

Original Article

Low frequency of HER2 expression in colorectal cancer: A Tunisian single-center study

Khouloud Ben Lazreg ^{1,2}, Wiem Majdoub ^{1,3}, Ahlem Bdioui ^{1,3}, Marwa Krifa ^{1,3}, Zayneb Lajmi ^{1,3}, Oussema Belkacem ⁴, Mariem Alaya ⁵, Sarra Mestiri ^{1,3}, Sihem Hmissa ^{1,3}, Nabiha Missaoui ^{3*}

¹ Pathology Department, Sahloul University Hospital, Sousse, Tunisia

² Pathology Department, Farhat Hached University Hospital, Sousse, Tunisia

³ Research Laboratory LR21ES03, Oncogenesis and Tumor Progression, Medicine Faculty of Sousse, University of Sousse, Sousse, Tunisia

⁴ Biopathology Department, Institut Paoli-Calmettes, Marseille, France

⁵ Pathology Department, Salah Azaiez Cancer Institute, Tunis, Tunisia

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Abstract



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HER2 expression is a potential theranostic and prognostic marker in some cancers, particularly in breast and gastric cancers. However, published data on HER2 expression in colorectal cancer (CRC) remain controversial. This study investigates the immunohistochemical and molecular expression of HER2 in primary CRC and evaluates its clinicopathological and prognostic significance in Tunisian patients. A retrospective analysis was conducted on 144 CRC patients. HER2 status was assessed by immunohistochemistry and tissue microarray analysis, following the diagnostic criteria for gastroesophageal adenocarcinoma. CRC cases with ambiguous results underwent chromogenic *in situ* hybridization. The mean patient age was 61.9 years (male-to-female ratio: 1.18:1). Tumors were classified as colonic (74.3%) or rectal (25.7%), with 45.8% located in the left colon. Stage III disease was identified in 37.5% of cases, and distant metastases were present in 13.9%. HER2 expression results were as follows: negative (score 0/1+) in 142 cases (98.6%), equivocal (score 2+) in one case (0.7%), and overexpressed (score 3+) in one case (0.7%). No HER2 gene amplification was detected, and none of the metastatic CRC cases showed HER2 immunostaining. These findings suggest that HER2 overexpression and amplification in CRC are rarer than previously reported, highlighting the need for multicenter Tunisian studies to validate these results. The variability in HER2 immunostaining criteria further underscores the importance of a standardized scoring system to ensure consistency in both diagnosis and research.

Keywords: Colorectal cancer, HER2, Immunohistochemistry, Chromogenic *in situ* hybridization, Scoring system, Theranostic marker, Tunisian patients.

1. Introduction

Colorectal cancer (CRC) represents a significant global public health issue, ranking third in incidence with 1,926,425 new cases and standing as the second leading cause of cancer-related mortality, with 904,019 deaths recorded in 2022 [1]. In Tunisia, a notable increase in CRC incidence has been reported, with rates reaching 14.6 per 100,000 men and 12.2 per 100,000 women [2]. In the era of molecular biology, the objective has shifted beyond the conventional anatomical classification of cancers towards a molecular classification, correlating these profiles with clinicopathological characteristics. CRC exhibits considerable histological heterogeneity and dynamic genetic alterations, with multiple tumor cell clones displaying distinct molecular profiles that respond variably to targeted therapies [3, 4]. This heterogeneity can evolve dynamically during disease progression and under therapeutic pressure, sometimes resulting in tumor progression despite ongoing treatment. Thus, CRC provides a promising framework for

the development of personalized oncology and the integration of theranostic biomarkers [5, 6].

Almost 20% of CRC patients are diagnosed with distant metastases, while 50% of those with non-metastatic disease who undergo curative treatment remain at high risk of recurrence [2, 7]. Advanced disease stages and metastatic relapses following curative treatment are the primary contributors to mortality in CRC patients. It is also noteworthy that patients who have exhausted all standard therapeutic options generally have a worse prognosis, even if they remain in relatively good health and continue to pursue additional therapeutic strategies [2, 8-10].

Recent advancements in therapeutic standards have led to an overall survival rate exceeding 30 months in genetically selected patients [8]. For many years, chemotherapy was the conventional treatment for metastatic CRC (mCRC). However, the advent of targeted therapies, notably those utilizing anti-EGFR (epidermal growth factor receptor) agents such as cetuximab and panitumumab,

* Corresponding author.

E-mail address: missaouinabiha@live.fr (N. Missaoui).

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which were approved in 2007 and 2008, respectively, have revolutionized the management of mCRC patients with *RAS* wild-type status [2, 11]. These therapies may be used in combination with chemotherapy or after chemotherapy failure. Despite these advancements, the EGFR expression level in CRC does not consistently correlate with therapeutic efficacy, suggesting the existence of primary and secondary resistance mechanisms [12].

Investigating the molecular profile of CRC has revealed mutations, particularly in the *RAS* gene, which contribute to resistance to anti-EGFR therapies [13, 14]. According to scientific societies, *RAS* status (*KRAS* and *NRAS* exons 2, 3, and 4) is the only validated predictive biomarker for response to anti-EGFR therapy [15]. Additional molecular alterations are under investigation to enhance the prediction of therapeutic responses. One such area of research focuses on the human epidermal growth factor receptor 2 (HER2), a member of the tyrosine kinase receptor family [13, 15-17].

HER2 is a member of the epidermal growth factor receptor (EGFR) family, which includes EGFR (ErbB1/HER1), HER3 (ErbB3), and HER4 (ErbB4) [18]. These receptors are expressed in various epithelial, mesenchymal, and neural tissues and play a crucial role in cellular development, proliferation, differentiation, and metabolism. Their functions are mediated through key signaling pathways, including the RAS/RAF/MAPK and PI3K/AKT pathways [19]. Typically, activation of these receptors occurs through homo- or heterodimerization of their tyrosine kinase domains, usually triggered by ligand binding. Notably, HER2 is unique among these receptors as it lacks a known ligand [19].

The *HER2 (ERBB2)* oncogene is located on the long arm of chromosome 17 (17q12; 35.109-35.138 Mb) [20]. The conversion of a proto-oncogene to an oncogene occurs through genetic alterations that affect its structure or regulatory expression. The most prevalent mechanism in human cancers is overexpression, characterized by increased receptor levels in tumor tissues. This overexpression can result from *ERBB2* gene amplification, transcription disruptions leading to uncontrolled protein production, or post-transcriptional modifications [21]. Activating mutations, such as V842I, V777L, and L755S in the kinase domain, as well as the extracellular domain mutation S310F, have been identified in various cancers, including CRC [22].

Over the last decade, HER2 has been extensively studied in various malignancies, notably breast and gastric cancers [23-25]. It has emerged as a potential key marker in CRC management, particularly in metastatic cases [15, 26]. Indeed, HER2 overexpression may represent an alternative mechanism of resistance to anti-EGFR treatments [8, 18, 27]. Furthermore, clinical trials assessing anti-HER2 therapy in mCRC patients have yielded promising results [28-31]. These findings have prompted further exploration of HER2 overexpression in CRC [32, 34]. Despite these promising results, study outcomes have been inconsistent [8]. In this study, we investigated the immunohistochemical and molecular expression of *HER2* in primary CRC at all stages diagnosed in Tunisian patients and explored its clinicopathological, prognostic, and therapeutic implications.

2. Materials and methods

2.1. Sample collection

We conducted a retrospective and descriptive study on CRC cases referred by the General Surgery Department and diagnosed by the Pathology Department at Sahloul University Hospital, Sousse, Tunisia. Data collection covered two years and six months, from January 1, 2020, to June 30, 2022.

We included primary CRC cases at all stages (I to IV) that underwent surgical resection with lymph node dissection. For rectal cancers, patients were included regardless of whether they had received neoadjuvant therapy. However, we excluded patients with non-carcinomatous colorectal tumors, recurrent CRC, or rectal cancer with a complete response to neoadjuvant therapy. Additionally, patients with synchronous or multiple colorectal tumors were excluded to ensure accuracy in HER2 assessment. Tumors too small for immunohistochemical analysis, such as small residual tumors following neoadjuvant therapy, were also excluded.

Ethical approval was obtained from the local Human Ethics Committee at Sahloul University Hospital, Sousse, Tunisia, in accordance with the Declaration of Helsinki.

2.2. Clinicopathological data

Clinicopathological data, including patient age, gender, tumor site and size, macroscopic appearance, distance from the nearest resection margin, presence of associated macroscopic lesions, and lymph node count after meticulous mesocolon dissection, were collected from pathology reports and clinical records. Additionally, we collected microscopic characteristics, including histological type, histological grade, tumor status (T), lymph node status (N), metastatic status (M), metastatic sites for metastatic cancers, TNM stage (pTNM or ypTNM), and vascular emboli and perineural invasion. Patient follow-up and outcomes were obtained from the Cancer Registry of Central Tunisia.

Histological diagnosis of all tumor cases was independently reviewed by two pathologists (KL and SH) using hematoxylin and eosin-stained sections, according to the 2019 World Health Organization (WHO) classification [34]. Histological grading of adenocarcinomas, not otherwise specified (NOS), followed the College of American Pathologists (CAP) recommendations. TNM staging including pathological TN (pTN) or post-neoadjuvant therapy pathological TN (ypTN), were carried out following the Eighth Edition of the American Joint Committee on Cancer (AJCC) Cancer Staging Manual [35].

All tissue samples underwent standard fixation in 10% buffered formalin and were subsequently embedded in paraffin. For each case, the most cellular tumor areas were identified using low magnification (x40). Necrotic areas and poorly fixed regions, such as border or crush artifacts, were excluded from the selection.

2.3. HER2 expression

HER2 expression was evaluated using immunohistochemistry on tissue microarrays (TMA) derived from archived samples as we previously published [36]. Additionally, whole-slide sections were prepared for 11 mucinous adenocarcinomas, as mucus pools compromised the preparation and interpretation of TMAs. In brief, antigen unmasking was performed on dewaxed and rehydrated sec-

tions using BOND™ Epitope Retrieval ER2 Solution (pH 9) at 100°C for 30 minutes. After blocking endogenous peroxidase activity with the Refine Detection Kit Peroxide Block, the slides were incubated with a pre-diluted rabbit monoclonal anti-c-erbB-2 primary antibody (clone SP3, BOND MAX Leica) for 15 minutes. Immunoreactivity was detected using the BOND-Polymer-Refine Detection Kit on a BOND MAX Leica system, in accordance with the manufacturer's instructions. The immunostaining was visualized with Diaminobenzidine, and the sections were briefly counterstained with hematoxylin and mounted [36].

2.4. Evaluation of HER2 expression

HER2 immunostaining was interpreted by two expert pathologists independently using an optical microscope. They evaluated the immunostaining type, extent, and intensity. Each tissue sample was assigned an HER2 expression score based on the diagnostic criteria established by Hofmann et al. [37] and adopted by the College of American Pathologists (CAP), American Society for Clinical Pathology (ASCP), and American Society of Clinical Oncology (ASCO) in the 2016 recommendations for gastroesophageal adenocarcinomas (GEA) [38]. In our study, given the small size of the tissue cylinders, we adhered to the CAP/ASCP/ASCO 2016 recommendations for GEA relevant to biopsies (GEA-b) [38]. For whole tissue sections, we followed the CAP/ASCP/ASCO 2016 guidelines for resection specimens [38]. According to these diagnostic criteria, isolated cytoplasmic/nuclear staining or basal/luminal immunostaining was deemed non-significant and therefore excluded [38].

2.5. HER2 gene amplification

HER2 2+ cases underwent additional chromogenic *in situ* hybridization (CISH) testing for gene amplification, as previously described [39]. Briefly, the ZytoDot SPEC ERBB2/CEN probe was applied to 3-μm-thick dewaxed and rehydrated sections following the manufacturer's protocol. Tumor samples were incubated with a cocktail of primary antibodies against digoxigenin and dinitrophenyl, followed by a cocktail of polymerized secondary antibodies: anti-HRP-GOAT and anti-AP-GOAT. Tissue sections were counterstained with hematoxylin, mounted in Faramount (DakoCytomation), and examined under an optical microscope [39].

DIG-labeled hybridization signals appeared as dark green dots (ERBB2 genomic region), while DNP-labeled signals appeared as dark red dots (CEP17). Slides were scanned at low magnification (x100 and x200) to assess heterogeneity. Signal visualization was performed at x400 magnification for clear detection. Interpretation was conducted in the invasive component, excluding necrotic areas, based on at least 200 non-overlapping nuclei. Results were analyzed according to GEA guidelines [38]. Tumors were classified as follows: amplified (≥ 6 copies per nucleus or HER2/CEP17 ratio ≥ 2 in 20 to 40 cells); non-amplified (< 4 copies per nucleus or HER2/CEP17 ratio < 2); equivocal (4 to 6 copies per nucleus or HER2/CEP17 ratio between 1.8 and 2). For equivocal cases, additional counting of at least 20 more nuclei in other tumor areas or sections was recommended [38].

2.6. Statistical analysis

Statistical analysis was performed using SPSS software

(Version 25.0, IBM Corp). Descriptive statistics included means for quantitative variables and absolute/relative frequencies (percentages) for qualitative variables.

3. Results

3.1. Clinicopathological characteristics

A total of 144 patients with CRC were included in the study. The cohort consisted of 78 males (54.2%) and 66 females (45.8%), with a sex ratio of 1.18. Patient ages ranged from 31 to 88 years, with a mean age of 61.9 years. The mean age was 61.4 years in males and 62.5 years in females. Patients younger than 40 years accounted for 6.9% of cases, with the highest frequency reported in the 60–69 year age group (25.7%). Table 1 presents the clinicopathological features of CRC patients.

CRC was diagnosed in 15.3% of patients following an episode of acute intestinal obstruction. Tumor sizes ranged from 1.3 cm to 19 cm, with an average of 5.3 cm. In our study, 107 cases (74.3%) involved colonic cancers, while 37 cases (25.7%) were rectal cancers.

The distribution of colonic tumors showed that descending colon tumors were the most common, accounting for 45.8% of cases ($n = 66$), followed by ascending colon tumors (22.9%) and transverse colon tumors (5.6%). Among rectal cancers, tumors were most frequently located in the upper rectum (11.8%), followed by the lower rectum (7.6%) and the middle rectum (6.3%).

In our study, the predominant histological type was adenocarcinoma NOS (formerly known as Lieberkühnian adenocarcinoma), accounting for 89.6%, followed by mucinous adenocarcinoma (9.7%) and serrated adenocarcinoma (0.7%). According to the CAP and the Royal College of Pathologists classification, the majority of adenocarcinoma NOS cases were classified as low-grade tumors (93.8%), with the remaining cases being categorized as high-grade tumors (Table 1).

Based on the degree of wall infiltration, tumors were classified as pT3 in 57.6% of cases ($n = 83$), pT4 in 27.8% of cases ($n = 40$), and pT2 in 14.6% of cases ($n = 21$). According to the Eighth Edition of the AJCC classification, colorectal tumors were most frequently diagnosed at stage III (37.5%, $n = 54$), followed by stage II (34%, $n = 49$) and stage IV (17.4%, $n = 25$). Stage I was the least frequent, representing 11.1% of cases.

In our study, 20 patients with CRC were diagnosed with metastasis. Distant metastases to a single organ were observed in 17 patients (11.8%). Peritoneal metastasis, with or without involvement of additional organs, was reported in three patients (2.1%). The remaining 124 tumors (86.1%) were non-metastatic at diagnosis. Among the metastatic cases, liver metastases were detected in 14 cases (70%), pulmonary metastases in two cases (10%), peritoneal metastases in three cases (15%), and ovarian metastasis in one case (5%).

3.2. Detection of HER2 overexpression

According to the GEA-validated diagnostic criteria, membranous HER2 expression was observed in four cases with a score of 1+ (2.8%), one case with a score of 2+ (0.7%), and one case with a score of 3+ (0.7%). The remaining 138 tumors (95.8%) exhibited no HER2 receptor expression (score 0) (Fig. 1). Based on these findings, CRC samples were classified into three categories: HER2-negative tumors (score 0/1+), accounting for 98.6% ($n =$

Table 1. Clinicopathological characteristics of CRC patients.

Parameters	N	Percentage (%)
Sex		
Male	78	54.2%
Female	66	45.8%
Age (Years)		
< 40	10	6.9%
40-49	16	11.1%
50-59	34	23.6%
60-69	37	25.7%
70-79	31	21.5%
≥ 80	16	11.1%
Acute intestinal obstruction		
Presence	22	15.3%
Absence	122	84.7%
Tumor size		
≤ 4 cm	57	39.6%
> 4 cm	87	60.4%
Tumor site		
Colonic	107	74.3%
Descending colon	66	45.8%
Ascending colon	33	22.9%
Transverse colon	8	5.6%
Rectal	37	25.7%
Upper rectum	17	11.8%
Lower rectum	11	7.6%
Middle rectum	9	6.3%
Growth pattern		
Exophytic	98	68.1%
Infiltrative	36	25%
Ulcerated	10	6.9%
Associated lesions		
Absence	105	72.9%
Presence	39	27.1%
≤ 100 polyps	34	23.6%
> 100 polyps	2	1.4%
Mucinous appendix tumor	2	1.4%
Colonic diverticula	1	0.7%
Surgical margin		
Clear	140	97.2%
Involved	4	2.8%
Histological type		
Adenocarcinoma NOS	129	89.6%
Mucinous adenocarcinoma	14	9.7%
Serrated adenocarcinoma	1	0.7%
Tumor grade		
Low-grade	135	93.8%
High-grade	9	6.2%
Vascular emboli		
Presence	69	47.9%
Absence	75	52.1%

Perineural invasion		
Presence	49	34%
Absence	95	66%
Degree of wall infiltration		
pT2	21	14.6%
pT3	83	57.6%
pT4	40	27.8%
Nodular metastasis		
pN0	73	50.7%
pN1	45	31.3%
pN2	26	18%
Distant metastasis		
Presence	20	13.9%
Absence	124	86.1%
Tumor stage		
Stage I	16	11.1%
Stage II	49	34%
Stage III	54	37.5%
Stage IV	25	17.4%

142); tumors with equivocal HER2 status (score 2+), representing 0.7% (n = 1); and HER2-overexpressing tumors (score 3+), also comprising 0.7% (n = 1). Additionally, *HER2* gene amplification was not detected in the equivocal HER2 CRC sample.

In our study, none of the metastatic CRC cases exhibited membranous HER2 immunostaining. Furthermore, cytoplasmic HER2 immunostaining without membranous labeling was observed in 16 CRC samples (11.1%) (Fig. 1).

3.3. Characteristics of CRC case HER2-overexpressing

The only case of HER2 overexpression (score 3+) was observed in a 37-year-old woman who presented with a mid-rectal tumor following neoadjuvant chemoradiotherapy. Initially, she was diagnosed with a mid-rectal tumor and a solitary hepatic lesion in segment II. The patient received neoadjuvant chemoradiotherapy according to the RAPIDO protocol, which resulted in an estimated 50% radiological response at the primary site and complete resolution of the hepatic lesion (M0).

Macroscopic examination revealed a residual tumor measuring 1.4 cm with a budding morphology. Both longitudinal and circumferential surgical margins were free of tumor. The tumor was classified as a low-grade, well-differentiated adenocarcinoma of the middle rectum. Therapeutic response was graded as TRG2 according to Dowrak's criteria. Perineural invasion was observed, but there were no evidence of vascular emboli. The final pathological stage was ypT3N0 (stage IIA), based on the Eighth Edition of the AJCC Cancer Staging Manual.

HER2 overexpression was further confirmed on the pre-treatment biopsy, which showed an immunohistochemical score of 3+ (Fig. 1), in accordance with the 2016 CAP/ASCO/ASCP guidelines for GEA-b. A HER2-overexpressing invasive breast carcinoma was included as a positive control on the same slide to validate the immunohistochemistry procedure.

Subsequent disease progression was marked by the appearance of secondary pulmonary nodules and recurrence

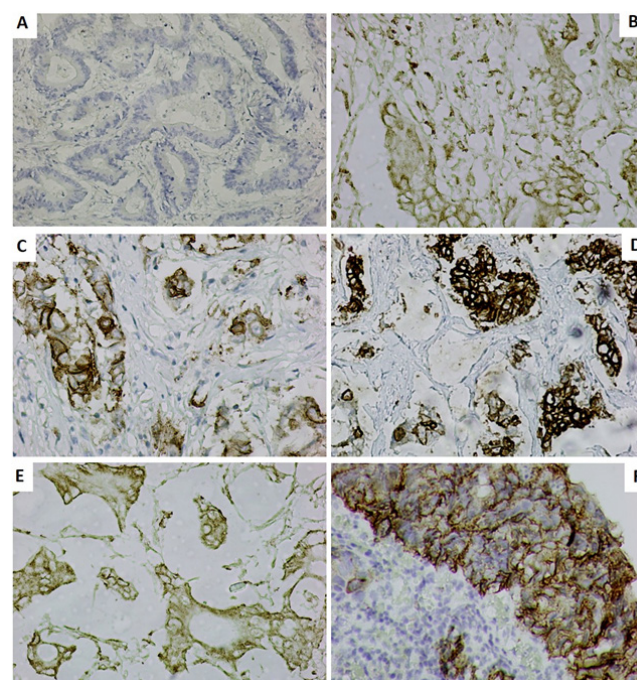


Fig. 1. HER2 expression in CRCs by immunohistochemistry. (A) Absence of HER2 staining (score 0) (x200). (B) HER2 expression (score 1+), showing faint granular basolateral membranous staining (x200). (C) HER2 expression (score 2+), showing moderate basolateral membranous staining (x100). (D) HER2 overexpression (score 3+), characterized by strong membranous staining (x100). (E) Granular cytoplasmic HER2 staining (x100). (F) HER2 expression on the pre-treatment biopsy of the HER2-overexpressing CRC case with strong membranous HER2 staining (x200).

of the hepatic lesion. The patient received three cycles of FOLFOX combined with Avastin, followed by FOLFIRI plus Avastin, but these regimens failed to produce clinical improvement. The tumor continued to progress, with the emergence of an osteosclerotic lesion in the L4 spinous process, pelvic presacral ascites, and a peritoneal carcinomatosis nodule. The patient is considered eligible for anti-

EGFR therapy. Pre-treatment molecular testing identified *KRAS* and *NRAS* mutations. Two years after diagnosis, the patient is still alive, but continues to experience recurrent metastatic disease.

4. Discussion

In our study, HER2 immunoexpression was absent in most CRC cases, with only 0.7% of tumors exhibiting HER2 overexpression. Additionally, low-level expression was observed in four cases, and one tumor exhibited an equivocal HER2 status without gene amplification. Furthermore, strong membranous HER2 overexpression was identified in one CRC case, consistent with findings from the corresponding pre-treatment biopsy. Cytoplasmic staining without membranous HER2 expression was observed in 11.1% of cases. No HER2 expression was detected in mCRC samples.

Various studies on CRC have evaluated HER2 status using tissue samples from surgical specimens, primary tumor biopsies, or metastatic lesions. Aside from the diagnostic criteria established for GEA [38], no specific guidelines currently exist for assessing HER2 in CRC biopsies. In our study, HER2 expression was assessed using TMA blocks containing 4 mm cores, which are comparable in size to biopsy samples. Therefore, we followed the recommendations for HER2 evaluation in biopsy specimens [38]. Previously, Conradi et al. proposed a minimum threshold of five cohesive tumor cells to define HER2 overexpression in biopsy samples, and recommended assessing HER2 on a representative section of the resected specimen [40]. More recently, Fujii et al. highlighted the challenges of accurately determining HER2 status due to tumor heterogeneity, and advocated for evaluating HER2 on complete, representative sections of the surgical specimen, as biopsy-based assessments may increase the risk of false-negative results [41]. Furthermore, proper tissue fixation is essential for reliable HER2 immunostaining. According to international guidelines, tumor samples from surgical specimens should be fixed in 10% neutral buffered formalin for 24 to 48 hours, starting within one hour of excision, to ensure optimal fixative penetration. Alcohol-based fixatives may cause false-positive results [42]. Additionally, it is important to maintain the paraffin embedding temperature below 60°C. Once formalin-fixed and paraffin-embedded, tumor samples remain stable for several decades, particularly when stored at room temperature not exceeding 27°C [42].

Assessing HER2 expression using the TMA technique relies on sample miniaturization. Although technically complex and requiring specialized training and expertise, the TMA method allows for cost-effective and high-throughput evaluation of large sample sets, enabling uniform analysis of multiple specimens on a single slide [43]. Nevertheless, this technique may lead to false-negative results, which can be mitigated by analyzing whole-tissue sections. Interestingly, Marx et al. reported that HER2 expression and amplification can be heterogeneous in CRC, recommending the evaluation of multiple regions from the same tumor to ensure diagnostic reliability [44]. Fujii et al. found an intratumoral heterogeneity rate of 36.8% among HER2-positive CRC cases [41]. In contrast, other studies have suggested that HER2 expression in CRC tends to be relatively homogeneous [45, 46]. Ingold Heppner et al. observed heterogeneous HER2 expression and amplifica-

tion in only four cases [45]. Similarly, in the HERACLES (HER2 Amplification for Colorectal Cancer Enhanced Stratification) clinical trials, only one case of intratumoral heterogeneity was reported [47].

In our study, using the monoclonal HER2 antibody clone SP3, 0.7% of CRCs overexpressed HER2 based on the GEA criteria proposed by Hofmann et al. [37]. Previously reported HER2 overexpression rates in CRC have varied widely, ranging from 1.3% to 82% [48]. A large-scale multicenter British study, which analyzed 3,256 stage II–IV primary CRC samples using the same scoring system as ours, found HER2 overexpression rates of 2.2% in stage IV tumors and 1.3% in stage II–III tumors [46]. Fonotto et al. reported a global membranous HER2 overexpression rate of 5%, significantly lower than the rate observed in breast cancer [8]. The Cancer Genome Atlas identified *HER2* gene amplification in 7% of CRC cases [49]. However, a 2015 meta-analysis involving 2,573 CRC samples estimated an overall HER2 overexpression rate at 16.2% (range: 3.9% to 54.8%), although not all included studies employed immunohistochemistry [50]. Among studies that performed immunohistochemistry, HER2 overexpression or amplification rates ranged from 2% to 18.3% [50]. These discrepancies in HER2 overexpression rates may be attributed to variations in fixation protocols and conditions, tumor volume analyzed, antibody clones used, scoring systems, positivity thresholds, and selection biases, particularly the heterogeneity of the clinicopathological characteristics of CRC samples [8,47,51].

Two standardized immunohistochemical kits commonly used to assess HER2 overexpression are the HerceptTest™ kit (DAKO), which employs the polyclonal antibody A485, and the PATHWAY™ kit (VENTANA-Roche), which utilizes the monoclonal antibody 4B5 [28]. The HERACLES clinical trial concluded that the 4B5 clone is superior for detecting HER2 overexpression using a 50% cell positivity cutoff. Specifically, the 4B5 clone exhibited fewer false negatives, ensuring greater sensitivity compared to the A485 polyclonal antibody [47]. Nevertheless, several studies have employed non-standardized HER2 antibodies, including the monoclonal antibody SP3 used in our study, applying either GEA diagnostic criteria [45] or HERACLES criteria [52], with reported HER2 overexpression rates ranging from 1.6% to 3.8%. Interestingly, Song et al. compared HER2 expression using the 4B5 and SP3 clones and found that 4B5 exhibited higher sensitivity and stronger staining intensity [52]. Beyond the pre-analytical factors previously described, several key methodological factors can influence results when using non-standardized immunohistochemistry techniques, including antigen retrieval conditions (buffer type, pH, temperature, and duration), antibody clone and concentration, incubation time, and detection method [42]. Such variations contribute to the substantial discrepancies observed in HER2 overexpression rates across different studies.

Multiple scoring systems have been proposed for assessing HER2 expression. Interestingly, Liu et al. compared GEA and HERACLES criteria and concluded that HERACLES system is more suitable for assessing HER2 expression, although both approaches reported similar HER2 amplification (4.1%) and overexpression (3.7%) rates [48]. Furthermore, HER2 overexpression was significantly associated with patient survival and other histoprosthetic factors, including left-sided CRC, advanced

lymph node status, and higher pTNM stage [48]. In a Chinese cohort of 664 CRC cases, Sun et al. applied the diagnostic criteria of HERACLES, GEA-s (for surgical specimens), and GEA-b (for applicable to biopsies). In addition, two other scoring systems, immune-reactive scores (IRS), were considered to evaluate the expression of HER2, including the IRS-plus system (IRS-p), and the IRS-multiply system (IRS-m), obtained by adding and multiplying intensity, staining type, and the percentage of positive cells, respectively [53]. These different scoring systems were applied to two 2-mm biopsy punches taken from the center of the tumor and the invasion margin [53]. The IRS-p score had the best specificity and sensitivity and correlated with histoprognostic factors, suggesting that it is the most suitable scoring system for CRC [53]. However, when using the GEA-b criteria, a HER2 overexpression rate of 2.71% was identified, which is higher than the rate reported in our study [53]. More recently, an international collaborative project developed harmonized diagnostic criteria for HER2-positive CRCs using IHC, FISH, and NGS [41]. Inspired by diagnostic criteria for HER2 expression in gastric and breast cancers, Fujii et al. proposed that a 10% threshold of HER2-positive cells is appropriate for diagnosing HER2-positive CRCs, considering the heterogeneous HER2 expression in CRC surgical specimens [41].

Similar to our findings, some previous studies have reported cytoplasmic HER2 expression [54-56]. Although guidelines for determining HER2 overexpression primarily focus on membranous staining, cytoplasmic staining was more frequently observed in CRCs, with reported frequencies ranging from 5% to 63% [8, 57]. Interestingly, Wang et al. reported membranous expression rates between 2.1% and 11%, while cytoplasmic overexpression ranged from 58% to 68.5% [58]. Nevertheless, most previous studies have found no significant correlation with key histoprognostic factors or survival, although some noted correlations with age, tumor size, lymph node status, and the non-mucinous histological type [54, 57, 59]. Furthermore, no significant association was found with *HER2* gene amplification [59]. The presence of cytoplasmic HER2 expression may be attributed to receptor internalization, dimerization, cytoplasmic phosphorylation, intense transcription, or the existence of a truncated HER2 protein [59].

In our study, both the pre-treatment biopsy and the surgical specimen of the CRC case showed the same HER2 status (score of 3+). However, Conradi et al. reported that among rectal cancer cases classified as HER2-negative on biopsy, 21% showed HER2 overexpression in surgical specimens, while 5% of cases that were HER2-positive on biopsy became negative in surgical samples, likely due to the effects of neoadjuvant therapies [40].

The patient exhibiting HER2 overexpression experienced multiple metastatic recurrences involving the lung, liver, bones, and peritoneum. Similarly, a meta-analysis by Pyo et al. demonstrated that HER2 overexpression is significantly associated with lymph node metastases and distant metastases [50]. Furthermore, a recent review highlighted a significant correlation between HER2 overexpression and the number of metastatic sites, with a particularly higher frequency of pulmonary metastases [51].

The prognostic value of HER2 overexpression in mCRCs remains controversial, as studies are limited by

the low prevalence of HER2 overexpression [58, 60]. Earlier studies failed to establish HER2 overexpression as an independent prognostic factor [58]. However, more recently, a significant association has been reported with early recurrences and shorter overall survival [58]. Similarly, Sawada et al. reported a poorer prognosis for HER2-positive mCRCs in terms of overall survival in patients with both mutated and wild-type *KRAS/BRAF* status [61].

Some limitations were present in our study. Firstly, we utilized a non-standardized HER2 antibody, the monoclonal antibody SP3. Additionally, the inclusion of samples from post-therapeutic resections may pose a limitation, particularly since the effect of neoadjuvant therapy on HER2 expression in CRCs is poorly documented in existing literature. However, excluding these specimens would have resulted in omitting many distal CRC cases, which are often associated with HER2 overexpression. Moreover, our sample size was too small to extrapolate our findings to the broader Tunisian population, highlighting the need for a multicenter study to further explore our results. Finally, we did not assess intratumoral heterogeneity in our study. Increasing the number of punch biopsies and/or verifying results with whole-section analyses could help strengthen our conclusions.

We observed lower HER2 overexpression and amplification rates in CRC compared to previous reports, highlighting the rarity of this molecular alteration in colorectal oncogenesis. Further multicenter studies in Tunisia are needed to confirm these findings. Additionally, inconsistencies in HER2 immunostaining criteria may cause diagnostic uncertainty; thus, establishing a standardized scoring system is crucial to guide future studies.

Author contributions

KL and NM worked on the study conception and data acquisition, analysis, and interpretation. WM, AB, MK, ZL, OB, MA and SM contributed to the study conception and data acquisition. SH secured the resources. NM supervised the study and contributed to the manuscript drafting. All authors have read and agreed to the published version of the manuscript.

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Ethical approval

Approval for the use of archival material for research purposes was obtained from the local Human Ethics Committee at Sahloul University Hospital, Sousse, Tunisia, and the study was conducted in accordance with the Declaration of Helsinki.

Informed consent

Not applicable.

Data availability

The supplementary data will be available to the readers when they send the request.

Conflict of interest

The authors declare no conflict of interest.

Abbreviations

AJCC: American Joint Committee on Cancer; CISH: chro-

mogenic *in situ* hybridization; CRC: colorectal carcinoma; EGFR: epidermal growth factor receptor; GEA: gastroesophageal adenocarcinomas; GEA-b: GEA relevant to biopsies; mCRC: metastatic CRC; TMA: tissue microarrays; WHO: World Health Organization.

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