advanced age or with important comorbidity the ones who would obtain more benefit of transforming emergency surgery into elective surgery.

Stenting has no demonstrated influence on survival although patients who present a stent related perforation have a higher risk of tumor recurrence and shorter disease free survival. In studies with perforation rates above 8%, higher recurrences rates in young patients<sup>[25]</sup> and lower disease free survival<sup>[32]</sup> have been shown. Each medical team must be well aware of their perforation rate in order to implement improvement measures if needed.

According to the literature, in these clinical setting, we have to choose between a treatment with more perioperative complications and another therapeutic strategy which might increase the risk of tumor recurrence. It seems cautious, as it has been suggested by others<sup>[23,32]</sup>, to consider emergency surgery and assume a higher initial complication rate in young patients without relevant co-morbidities avoiding the risk of local recurrence and stenting, accepting the risk of local recurrence but with a lesser perioperative complications rate, in old patients (> 70 years) with high surgical risk (ASA III/IV).

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## Role of self expandable stents in management of colorectal cancers

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### Abstract

Acute malignant colorectal obstruction is a complication of colorectal cancer that can occur in 7%-29% of

patients. Self-expanding metallic stent placement for malignant colorectal obstruction has gained popularity as a safe and effective procedure for relieving obstruction. This technique can be used in the palliation of malignant colorectal obstruction, as a bridge to elective surgery for resectable colorectal cancers, palliation of extracolonic malignant obstruction, and for nonmalignant etiologies such as anastomotic strictures, Crohn's disease, radiation therapy, and diverticular diseases. Self-expanding metallic stent has its own advantages and disadvantages over the surgery in these indications. During the insertion of the self-expanding metallic stent, and in the follow-up, short term and long term morbidities should be kept in mind. The most important complications of the stents are perforation, stent obstruction, stent migration, and bleeding. Additionally, given the high risk of perforation, if a patient is treated or being considered for treatment with antiangiogenic agents such as bevacizumab, it is not recommended to use self-expanding metallic stent as a palliative treatment for obstruction. Therefore, there is a need for careful clinical evaluation for each patient who is a candidate for this procedure. The purpose of this review was to evaluate self-expanding metallic stent in the management of the obstruction of the colon due to the colorectal and extracolonic obstruction.

**Key words:** Colorectal cancer; Obstruction; Metallic stents; Self-expandable; Extracolonic obstruction

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**Core tip:** Self-expanding metallic stent placement for malignant colorectal obstruction has gained popularity as a safe and effective procedure for relieving obstruction. This technique can be used in the palliation of malignant colorectal obstruction, as a bridge to elective surgery for resectable colorectal cancers, palliation of extracolonic malignant obstruction, and for nonmalignant etiologies such as anastomotic strictures, Crohn's disease, radiation therapy, and diverticular diseases. In this review we

aimed to evaluate the placement technique, indications and complications of self-expanding metallic stent in colorectal obstructions.

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## INTRODUCTION

Colorectal cancers are one of the most common cancers worldwide, and it is the second most common diagnosed cancer in women and third in men<sup>[1]</sup>. Acute malignant colorectal obstruction is a complication of colorectal cancer that can occur in 7%-29% of patients<sup>[2]</sup>. It is a life-threatening condition that needs prompt evaluation. Large bowel obstruction causes colonic dilatation, bacterial translocation, and electrolyte and fluid imbalance, and has an increased risk of colonic necrosis and perforation<sup>[3]</sup>. The main treatment of malignant colonic obstruction is resection of the tumor; however, in the past two decades, the use of self-expanding metallic stents (SEMS) has drawn interest since it was first reported in 1991 by Dohmoto<sup>[4]</sup> for palliation of malignant colonic obstruction.

The major indications of SEMS for colonic stenting are palliation of malignant obstruction and preoperative decompression<sup>[5]</sup>. Additionally, extracolonic obstructions due to other malignancies and some benign diseases have been shown to be treated by SEMS<sup>[3]</sup>. Although SEMS placement for treating malignant obstruction seems safe and effective and has some advantages over surgery, short term and long term morbidities should be kept in mind. In this review, we aimed to evaluate SEMS in the treatment of colorectal and extracolonic cancers with advantages and disadvantages of this technique over surgery.

## STENT PLACEMENT TECHNIQUE

SEMS placement can be performed by using endoscopic guidance with or without the use of fluoroscopy. It can be inserted through the scope (TTS) or over the guidewire<sup>[5]</sup>. Most of the SEMS are inserted endoscopically with TTS with the use of fluoroscopy<sup>[6]</sup>. SEMS placement with endoscope has advantages over the radiologic placement when the obstruction is proximal to the rectosigmoid region or in the presence of a tortuous colon. Kim *et al.*<sup>[7]</sup> evaluated the technical feasibility and clinical effectiveness of fluoroscopically guided placement of SEMS in 42 patients for acute malignant colorectal obstruction; clinical success was achieved in 98% of the patients. They stated that fluoroscopically guided placement was feasible without endoscopic assistance,

even in lesions proximal to the splenic flexure and transverse colon. In a multicenter retrospective study, Geraghty *et al.*<sup>[8]</sup> aimed to determine the outcomes after SEMS; TTS endoscopy technique was found to be more successful than radiological placement alone (90.3% vs 74.8%,  $P < 0.001$ ) for large bowel obstruction. In another retrospective study, Kim *et al.*<sup>[9]</sup> compared the SEMS placement technique in 111 patients; while the technical success rate was significantly higher in the endoscopic method than in the radiologic method (100% vs 92.1%, respectively,  $P = 0.038$ ), the clinical success rate did not differ significantly between the two groups (91.8% vs 97.1%, respectively,  $P = 0.424$ ). They concluded that endoscopic and radiologic placement technique have their own advantages and disadvantages, but when an obstructive lesion is located in the tortuous, curved angulation of the sigmoid or descending colons, it is more difficult to pass the stenotic lesion using the radiologic method alone.

Bowel preparation before stent placement is not necessary, and oral bowel cleansing is contraindicated in symptomatic bowel obstruction, but enema can be used for facilitating the stent placement by preparing the bowel distal to the stenosis<sup>[5]</sup>.

Antibiotic prophylaxis before SEMS placement is not recommended routinely because of the low risk of fever and bacteremia after the insertion<sup>[5]</sup>. However, antibiotic prophylaxis should be considered especially in patients with complete obstruction who have dilated colon and a risk of microperforation during insertion<sup>[10]</sup>.

Operator experience is an important matter in the placement of the stents. In a retrospective study, SEMS placement was performed in 334 patients, and technical and clinical success was higher for operators who had performed more than 10 procedures<sup>[8]</sup>. In another study, Small *et al.*<sup>[11]</sup> reported that the complication rate was higher when stents were placed by endoscopists who were not experienced in pancreaticobiliary endoscopy.

Technical success is usually defined as stent placement appropriately across the entire length of the stenosis, and clinical success is defined as resolution of colonic obstruction within the first days after the stent placement<sup>[6]</sup>. Technical and clinical success rates vary between the studies. In a systematic review focusing on 88 studies published in 2007 by Watt *et al.*<sup>[12]</sup> the median rate of technical success was 96.2%, ranging from 66.6% to 100%, and clinical success was achieved in 92% of the cases, ranging from 46% to 100%. It was stated that the etiology of the primary obstruction and indication for the stent placement appeared to have little effect on the rates of technical and clinical success. In a recent meta-analysis that included seven randomized clinical trials, pooled data showed a mean success rate of 76.9% (range: 46.7%-100%)<sup>[13]</sup>. In another meta-analysis, Cennamo *et al.*<sup>[14]</sup> compared randomized trials in terms of endoscopic stenting and surgical decompression for colorectal cancer obstruction; the stents were successfully inserted in 73.5% of patients, with

clinical relief of obstruction in 72% of patients.

Covered and uncovered SEMS can be used for colonic stenting. In a meta-analysis, in which Zhang *et al.*<sup>[15]</sup> compared covered and uncovered stents, uncovered stents were found to be associated with a lower late migration rate, a higher tumor ingrowth rate, and a prolonged stent patency. No significant difference was found in technical success, clinical success, tumor overgrowth, early migration, perforation and overall complications between type of stents. In another meta-analysis including a total of 1376 patients, Yang *et al.*<sup>[16]</sup> compared covered and uncovered SEMS in terms of technical success, clinical success and stent patency, and no significant difference was found between the two groups. Uncovered stents were found to be more prone to tumor ingrowth, but covered stents had the higher risk of stent migration over uncovered stents. Each type of stent have their own advantages and disadvantages. The main advantage of covered stents is a reduction in the risk of tissue ingrowth, whereas they are more prone to migrate.

## INDICATIONS OF SEMS

### **Palliation of malignant obstruction**

Acute malignant colorectal obstruction is a complication of colorectal cancer that can occur in 7%-29% of patients<sup>[2]</sup>. Bowel obstruction can be caused by intrinsic disease or extrinsic compression. Large bowel obstruction causes colonic dilatation, bacterial translocation, electrolyte and fluid imbalance, and has an increased risk of colonic necrosis and perforation, so this gastrointestinal emergency needs urgent evaluation. The main treatment modalities for malignant colorectal obstruction are surgical resection or diverting colostomy. Resection is a suitable procedure in patients with less advanced cancer. Permanent stoma creation is a procedure for relieving symptoms of obstruction in patients with nonresectable tumors<sup>[12]</sup>. Emergent surgery should be performed for the patients with colonic perforation and ischemia/necrosis. If there are no signs of systemic toxicity, SEMS can be performed in patients with a partial obstruction or with complete obstruction. SEMS is an alternative procedure for relieving the obstruction of the colon. In the literature, several studies have been published showing the feasibility and safety of SEMS in the management of acute malignant obstruction. In 2007, Watt *et al.*<sup>[12]</sup> compared the safety and efficacy of SEMS with surgery through a systematic review. SEMS was found to be effective and safe in overcoming left-sided malignant colorectal obstructions, with high levels of technical and clinical success, shorter hospital stay, and lower rate of serious adverse events than surgery. Zhao *et al.*<sup>[17]</sup> compared surgery with SEMS in the relief of obstruction in a meta-analysis, and the SEMS group showed a lower clinical success rate (99.8% vs 93.1%,  $P = 0.0009$ ) but shorter length of hospital stay (18.84 d vs 9.55,  $P < 0.00001$ ) and time to initiation of chemotherapy (33.36 d vs 15.53 d,  $P < 0.00001$ ), and

lower rate of stoma formation (54.0% vs 12.7%,  $P < 0.00001$ ). Hospital mortality was significantly lower in the SEMS group, and no difference was found in overall complications between the two groups. Surgery was found to be associated with short term complications and SEMS with late term complications<sup>[17]</sup>. Liang *et al.*<sup>[18]</sup> compared SEMS with surgery in the same indication mentioned above in a meta-analysis; the success rate of SEMS was found to be 93.9%, and no significant difference was found in mortality between the groups. The hospitalization time was shorter in the SEMS group ( $P < 0.01$ ); however, long term complications were higher than surgery ( $P = 0.03$ ). However, it was mentioned that all of the studies reported only the complications of colostomy or Hartmann's procedure, and none of them considered the complications of the stoma. They stated that morbidity and mortality would be much higher in the multi-stage surgery than with SEMS. In a recent study Young *et al.*<sup>[19]</sup> compared the stent insertion and surgical decompression in patients with incurable large bowel obstruction in terms of improving quality of life. Stent related perforations or deaths were not reported. They found that surgery group had significantly reduced quality of life compared with the stent group. The patients in the stent group was found to have significantly lower permanent stoma rates, reductions in post procedure stay, earlier return of bowel function and shorter hospital stay. Thirty-day mortality for the stent group was 8% and for the surgery was 15% ( $P = 0.67$ ). No significant difference was found in survival rates between treatment groups ( $P = 0.61$ )<sup>[19]</sup>.

### **Placement of SEMS as a bridge to elective surgery**

SEMS have been suggested to relieve colon obstruction and act as a "bridge to surgery" for resectable colon cancers. There are conflicting results on this subject. In the literature, systematic reviews with meta-analysis have been published in order to evaluate preoperative SEMS placement as a bridge to elective surgery with emergency resection for acute malignant left-sided colonic obstruction. In the most recent meta-analysis that included seven randomized clinical trials, Huang compared emergency surgery and SEMS group. The pooled data showed a mean success rate of colonic stent placement of 76.9% (range: 46.7%-100%). Compared with the emergency surgery group, the SEMS group achieved significantly lower rates of permanent stoma (9% vs 27.4%,  $P < 0.01$ ), primary anastomosis (67.2% vs 55.1%,  $P < 0.01$ ), lower overall complications (33.1% vs 53.9%,  $P = 0.03$ ) and lower wound infections (6.7% vs 18.1%,  $P < 0.01$ ). No significant difference was found between the two groups in anastomotic leakage, mortality, or intra-abdominal infection. In this setting, SEMS placement for relieving obstructive symptoms allows time for the optimization of the medical condition, bowel preparation, and staging the disease<sup>[13]</sup>. Although there are some advantages of SEMS placement preoperatively compared to the emergency surgery, long term oncological outcome, especially in patients with

resectable colon cancer, should be kept in mind.

There has been a major concern about the oncological outcome of the patients with resectable colon cancer who received SEMS placement as a bridge to surgery. In the literature, it was shown that placement of SEMS preoperatively in patients with resectable colon cancer impairs the oncological outcome, because of the dissemination of cancer cells during the procedure<sup>[20]</sup>, and because stent placement will be complicated by perforation and associated with ulceration as well as perineural and lymph node invasion of the tissues<sup>[21]</sup>. Alcántara *et al.*<sup>[22]</sup> compared short-term results and long-term outcomes of patients who underwent stent placement preoperatively with intraoperative colonic lavage with primary anastomosis. More relapses occurred in the SEMS group, but this finding was not significant, and no differences were found in survival. In another study, Sloothaak *et al.*<sup>[23]</sup> compared 5-year overall recurrence rates in the SEMS placement as a bridge to surgery group with the emergency surgery group; the SEMS group was found to have higher recurrence rate (42% vs 25%,  $P = 0.027$ ). In a larger prospective study that evaluated the long-term oncological outcome between the same groups, in patients aged  $\leq 75$  years, stent as a bridge to surgery was associated with a higher local recurrence rate compared with emergency surgery (32% vs 8%,  $P = 0.038$ ) without a difference in the overall survival rates<sup>[24]</sup>. These findings suggest that use of SEMS in the treatment of curable patients with left-sided malignant colonic obstruction will impair the oncologic outcome. In the recent guidelines, as stent seems to impact the oncological safety with no reduction in postoperative mortality, SEMS as a bridge to elective surgery in curable patients with left-sided malignant colonic obstruction is not recommended. However, this procedure may be a good option for selected patients with a high risk of postoperative mortality, and patients over 70 years old and/or with American Society of Anesthesiologists score  $\geq III$ <sup>[5]</sup>.

### **Palliation of extracolonic malignant obstruction**

Colonic obstructions also can occur due to tumor invasion, peritoneal seeding, or extraluminal compression resulting from advanced extracolonic malignancy<sup>[25]</sup>. Outcomes of SEMS placement in the treatment of extracolonic malignancies are unclear. There have been published studies that compared the clinical outcomes of SEMS between patients with colon cancer and with extracolonic malignancies. Kim *et al.*<sup>[25]</sup> performed SEMS placement for colorectal cancer in 149 patients and for extracolonic malignancy in 60 patients. Advanced gastric cancer, pancreatic cancer, and ovarian cancer were the most common causes of obstruction in that study. The clinical success rates, complications, and stent patency were similar between the two groups. In another study, Kim *et al.*<sup>[26]</sup> evaluated the clinical outcomes and complications of SEMS compared with emergency surgery for relieving obstruction; technical and clinical success rates were higher in the emergency surgery

group. SEMS related complications occurred in 64.5% of the patients, including reobstruction (36.8%), stent migration (10.5%), perforation (13.2%), and bleeding (3.9%). In a retrospective study of palliative stent placement for extracolonic malignancies, clinical success was significantly higher in patients with colorectal cancer than in those with extracolonic malignancies (94.1% vs 20%,  $P < 0.0001$ ). Two procedure related deaths occurred in the extracolonic malignancy group. Colon stenting for this purpose was found to be less successful in comparison with patients with colorectal cancer<sup>[27]</sup>.

### **SEMS for nonmalignant etiologies**

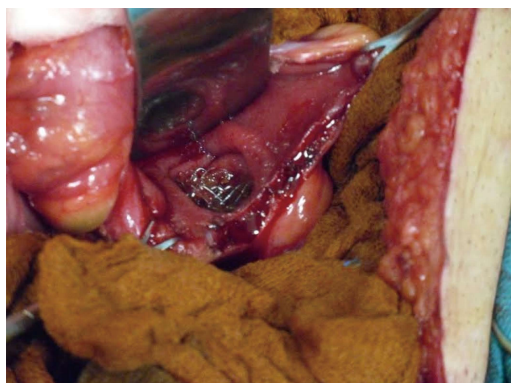
Colonic stents have been used in a variety of non-malignant conditions as colonic strictures, including anastomotic strictures, Crohn's disease, radiation therapy, and diverticular disease<sup>[3]</sup>. In a retrospective study, Keränen *et al.*<sup>[28]</sup> evaluated a total of 21 patients with 23 SEMS procedures for benign colorectal obstruction; eight of the patients had an obstruction in the surgical anastomosis, two patients had anastomotic strictures due to Crohn's disease, 10 patients had the obstruction due to diverticular disease, and one patient had a stricture after radiation therapy. Technical success was achieved in all patients, and clinical success was achieved in 76% of the patients; complications occurred for 9 patients in 10 out of 23 procedures. They concluded that SEMS placement for benign colon strictures may be a good option for the patients who are not fit for surgery. Pommergaard *et al.*<sup>[29]</sup> performed a retrospective study that included 45 patients with benign and malignant colonic obstruction: Technical and clinical success was 97.4% of the patients with malignant etiology, complications occurred in 21%, and mortality rate was 2.6%. For benign etiology, technical success was 85.7%, and clinical success was 71.4%, and complications occurred in 71.4% in this group with a mortality rate of 28.6%.

## **COMPLICATIONS OF SEMS**

Stent related complications can occur in patients with malignant colon obstruction in the palliative or bridge to surgery setting. The most important complications of the stents are perforation, stent obstruction, stent migration, and bleeding. The most seen complication is the stent obstruction because of the tumor ingrowth or overgrowth<sup>[30]</sup>. The main stent related complications are discussed above.

### **Perforation**

The incidence of colonic perforation after SEMS placement varies between the studies. Perforation is the most feared complication of SEMS. In a review that included a total of 2287 patients, Datye *et al.*<sup>[31]</sup> found overall perforation rate was 4.9%. No significant difference was found in the perforation rates for palliation and bridge to surgery (4.8% vs 5.4%,  $P = 0.66$ ). The mortality rate after perforation was 16.2%. Most of the perforations



**Figure 1** Perforation of the rectum due to the self-expanding metallic stent detected intraoperatively.



**Figure 2** Occluded self-expanding metallic stent due to the tumor ingrowth.

(over 80%) occurred within 30 d of stent placement, and almost half of these were noted during or within one day of the procedure; the majority of them were related to dilation, the guidewire, or the stent. In another systematic review, Watt *et al*<sup>[12]</sup> reported the median rate of perforation caused by either the guidewire or stent was 4.5% (range: 0%-83%). The perforation rate was not found to be affected by the indication for stent placement. Colon perforation can be immediate or delayed, and is more likely to occur in the distal colon where sharp angulation and redundancy make stent deployment challenging<sup>[32]</sup>. Baron *et al*<sup>[10]</sup> identified the reasons that can cause perforation after stent placement in four different types: (1) guidewire or catheter malpositioning; (2) dilation of the stricture before or after stent placement; (3) stent-induced perforation; and (4) caused by proximal colonic distention away from the site of stent placement because of inadequate colonic decompression or excessive air insufflation. Delayed perforation can be tumor related, drug related (bevacizumab), and stent related<sup>[33]</sup>. Figure 1 shows the perforation of the rectum due to the SEMS intraoperatively.

In the literature, published results have shown that patients who have undergone palliative stenting can be treated with chemotherapy without antiangiogenic agents<sup>[34]</sup>. Safety of SEMS in the colon or rectum of patients who are receiving the anti-angiogenic agent bevacizumab as a component of chemotherapy has been studied in the literature. Radiotherapy and bevacizumab may increase the risk of perforation. In a retrospective study that includes 201 patients undergoing stenting for incurable malignant obstruction, bevacizumab therapy was found to increase the risk of perforation by 19.6-fold over patients who did not receive bevacizumab<sup>[35]</sup>. In another review, Small *et al*<sup>[11]</sup> determined long-term efficacy, incidence of complications, and risk factors of SEMS placement for colonic obstruction; the incidence of perforation was higher in patients with bevacizumab treatment compared with untreated patients (15.4% vs 6.8%). The complication rate was found to be associated with SEMS placement in men, completely obstructed bowel, with balloon-dilated strictures, and with post-stent bevacizumab treatment. Given the high risk of

perforation, if a patient is treated or considered to be treated with antiangiogenic agents like bevacizumab, it is not recommended to use SEMS as a palliative treatment for obstruction<sup>[34]</sup>. However, there is no strong evidence for the newer antiangiogenic agents like aflibercept and regorafenib, and because of the similar mechanisms, perforation risk should be kept in mind<sup>[5]</sup>. Based upon these data, it is suggested that colonic stent placement be avoided if possible in patients who are or who will be receiving bevacizumab.

### Stent obstruction

The most common complication is stent obstruction because of the tumor ingrowth or overgrowth<sup>[31]</sup>. Figure 2 shows the occluded SEMS due to the tumor ingrowth. In a meta-analysis that included 13 studies, 11 of them reported stent related complications, rate of perforation was 10.1%, stent migration was 9.2%, and stent obstruction was 18.3%<sup>[17]</sup>. It is believed that covered stents provide resistance to tumor ingrowth, thus helping to reduce reconstruction events, while uncovered stents are believed to minimize stent migration<sup>[12,36,37]</sup>. For the uncovered stents, the main disadvantage is the tumor ingrowth, but the membrane of the covered stents can provide a barrier to prevent this. In a systematic review that compared covered SEMS with uncovered SEMS, uncovered SEMS showed a higher tumour ingrowth rate (RR = 5.99; 95%CI: 2.23-16.10,  $P = 0.0004$ )<sup>[15]</sup>. The factors that are associated with the stent obstruction are: Demographic factors, underlying malignancy, length of stent, site of stricture, degree of stent expansion, and chemotherapy after stent insertion<sup>[30]</sup>. However, Im *et al*<sup>[38]</sup> performed a study in order to evaluate clinical outcomes, long term complications, and patency of SEMS in patients with malignant colorectal obstruction, and stent patency was not found to be associated with demographic characteristics of patients, site of obstruction, or palliative chemotherapy. In a retrospective study, Suh *et al*<sup>[30]</sup> analyzed the predictive factors for stent occlusion, and insufficient stent expansion (< 70%) 48 h after stent insertion was significantly associated with stent occlusion during the follow-up.

If SEMS is inserted for the relief of obstruction in advanced and incurable colorectal cancer, the stent patency should be maintained until the death of the patients<sup>[30]</sup>. but if it is used in the preoperative setting, after 1-2 wk, the stent will be removed en bloc at the time of surgical resection<sup>[6]</sup>. In a systematic review, 14 studies reported duration of patency; the median of reported study mean durations was 106 d (range: 68-288 d) in the palliative stent population<sup>[12]</sup>. Suh *et al*<sup>[30]</sup> reported stent patency mean and median 184 and 141 d respectively.

There have been no accurate data in the management of occluded SEMS in malignant colorectal obstruction. In most of the patients with stent obstruction, this can be treated by stent-in-stent placement. In a retrospective case series, Yoon *et al*<sup>[39]</sup> determined the effectiveness of stent-in-stent SEMS insertion for the treatment of SEMS obstruction in cases with malignant colorectal obstruction. In this study the clinical success was reported in 75% of the cases; 9 of them had persistent symptoms, 8 of them underwent palliative surgery, but at the end of the follow-up, 16 of 36 patients (44.4%) remained free of obstruction symptoms until death. The success rate was found to be slightly lower than that of primary SEMS placement<sup>[40]</sup>. In another study, Yoon *et al*<sup>[39]</sup> compared the clinical outcomes of the patients who underwent second intervention because of the obstruction of the first successful SEMS placement for colorectal obstruction with second SEMS insertion or palliative surgery. No significant difference was found in the median overall survival (8.2 mo vs 15.5 mo) and progression-free survival (4.0 mo vs 2.7 mo) between the stent and surgery groups. However, the median lumen patency in the stent group was 3.4 mo and 7.9 mo in the surgery ( $P = 0.003$ ). Male gender and having an obstruction in the right colon were identified as prognostic factors of lumen patency in second SEMS; additional chemotherapy after a second intervention was found to be a prognostic factor with a longer lumen patency in the palliative surgery group.

### Stent migration

In a systematic review including 54 studies, Watt *et al*<sup>[12]</sup> evaluated stent for all indications reported that median rate of migration was 11%, ranging from 0% to 50%. Stent migration can occur at any time following the insertion, but is usually detected within one week of insertion. Migrations tend to occur with stents which are too narrow in diameter and/or too short in relation to the stricture they are placed in<sup>[41]</sup>. In another systematic review, Khot *et al*<sup>[42]</sup> reported stent migration in 54 (10%) of 551 technically successful cases; 26% of the stent migration occurred within 3 d, and the remaining occurred after 3 d. Factors that were associated with the migration were laser pretreatment, chemotherapy, and benign tumor. Covered and small diameter (< 24 mm) SEMS were also found to be associated with stent migration<sup>[15,35,36]</sup>. Chemotherapy with the mechanism of tumor shrinkage increases the stent migration<sup>[43-45]</sup>.

### Others

After the SEMS placement, abdominal pain and bleeding can occur in the follow-up. Bleeding is usually minor after the procedure, and generally no intervention will be required. Abdominal or rectal pain is common and varies between 7.4% and up to 62.5% in patients with SEMS placement within 5 cm of the anal verge<sup>[46,47]</sup>. Mild abdominal pain generally requires no specific treatment; if needed, use of analgesics will be enough for relieving the pain.

## CONCLUSION

SEMS placement can be an alternative method in the treatment of patients with colorectal cancer who have acute malignant colorectal obstruction. SEMS offers favourable results compared to surgery in the setting of colorectal obstruction in advanced disease. Use of SEMS in the treatment of curable patients with left-sided malignant colonic obstruction will impair the oncologic outcome; therefore, SEMS as a bridge to elective surgery in curable patients with left-sided malignant colonic obstruction is not recommended. Although SEMS placement seems to be safe and effective and has some advantages over surgery, short term and long term morbidities should be kept in mind, and it will be preferred for patients who are at increased risk for complications of emergency surgery.

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## Role of microRNA-7 in digestive system malignancy

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### Abstract

There are several malignancies of the digestive system (including gastric, pancreatic and colorectal cancers, and hepatocellular carcinoma), which are the most common types of cancer and a major cause of death worldwide. MicroRNA (miR)-7 is abundant in the pancreas, playing an important role in pancreatic development and endocrine function. Expression of miR-7 is downregulated in digestive system malignancies compared with normal tissue. Although there are contrasting results for miR-7 expression, almost all research reveals that miR-7 is a tumor suppressor, by targeting various genes in specific pathways. Moreover, miR-7 can target different genes simultaneously in different malignancies of the digestive system. By acting on many cytokines, miR-7 is also involved in many gastrointestinal inflammatory diseases as a significant carcinogenic factor. Consequently, miR-7 might be a biomarker or therapeutic target gene in digestive system malignancies.

**Key words:** MicroRNA-7; Digestive system malignancy; Tumor biomarker; Target gene; Inflammation

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**Core tip:** MicroRNA (miR)-7 targets different genes in various complicated pathways and plays diagnostic, prognostic, anti-metastatic, and therapeutic roles in digestive system malignancies. MiR-7 might be a biomarker or therapeutic target gene in digestive system malignancies, even in the precancerous lesions (inflammatory disease).

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in digestive system malignancy. *World J Gastrointest Oncol* 2016; 8(1): 121-127 Available from: URL: <http://www.wjgnet.com/1948-5204/full/v8/i1/121.htm> DOI: <http://dx.doi.org/10.4251/wjgo.v8.i1.121>

## INTRODUCTION

MicroRNAs are small noncoding RNAs consisting of 18-25 nucleotides that post-transcriptionally regulate expression of target genes, and are involved in cell proliferation, epithelial-mesenchymal transition (EMT), apoptosis, migration, invasion and metastasis<sup>[1-3]</sup>. miRNAs have emerged as potential critical regulators of carcinogenesis and tumor progression<sup>[4,5]</sup>.

The digestive system is composed of many ducts and glands, and because of its complicated physiology and anatomy, numerous diseases may occur, especially malignancies including the third, fourth and eighth most common cancers worldwide: Colorectal cancer (CRC), gastric cancer (GC) and esophageal cancer, respectively<sup>[6,7]</sup>, as wells as the leading cause of cancer-related death: Pancreatic cancer (PC)<sup>[8]</sup>. According to the 2014 cancer statistics, the combined cancer mortality rates have been continuously declining for the past two decades. However, the incidence of some digestive system malignancies, including cancers of the esophagus, liver, anus and pancreas, is increasing. Moreover, with rising death rates for cancers of the liver, anus and pancreas, and other non-digestive cancers, cancer is still the second leading cause of death following heart disease<sup>[8]</sup>. Therefore, it is necessary for us to explore novel molecular mechanisms, and screen for the most effective therapeutic methods to avoid the majority of patients succumbing to these digestive malignancies.

MicroRNA (miR)-7 is an evolutionarily conserved miRNA that is involved in the development of the eye and pancreas in *Drosophila*. Li *et al*<sup>[9]</sup> reported that miR-7 is repressed by the transcription factor Yan, which is degraded while mediating epidermal growth factor receptor (EGFR) signaling. Also, miR-7 is expressed abundantly in human pancreas and endocrine cells and has a specific role in endocrine cell differentiation and function<sup>[10]</sup>. It has been demonstrated that miR-7 is a tumor suppressor in breast, lung and ovarian cancers, and glioblastoma, mainly focusing on its relationship with EGFR<sup>[11-15]</sup>. Accumulating evidence shows that miR-7 can simultaneously target a variety of mRNAs involved in diverse signaling pathways in different tumors. However, no specific review has described the role of miR-7 in digestive tract malignancies. In this review, we focus on current research on miR-7 in order to elucidate its role in digestive system malignancies or their precancerous lesions, with reference to its expression, signaling pathways, and role as a circulatory biomarker.

## EXPRESSION OF MIR-7

By comparing the differential expression of miRNAs in

pancreatic islets (endocrine) and acinar (exocrine) tissue in rats, using microarray and quantitative polymerase chain reaction (qPCR), Bravo-Egana *et al*<sup>[16]</sup> revealed that miR-7 was ranked highest among the 17 miRNAs preferentially expressed in islets, suggesting that it acts as an endocrine miRNA. Another two studies reported that miR-7 was expressed at a high level during human pancreatic islet development<sup>[10,17]</sup>. For malignancy, it has been demonstrated that miR-7 is downregulated in cancer tissue of digestive malignancies such as GC<sup>[18-20]</sup>, CRC<sup>[21,22]</sup> and hepatocellular carcinoma (HCC)<sup>[23]</sup> by comparison with normal tissues, suggesting that it acts as a suppressor. A similar conclusion was drawn in a study of hydroxycamptothecin-resistant GC cells<sup>[24]</sup>. In some inflammatory diseases, such as gastritis and Crohn's disease<sup>[25]</sup>, the level of miR-7 is also lower than that in normal tissue, which suggests that it is an inflammation-related miRNA participating in the process of digestive cancer.

In contrast, using the same method, Suto *et al*<sup>[26]</sup> discovered that miR-7 level was higher in CRC tissue than in adjacent normal tissue, induced by EGFR mutations. However, it was found that the aforementioned results would be opposite when the EGFR protein expression was positive in CRC. Finally, they concluded that low miR-7 expression resulted in poorer prognosis than high expression. Ahmed *et al*<sup>[27]</sup> identified the expression of miR-7 in stool samples from 40 cases of colon cancer (TNM stages 1-4), and found that miR-7 was one of the 12 increased miRNAs, which they then recognized as a diagnostic gene. In HCC, Fang *et al*<sup>[28]</sup> speculated that owing to inactivation of the transcriptional regulators and/or failure to promote miR-7 expression, there is no alteration of its expression between tumor and adjacent normal tissues. However, miR-7 and miR-21 are overexpressed in esophageal squamous cell carcinoma (ESCC) and related to its differentiation<sup>[29]</sup>.

From Table 1, we can speculate the reasons for the divergent views about the expression of miR-7 under different conditions, including<sup>[30]</sup>: (1) heterogeneity of different malignancies/diseases; (2) different study sample sizes; and (3) the standards were not the same (*e.g.*, whether or not to include patients with prior cytotoxic therapy). Based on the published studies, we conclude that miR-7 could be an oncogene or tumor suppressor in the digestive system depending on the specific gene targeted (Table 2).

## GC

The pathogenesis of GC has been extensively studied, and there is a consensus that intestinal gastric carcinogenesis is a multistep process starting with chronic gastritis triggered by *Helicobacter pylori*, progressing through atrophy, intestinal metaplasia and dysplasia to carcinoma (Correa model)<sup>[31]</sup>. Thus, inflammation is a significant event in gastric carcinogenesis, whereas miR-7 is an inflammation-mediated miRNA inversely

**Table 1** Expression of microRNA-7 in the digestive system

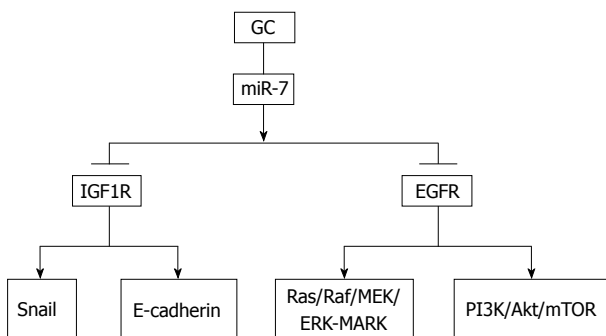
Cancer	Sample	Sap No.	Method	Exp	Role	Ref.
Colon	Stool	60	qPCR	↑	Diagnostic	[27]
CRC	Tissue	80	qPCR	↓	Diagnostic/therapeutic	[21]
CRC	Tissue	8	RT-PCR	↓	Therapeutic	[22]
CRC	Tissue	105	qRT-PCR	↑	Prognostic	[26]
ESCC	Tissue	34	Microarray/qRT-PCR	↑	Differentiation	[29]
GC	Tissue	40	ISH/IHC	↓	Inhibits metastasis/EMT	[18]
GC	Tissue	23	Microarray	↓	Inhibits invasion/metastasis	[19]
			qRT-PCR			
GC	Tissue	28	RT-PCR	↓	Represses inflammation	[20]
HCC	Tissue	10	Microarray	-	Therapeutic/diagnostic/prognostic	[28]
			qRT-PCR			
HCC	Tissue	12	qRT-PCR	↓	Tumor suppressor	[23]
HCC	Tissue	429	Chip assay	↓	Prognostic	[43]
CD	Tissue	-	RT-PCR	↓	Therapeutic	[25]

↓: MiR-7 is downregulated; ↑: MiR-7 is upregulated; -: There is no alteration for expression of miR-7, or no mention. Sap No.: Sample number; Exp: Expression; ISH/IHC: *In situ* hybridization/immunohistochemistry; CRC: Colorectal cancer; GC: Gastric cancer; HCC: Hepatocellular carcinoma; ESCC: Esophageal squamous cell carcinoma; EMT: Epithelial-mesenchymal transition; qPCR: Quantitative polymerase chain reaction.

**Table 2** Function of microRNA-7 by targeting diverse genes

Cells	Function of miR-7	Target	Ref.
CCA	Reduces migration, invasion and metastasis	LAT1	[41]
CRC	Inhibits proliferation, invasion and metastasis, and induces G1 arrest	PAX6	[21]
CRC	Inhibits proliferation and induces apoptosis	XRCC2	[22]
CRC	Suppresses proliferation, induces G1 arrest, and induces apoptosis	YY1	[37]
GC	Suppresses invasion and metastasis	IGF1R	[18]
GC	Inhibits proliferation, invasion and metastasis	EGFR	[19]
HCC	Decreases invasion and migration	PIK3CD/mTOR/p70S6K	[28]
HCC	Suppresses colony formation and induces cell cycle arrest	CUL5	[23]

CCA: Cholangiocarcinoma; CRC: Colorectal cancer; GC: Gastric cancer; HCC: Hepatocellular carcinoma; miR-7: MicroRNA; XRCC2: X-ray repair complementing defective repair in Chinese hamster cells 2; IGF1R: Insulin-like growth factor 1 receptor; EGFR: Epidermal growth factor receptor; mTOR: Mammalian target of rapamycin; CUL5: Cullin 5.



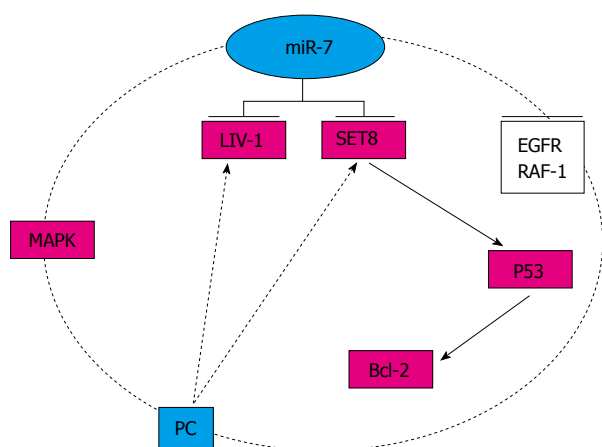
**Figure 1** Pathway of microRNA-7 in gastric cancer. It has been revealed that miR-7 targets mainly IGF1R and EGFR. IGF1R: Insulin-like growth factor 1 receptor; EGFR: Epidermal growth factor receptor; GC: Gastric cancer; miR-7: MicroRNA-7; PI3K: Phosphoinositide 3-kinase; mTOR: Mammalian target of rapamycin.

correlated with many proinflammatory cytokines and inflammatory factors such as interleukin-1 $\beta$  and tumor necrosis factor- $\alpha$ . Three genes, *LPHN2*, *BASP1* and *MAFG*, targeted by miR-7 are induced in the cyclooxygenase (COX)-2/prostaglandin (PG) E2 pathways, which shows that miR-7 plays a significant part in gastric tumorigenesis with an inflammatory response<sup>[20]</sup>.

MiR-7 suppresses GC cell invasion and metastasis both *in vitro* and *in vivo* by targeting the miR-7/insulin-like growth factor 1 receptor/Snail axis, which shows its EMT function and suggests that it can act as a therapeutic biomarker to prevent GC metastasis<sup>[18]</sup>. Xie *et al.*<sup>[19]</sup> demonstrated that restoration of miR-7 significantly inhibited tumor cell viability, invasion and migration by suppressing EGFR expression. These results suggest that targeting miR-7 is a potential therapeutic option for GC (Figure 1).

## PC

PC is one of the major leading causes of cancer mortality; the 5-year survival rate for pancreatic adenocarcinoma is < 5%, and most patients die within the first 2 years<sup>[8]</sup>. Therefore, there is an urgent need to explore novel therapeutic methods. In accordance with the expression of miR-7 in the pancreas, miR-7-3, which is one of the three endogenous genes potentially transcribed in the human genome, is upregulated by targeting mitogen-activated protein kinase (MAPK), suggesting that miR-7 is negatively modulated by an EGFR-MAPK feedback loop<sup>[32]</sup>. In an *in vitro* study, in

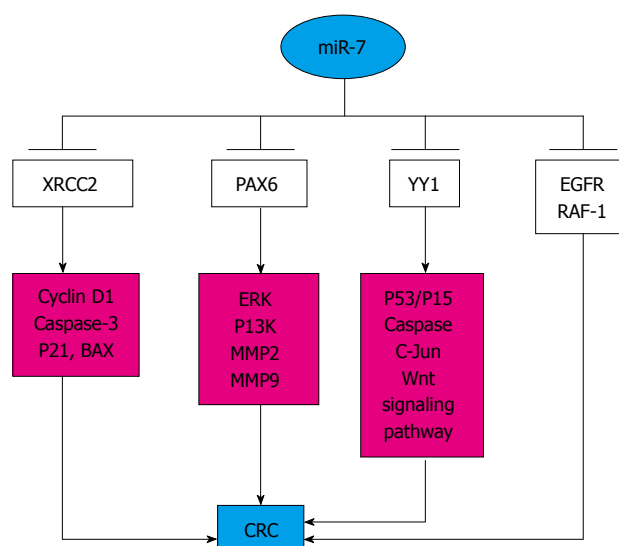


**Figure 2** Pathway of microRNA-7 in pancreatic cancer. In PC, there is an EGFR-MAPK-miR-7 negative feedback loop, and LIV-1 and SET8 are two other targets. EGFR: Epidermal growth factor receptor; MAPK: Mitogen-activated protein kinase; PC: Pancreatic cancer; miR-7: MicroRNA-7; SET8: SET domain containing 8.

which miR-7 targeted SET domain containing 8 leading to increased p53 expression and decreased Bcl-2 level, curcumin suppressed cell growth, migration and invasion, and induced apoptosis in PC cells, indicating that targeting miR-7 is a useful therapeutic option for PC<sup>[33]</sup>. Although knockdown of LIV-1 (a zinc transporter) can upregulate expression of miR-7 in PC cells, the exact role of miR-7 in the maintenance of cancer-stem-cell-related phenotypes in PC remains unclear<sup>[34]</sup>. Future research will focus on identifying the exact pathway of miR-7 in PC, and only in this way, can research proceed from bench to bedside (Figure 2).

## CRC

CRC is related to the mutation of genes such as P53, APC, SMAD4, PIK3CA, KRAS, ARID1A, SOX9 and FAM123B. Some minimal tailoring of therapy (selecting a chemotherapeutic agent based on toxicity, or not using anti-EGFR in those with KRAS-mutated tumors) can be offered to patients, however, the dream of truly individualized therapy remains elusive<sup>[35,36]</sup>. Based on the present studies, miR-7 can target specific genes to modulate the correlated pathways, and its decreased expression continuously participates in the process of CRC. MiR-7 is a tumor suppressor, which is mediated through the YY1-P53-Wnt signaling pathway, and plays pivotal roles in many cellular processes, such as development, differentiation, proliferation and apoptosis<sup>[37]</sup>. By targeting EGFR and *v-raf-1* murine leukemia viral oncogene homolog 1 (RAF-1), a low level of miR-7 suggests poor prognosis for CRC, and miR-7 precursor, alone or in combination with a monoclonal antibody, could be a novel therapy against CRC<sup>[26]</sup>. XRCC2 (X-ray repair complementing defective repair in Chinese hamster cells 2) participates in homologous recombination, and its relationship with miR-7 has been studied. *In vitro*, overexpression of miR-7 suppressed

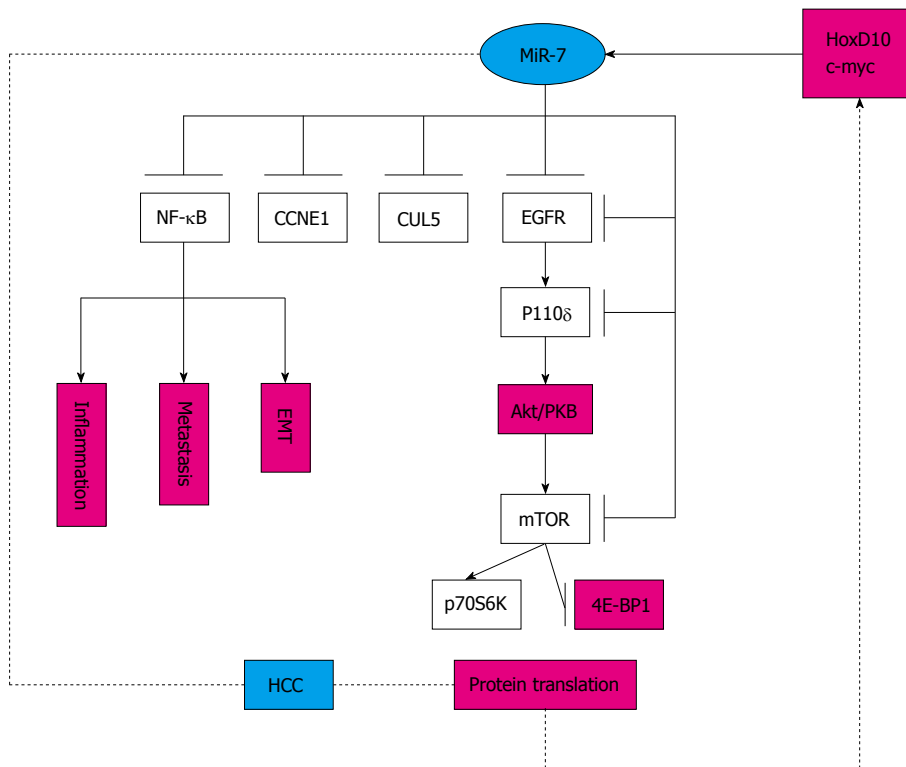


**Figure 3** Pathway of microRNA-7 in colorectal cancer. MiR-7 can target various genes involving different pathways and act as a suppressor. CRC: Colorectal cancer; EGFR: Epidermal growth factor receptor; miR-7: MicroRNA-7. XRCC2: X-ray repair complementing defective repair in Chinese hamster cells 2; ERK: Extracellular signal-regulated kinase.

proliferation and induced apoptosis of CRC cells by directly targeting XRCC2 through decreasing cyclin D1 and increasing p21, caspase-3 and BAX expression<sup>[22]</sup>. In addition, the expression of paired box (PAX) 6 is inversely correlated with that of miR-7, and simultaneous activation of the extracellular signal-regulated kinase and phosphoinositide 3-kinase (PI3K) signaling pathways and regulation of the levels of matrix metalloproteinase (MMP) 2 and MMP9 could modulate the expression of PAX6 and miR-7 in opposing ways, which suggests that miR-7 is a promising therapeutic target for CRC<sup>[21]</sup>. Thus, further mechanisms mediated by miR-7 should be explored, which could be a promising approach for individually tailored therapy of CRC (Figure 3).

## HCC

HCC, the third most common cause of cancer mortality worldwide, which develops from activation of cellular oncogenic pathways and abrogation of tumor suppressor pathways including the p53/p21<sup>WAF1</sup> pathway, the p16<sup>INK4a</sup>/CDK4/RB1/E2F pathway, the Wnt/ $\beta$ -catenin signaling pathway, transforming growth factor- $\alpha$ , c-myc, transcription factor NF- $\kappa$ B, insulin/IGF-I, and receptor tyrosine kinases and their downstream activators<sup>[38,39]</sup>. Several studies have shown that miR-7 participates in several pathways by targeting different genes in HCC. MiR-7 regulates the PI3K/Akt/mammalian target of rapamycin *in vitro* and *in vivo*, which functions downstream of EGFR, suggesting that miR-7 is a potential target for treating or diagnosing/prognosing HCC<sup>[28]</sup>. Likewise, ectopic expression of cullin 5, a novel target gene of miR-7, inhibits HCC cell proliferation, arrests cell cycle progression, and suppresses colony formation, although the exact pathway remains unclear<sup>[23]</sup>. Moreover,



**Figure 4** Pathway of miR-7 in hepatocellular carcinoma. MiR-7 can target various genes in the specific signaling pathway. HCC: Hepatocellular carcinoma; miR-7: MicroRNA-7; NF-κB: Nuclear factor κB; CCNE1: Cyclin E1; CUL5: Cullin 5; EGFR: Epidermal growth factor receptor; mTOR: Mammalian target of rapamycin; EMT: Epithelial-mesenchymal transition.

a member of the highly conserved cyclin family, CCNE1 (cyclin E1), is inversely correlated with miR-7 expression in HCC cell lines and clinical samples, indicating that it is a downstream mediator for miR-7, and miR-7 might be a candidate for the treatment of HCC<sup>[40]</sup>. Most studies in this field have been *in vitro* experiments, except one<sup>[28]</sup>. The detailed mechanisms remain to be elucidated, thus, the exact role of miR-7 in HCC needs further research (Figure 4).

## OTHER DIGESTIVE MALIGNANCIES

MiR-7 also plays a role in other digestive tract malignancies such as cholangiocarcinoma and ESCC<sup>[29,41]</sup>. However, the expression and exact role of miR-7 in these two malignancies need to be verified.

## INFLAMMATORY DISEASE

Inflammation makes a significant contribution to carcinogenesis and progression of malignancies<sup>[42]</sup>. In some conditions, inflammation such as chronic atrophic gastritis is defined as a precancerous lesion of GC. MiR-7 also participates in some inflammatory diseases, in addition to malignancies. The role of miR-7 in the progression from chronic inflammation to GC has been studied more thoroughly compared with other inflammatory diseases. Using established mouse models, Kong *et al.*<sup>[20]</sup> have demonstrated that downregulation of miR-7 induced by PGE2 associated with inflammation, and activation

of EGFR are critical steps in gastric carcinogenesis. Although the COX-2/mPGES-1/PGE2/EP2 pathway has been identified in gastric tumorigenesis, whether there is a similar mechanism mediated by miR-7 has not been established in other malignancies. It has been revealed that the expression of miR-7 is decreased in actively inflamed colonic tissues from patients with Crohn's disease, which is regulated by hCD98<sup>[25]</sup>. Similarly, chronic hepatitis has an important influence on HCC development, and hepatocyte nuclear factor 4α and NF-κB form a feedback circuit, for which miR-7 and miR-124 could be the targets<sup>[43]</sup>. These findings suggest that miR-7 is involved in many inflammatory diseases by activating many inflammatory/proinflammatory cytokines, and it will be intriguing to demonstrate the role of miR-7 in the regulation of alimentary inflammatory responses and carcinogenesis.

## CIRCULATORY BIOMARKER

The diagnostic and prognostic biomarkers for some digestive malignancies including GC and CRC are still limited. Common circulatory markers such as carcinoembryonic antigen (CEA) and carbohydrate antigen 19-9 have inadequate sensitivity, therefore, exploring specific biomarkers is a significant breakthrough.

MiRNAs are stable in serum, plasma and body fluids (*e.g.*, stools and gastric juice), and their expression differs between tumor and non-tumor tissue. Some miRNAs, like miR-21, have been subjected to meta-

analysis and concluded to be diagnostic biomarkers for GC<sup>[44]</sup>. Wang *et al.*<sup>[45]</sup> designed their study with three phases. In the discovery phase, they detected 723 miRNAs in 80 serum samples using microarrays; in the training phase they experimented on another 112 plasma samples using qPCR; and finally, they confirmed the results with 49 samples using a logistic model, and screened miR-7 as one of a panel that yielded high diagnostic accuracy to diagnose CRC. Compared with CEA, miR-7 has a higher receiver operating characteristic curve, sensitivity and specificity (0.897, 82% and 89%, respectively). Similarly, by analyzing the serum from 12 acute pancreatitis patients and three healthy controls, Liu *et al.*<sup>[46]</sup> identified miR-7 as one of the three diagnostic and prognostic biomarkers. Although several systematic reviews<sup>[44,47-49]</sup> have investigated biomarkers for GC, none has shown that miR-7 could be a biomarker of GC.

## CONCLUSION

Several studies have identified possible mechanisms mediated by miR-7 in specific malignancies of the digestive system, including some inflammatory diseases. No study has investigated miR-7 comprehensively, which may explain why different studies have discovered different targets for miR-7, or it may be because miRNA can form one-to-one, one-to-multiple or multiple-to-one relationships with its target genes<sup>[50]</sup>. Disruption of homeostasis in the digestive system is due to many pathways acting together in a complicated manner, which contributes to the progression from inflammatory diseases to malignancy. Furthermore, the genetic abnormalities in tumors are highly heterogeneous, and no two tumors are exactly alike, which raises a serious challenge. Consequently, more research should be conducted to verify whether miR-7 could be a biomarker or therapeutic target gene for digestive system malignancies.

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## Retrospective Study

# Impact of *RAS* and *BRAF* mutations on carcinoembryonic antigen production and pattern of colorectal metastases

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**Institutional review board statement:** This study was reviewed and approved by the City of Hope National Medical Center.

**Informed consent statement:** Patients were not required to give informed consent to the study because the analysis used anonymous clinical data.

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## Abstract

**AIM:** To investigate the impact of *RAS* and *BRAF* mutations on the pattern of metastatic disease and carcinoembryonic antigen (CEA) production.

**METHODS:** In this retrospective study, we investigated the impact of *RAS* and *BRAF* mutational status on pattern of metastatic disease and CEA production. Only patients presenting with a newly diagnosed metastatic colorectal cancer (CRC) were included. Patients' characteristics, primary tumor location, site of metastatic disease and CEA at presentation were compared between those with and without *RAS* and *BRAF* mutations.

**RESULTS:** Among 174 patients, mutations in *KRAS*, *NRAS* and *BRAF* were detected in 47%, 3% and 6% respectively. *RAS* mutations (*KRAS* and *NRAS*) were more likely to be found in African American patients (87% vs 13%; *P* value = 0.0158). *RAS* mutations were associated with a higher likelihood of a normal CEA (< 5 ng/mL) at presentation. *BRAF* mutations were more likely to occur in females. We were not able to confirm

any association between mutational status and site of metastatic disease at initial diagnosis.

**CONCLUSION:** No association was found between *RAS* and *BRAF* mutations and sites of metastatic disease at the time of initial diagnosis in our cohort. Patients with *RAS* mutations were more likely to present with CEA levels < 5 ng/mL. These findings may have clinical implications on surveillance strategies for *RAS* mutant patients with earlier stages of CRC.

**Key words:** *RAS*; *BRAF*; Carcinoembryonic antigen; Pattern of metastatic disease; Surveillance

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**Core tip:** We investigated the impact of *RAS* and *BRAF* mutations on pattern of colorectal cancer (CRC) metastases and carcinoembryonic antigen (CEA) production. Patients with *RAS* mutations were more likely to present with CEA levels < 5 ng/mL. No association was found between *RAS* and *BRAF* mutations and sites of metastatic disease at the time of initial diagnosis in our cohort. Our study is the first study to link low CEA production with a *RAS* mutant status at the time of initial presentation of metastatic CRC. These findings may have clinical implications on surveillance strategies for *RAS* mutant patients with earlier stages of CRC.

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## INTRODUCTION

Colorectal cancer (CRC) continues to be the second leading cause of cancer-related death in the United States. It is projected that 136830 individuals will be diagnosed with CRC in 2014 in the United States, 50310 of whom will succumb to this disease<sup>[1]</sup>. While significant progress has been made in the treatment of metastatic CRC (mCRC) over the last two decades, cure amongst these patients remains rare and is only achievable in approximately 20% of patients who are amenable to metastases resection<sup>[2,3]</sup>.

It is estimated that 20% of patients with CRC present with metastatic disease while another 30% develop metastatic disease after an initial presentation with local or regional disease<sup>[2,4]</sup>. Patients with limited oligometastatic disease are the ones who benefit the most from aggressive surgical strategies<sup>[5]</sup>. Therefore, early identification of metastatic disease remains key in improving the outcome of patients with metastatic disease. Indeed, intensive surveillance strategies in

patients with earlier stages of CRC have been associated with an increased rate of metastectomies in several prospective and retrospective clinical trials<sup>[6]</sup>. However, these surveillance strategies are not standardized amongst different medical societies and do not take into account the molecular heterogeneity of CRC<sup>[7]</sup>. It has been recently shown that certain oncogenic alterations have significant impact on disease biology, response to treatment, and overall outcome. For example, *BRAF* mutations, present in 5%-10% of CRCs, are associated with worse prognosis, a worse overall survival after disease recurrence, and a tendency to metastasize to the peritoneum and distant lymph nodes<sup>[8,9]</sup>. The impact of *KRAS* and *NRAS* mutations, which occur in approximately 50% of CRCs, on the pattern of metastatic disease at initial presentation has been more controversial<sup>[10-13]</sup>.

To better understand the impact of the commonly tested *RAS* (*KRAS* and *NRAS*) and *BRAF* mutations on metastatic disease pattern and on surveillance strategies, we conducted a single institute retrospective study that investigates the impact of *RAS* and *BRAF* mutations on the pattern of metastatic disease and carcinoembryonic antigen (CEA) production.

## MATERIALS AND METHODS

### Study population

We retrospectively reviewed all cases with metastatic colon cancer patients who presented to City of Hope Comprehensive Cancer Center from 2007 to 2014. Inclusion on study required all the following criteria: (1) confirmed CRC by pathology; (2) availability of imaging studies confirming metastatic disease at the time of presentation; (3) availability of *KRAS* or *BRAF* testing by PCR or by ONCO44 or ONCO48 next generation sequencing; and (4) available CEA level at the time of presentation of metastatic CRC.

Patients' characteristics including age, gender, race, location of the primary tumor, CEA, and sites of metastatic disease at the time of presentation were reviewed and collected from corresponding electronic medical records. Primary tumor location was categorized as right or transverse colon, left colon, and rectum. Metastatic sites were categorized into 3 groups: (1) lung; (2) liver; and (3) mesenteric or distal lymph nodes or peritoneum. The study was approved by the local institutional review board.

### *RAS* and *BRAF* analysis

To allow for a more powerful sample size, we included *RAS* and *BRAF* analysis performed by either a CLIA certified next generation sequencing or a CLIA certified PCR assay.

**Onco 44:** Genomic DNA is extracted from micro-dissected cells from formalin-fixed, paraffin-embedded tissue with minimum 30% tumor cellularity. A targeted DNA library is generated using the Ion AmpliSeq™ Cancer

Table 1 *RAS* and *BRAF* status and patient demographics

		All		<i>BRAF</i> MT		<i>BRAF</i> WT		<i>P</i>	<i>RAS</i> MT		<i>RAS</i> WT		<i>P</i>
		<i>n</i>	%	<i>n</i>	%	<i>n</i>	%		<i>n</i>	%	<i>n</i>	%	
Age	< 60	87	50	5	6	82	94	1.00	44	51	43	49	1.00
	≥ 60	87	50	6	7	81	93		43	49	44	51	
Gender	Male	103	59	3	3	100	97	0.052	49	48	54	52	0.54
	Female	71	41	8	11	63	89		38	54	33	46	
Race	White	122	70	7	6	115	94	0.53	57	47	65	53	0.015
	Asian, PI	41	24	4	10	37	90		23	56	18	44	
	Black	8	5	0	--	8	100		7	87	1	13	
	Unknown	3	2	0	--	3	100		0	--	3	100	

*n*: Number of patients; PI: Pacific Islander; MT: Mutant; WT: Wild type.

Hotspot Panel Kit, and sequenced by semiconductor-based next-generation sequencing technology on an Ion Torrent PGM. The Onco 44 panel is designed to target 713 mutations in 44 key cancer genes that include *KRAS*, *NRAS*, and *BRAF*. Tested *KRAS* mutations include codon 12, 13, 61 and 146. Tested *NRAS* mutations include codon 12, 13, 61.

**Onco 48:** The Onco48 Panel is designed to target 2800 mutations in 48 key cancer genes. The difference between Onco 44 and 48 is the additional sequencing of 4 target genes: *EZH2*, *GNA11*, *GNAQ*, and *IDH2*. In addition, the Onco48 panel identifies the rare *KRAS* codon 117 and *NRAS* codon 146 mutations.

***KRAS*-PCR:** DNA was extracted from micro-dissected cells from formalin-fixed, paraffin-embedded tissue with minimum 30% tumor cellularity. A PCR based fragment analysis with 5% sensitivity using "Shift Termination" technology was used to detect mutations in the *KRAS* gene. This assay is CLIA approved and detects 6 mutations on codon 12 and 1 mutation on codon 13 of exon 2.

***BRAF*:** Genomic DNA is extracted from micro-dissected cells from formalin-fixed, paraffin-embedded tissue with minimum 30% tumor cellularity. A real-time PCR assay with 1% sensitivity was performed to detect the c.1799 T > A (V600E) mutation in the *BRAF* gene.

#### CEA assay

CEA was tested *via* Siemens Advia Centaur chemiluminescent immunoassay and normal range is 0.5 ng/mL to 4.5 ng/mL.

#### Statistical analysis

We tested for differences in proportions between rate of mutations vs clinical and demographic factors with Fisher's Exact Tests. We also tested for differences in proportions between rate of mutations vs site of metastatic disease, location of primary disease, and CEA (cut point of 5 ng/mL) with Fisher's Exact Tests. For testing the association between metastases site and CEA as a continuous variable, we transformed CEA using

the natural logarithm and used it as the independent variable in a logistic regression. The dependent variable in the logistic regression was presence or absence of a given metastases location.

*KRAS* and *NRAS* mutations were categorized under *RAS* mutations, irrespective of the testing methodology. Comparative analysis was performed on 4 distinct subgroups: *RAS* mutant, *RAS* wild type, *BRAF* mutant, and *BRAF* wild type populations.

## RESULTS

The study population consisted of 174 patients who presented with metastatic colon cancer patients and documented *RAS* and *BRAF* mutational analysis. Genomic evaluation for *KRAS*, *NRAS*, and *BRAF* was performed by next generation sequencing using ONCO44 or ONCO48 in 122 patients. 52 patients were evaluated for *KRAS* (no *NRAS* evaluation) and *BRAF* mutation by PCR. Eighty-seven (50%) of patients had an identifiable *RAS* mutations (47% *KRAS* and 3% *NRAS*). Only 11 patients (6%) had *BRAF* mutation (Table 1).

#### *RAS* and *BRAF* mutations and patients' demographics

The median age of the study population was 60 years (range 23 to 87 years). There was no difference in *RAS* or *BRAF* mutation status by age, or gender. However, females had a trend towards a higher incidence of *BRAF* mutation. No distinct variations were noted in *KRAS* or *BRAF* mutations by race, with the exception of an increased rate of *RAS* mutations among African Americans. However, African American representation on this study was low (5%), limiting the interpretation of this finding (Table 1).

#### *RAS* and *BRAF* status, primary tumor location and pattern of metastases

There was no difference in primary tumor sites by *KRAS* or *BRAF* status, with the exception of a lower likelihood of *BRAF* mutations among rectal cancers. In addition, no difference in tumor spread pattern at the time of metastatic disease presentation was noted among the 4 molecular subgroups (Table 2).

**Table 2** *RAS* and *BRAF* status and primary tumor location and pattern of metastasis

		All		<i>BRAF</i> MT		<i>BRAF</i> WT		<i>P</i>	<i>RAS</i> MT		<i>RAS</i> WT		<i>P</i>
		<i>n</i>	%	<i>n</i>	%	<i>n</i>	%		<i>n</i>	%	<i>n</i>	%	
Primary lesion	Rectal	43	25	0	--	43	100	0.022	23	53	20	47	0.23
	Left colon	79	45	5	6	74	94		34	43	45	57	
	Right colon	52	30	6	12	46	88		30	58	22	42	
Site of metastasis	Lung	72	42	3	4	69	96	0.36	41	57	31	42	0.17
	Liver	98	56	5	5	93	95	0.54	46	47	52	53	0.44
	Peritoneal	49	28	5	10	44	90	0.3	23	47	26	53	0.74

*n*: Number of patients; MT: Mutant; WT: Wild type.

**Table 3** *RAS* and *BRAF* status and carcinoembryonic antigen levels

		All		<i>BRAF</i> MT		<i>BRAF</i> WT		<i>P</i>	<i>RAS</i> MT		<i>RAS</i> WT		<i>P</i>
		<i>n</i>	%	<i>n</i>	%	<i>n</i>	%		<i>n</i>	%	<i>n</i>	%	
< 5 ng/mL		60	34	4	7	56	93	1.00	37	62	23	38	0.037
≥ 5 ng/mL		114	66	7	6	107	94		64	56	50	44	

*n*: Number of patients; MT: Mutant; WT: Wild type.

### ***RAS* and *BRAF* status and CEA production**

Thirty-four percent of the total cohort were non-CEA producers (CEA < 5 ng/mL). Patients with liver metastases were more likely to produce CEA (OR = 0.639; *P* < 0.0001) while patients with peritoneal/mesenteric metastases were less likely to produce CEA (OR = 1.315; *P* = 0.0010). Patients with *RAS* mutation were more likely to be low-CEA producers at the time of metastatic disease presentation (Table 3). There was no significant association between *BRAF* mutation status and CEA production.

## **DISCUSSION**

In this study we sought to explore correlations between *RAS* and *BRAF* mutational status, patient demographics, metastatic disease pattern, and CEA production. No distinct demographic characteristics were associated with *RAS* or *BRAF* status, with the exception of *BRAF* mutations which were less likely to occur with a rectal primary. Although not statistically significant, females were more likely to harbor a *BRAF* mutation. These findings are consistent with prior reports<sup>[9,12,14,15]</sup>. We were not able to confirm an association between *BRAF* mutations and age or a right colon primary, contrary to previous reports<sup>[9,12,14,15]</sup>. This discordance is likely related to our more limited sample size, especially that the percentages of *RAS*-mutant and *RAS*-wild type patients with right colonic primaries were in line with the above referenced studies. We also investigated the impact of race on *RAS* and *BRAF* mutational status. The only positive association was for *RAS* mutation and African American race. Several studies have previously evaluated the impact of race on *RAS* and *BRAF* mutational status<sup>[16,17]</sup>. The N0147 adjuvant clinical trial in patients with stage III colon cancer reported an

increased likelihood of *BRAF* mutation amongst White and an increased *KRAS* mutation frequency in African Americans<sup>[18]</sup>. In addition, N0147 reported a lower frequency of *KRAS* mutations in Asians, a finding not supported by our study.

Contrary to the current literature, we did not find an association between *BRAF* mutation and peritoneal metastases at the time of presentation, likely due to our small *BRAF* mutant sample size. Several studies have reported an increased likelihood of peritoneal dissemination in *BRAF* mutant mCRC patients<sup>[8,9,19]</sup>. Yaeger *et al*<sup>[9]</sup> reported that patients with *BRAF* mutations were more likely to present with peritoneal metastases at initial diagnosis and less likely to have liver-limited metastases. Moreover, the 2-year cumulative incidence of peritoneal metastases was higher with *BRAF* mutated tumors<sup>[9]</sup>. Tran *et al*<sup>[8]</sup> reported a higher rate of peritoneal and distant lymph node metastases and a lower rate of lung metastases in *BRAF* mutated tumors. Similarly, Russo *et al*<sup>[19]</sup> reported a higher likelihood of *BRAF* mutations in patients with distant lymph node metastases at the site of first recurrence. Finally, Kawazoe *et al*<sup>[12]</sup> retrospectively studied the clinical-pathological features of *BRAF* mutations in Japanese patients with metastatic CRC and found that peritoneal metastases are more frequently observed in *BRAF* mutated patients. Since the presence of peritoneal metastases has been identified as a poor prognostic factor, a higher incidence of peritoneal metastases in *BRAF* tumors may partly explain the poor prognosis associated with this subgroup<sup>[12,20,21]</sup>. These studies are summarized in Table 4.

Our study did not confirm an association between *RAS* mutations and lung metastases at initial mCRC presentation. There is discordance among studies on the impact of *RAS* mutational status on lung metastases at the time of initial mCRC presentation. However,

**Table 4** *BRAF* status and pattern of colon cancer metastases

Ref.	n (% <i>BRAF</i> )	End point	% <i>BRAF</i> MT vs % <i>BRAF</i> WT	P
Tran <i>et al</i> <sup>[8]</sup>	524 (11%)	Rate of peritoneal metastases	46% vs 24%	0.001
		Rate of distant lymph node metastases	53% vs 38%	0.008
		Rate of lung metastases	35% vs 49%	0.049
Yaeger <i>et al</i> <sup>[9]</sup>	515 (18%)	Peritoneal involvement at presentation	26% vs 14%	< 0.01
Kawazoe <i>et al</i> <sup>[12]</sup>	264 (5%)	Peritoneal metastasis	50% vs 18%	0.009

n: Total number of patients; %*BRAF*: %patients with *BRAF* mutation; MT: Mutant; WT: Wild type.

**Table 5** *RAS* status and pattern of colon cancer metastases

Ref.	n (%MT)	Results	P
Cejas <i>et al</i> <sup>[29]</sup>	110 (34% <i>KRAS</i> MT)	Frequency of <i>KRAS</i> mutation in primary tumor of patients with lung vs liver metastases	0.054
Tie <i>et al</i> <sup>[10]</sup>	Cohort A 161 (48.4% <i>KRAS</i> MT)	59% vs 32%	0.003
		Mutation frequencies in lung in <i>KRAS</i> MT vs WT	
		62% vs 38%	0.003
Kim <i>et al</i> <sup>[23]</sup>	Cohort C 859 (33.8% <i>KRAS</i> MT) 143 (43.4% <i>KRAS</i> MT)	Mutation frequencies in brain in <i>KRAS</i> MT vs WT	0.007
		56.5% vs 43.5%	0.003
		Relapse in lung in <i>KRAS</i> MT	
		HR 2.1, 95%CI: 1.2-3.5	0.007
		Lung as initial metastatic site in <i>KRAS</i> MT vs WT	0.003
Vauthey <i>et al</i> <sup>[25]</sup>	193 (18% All <i>RAS</i> MT)	45.3% vs 22.1%	< 0.001
		Liver as initial metastatic site in <i>KRAS</i> MT vs WT	
		37.3% vs 70.6%	< 0.001
Yaeger <i>et al</i> <sup>[11]</sup>	918 (48% All <i>RAS</i> MT)	Distant lymph node as initial metastatic site in <i>KRAS</i> MT vs WT	0.025
		6.7% vs 19.1%	< 0.001
		3-yr lung RFS rate in patients undergoing curative resection of liver metastases in <i>RAS</i> MT vs WT	
Kemeny <i>et al</i> <sup>[24]</sup>	169 (30% <i>KRAS</i> MT)	34.6% vs 59.3%	< 0.01
		Lung as site of first metastasis in <i>RAS</i> MT vs WT	< 0.01
		22% vs 0%	< 0.001
		Cumulative incidence of lung as subsequent metastasis at 2 yr after diagnosis in <i>RAS</i> MT vs WT	
		32.5% vs 19%	< 0.01
Pereira <i>et al</i> <sup>[13]</sup>	494 (41% <i>KRAS</i> MT)	3-yr cumulative recurrence rate to lung after hepatic resection and HAI in <i>KRAS</i> MT vs WT	0.05
		58% vs 32%	< 0.01
		3-yr cumulative recurrence rate to brain after hepatic resection and HAI in <i>KRAS</i> MT vs WT	
Pereira <i>et al</i> <sup>[13]</sup>	494 (41% <i>KRAS</i> MT)	14.5% vs 2%	< 0.01
		3-yr cumulative recurrence rate to bone after hepatic resection and HAI in <i>KRAS</i> MT vs WT	0.002
Pereira <i>et al</i> <sup>[13]</sup>	494 (41% <i>KRAS</i> MT)	13.4% vs 2%	0.002
		Time to lung metastasis (median months) in <i>KRAS</i> MT vs WT	
		15.2 vs 22.4 (HR 1.4)	

n: Total number of patients; %MT: %patients with mutation; MT: Mutant; WT: Wild type; RFS: Recurrence free survival; HAI: Hepatic arterial infusion.

clinical studies have consistently shown an association between *KRAS* mutation and lifetime likelihood of lung metastases in patients with mCRC, but not at initial presentation (Table 5). In our previous study, conducted on a different patient data set, Sharma *et al*<sup>[22]</sup> reported no predictive role for *KRAS* mutations on the site(s) of metastatic disease at the time of presentation. Pereira *et al*<sup>[13]</sup> retrospectively evaluated patients with mCRC who were tested for *KRAS* mutation at MD Anderson Cancer Center. They did not report an increase rate of lung

metastases in *KRAS* mutated patients at the time of diagnosis of mCRC. However, *KRAS* mutation was found to have a shorter time to lung metastases and a two-fold greater odd of developing lifetime lung metastases in a cohort of a liver-limited CRC. However, several other studies reported that *KRAS* mutant patients were more likely to present with lung metastases than *KRAS* wild type patients. Kim *et al*<sup>[23]</sup> reported on the initial metastatic disease patterns in South Korean patients with mCRC. Lung metastases were more frequent

as the initial metastatic site in *KRAS* mutant patients while liver and distant lymph node metastases were less likely<sup>[23]</sup>. Yaeger *et al.*<sup>[11]</sup> reported on the impact of *KRAS* mutations on the pattern of metastatic spread in CRC. In this retrospective study, *KRAS* mutant patients had a higher incidence of lung metastases at initial presentation compared to *KRAS* wild type patients. In addition, *KRAS* mutated patients had higher cumulative incidence of lung, bone and brain metastases at two years from initial mCRC presentation. Fewer patients had liver-limited disease at the initial presentation in *KRAS* mutated patients than *KRAS* wild type patients<sup>[11]</sup>. *KRAS* mutations have also been associated with a higher risk of lung relapse while *NRAS* mutations were associated with increased local recurrence after curative resection of primary CRC or after curative intent hepatectomy<sup>[10,24,25]</sup>. Review of patients with stage II and III primary CRC who participated in VICTOR clinical trial showed an association between *KRAS* mutations and an increased relapse rate in the lung. Relapse in the liver was similar between *KRAS* mutant and wild type patients<sup>[10]</sup>. Kemeny *et al.*<sup>[24]</sup> reported on the pattern of metastatic disease recurrence in patients who underwent hepatic resection and adjuvant HAI plus systemic chemotherapy. The three-year cumulative incidence of lung metastases was higher in the *KRAS* mutant patients. The cumulative incidence of bone and brain metastases was also increased in the *KRAS* mutant patients. Similarly, Vauthey *et al.*<sup>[25]</sup> reported that patients with *KRAS* mutant tumors who underwent curative intent liver resection at MD Anderson cancer center had a lower three-year lung RFS in comparison to patients with *KRAS* wild type tumors. Based on the above studies (summarized in Table 5), *KRAS* mutant mCRC patients have an increased lifetime risk of developing lung metastases. However, the impact of *KRAS* mutational status on the incidence of lung metastases at the initial time of diagnosis of metastatic disease remains controversial. Whether the lack of association between lung metastases at presentation and *KRAS* mutations is related to a limited sample size on those studies vs being the result of tumor biology remains unclear.

We have studied the impact of *RAS* and *BRAF* mutational status on CEA levels at the time of initial diagnosis of metastatic disease. We did not find any difference in CEA levels between *BRAF* mutant and *BRAF* wild type mCRC at initial presentation. In contrast, *RAS* mutant mCRC patients were more likely to be non-CEA producers (62% *RAS*-MT vs 38% *RAS*-WT) (Table 3). Our findings are in contrast to a study by Selcukbiricik *et al.*<sup>[26]</sup> which reported a higher percentage of patients with CEA > 5 ng/mL among the *KRAS* mutant cohort. Selcukbiricik study was limited by stage heterogeneity (stages I-IV) and did not include an analysis of the impact of *RAS* mutation within the stage IV disease cohort. Our study also showed an association between CEA levels and site of metastatic disease. CEA was more likely to be elevated in patients with liver metastases

and lower in patients with peritoneal or mesenteric recurrence, which is consistent with prior reports<sup>[27]</sup>.

Our study has several limitations. This is a single institution study with a relatively small size. Modest associations between *RAS* and *BRAF* status and other clinical variables may have therefore been missed due to the lack of adequate power. In addition, the diagnosis of metastatic disease on this study could have been made during surveillance for disease recurrence or during the work-up of symptomatic disease. Therefore, the conclusions derived from this study may not be clearly generalizable to the surveillance population or to the population presenting with symptomatic stage IV disease. Other limitations include the inclusion of patients with *KRAS* PCR mutation assay (no ONCO48 analysis). This implies that some patients may have been assigned to the *RAS* wild type subgroup without ruling out the possibility of *NRAS* or non-exon 2 *KRAS* mutations. The likelihood of this event impacting our overall results is low as only 52 patients (30%) of our study population was analyzed by *KRAS*-PCR only. Given that less than 10% of the general population carries a non-exon 2 *KRAS* mutation or *NRAS* mutations, we expect that less than 10 patients may have been inappropriately labeled.

In summary, our study is the first study to link low CEA production with a *RAS* mutant status at the time of initial presentation of metastatic CRC. If validated in larger studies, especially in surveillance settings, our findings would have major clinical significance. It has been recently confirmed that *RAS* mutations increase the risk of systemic disease recurrence after a curative resection in patients with stage III colon cancer<sup>[28]</sup>. Reliable screening strategies are especially important in this high risk population in order to diagnosis early recurrence and increase the likelihood of curative-intent metastectomies. If CEA is confirmed as a less reliable screening strategy, intense radiographic screening will be especially important as a complement to CEA screening in this population.

## COMMENTS

### Background

It is estimated that 20% of patients with colorectal cancer (CRC) present with metastatic disease while another 30% develop metastatic disease after an initial presentation with local or regional disease. Patients with limited oligometastatic disease are the ones who benefit the most from aggressive surgical strategies. Therefore, early identification of metastatic disease remains key in improving outcome. It has been recently shown that certain oncogenic alterations have significant impact on disease biology, response to treatment, and overall outcome. To better understand the impact of the commonly presented *RAS* (*KRAS* and *NRAS*) and *BRAF* mutations on metastatic disease pattern and on surveillance strategies, the authors conducted a single institute retrospective study that investigates the impact of *RAS* and *BRAF* mutations on the pattern of metastatic disease and carcinoembryonic antigen (CEA) production.

### Research frontiers

*BRAF* mutations, present in 5%-10% of CRCs, are associated with worse prognosis, a worse overall survival after disease recurrence, and a tendency to metastasize to the peritoneum and distant lymph nodes. The impact of *KRAS* and *NRAS* mutations, which occur in approximately 50% of CRCs, on the

pattern of metastatic disease at initial presentation has been more controversial. No studies have reported on the impact of either *RAS* or *BRAF* mutations on CEA production.

# Innovations and breakthroughs

The authors did not find any difference in CEA levels between *BRAF* mutant and *BRAF* wild type mCRC at initial presentation. In contrast, *RAS* mutant mCRC patients were more likely to be non-CEA producers (62% *RAS*-MT vs 38% *RAS*-WT).

# Applications

The study is the first study to link low CEA production with a *RAS* mutant status at the time of initial presentation of metastatic CRC. If validated in larger studies, especially in surveillance settings, the authors' findings may indicate that CEA surveillance is less reliable in curatively resected *RAS* mutant CRC patients. Alternative surveillance strategies may be required in this patients population.

# Terminology

The ONCO 44/48 is the next-generation sequencing technology at the City of Hope which is designed to target 713 mutations in 44 and 48 key cancer genes.

# Peer-review

It is a well-written paper.

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