



Medizinische Universität Graz

Gastric Cancer

Minisymposium: Patológia Gastrointestinálneho Traktu

SD-IAP, Košice, Slovakia, 6-7 June 2019



Cord Langner MD
Diagnostic & Research Centre for Molecular
BioMedicine
Institute of Pathology
Medical University of Graz, Austria



Agenda

- **Classification of gastric cancer**
 - Histology
 - Molecular pathology
- **Predictive pathology**
 - HER2
 - PD-L1
 - Microsatellite instability
- **Sporadic vs hereditary gastric cancer**
- **Take home messages**

Agenda



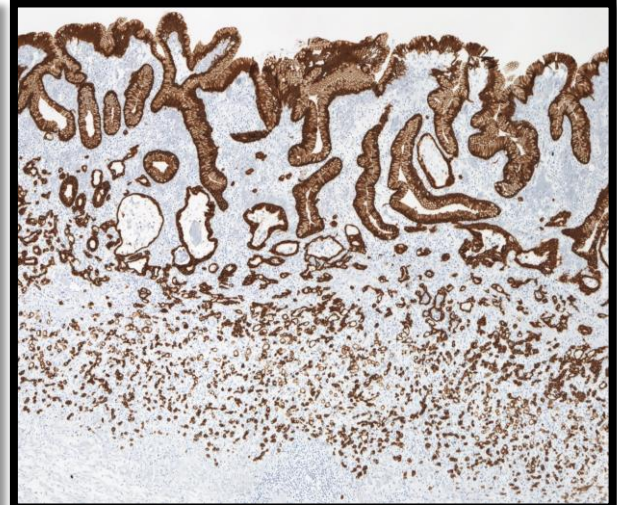
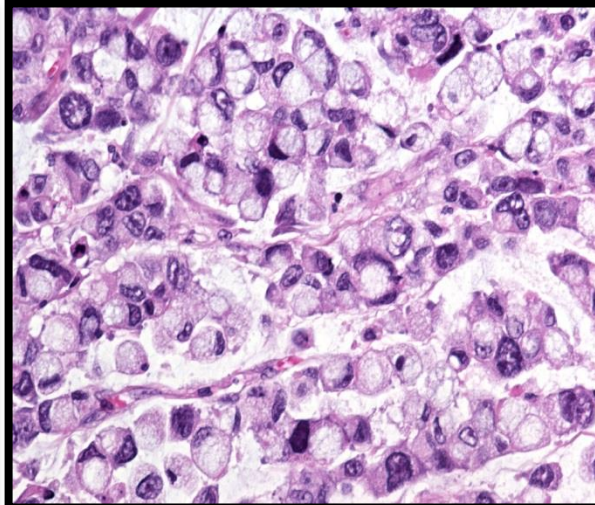
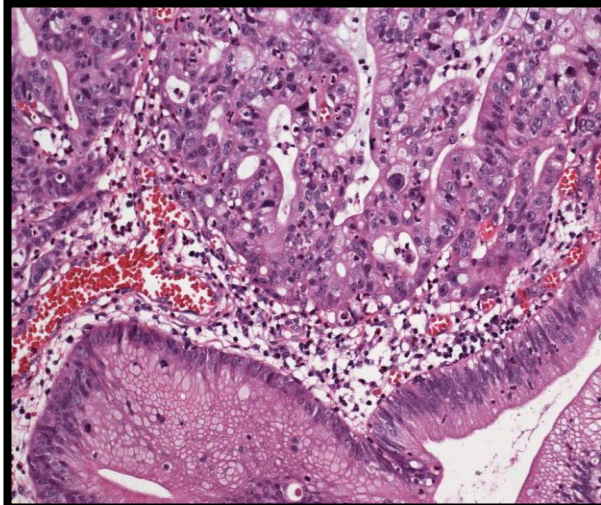
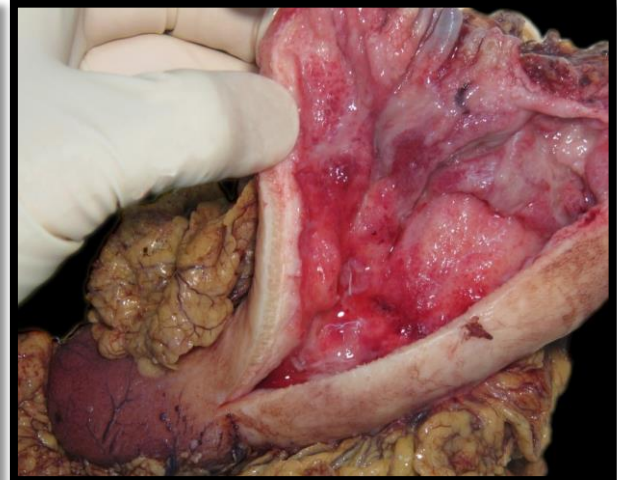
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 - Molecular pathology
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- Take home messages

Lauren Classification



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Lauren classification and individualized chemotherapy in gastric cancer (Review)

JUNLI MA^{1,2}, HONG SHEN^{2,3}, LINDA KAPESA¹ and SHAN ZENG^{1,2}



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	Intestinal Type GC	Diffuse Type GC
Macroscopy	Well circumscribed, antrum > corpus	Poorly circumscribed, corpus > antrum
Histology	Glandular (or solid), cell adhesion, often in association with intestinal metaplasia	Non-cohesive tumour cell growth, lack of cell adhesion, signet-ring cell carcinomas
Clinical characteristics	Elderly patients, male > female, more prevalent in high-risk areas	Younger patients, female > male, more prevalent in low-risk areas
Aetiology	Helicobacter pylori (Correa's cascade)	Chronic inflammation, HDGC
Metastasis	Liver > peritoneum	Peritoneum > liver
Biomarkers	CDX-2 (MUC2), MSI, HER2	CDH1 (loss of E-cadherin), MSS

WHO Classification

Epithelial tumours

Intraepithelial neoplasia – Adenoma	8140/0 ²
Carcinoma	
Adenocarcinoma	8140/3
intestinal type	8144/3
diffuse type	8145/3
Papillary adenocarcinoma	8260/3
Tubular adenocarcinoma	8211/3
Mucinous adenocarcinoma	8480/3
Signet-ring cell carcinoma	8490/3
Adenosquamous carcinoma	8560/3
Squamous cell carcinoma	8070/3
Small cell carcinoma	8041/3
Undifferentiated carcinoma	8020/3
Others	
Carcinoid (well differentiated endocrine neoplasm)	8240/3

Non-epithelial tumours

Leiomyoma	8890/0
Schwannoma	9560/0
Granular cell tumour	9580/0
Glomus tumour	8711/0
Leiomyosarcoma	8890/3
GI stromal tumour	8936/1
benign	8936/0
uncertain malignant potential	8936/1
malignant	8936/3
Kaposi sarcoma	9140/3
Others	
Malignant lymphomas	
Marginal zone B-cell lymphoma of MALT-type	9699/3
Mantle cell lymphoma	9673/3
Diffuse large B-cell lymphoma	9680/3
Others	

Secondary tumours

¹ The classification is modified from the previous WHO histological classification of tumours {2066} taking into account changes in our understanding of these lesions. In the case of endocrine neoplasms, the classification is based on the recent WHO clinicopathological classification {1784}, but has been simplified to be of more practical utility in morphological classification.

² Morphology code of the International Classification of Diseases for Oncology (ICD-O) {542} and the Systematized Nomenclature of Medicine (<http://snomed.org>). Behaviour is coded /0 for benign tumours, /3 for malignant tumours, and /1 for unspecified, borderline or uncertain behaviour. Intraepithelial neoplasia does not have a generic code in ICD-O. ICD-O codes are available only for lesions categorized as glandular intraepithelial neoplasia grade III (8148/2), and adenocarcinoma in situ (8140/2).

WHO Classification

Epithelial tumours

Premalignant lesions

Adenoma	8140/0
Intraepithelial neoplasia (dysplasia), low grade	8148/0*
Intraepithelial neoplasia (dysplasia), high grade	8148/2*

Carcinoma

Adenocarcinoma	8140/3
Papillary adenocarcinoma	8260/3
Tubular adenocarcinoma	8211/3
Mucinous adenocarcinoma	8480/3
Poorly cohesive carcinoma (including signet ring cell carcinoma and other variants)	8490/3*
Mixed adenocarcinoma	8255/3
Adenosquamous carcinoma	8560/3
Carcinoma with lymphoid stroma (medullary carcinoma)	8512/3
Hepatoid adenocarcinoma	8576/3
Squamous cell carcinoma	8070/3
Undifferentiated carcinoma	8020/3

Neuroendocrine neoplasms^b

Neuroendocrine tumour (NET)	
NET G1 (carcinoid)	8240/3
NET G2	8249/3

Neuroendocrine carcinoma (NEC)	8246/3
Large cell NEC	8013/3
Small cell NEC	8041/3
Mixed adenoneuroendocrine carcinoma	8244/3
EC cell, serotonin-producing NET	8241/3
Gastrin-producing NET (gastrinoma)	8153/3

Mesenchymal tumours

Glomus tumour	8711/0
Granular cell tumour	9580/0
Leiomyoma	8890/0
Plexiform fibromyxoma	8811/0*
Schwannoma	9560/0
Inflammatory myofibroblastic tumour	8825/1
Gastrointestinal stromal tumour	8936/3
Kaposi sarcoma	9140/3
Leiomyosarcoma	8890/3
Synovial sarcoma	9040/3

Lymphomas

Secondary tumours

**WHO Classification of Tumours of the Digestive System, 4th edition
(Bosmann FT, Carneiro F, Hruban RH, Theise ND) IARC Press 2010**



WHO Classification

- **Poorly cohesive carcinomas** are composed of neoplastic cells that are isolated or arranged in small aggregates. These encompass:
 - **Signet-ring cell type** is defined as a tumour composed predominantly or exclusively of signet-ring cells, characterized by a central optically clear, globoid droplet of cytoplasmic mucin with an eccentrically placed nucleus
 - **Other cellular variants** of poorly cohesive carcinoma include tumours composed of neoplastic cells resembling histiocytes or lymphocytes; others have deeply eosinophilic cytoplasm; some poorly cohesive cells may show irregular bizarre nuclei
- **Mixed carcinomas** display a mixture of discrete morphologically identifiable glandular /tubular/papillary) and signet-ring/poorly cohesive cellular histological components (any component should be reported)

**WHO Classification of Tumours of the Digestive System, 4th edition
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Gastric poorly cohesive carcinoma: a correlative study of mutational signatures and prognostic significance based on histopathological subtypes

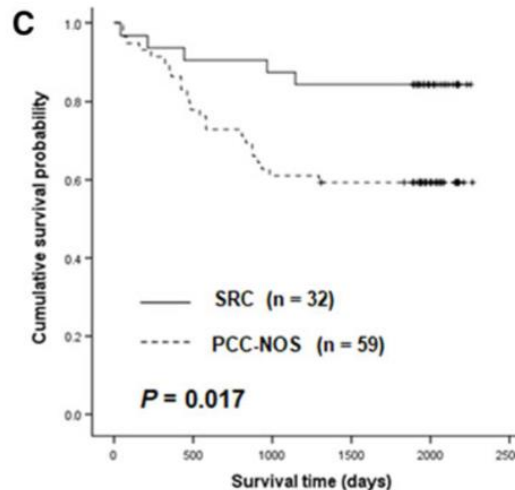
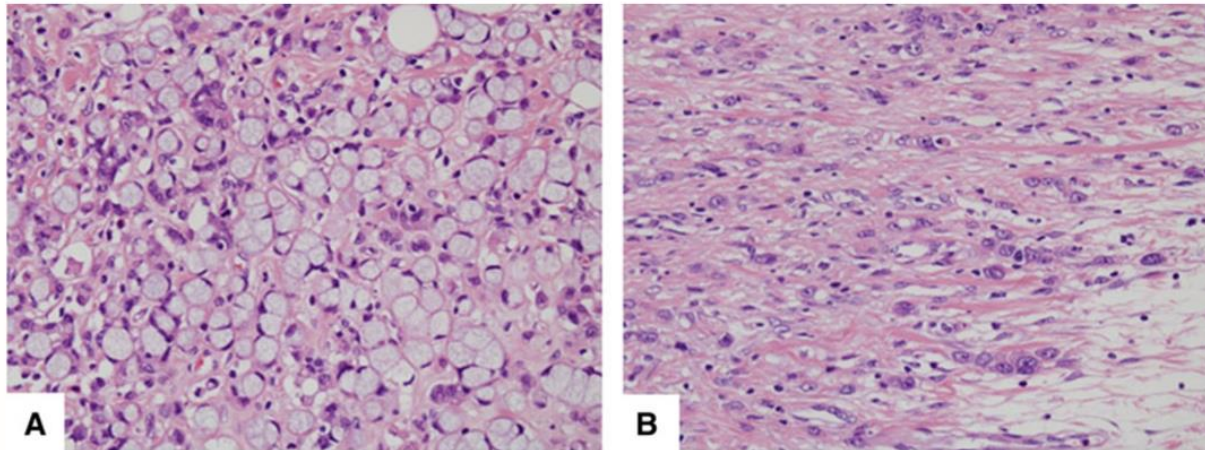


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Gastric poorly cohesive carcinoma: a correlative study of mutational signatures and prognostic significance based on histopathological subtypes



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Table 3. Relationship of five gene mutations and morphological features of 91 gastric poorly cohesive carcinomas

		Gastric poorly cohesive carcinoma, <i>n</i> (%)				
		SRC-predominant		PCC-NOS-predominant		
Genes	<i>n</i>	Pure SRC	Mixed SRC	Pure PCC-NOS	Mixed PCC-NOS	<i>P</i> -value*
<i>RHOA</i>						
Wild type	76	29 (38.2)	3 (3.9)	23 (30.3)	21 (27.6)	0.002
Mutant	15	0 (0.0)	0 (0.0)	1 (6.7)	14 (93.3)	
<i>BRAF</i>						
Wild type	75	27 (36.0)	3 (4.0)	21 (28.0)	24 (32.0)	0.036
Mutant	16	2 (12.5)	0 (0.0)	3 (18.3)	11 (68.8)	
<i>PI3CA</i>						
Wild type	71	27 (38.0)	2 (2.8)	19 (26.8)	23 (32.4)	0.033
Mutant	20	2 (10.0)	1 (5.0)	5 (25.0)	12 (60.0)	
<i>SMAD4</i>						
Wild type	79	28 (35.4)	3 (3.8)	21 (26.6)	27 (34.2)	0.050
Mutant	12	1 (8.3)	0 (0.0)	3 (25.0)	8 (66.7)	
<i>TP53</i>						
Wild type	54	21 (38.9)	3 (5.6)	15 (27.8)	15 (27.8)	0.025
Mutant	37	8 (21.6)	0 (0.0)	9 (24.3)	20 (54.1)	

PCC-NOS, Poorly cohesive carcinoma (not otherwise specified); SRC, Signet ring cell.



Consensus on the pathological definition and classification of poorly cohesive gastric carcinoma

C. Mariette¹ · F. Carneiro² · H. I. Grabsch^{3,4} · R. S. van der Post⁵ · W. Allum⁶ · Giovanni de Manzoni⁷ on behalf of European Chapter of International Gastric Cancer Association

Table 2 Comparison of different classifications of gastric cancer (Laurén, Nakamura, WHO and Japanese classifications)

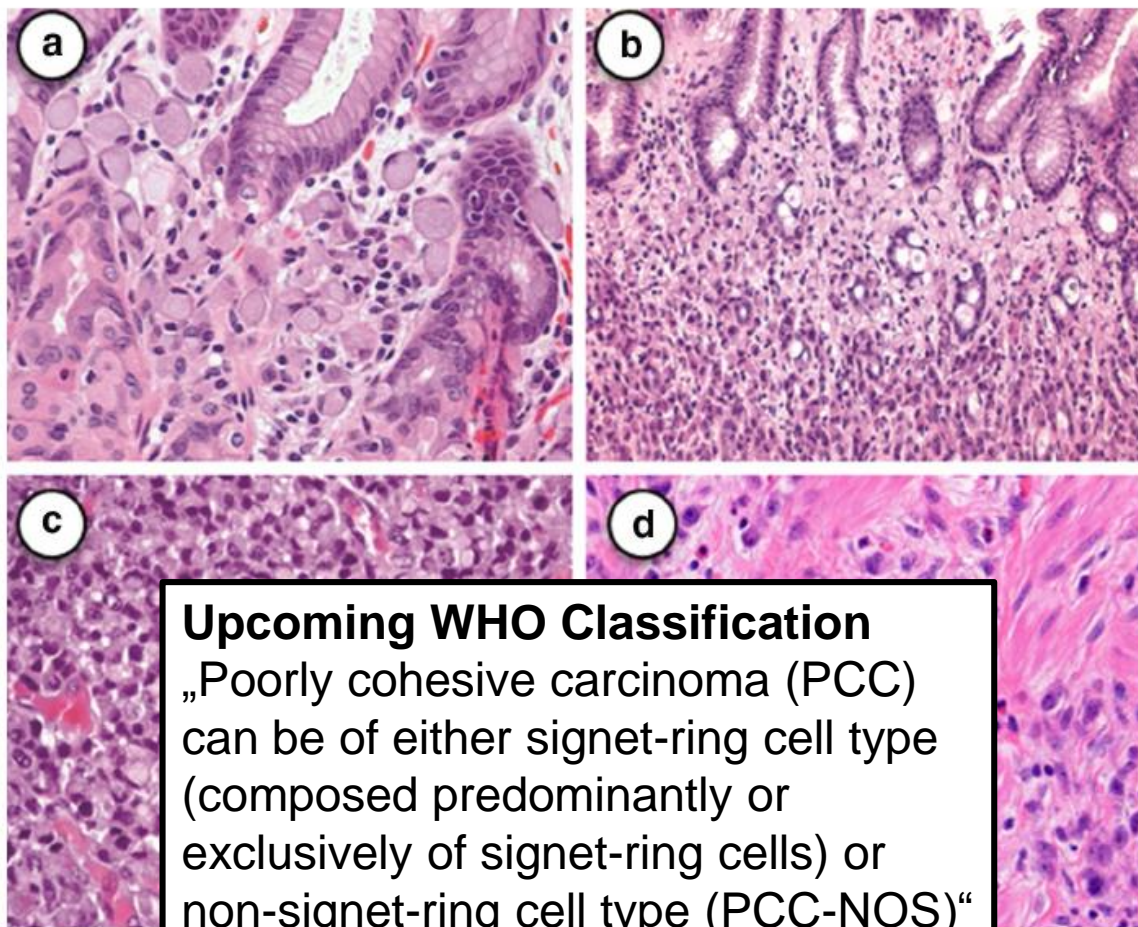
Laurén (1965)	Nakamura (1968)	WHO (2010)	Japanese classification (2017)
Intestinal	Differentiated	Common type: Papillary Tubular	Common type Papillary: pap Tubular 1 (well-differentiated): tub1 Tubular 2 (moderately differentiated):
Intestinal/diffuse	Differentiated undifferentiated	<p>To standardize the definition of SRC cancers, we propose that only WHO PC carcinomas with more than 90% poorly cohesive cells having classical signet ring cell morphology should be classified as SRC carcinomas.</p> <p>We propose to use the following subclassification of PC and SRC carcinomas (Fig. 3):</p> <ul style="list-style-type: none">– Signet ring cell (SRC) type (> 90% of signet ring cells)– Combined poorly cohesive NOS and SRC carcinoma (PC-NOS/SRC; <90% but > 10% of signet ring cells)– Poorly cohesive NOS (PC-NOS; <10% of signet ring cells)	ous
Diffuse	Undifferentiated		arcinoma: sig 2 (non-solid type): por2
Mixed	Undifferentiated		ption according to the propor-
Indeterminate	Undifferentiated		or2 > sig > tub2) 1 (solid type): por1 erentiated carcinoma



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Fig. 3 Poorly cohesive gastric carcinoma, examples of morphology. **a** Signet ring cell carcinoma (SRCC) (> 90% of signet ring cells): classical signet ring cells are seen at the superficial layer of gastric mucosa; **b** combined PCC-NOS and SRCC (PCC-NOS/ SRC) (< 90% but > 10% of signet ring cells): this case has two components, the superficial part is composed of classical signet ring cells and the deeper part is composed by poorly cohesive, non-signet ring cells; **c** combined PCC-NOS and SRCC (PCC-NOS/ SRC) (< 90% but > 10% of signet ring cells): in this case, the two cell types (signet ring and poorly cohesive cells) are intermingled; **d** poorly cohesive carcinoma NOS (PCC-NOS) (< 10% of signet ring cells): the poorly cohesive, non-signet ring cells, are invading the muscle layer (H&E, original magnifications ×200–400)



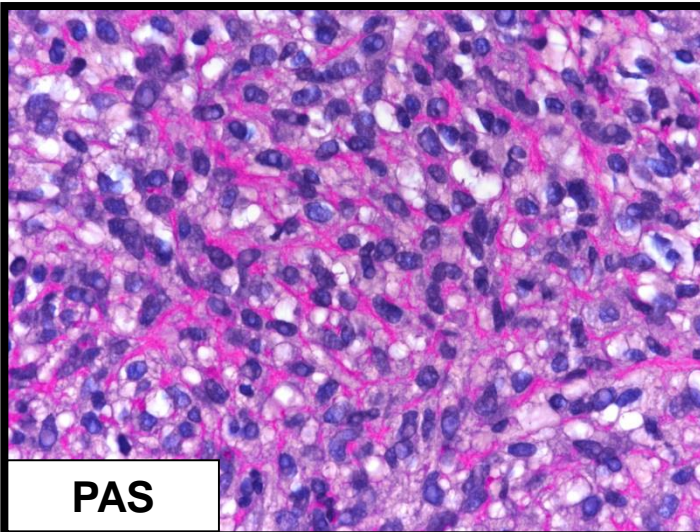
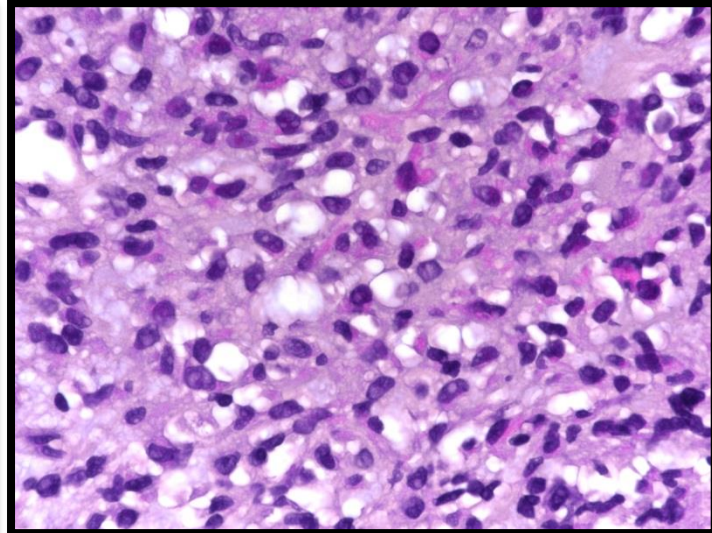
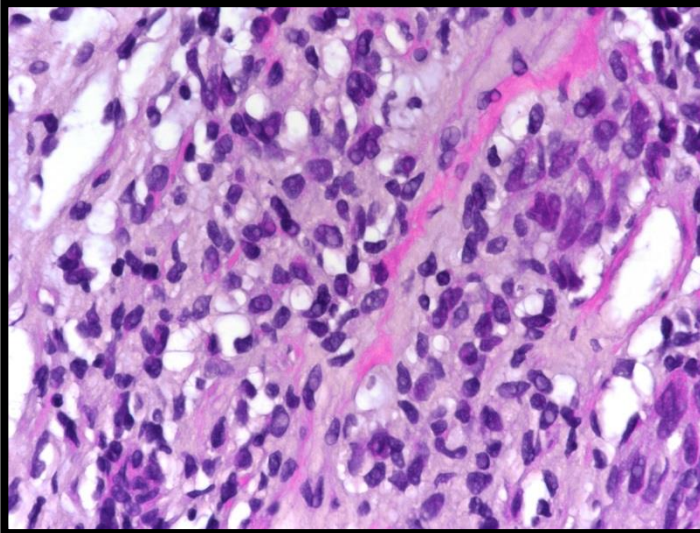
Upcoming WHO Classification

„Poorly cohesive carcinoma (PCC) can be of either signet-ring cell type (composed predominantly or exclusively of signet-ring cells) or non-signet-ring cell type (PCC-NOS)“



A potential pitfall...

Gastric ulceration suspicious for malignancy

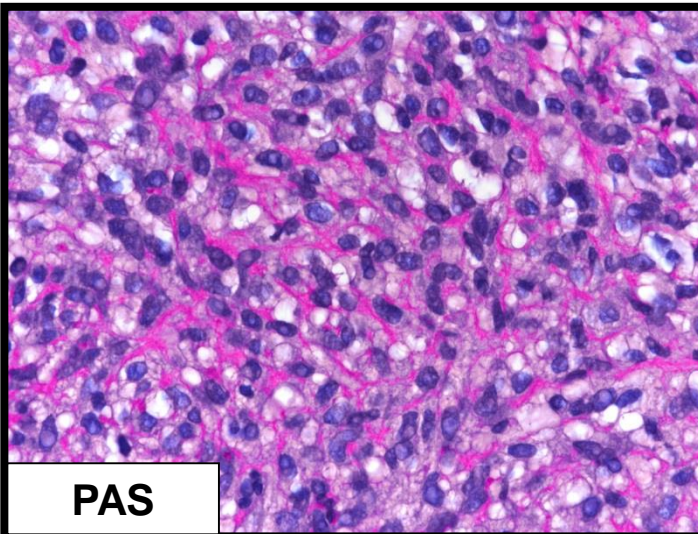
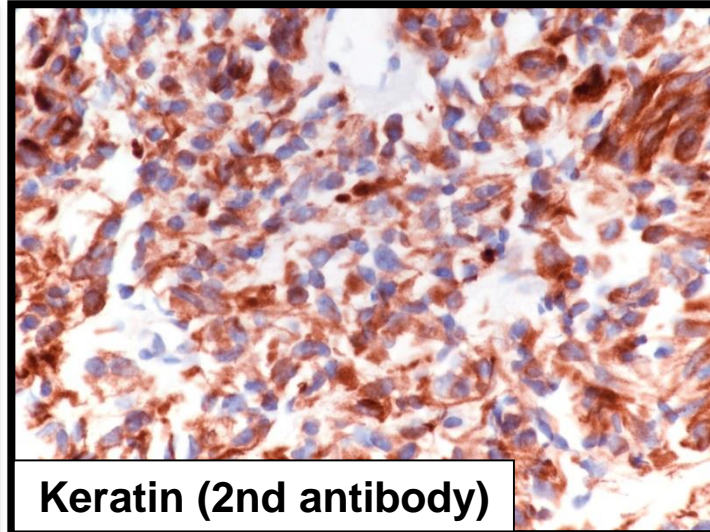
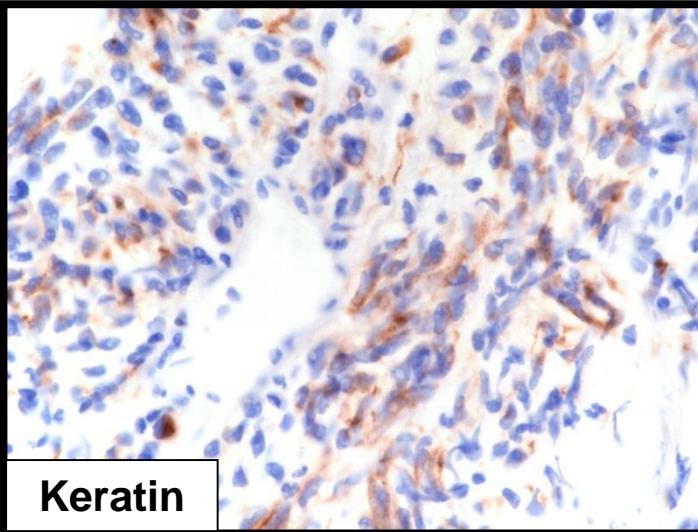


PAS

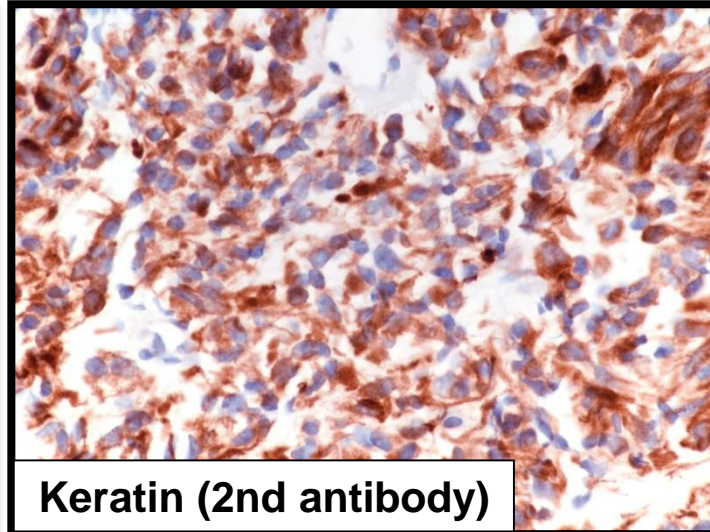
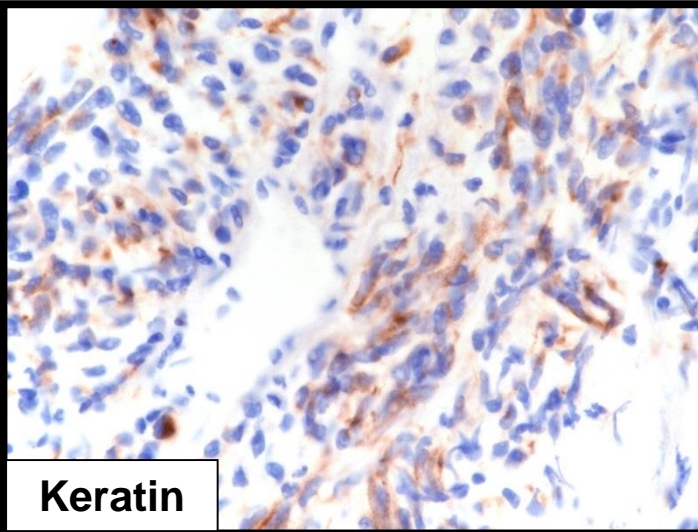
Poorly cohesive
adenocarcinoma?

Better do keratin
staining!

Gastric ulceration suspicious for malignancy



Gastric ulceration suspicious for malignancy

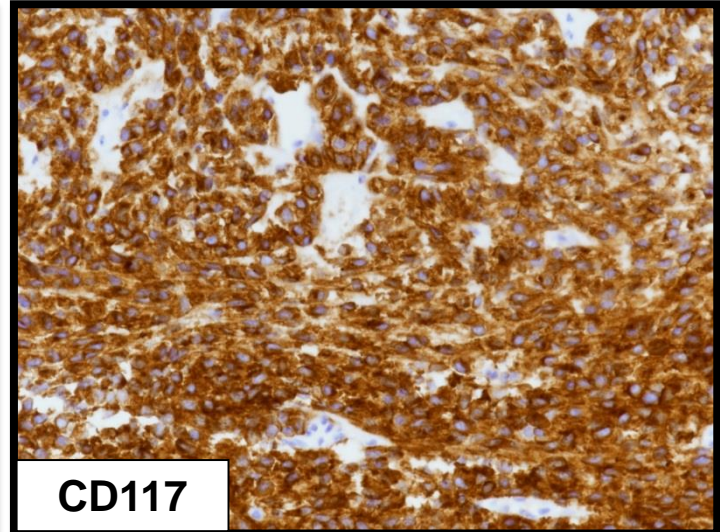
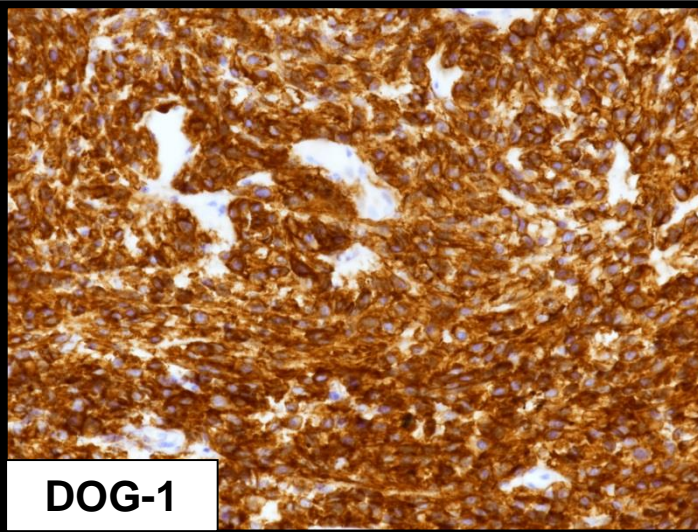


**Poorly cohesive
adenocarcinoma?
Better do additional
staining!**

Gastric ulceration suspicious for malignancy



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Final diagnosis:
epitheloid (keratin
positive) GIST
PDGFRalpha
mutation positive



Towards a molecular classification of gastric cancer...



Genetics and Molecular Pathogenesis of Gastric Adenocarcinoma

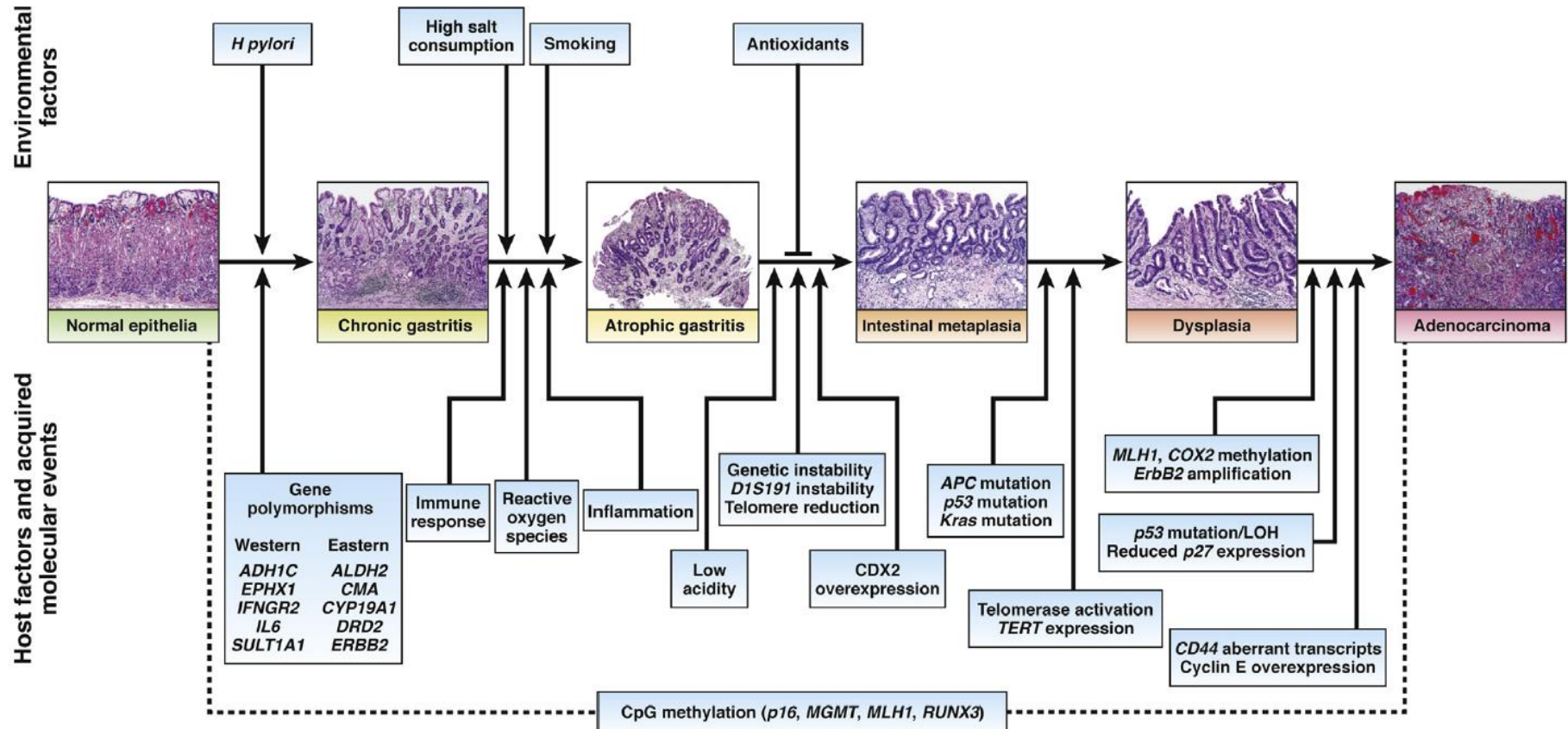
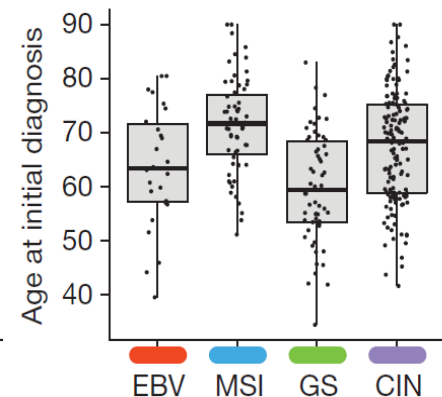
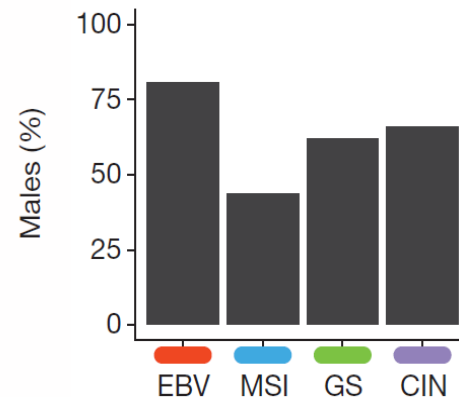
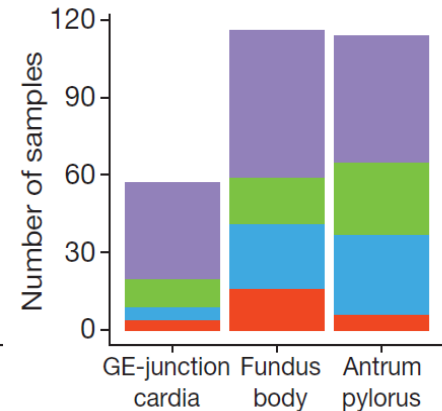
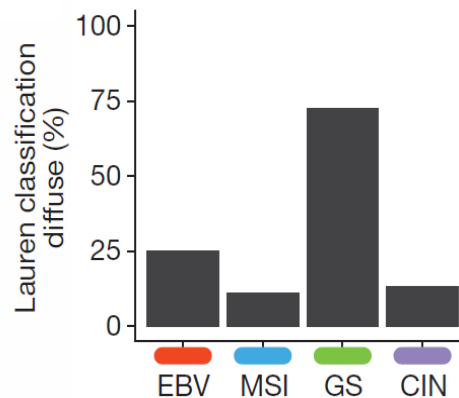
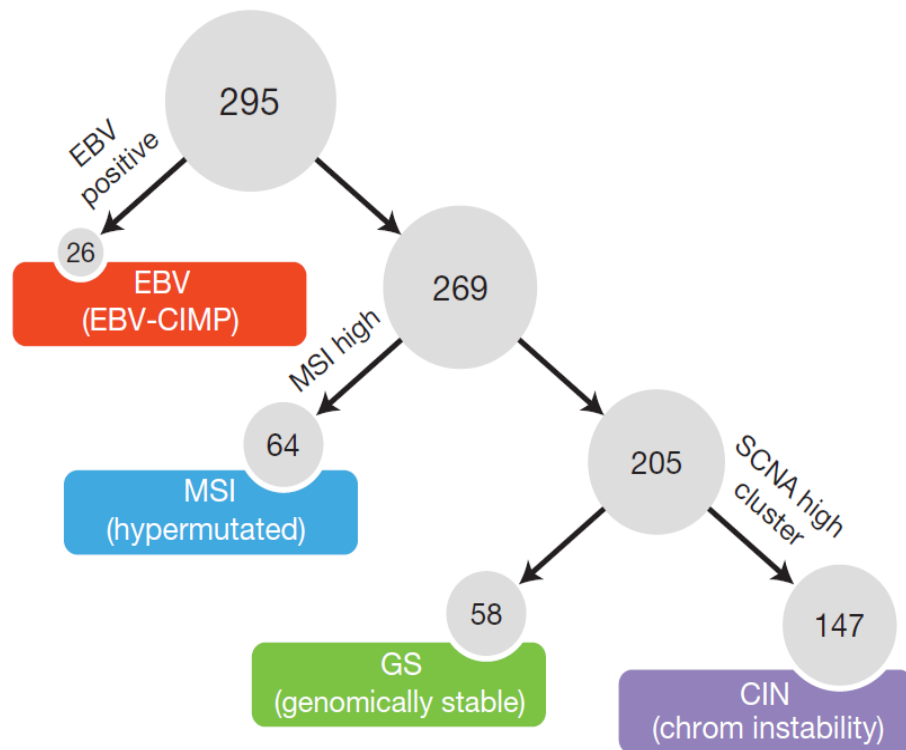
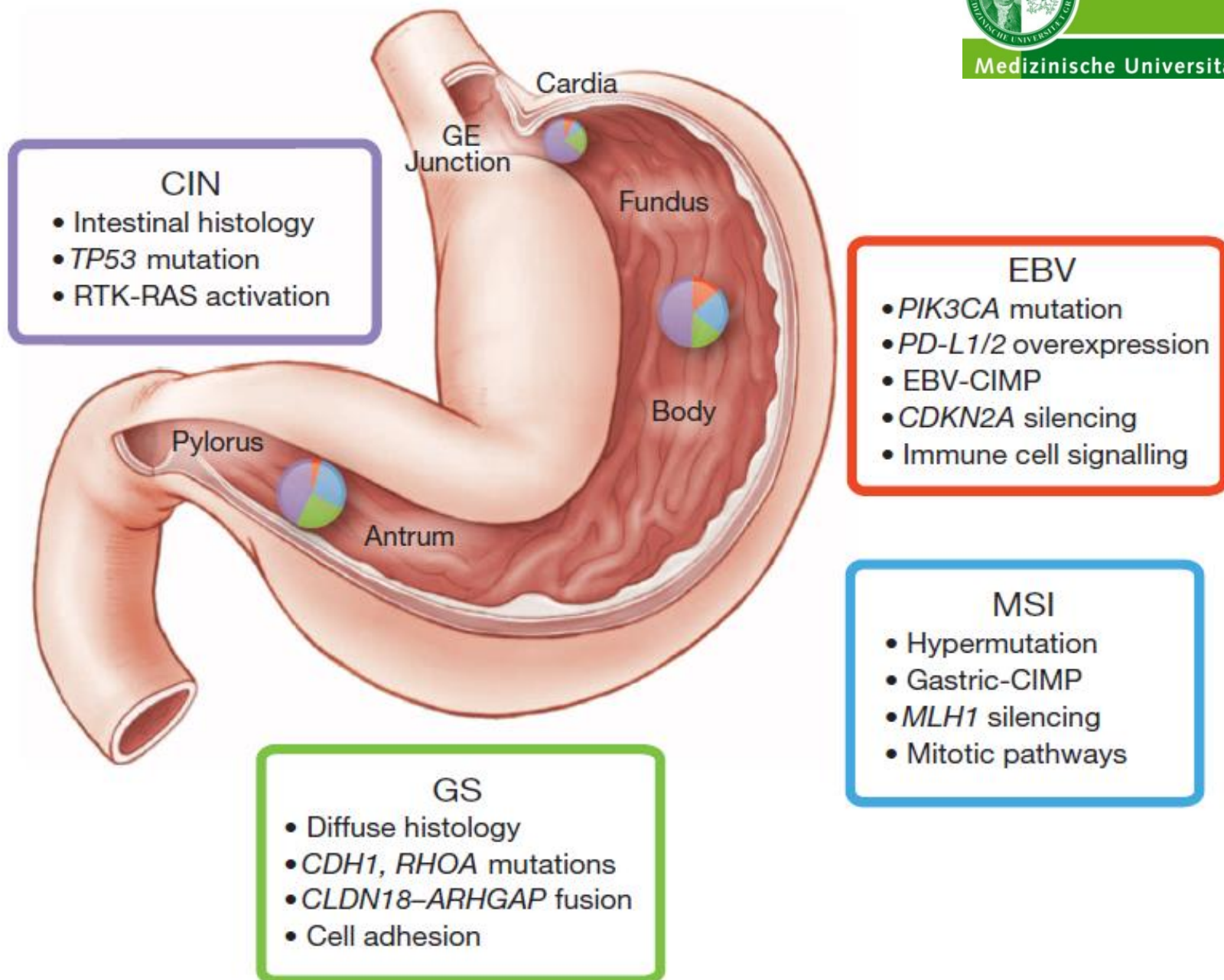


Figure 1. Cause and pathogenesis of intestinal-type GC. A summary of current knowledge of the cause and pathogenesis of intestinal type GC is shown, including host and environmental factors as well as acquired molecular events.^{52,143–145} GC, gastric cancer.

Comprehensive molecular characterization of gastric adenocarcinoma

The Cancer Genome Atlas Research Network*





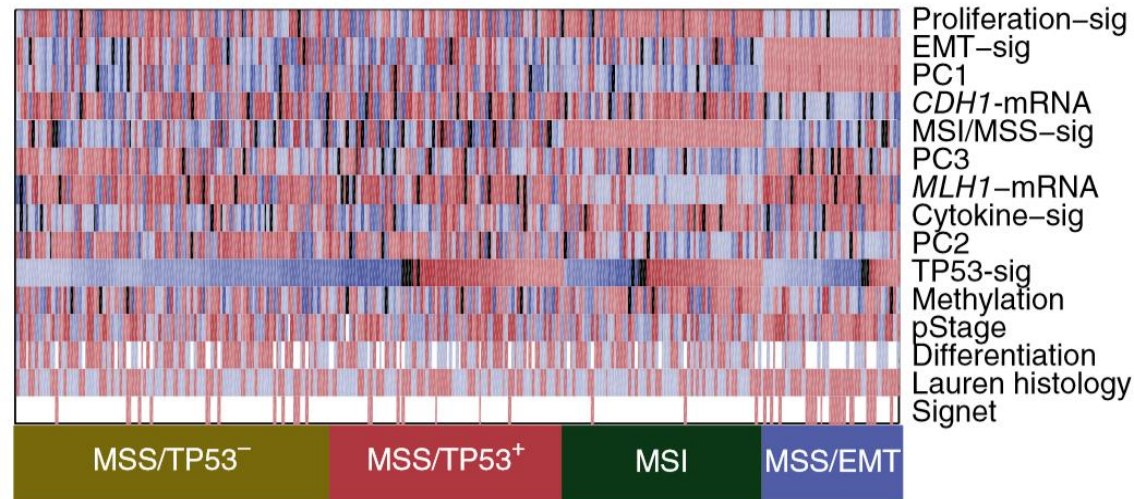
Molecular analysis of gastric cancer identifies subtypes associated with distinct clinical outcomes



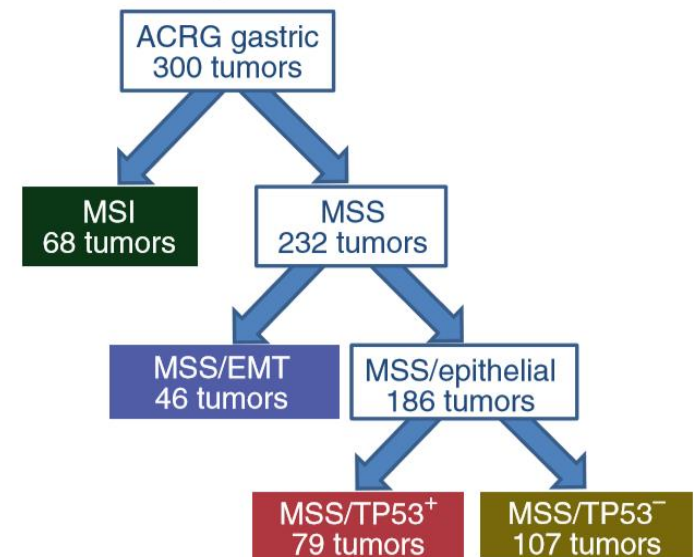
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ACRG gastric tumors



ACRG gastric tumors



ACRG: Asian Cancer Research Group

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Table 1 The four molecular subtypes and patient characteristics.

Characteristics	MSS/TP53 ⁻	MSS/TP53 ⁺	MSI	MSS/EMT	<i>P</i> value
<i>N</i>	107 (35.7%)	79 (26.3%)	68 (22.7%)	46 (15.3%)	
Median age	65 (30–82)	64 (24–81)	66 (31–84)	53 (28–86)	0.0324 ^a
Sex					
Male	70 (65.4%)	57 (72.2%)	45 (66.2%)	27 (58.7%)	0.4863
Female	37 (34.6%)	22 (27.8%)	23 (33.8%)	19 (41.3%)	
Location of tumor					
Antrum	61 (57.0%)	26 (32.9%)	51 (75.0%)	17 (37.0%)	<0.0001
Body	37 (34.6%)	36 (45.6%)	13 (19.1%)	21 (45.6%)	
Cardia, GE junction	9 (8.4%)	14 (17.7%)	4 (5.9%)	5 (10.9%)	
Whole, multicentric	0 (0.0%)	3 (3.8%)	0 (0.0%)	3 (6.5%)	
Grade and WHO classification					
W/D and M/D tubular	54 (50.5%)	32 (40.5%)	33 (48.5%)	4 (8.7%)	< 0.0001
P/D tubular	37 (34.6%)	31 (39.2%)	29 (42.7%)	19 (41.3%)	
Signet ring cell	9 (8.4%)	5 (6.3%)	3 (4.4%)	20 (43.5%)	
Mucinous	4 (3.7%)	3 (3.8%)	0 (0.0%)	1 (2.2%)	
Others	3 (2.8%)	8 (10.1%)	3 (4.4%)	2 (4.3%)	

Molecular analysis of gastric cancer identifies subtypes associated with distinct clinical outcomes



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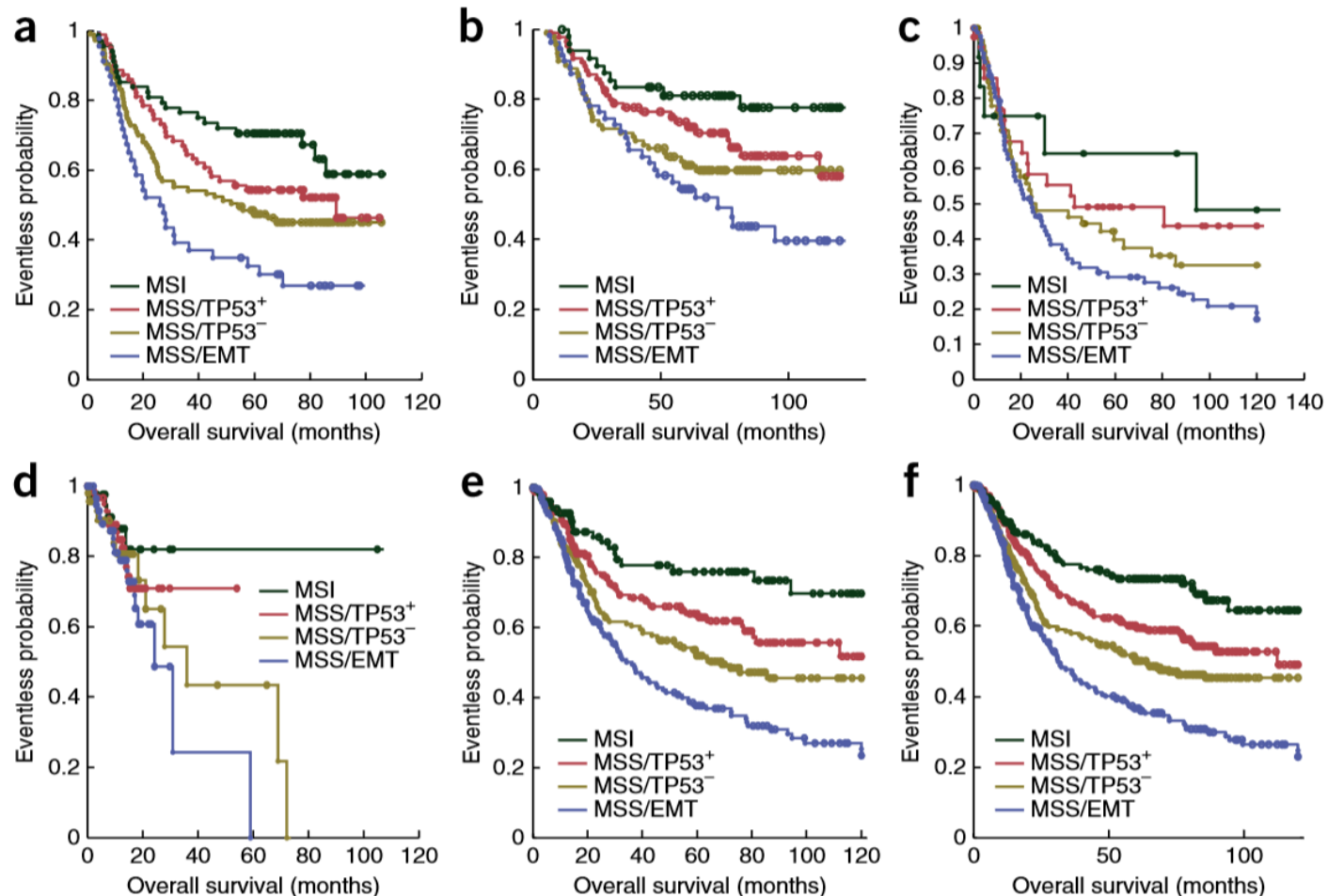
Characteristics	MSS/TP53 ⁻	MSS/TP53 ⁺	MSI	MSS/EMT	<i>P</i> value
Lauren type					
Intestinal	58 (54.2%)	38 (48.1%)	42 (61.8%)	8 (17.4%)	<0.0001
Diffuse	42 (39.3%)	36 (45.6%)	20 (29.4%)	37 (80.4%)	
Mixed	7 (6.5%)	4 (5.1%)	5 (7.4%)	1 (2.2%)	
Missing	0 (0.0%)	1 (1.2%)	1 (1.0%)	0 (0.0%)	
pT stage					
T2	70 (65.4%)	57 (72.1%)	47 (69.1%)	14 (30.4%)	0.0003
T3	29 (27.1%)	18 (22.8%)	17 (25.0%)	27 (58.7%)	
T4	8 (7.5%)	4 (5.1%)	4 (5.9%)	5 (10.9%)	
pN Stage					
N0	12 (11.2%)	4 (5.1%)	16 (23.5%)	6 (13.0%)	0.0058
N1	41 (38.3%)	45 (57.0%)	31 (45.6%)	14 (30.4%)	
N2	31 (29.0%)	19 (24.0%)	15 (22.1%)	15 (32.6%)	
N3	23 (21.5%)	11 (13.9%)	6 (8.8%)	11 (23.9%)	
EBV					
Positive	2 (1.9%)	12 (15.2%)	0 (0.0%)	4 (8.7%)	0.0002
Negative	94 (87.9%)	60 (75.9%)	63 (92.6%)	40 (87.0%)	
Missing	11 (10.2%)	7 (8.9%)	5 (7.4%)	2(4.3%)	

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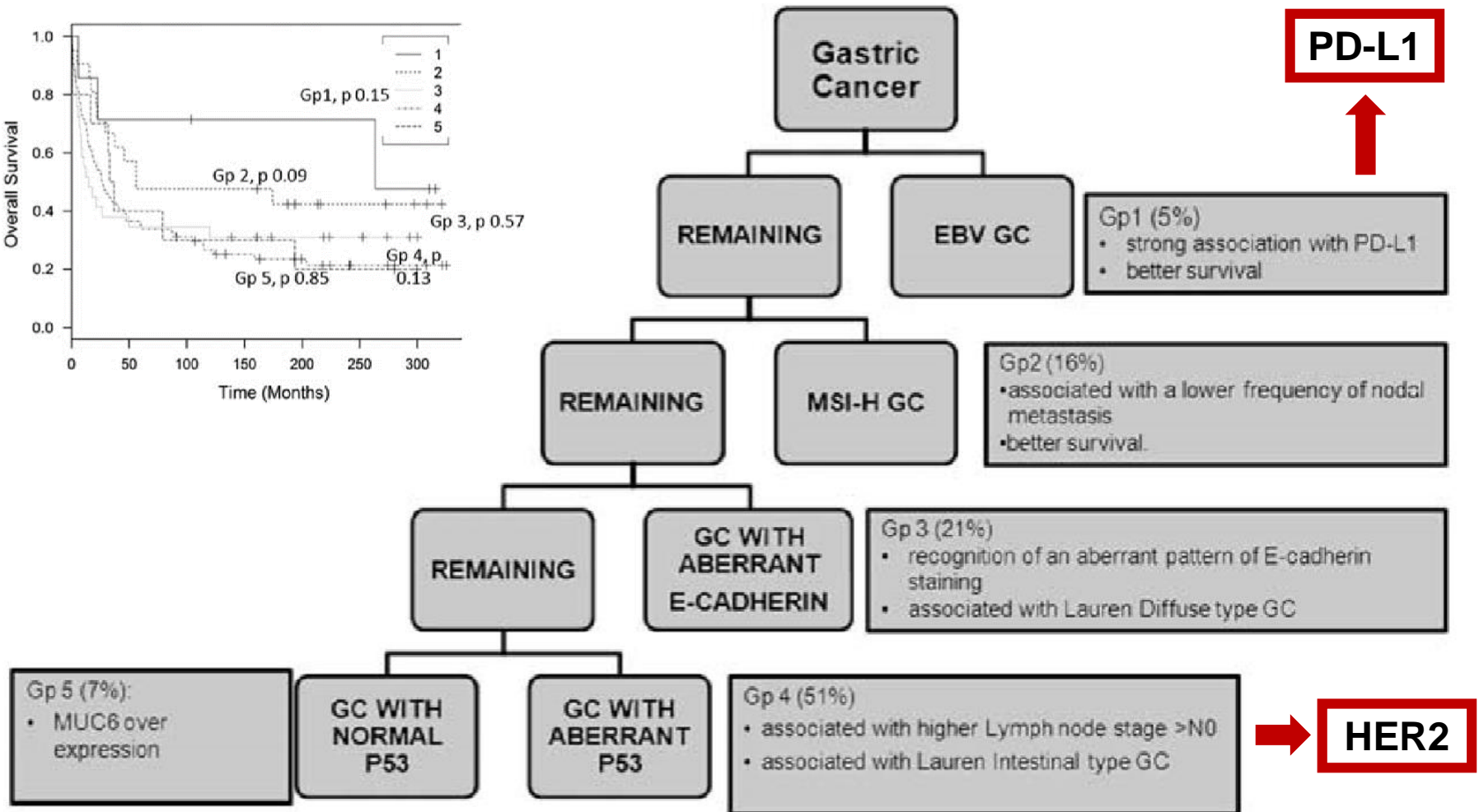
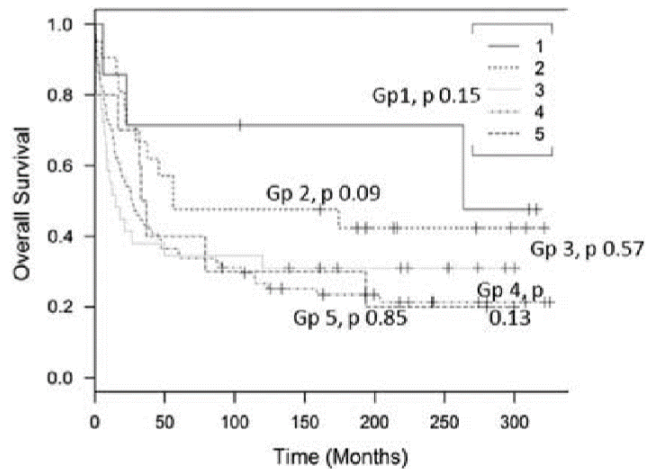


A protein and mRNA expression-based classification of gastric cancer

Namrata Setia¹, Agoston T Agoston², Hye S Han^{1,3}, John T Mullen⁴, Dan G Duda⁵, Jeffrey W Clark⁶, Vikram Deshpande¹, Mari Mino-Kenudson¹, Amitabh Srivastava², Jochen K Lennerz¹, Theodore S Hong⁵, Eunice L Kwak^{6,*} and Gregory Y Lauwers^{1,*}



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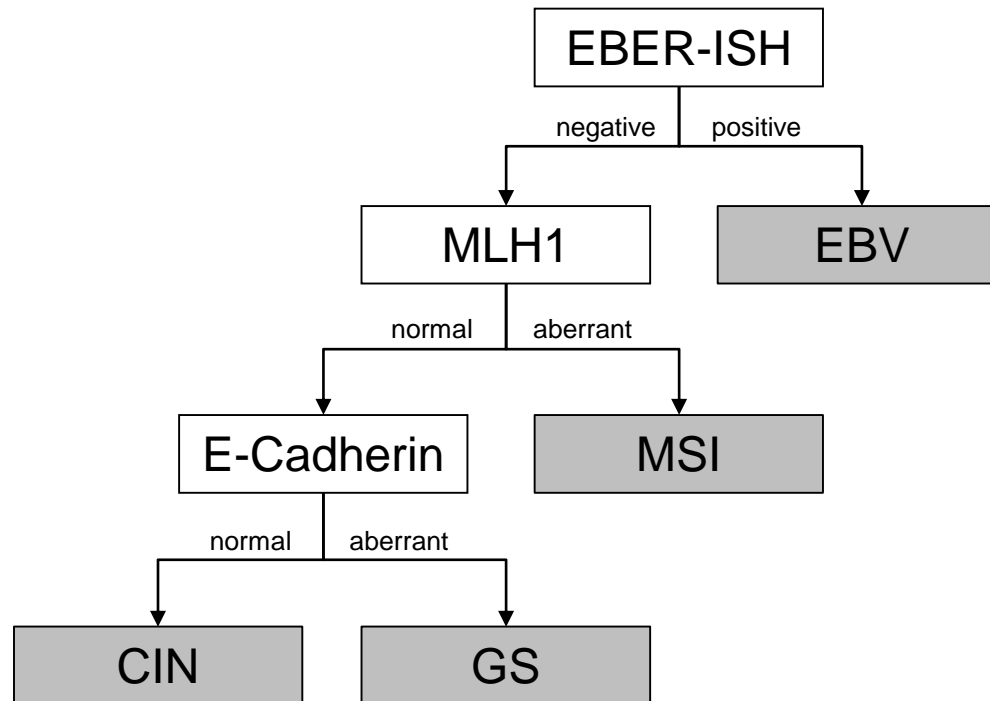


High-throughput Protein and mRNA Expression-based Classification of Gastric Cancers Can Identify Clinically Distinct Subtypes, Concordant With Recent Molecular Classifications



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Sangjeong Ahn, MD, PhD,† So-Jeong Lee, MD,* Yonugkeum Kim, MD,* Ahrong Kim, MD,*
Nari Shin, MD,‡ Kyung Un Choi, MD, PhD,* Chang-Hun Lee, MD, PhD,*
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Gregory Y. Lauwers, MD,# and Do Youn Park, MD, PhD**

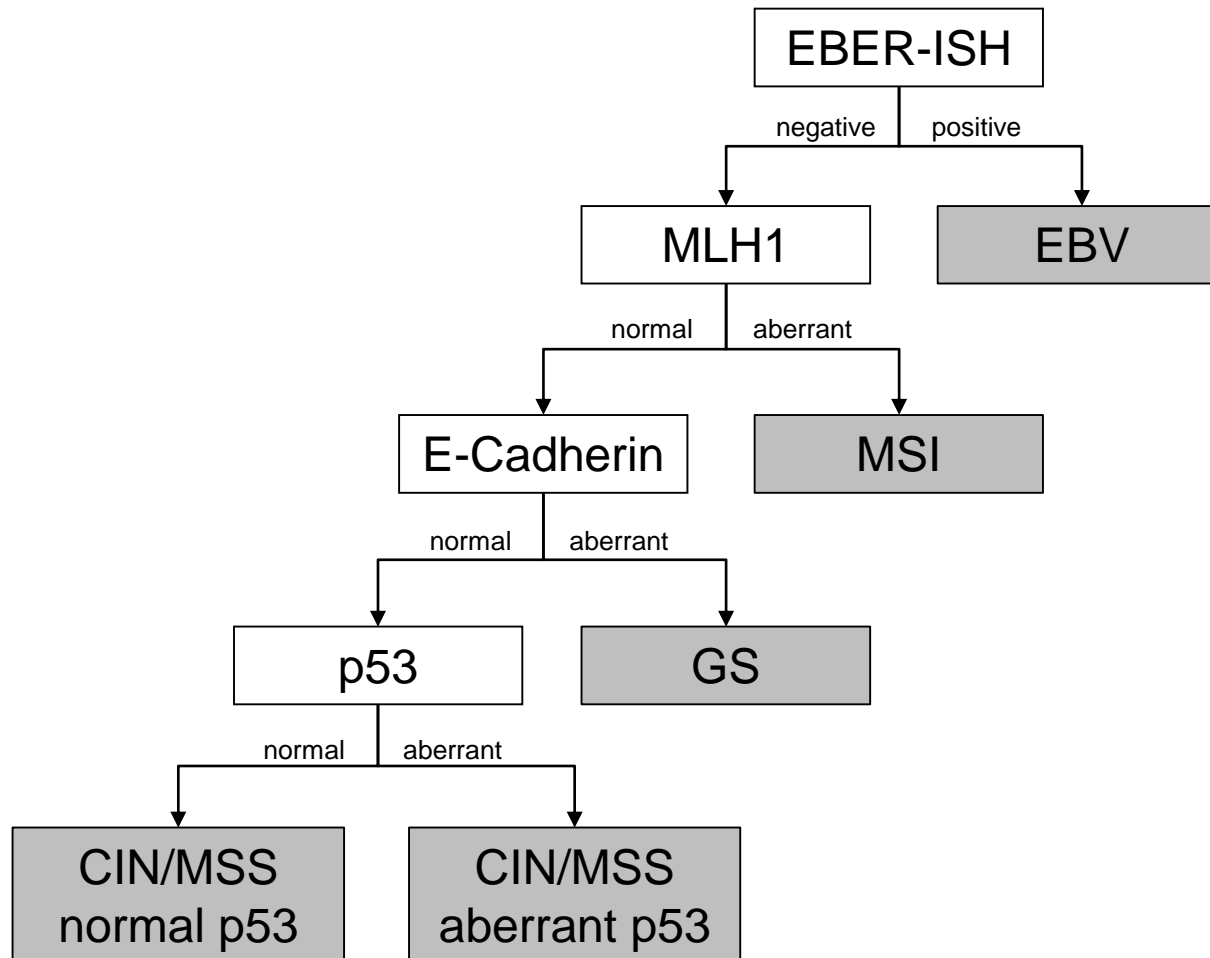


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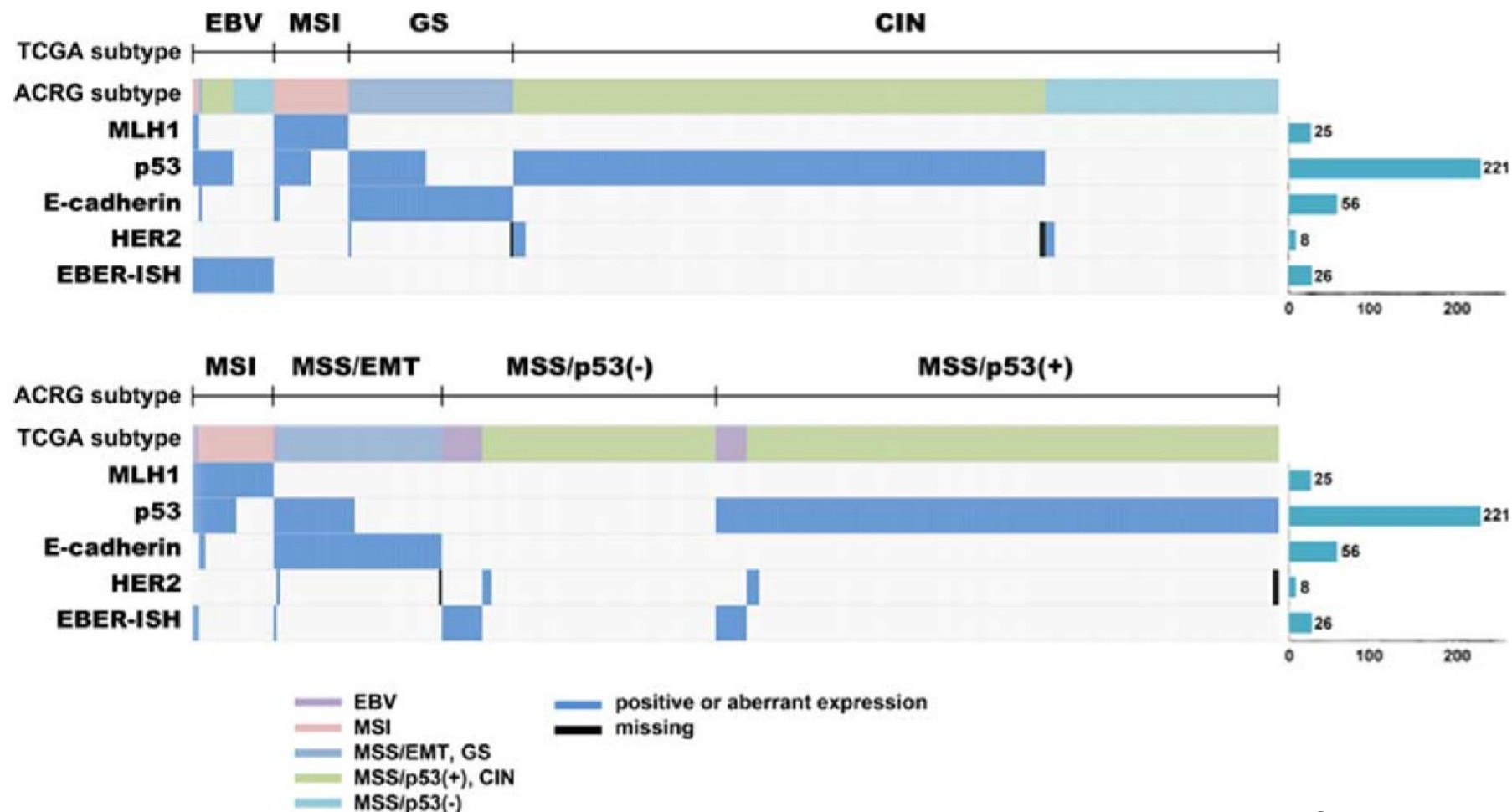


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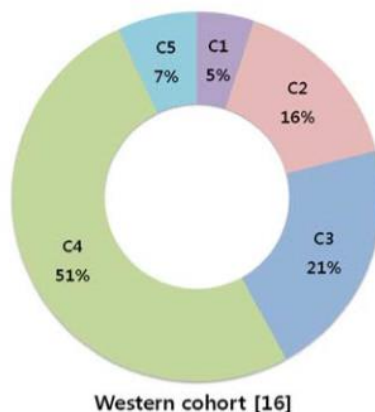
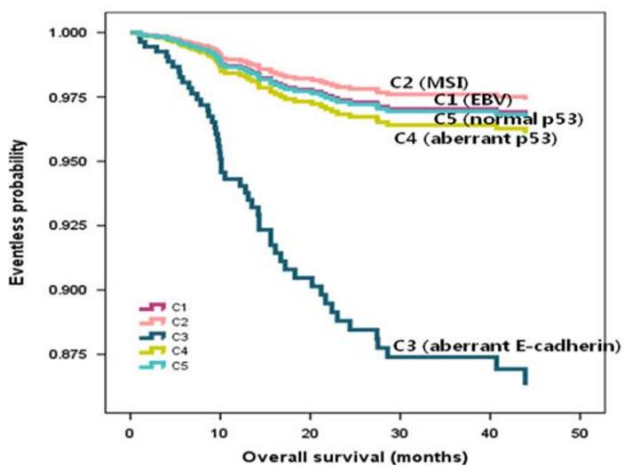
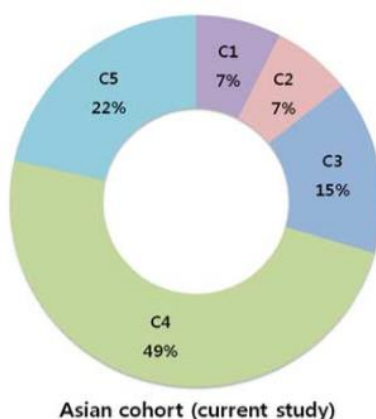
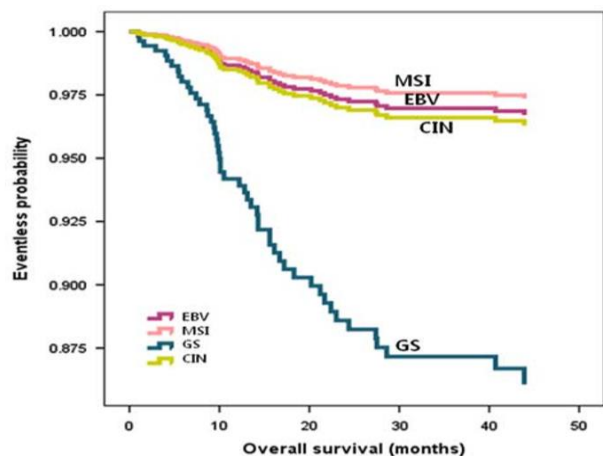


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C1 (EBV tumors)
<ul style="list-style-type: none"> - Male predominance - Body location - Mostly poorly differentiated type - Best prognosis - Molecular features: <i>PIK3CA</i>, <i>ARID1A</i>, <i>BCOR</i> mutation <i>CDKN2A</i> (p16) promoter hypermethylation <i>PD-L1</i>, <i>PD-L2</i>, <i>JAK2</i> amplification
C2 (MSI tumors)
<ul style="list-style-type: none"> - Old age - Distal location - Mostly Well- and moderately differentiated type - Gastric type by mucin phenotype - Better prognosis - Molecular features: <i>MLH1</i> promoter hypermethylation Hypermutation (occasional mutations in <i>PIK3CA</i>, <i>ERBB2</i>, <i>ERBB3</i>, <i>EGFR</i>, <i>ARID1</i>)
C3 (EMT tumors)
<ul style="list-style-type: none"> - Younger age - Mostly diffuse type by Lauren classification - Advanced T and N stage - Worst prognosis - Molecular features: <i>CDH1</i>, <i>RHOA</i> mutations lower number of mutations
C4 (aberrant p53 expression tumors)
<ul style="list-style-type: none"> - Intermediate prognosis - Molecular features: high <i>TP53</i> mutation <i>HER2</i>, <i>EGFR</i>, <i>CCNE1</i>, <i>CCND1</i>, <i>MDM2</i>, <i>ROBO2</i>, <i>GATA6</i>, <i>MYC</i> amplification
C5 (normal p53 expression tumors)
<ul style="list-style-type: none"> - Intermediate prognosis - Molecular features: intermediate level of mutations (<i>APC/KRAS/ARID1/PI3K/SMAD4</i>)

Agenda



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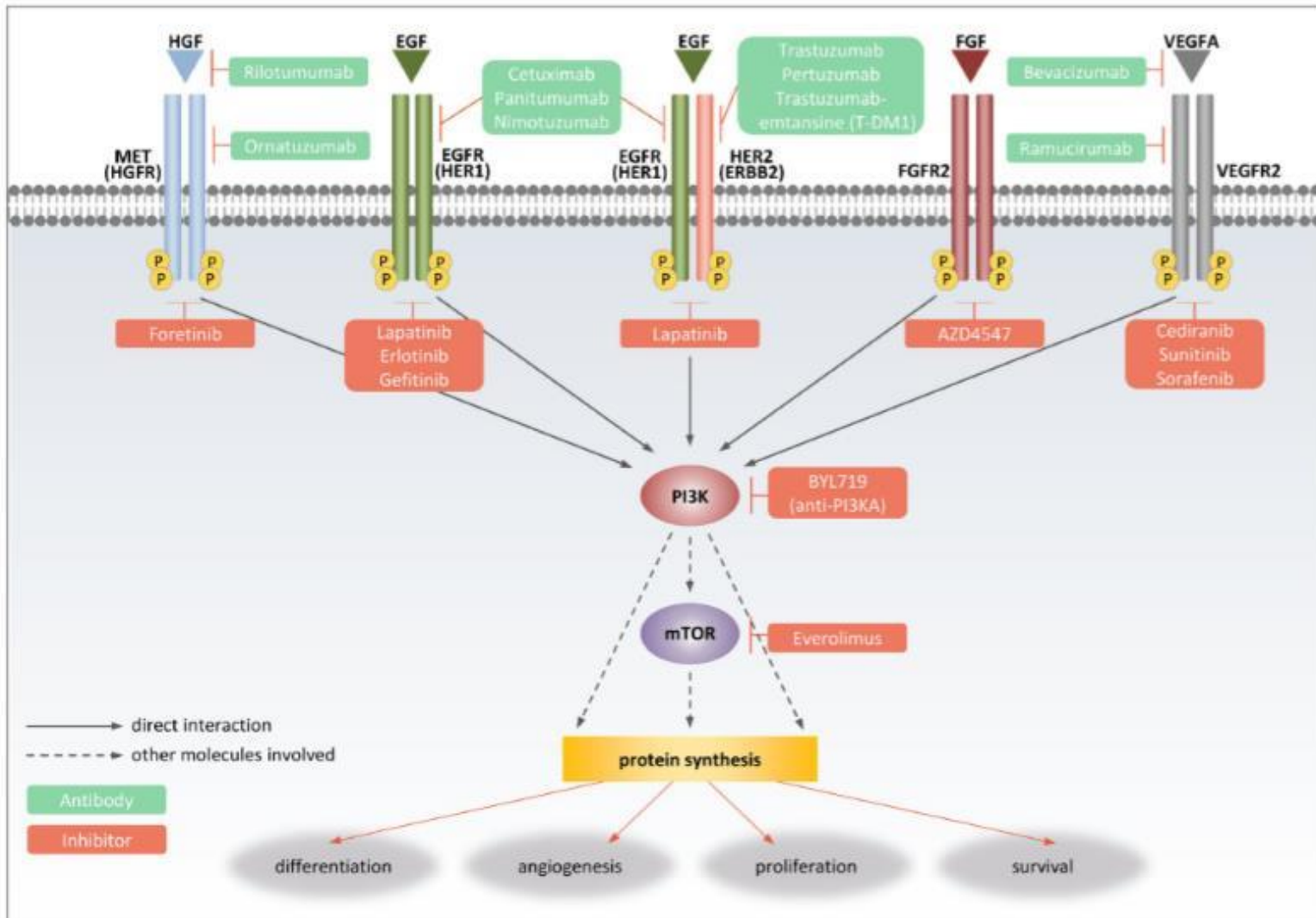
- Classification of gastric cancer
 - Histology
 - Molecular pathology
- **Predictive pathology**
 - HER2
 - PD-L1
 - Microsatellite instability
- Sporadic vs hereditary gastric cancer
- Take home messages

Biomarkers for gastric cancer: prognostic, predictive or targets of therapy?

Cecília Durães • Gabriela M. Almeida • Raquel Seruca •
Carla Oliveira • Fátima Carneiro



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HER2 testing in gastric cancer: a practical approach

Josef Rüschoff^{1,2}, Wedad Hanna³, Michael Bilous⁴, Manfred Hofmann², Robert Y Osamura⁵,
Frédérique Penault-Llorca⁶, Marc van de Vijver⁷ and Giuseppe Viale⁸

Table 2 Comparison of differences between human epidermal growth factor receptor 2 (HER2) scoring in gastric and breast cancer²⁹

		Gastric cancer	Breast cancer
Immunohistochemical scoring	Extent	Biopsy specimens ≥ 5 cells	$\geq 10\%$ ($\geq 30\%$) ^a
	(Area cutoff) Circularity	Resection specimens: $\geq 10\%$ Mostly missing (often only lateral in immunohistochemistry 2+/3+)	A must in immunohistochemistry 2+/3+
(Fluorescence) <i>in situ</i> hybridization analysis	Cell number	20 cohesive tumor cells showing highest gene count (add 20 new if ratio 1.8–2.2)	20 cohesive tumor cells showing highest gene count (add 20 new if ratio 1.8–2.2)
	Amplification	Ratio ≥ 2.0	Ratio ≥ 2.0 (≥ 2.2) ^a
HER2 positivity	Tumor type	About 30% of intestinal type gastric cancer about 15% of mixed type about 5% of diffuse type (signet ring type typically negative)	15–25% of ductal type (grade 2/3); almost never in subtypes such as lobular, medullary, and ductal grade 1
	Tumor location	About 30% at cardiac/gastro-esophageal junction About 15% of gastric cancer	No correlation
Patient selection	Fluorescence <i>in situ</i> hybridization vs immunohistochemistry	Immunohistochemistry more predictive than fluorescence <i>in situ</i> hybridization: immunohistochemistry primary test ^b fluorescence <i>in situ</i> hybridization only if immunohistochemistry 2+	Fluorescence <i>in situ</i> hybridization/immunohistochemistry equally predictive

^a According to the American Society of Clinical Oncology/College of American Pathologists.³⁰

^b According to approval by the European Medicines Agency.²⁷



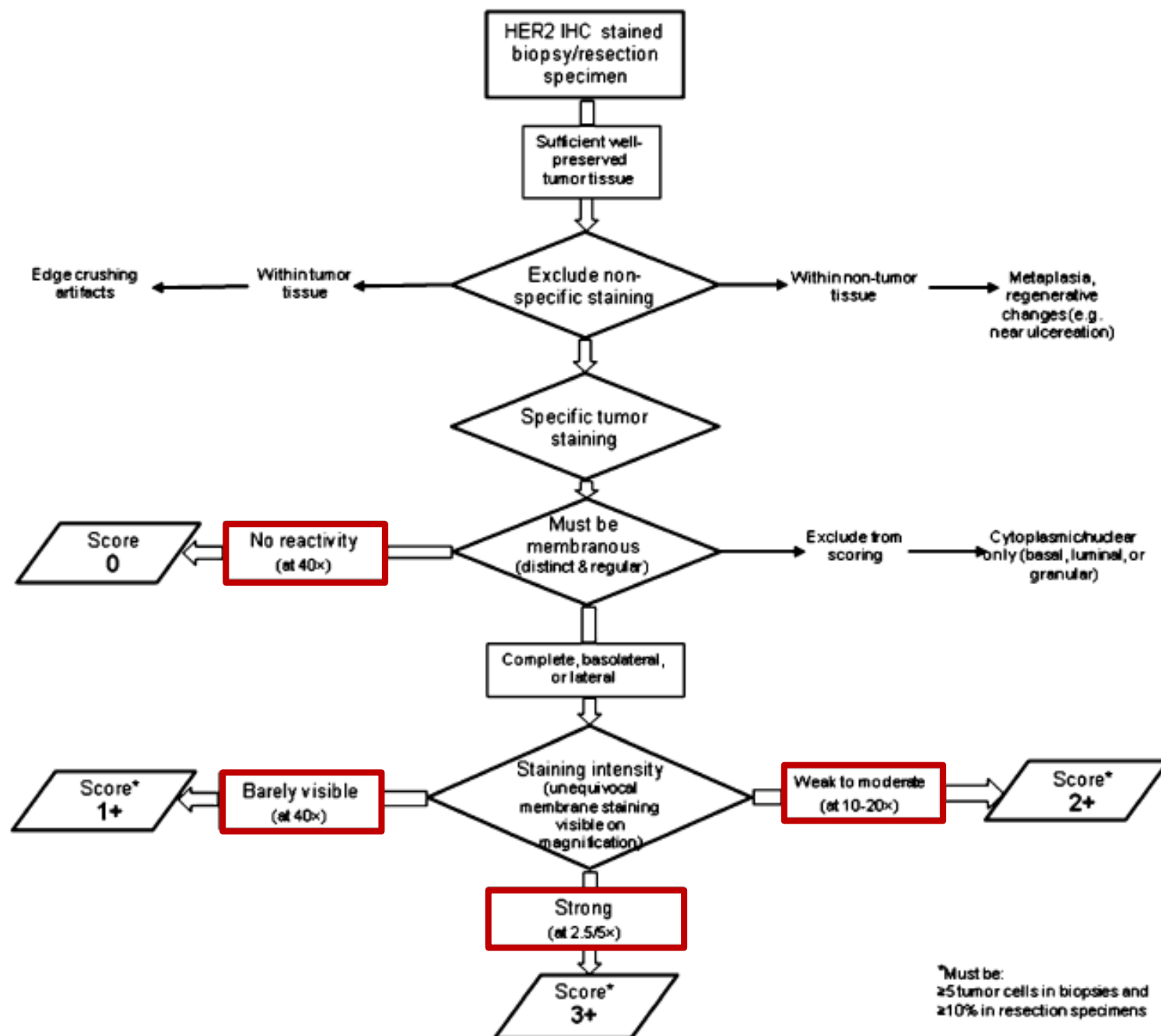
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Table 1 Human epidermal growth factor receptor 2 (HER2) scoring criteria for gastric cancer

Score	Surgical specimen-staining pattern	Biopsy specimen-staining pattern	HER2 overexpression assessment
0	No reactivity or membranous reactivity in <10% of tumor cells	No reactivity or no membranous reactivity in any tumor cell	Negative
1+	Faint/barely perceptible membranous reactivity in ≥10% of tumor cells; cells are reactive only in part of their membrane	Tumor cell cluster with a faint/barely perceptible membranous reactivity irrespective of percentage of tumor cells stained	Negative
2+	Weak to moderate complete, basolateral, or lateral membranous reactivity in ≥10% of tumor cells	Tumor cell cluster with a weak to moderate complete, basolateral, or lateral membranous reactivity irrespective of percentage of tumor cells stained	Equivocal
3+	Strong complete, basolateral, or lateral membranous reactivity in ≥10% of tumor cells	Tumor cell cluster with a strong complete, basolateral, or lateral membranous reactivity irrespective of percentage of tumor cells stained	Positive

**The „magnification rule“ should be
used to assess HER2 positivity**



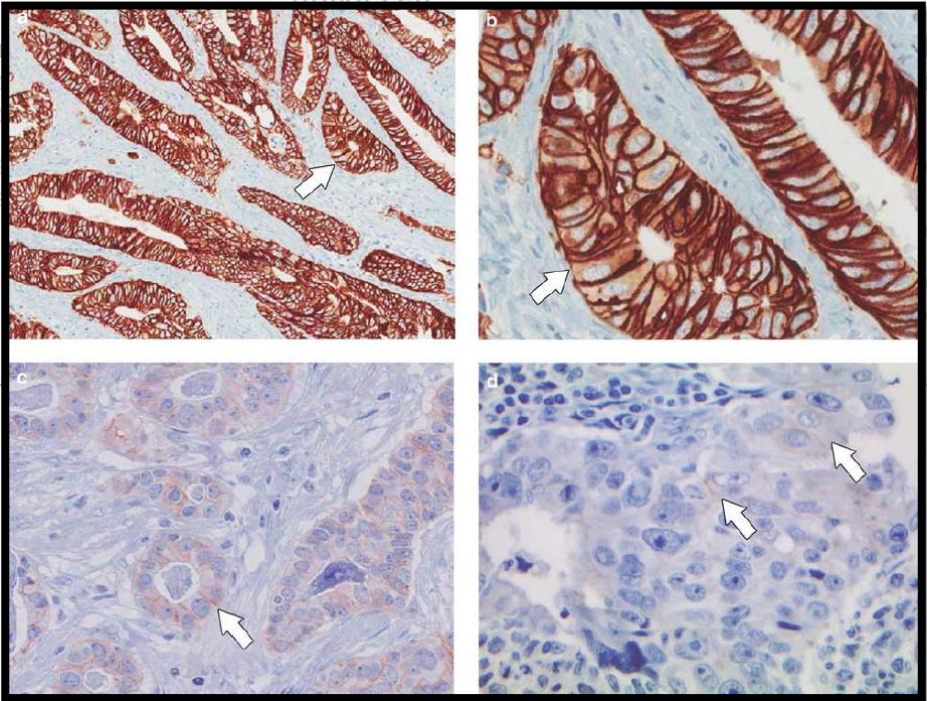


HER2 testing in gastric cancer: a practical approach

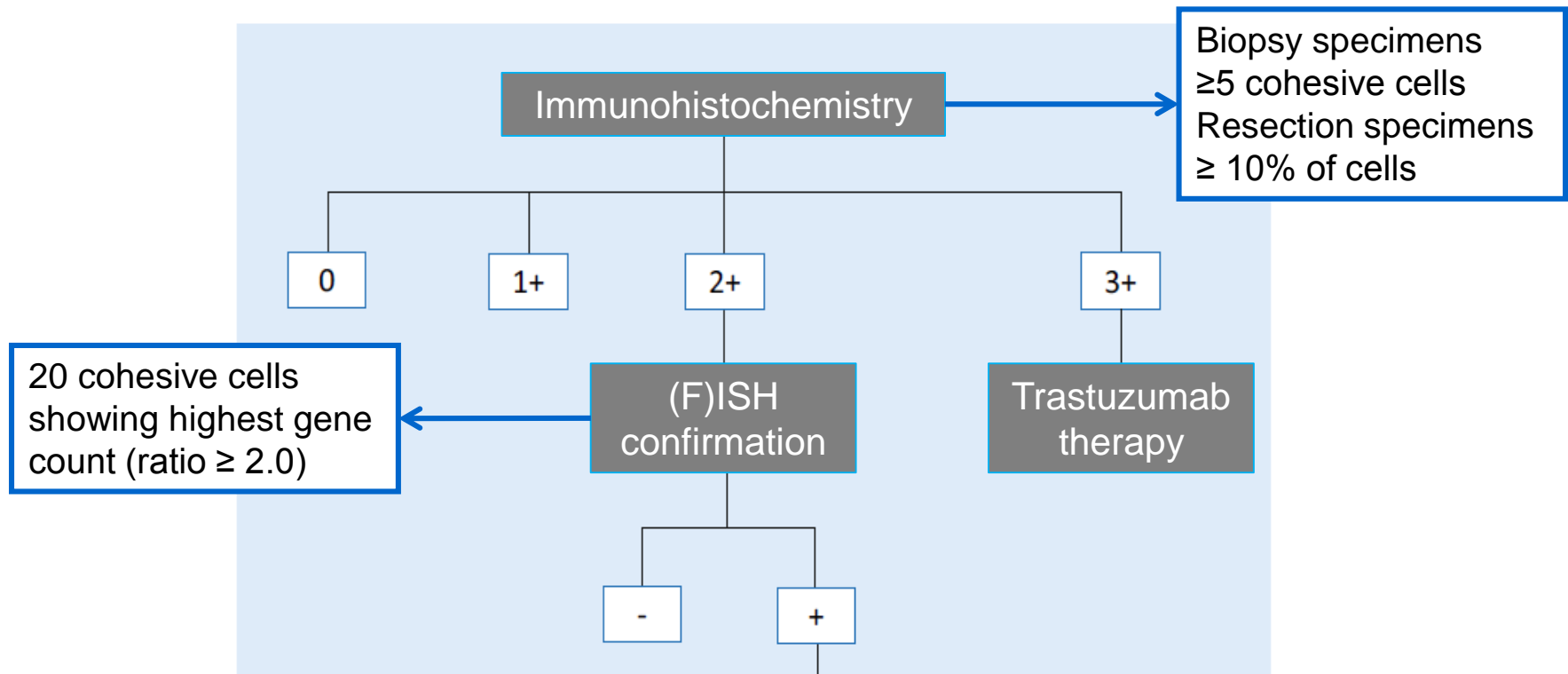
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2+	Weak to moderate complete or lateral membranous reactivity in ≥10% of tumor cells	Weak to moderate complete or lateral membranous reactivity in ≥10% of tumor cells	Equivocal
3+	Strong complete, basolateral membranous reactivity in ≥10% of tumor cells	Strong complete, basolateral membranous reactivity in ≥10% of tumor cells	Positive



HER2 Testing Algorithm



“Herceptin (trastuzumab) should only be used in patients with metastatic gastric cancer (adenocarcinoma of stomach and gastroesophageal junction) whose tumours have HER2 overexpression as defined by IHC2+ and a confirmatory FISH+ result, or IHC 3+, as determined by an accurate and validated assay”



HER2 testing in gastric cancer: a practical approach

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Table 3 Human epidermal growth factor receptor 2 (HER2) testing recommendations in gastric cancer, (a) immunohistochemistry and (b) *in situ* hybridization

(a) Immunohistochemistry

Testing recommendations

- Representative surgical samples or an adequate number of viable biopsy specimens (ideally six to eight) are required
 - If few biopsies are available, all viable specimens should be tested
- Immunohistochemistry should be the initial HER2 testing methodology for gastric cancer and bright-field methodologies are preferred wherever possible
 - HER2-positive per European Medicines Agency license: immunohistochemistry 3+ or immunohistochemistry 2+/fluorescence *in situ* hybridization-positive or immunohistochemistry 2+/silver *in situ* hybridization-positive
 - Borderline immunohistochemistry 1+/immunohistochemistry 2+ cases and samples with focal and intense membranous reactivity in < 10% cells may also be retested with fluorescence *in situ* hybridization or silver *in situ* hybridization (scores for both assays should be indicated separately on the report)
- Validated immunohistochemistry HER2 assays should be used

Scoring recommendations

- Due to the tumor heterogeneity (focal areas of positivity) and incomplete membrane staining commonly seen in gastric cancer, the gastric cancer-specific scoring criteria should be adhered to:
 - Surgical specimen cutoff: complete, basolateral, or lateral membranous reactivity in $\geq 10\%$ of cells
 - Biopsy specimen cutoff: complete, basolateral, or lateral membranous reactivity in ≥ 5 clustered cells
- The 'magnification rule' should be used in conjunction with the scoring criteria
- Borderline cases (immunohistochemistry 1+/immunohistochemistry 2+ or focal staining in < 10% cells) that score fluorescence *in situ* hybridization-positive or silver *in situ* hybridization-positive may be considered HER2-positive (scores for both assays should be indicated separately on the report)



HER2 testing in gastric cancer: a practical approach

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(b) In situ hybridization

Testing recommendations

- Tumor samples classified as immunohistochemistry 2+ should be retested by fluorescence *in situ* hybridization or silver *in situ* hybridization to assess HER2 status
- Silver *in situ* hybridization is a more suitable methodology than fluorescence *in situ* hybridization for assessing HER2 status in gastric tumor samples as it is a bright-field methodology and thus allows for rapid identification of HER2-positive tumor foci within a heterogeneous sample
- Validated *in situ* hybridization HER2 assays should be used

Scoring recommendations

- The definition of fluorescence *in situ* hybridization or silver *in situ* hybridization positivity in gastric or gastro–esophageal junction cancer is a HER2:chromosome 17 ratio of ≥ 2.0
- The entire case should be screened for amplified regions (particularly important for fluorescence *in situ* hybridization samples where a bright-field image is not available)
- At least 20 evaluable, non-overlapping cells in the invasive component should be counted initially
- In borderline amplification cases, ~20 additional cells should be recounted or scoring should be performed in an alternative area of tissue
- The overall HER2 gene count is important:
 - >6 HER2 gene copies using single probe: considered positive
 - Four to six HER2 gene copies: dual probe test advised and the ratio should be recalculated by counting an additional 20 cells

Ensuring quality and timely HER2 testing results

- The use of validated immunohistochemistry and *in situ* hybridization tests is strongly recommended and appropriate controls should be included in each run
- Turnaround time from initial diagnosis to reporting of results should ideally not exceed 5 working days and a multidisciplinary approach is required
- Centralized testing is recommended wherever possible and all laboratories should participate in validated quality assurance programs

Significant intratumoral heterogeneity of human epidermal growth factor receptor 2 status in gastric cancer: A comparative study of immunohistochemistry, FISH, and dual-color *in situ* hybridization

Kazuki Kanayama,¹ Hiroshi Imai,¹ Misao Yoneda,² Yoshifumi S. Hirokawa¹ and Taizo Shiraishi¹

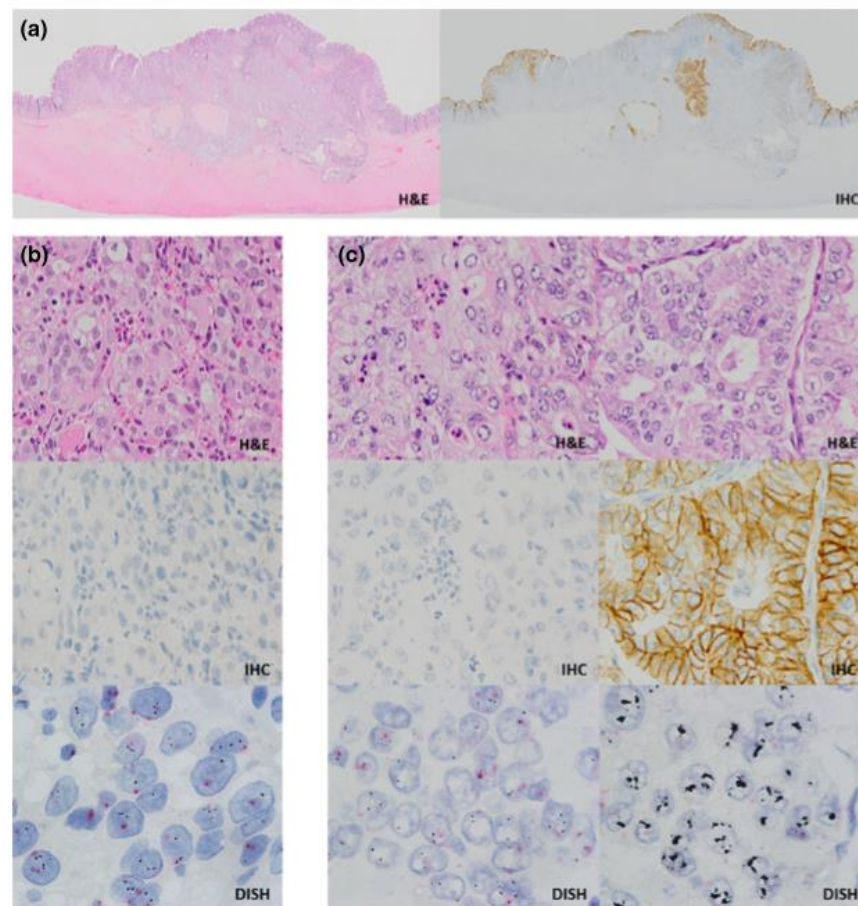
Table 2. Comparison of FISH and dual-color *in situ* hybridization (DISH) results for assessment of human epidermal growth factor receptor 2 status in biopsy specimens

IHC score	FISH		DISH		Total
	Unamplified	Amplified	Unamplified	Amplified	
0	74	0	74	0	74
1+	18	0	18	0	18
2+	5	4	5	4	9
3+	0	7	0	7	7
Total	97	11	97	11	108

IHC, immunohistochemistry.

Table 3. Concordance of human epidermal growth factor receptor 2 (HER2) immunohistochemistry (IHC) between biopsy and surgical resection specimens

	Score	HER2 IHC in surgical resection			Total
		0 or 1+	2+	3+	
HER2 IHC in biopsy	0 or 1+	50	9	1	60
	2+	2	4	1	7
	3+	0	1	2	3
Total		52	14	4	70



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Table 5. Discordant and concordant cases of human epidermal growth factor receptor 2 (HER2) status between biopsy and surgical resection specimens

Case no.		Biopsy		Surgical resection			Amplified area, %
		HER2 IHC	HER2 status (HER2/CEP17 ratio)	WHO classification	HER2 IHC	HER2 status (HER2/CEP17 ratio)	
Discordant cases							
10	0	Unamplified (1.13)	Tubular	2+ Heterogeneous	Heterogeneous (2.96)	Tubular	17.4
15	0	Unamplified (1.17)	Tubular	2+ Heterogeneous	Heterogeneous (3.36)	Tubular	5.4
38	0	Unamplified (1.13)	Poorly cohesive	2+ Heterogeneous	Heterogeneous (4.02)	Poorly cohesive (tubular component)	9.3
71	2+ Heterogeneous	Unamplified (1.11)	Tubular	2+	Homogeneous (3.61)	Tubular	89.9
79	1+	Unamplified (1.10)	Tubular	2+ Heterogeneous	Heterogeneous (2.68)	Papillary	12.2
87	0	Unamplified (1.36)	Tubular	3+ Heterogeneous	Heterogeneous (7.69)	Tubular	5.3
Concordant cases							
6	3+	Amplified (7.62)	Poorly cohesive	3+	Homogeneous (8.69)	Tubular (poorly component)	100.0
41	3+ Heterogeneous	Amplified heterogeneous (8.92)	Tubular	3+ Heterogeneous	Heterogeneous (8.86)	Tubular	12.4
58	2+ Heterogeneous	Amplified (3.25)	Tubular	2+ Heterogeneous	Homogeneous (3.42)	Tubular	100.0
64	2+ Heterogeneous	Amplified (2.60)	Tubular	2+ Heterogeneous	Homogeneous (2.20)	Tubular	100.0
72	2+	Amplified (4.29)	Tubular	3+	Homogeneous (4.60)	Tubular	100.0
85	3+ Heterogeneous	Amplified heterogeneous (4.40)	Tubular	2+ Heterogeneous	Heterogeneous (2.75)	Tubular	47.9

HER2 Testing and Clinical Decision Making in Gastroesophageal Adenocarcinoma: Guideline From the College of American Pathologists, American Society for Clinical Pathology, and the American Society of Clinical Oncology

Angela N. Bartley, Mary Kay Washington, Carol Colasacco, Christina B. Ventura, Nofisat Ismaila, Al B. Benson III, Alfredo Carrato, Margaret L. Gulley, Dhanpat Jain, Sanjay Kakar, Helen J. Mackay, Catherine Streutker, Laura Tang, Megan Troxell, and Jaffer A. Ajani



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Key Points and Recommendations for Pathologists

Recommendation 2.1: Laboratories/pathologists must specify the antibodies and probes used for the test and ensure that assays are appropriately validated for HER2 IHC and ISH on GEA specimens (Type: evidence based; Quality of evidence: moderate/intermediate; Strength of recommendation: strong).

Recommendation 2.2: When GEA HER2 status is being evaluated, laboratories/pathologists should perform/order IHC testing first, followed by ISH when IHC result is 2+ (equivocal). Positive (3+) or negative (0 or 1+) HER2 IHC results do not require further ISH testing (Type: evidence based; Quality of evidence: high; Strength of recommendation: strong).

Recommendation 2.3: Pathologists should use the Ruschhoff/Hofmann method in scoring HER2 IHC and ISH results for GEA (Type: evidence based; Quality of evidence: moderate/intermediate; Strength of recommendation: strong).

Recommendation 2.4: Pathologists should select the tissue block with the areas of lowest grade tumor morphology in biopsy and resection specimens. More than one tissue block may be selected if different morphologic patterns are present (Type: evidence based; Quality of evidence: moderate/intermediate; Strength of recommendation: recommendation/moderate).

Recommendation 2.5: Laboratories should report HER2 test results in GEA specimens in accordance with the CAP “Template for Reporting Results of *HER2 (ERBB2)* Biomarker Testing of Specimens From Patients With Adenocarcinoma of the Stomach or Esophagogastric Junction” (Type: evidence based; Quality of evidence: moderate/intermediate; Strength of recommendation: strong).

Recommendation 2.6: Pathologists should identify areas of invasive adenocarcinoma and also mark areas with strongest intensity of HER2 expression by IHC in GEA specimen for subsequent ISH scoring when required (Type: evidence based; Quality of evidence: moderate/intermediate; Strength of recommendation: strong).

(continued on following page)

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Recommendation 2.4

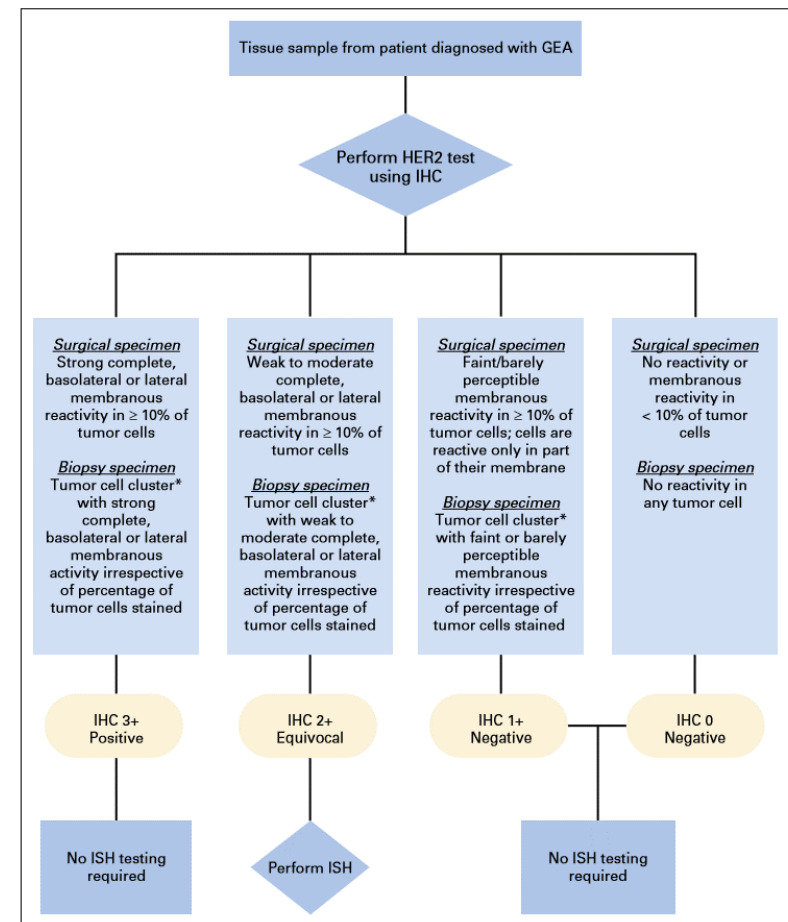
Pathologists should select the tissue block with the areas of lowest grade tumor morphology in biopsy and resection specimens. More than one tissue block may be selected if different morphologic patterns are present (Type: evidence based; Quality of evidence: moderate/intermediate; Strength of recommendation: recommendation/moderate).

As mentioned previously, studies show that HER2 over-expression is strongly associated with the intestinal phenotype, and less frequently with the diffuse (signet ring cell) phenotype of GEA. The rates of HER2 positivity vary for intestinal (3% to 23.5%), diffuse (0% to 6%), and mixed histology (0% to 20%) cancers.^{36,85-88}

HER2 positivity seems to be more strongly associated with low-grade than high-grade tumors and varies from 15% to 45% for low grade, and 6% to 28% for high grade, in different studies.^{36,86,89-91} When choosing a tissue block, selecting one with the lower grade or intestinal morphology appears more likely to yield HER2-positive results and is thus recommended. If the cancer comprises substantially different grades or histologic patterns, it is reasonable to test different areas, which may require selection of more than one block.



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Table 3. Scoring Guidelines for Interpretation of HER2 Immunohistochemistry in Gastric Carcinoma

Surgical Specimen-Staining Pattern	Biopsy Specimen-Staining Pattern	Score	HER2 Expression Assessment
No reactivity or membranous reactivity in < 10% of tumor cells	No reactivity or no membranous reactivity in any tumor cell	0	Negative
Faint/barely perceptible membranous reactivity in $\geq 10\%$ of tumor cells; cells are reactive only in part of their membrane	Tumor cell cluster* with a faint/barely perceptible membranous reactivity irrespective of percentage of tumor cells stained	1+	Negative
Weak to moderate complete, basolateral or lateral membranous reactivity in $\geq 10\%$ of tumor cells	Tumor cell cluster* with a weak to moderate complete, basolateral or lateral membranous reactivity irrespective of percentage of tumor cells stained	2+	Equivocal
Strong complete, basolateral or lateral membranous reactivity in $\geq 10\%$ of tumor cells	Tumor cell cluster* with a strong complete, basolateral or lateral membranous reactivity irrespective of percentage of tumor cells stained	3+	Positive

NOTE. Hofmann M, et al: Histopathology 52:797-805, 2008.¹³

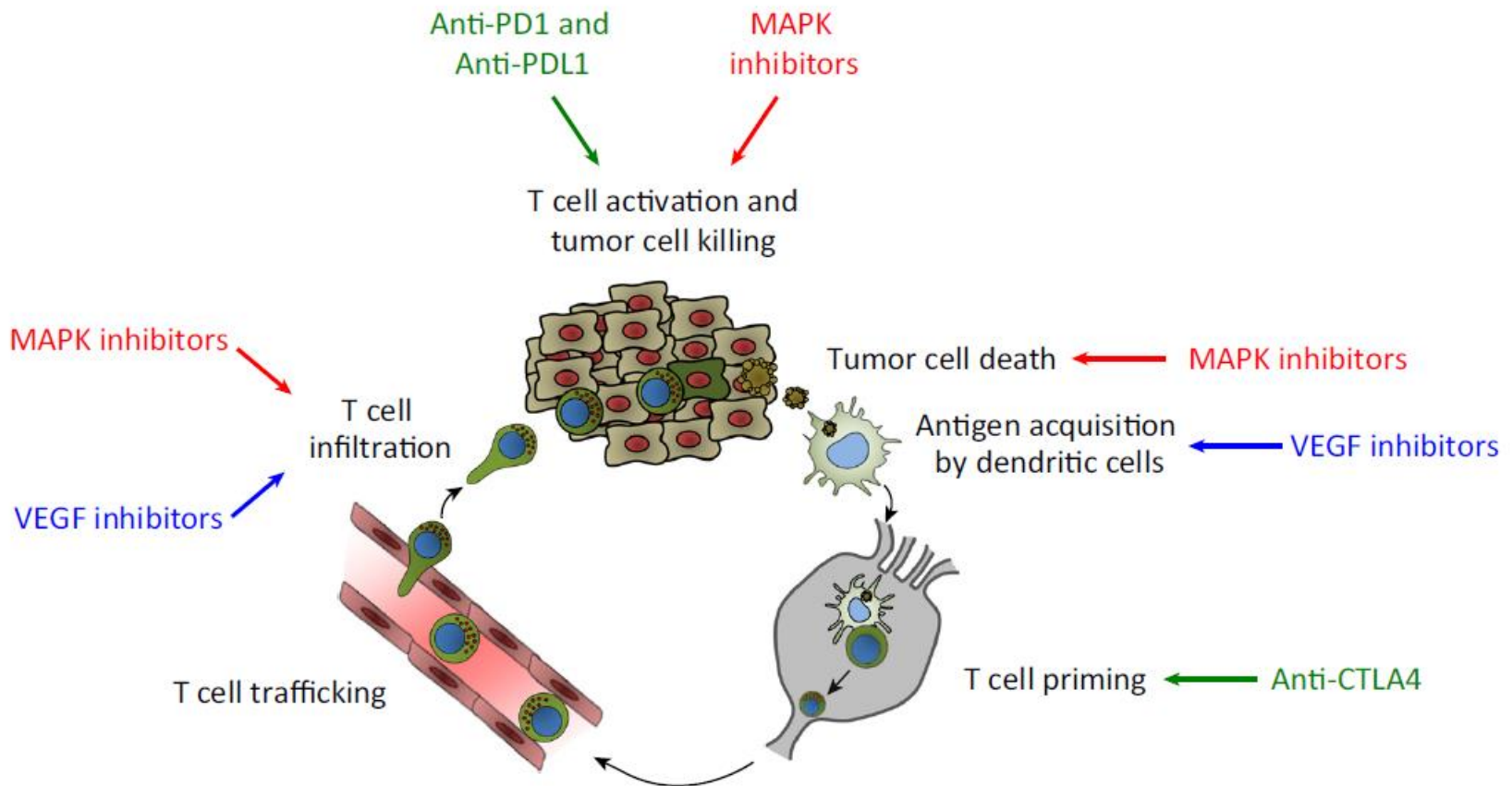
*Tumor cell cluster (≥ 5 neoplastic cells).

Targeted Therapy and Checkpoint Immunotherapy Combinations for the Treatment of Cancer

Paul E. Hughes,¹ Sean Caenepeel,¹ and Lawren C. Wu^{2,*}



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Clinicopathological features of programmed death ligand 1 expression with tumor-infiltrating lymphocyte, mismatch repair, and Epstein–Barr virus status in a large cohort of gastric cancer patients


Akihito Kawazoe^{1,2,3} · Takeshi Kuwata^{1,5} · Yasutoshi Kuboki² · Kohei Shitara² · Akiko Kawano Nagatsuma¹ · Masaaki Aizawa⁴ · Takayuki Yoshino² · Toshihiko Doi² · Atsushi Ohtsu^{2,3} · Atsushi Ochiai¹ 

Table 1 Prevalence of programmed death ligand 1 (*PD-L1*) expression according to mismatch repair (*MMR*) status and Epstein–Barr virus (*EBV*) status

	All (<i>N</i> = 487)	P- <i>MMR</i> (<i>n</i> = 462)	D- <i>MMR</i> (<i>n</i> = 25)	<i>P</i>	EBV negative (<i>n</i> = 462)	EBV positive (<i>n</i> = 25)	<i>P</i>
TCs							
No PD-L1 expression in TCs	376 (77.2 %)	369 (79.9 %)	7 (28.0 %)	<0.001	364 (78.8 %)	12 (48.0 %)	0.001
PD-L1 expression in TCs	111 (22.8 %)	93 (20.1 %)	18 (72.0 %)		98 (21.2 %)	13 (52.0 %)	
IHC score 1+	67 (13.8 %)	58 (12.5 %)	9 (36.0 %)	<0.001	60 (13.0 %)	7 (28.0 %)	0.022
IHC score 2+	23 (4.7 %)	19 (4.1 %)	4 (16.0 %)		20 (4.3 %)	3 (12.0 %)	
IHC score 3+	21 (4.3 %)	16 (3.5 %)	5 (20.0 %)		18 (3.9 %)	3 (12.0 %)	
TIICs							
No PD-L1 expression in TIICs	188 (38.6 %)	187 (40.5 %)	1 (4.0 %)	<0.001	183 (39.6 %)	5 (20.0 %)	0.050
PD-L1 expression in TIICs	299 (61.4 %)	275 (59.5 %)	24 (96.0 %)		279 (60.4 %)	20 (80.0 %)	
IHC score 1+	278 (57.1 %)	260 (56.3 %)	18 (72.0 %)	<0.001	259 (56.1 %)	19 (76.0 %)	1.00
IHC score 2+	19 (3.9 %)	14 (3.0 %)	5 (20.0 %)		18 (3.9 %)	1 (4.0 %)	
IHC score 3+	2 (0.4 %)	1 (0.2 %)	1 (4.0 %)		2 (0.4 %)	0 (0 %)	

D-*MMR* MMR deficient, *IHC* immunohistochemistry, P-*MMR* MMR proficient, *TCs* tumor cells, *TIICs* tumor-infiltrating immune cells

Clinicopathological features of programmed death ligand 1 expression with tumor-infiltrating lymphocyte, mismatch repair, and Epstein–Barr virus status in a large cohort of gastric cancer patients



Akihito Kawazoe^{1,2,3} · Takeshi Kuwata^{1,5} · Yasutoshi Kuboki² · Kohei Shitara² · Akiko Kawano Nagatsuma¹ · Masaaki Aizawa⁴ · Takayuki Yoshino² · Toshihiko Doi² · Atsushi Ohtsu^{2,3} · Atsushi Ochiai¹ 

Table 1 Prevalence of programmed death ligand 1 (*PD-L1*) expression according to mismatch repair (*MMR*) status and Epstein–Barr virus (*EBV*) status

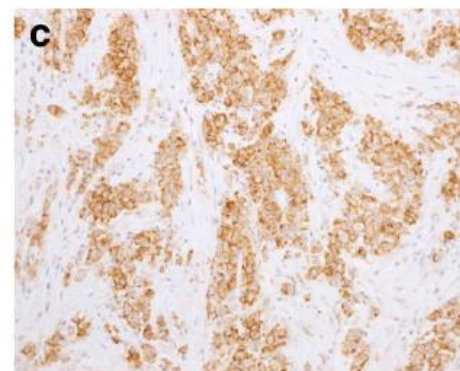
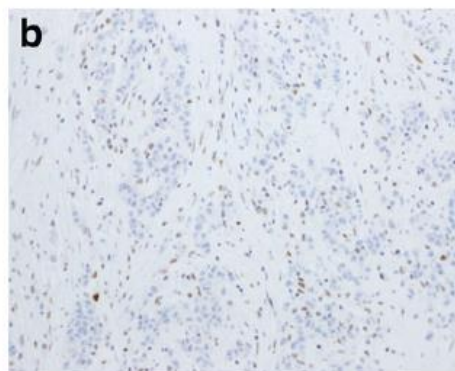
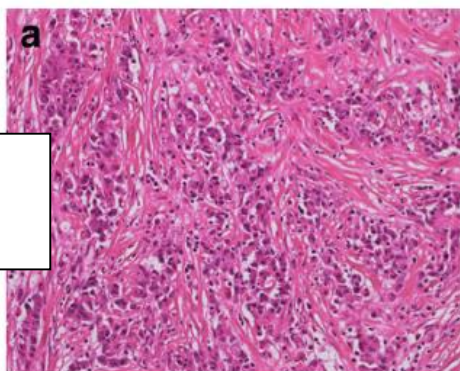
	All (<i>N</i> = 487)	P- <i>MMR</i> (<i>n</i> = 462)	D- <i>MMR</i> (<i>n</i> = 25)	<i>P</i>	EBV negative (<i>n</i> = 462)	EBV positive (<i>n</i> = 25)	<i>P</i>
TCs							
No PD-L1 expression in TCs	376 (77.2 %)	369 (79.9 %)	7 (28.0 %)	<0.001	364 (78.8 %)	12 (48.0 %)	0.001
PD-L1 expression in TCs	111 (22.8 %)	93 (20.1 %)	18 (72.0 %)		98 (21.2 %)	13 (52.0 %)	
IHC score 1+	67 (13.8 %)	58 (12.5 %)	9 (36.0 %)	<0.001	60 (13.0 %)	7 (28.0 %)	0.022
IHC score 2+	23 (4.7 %)	19 (4.1 %)	4 (16.0 %)		20 (4.3 %)	3 (12.0 %)	
IHC score 3+	21 (4.3 %)	16 (3.5 %)	5 (20.0 %)		18 (3.9 %)	3 (12.0 %)	
TIICs							
No PD-L1 expression in TIICs	188 (38.6 %)	187 (40.5 %)	1 (4.0 %)	<0.001	183 (39.6 %)	5 (20.0 %)	0.050
PD-L1 expression in TIICs	299 (61.4 %)	275 (59.5 %)	24 (96.0 %)		279 (60.4 %)	20 (80.0 %)	
IHC score 1+	278 (57.1 %)	260 (56.3 %)	18 (72.0 %)	<0.001	259 (56.1 %)	19 (76.0 %)	1.00
IHC score 2+	19 (3.9 %)	14 (3.0 %)	5 (20.0 %)		18 (3.9 %)	1 (4.0 %)	
IHC score 3+	2 (0.4 %)	1 (0.2 %)	1 (4.0 %)		2 (0.4 %)	0 (0 %)	

D-*MMR* MMR deficient, IHC immunohistochemistry, P-*MMR* MMR proficient, TCs tumor cells, TIICs tumor-infiltrating immune cells

Clinicopathological features of programmed death ligand 1 expression with tumor-infiltrating lymphocyte, mismatch repair, and Epstein–Barr virus status in a large cohort of gastric cancer patients

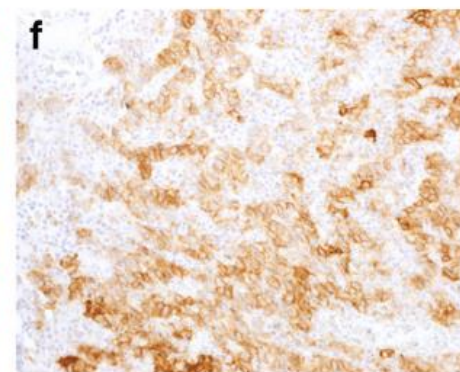
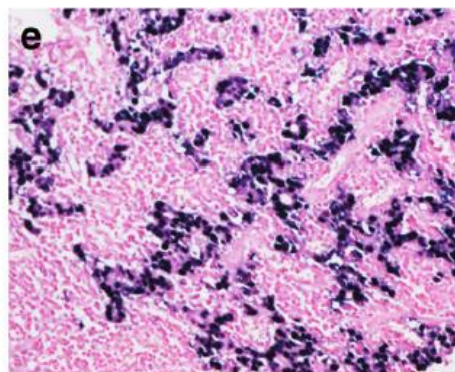
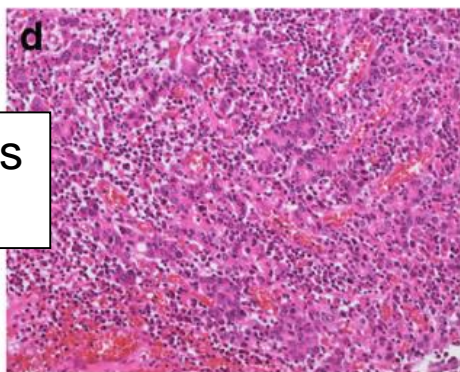
Akihito Kawazoe^{1,2,3} · Takeshi Kuwata^{1,5} · Yasutoshi Kuboki² · Kohei Shitara² · Akiko Kawano Nagatsuma¹ · Masaaki Aizawa⁴ · Takayuki Yoshino² · Toshihiko Doi² · Atsushi Ohtsu^{2,3} · Atsushi Ochiai¹ 

Panel 1



MSI-H
GC

Panel 2



EBV pos
GC

Clinicopathological features of programmed death ligand 1 expression with tumor-infiltrating lymphocyte, mismatch repair, and Epstein–Barr virus status in a large cohort of gastric cancer patients


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Table 3 Association between programmed death ligand 1 (*PD-L1*) expression and tumor-infiltrating lymphocytes

	CD3		CD4		CD8		FOXP3	
	High	Low	High	Low	High	Low	High	Low
PD-L1 in TCs								
Positive	86 (77 %)	25 (23 %)	69 (62 %)	42 (38 %)	87 (78 %)	24 (22 %)	84 (76 %)	27 (24 %)
Negative	157 (42 %)	219 (58 %)	175 (47 %)	201 (53 %)	157 (42 %)	219 (58 %)	158 (42 %)	218 (58 %)
<i>P</i>	<0.001		0.004		<0.001		<0.001	
PD-L1 in TIICs								
Positive	188 (63 %)	111 (37 %)	164 (55 %)	135 (45 %)	193 (65 %)	106 (35 %)	179 (60 %)	120 (40 %)
Negative	55 (29 %)	133 (71 %)	80 (43 %)	108 (57 %)	51 (27 %)	137 (73 %)	63 (33 %)	125 (67 %)
<i>P</i>	<0.001		0.008		<0.001		<0.001	

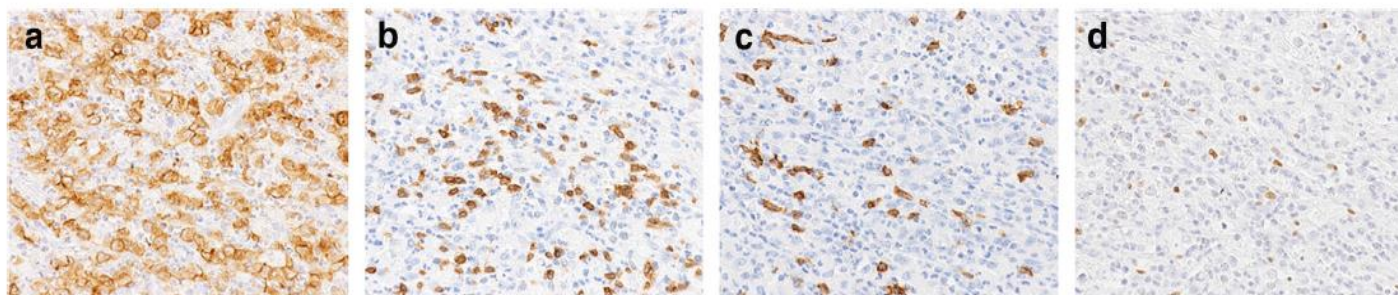
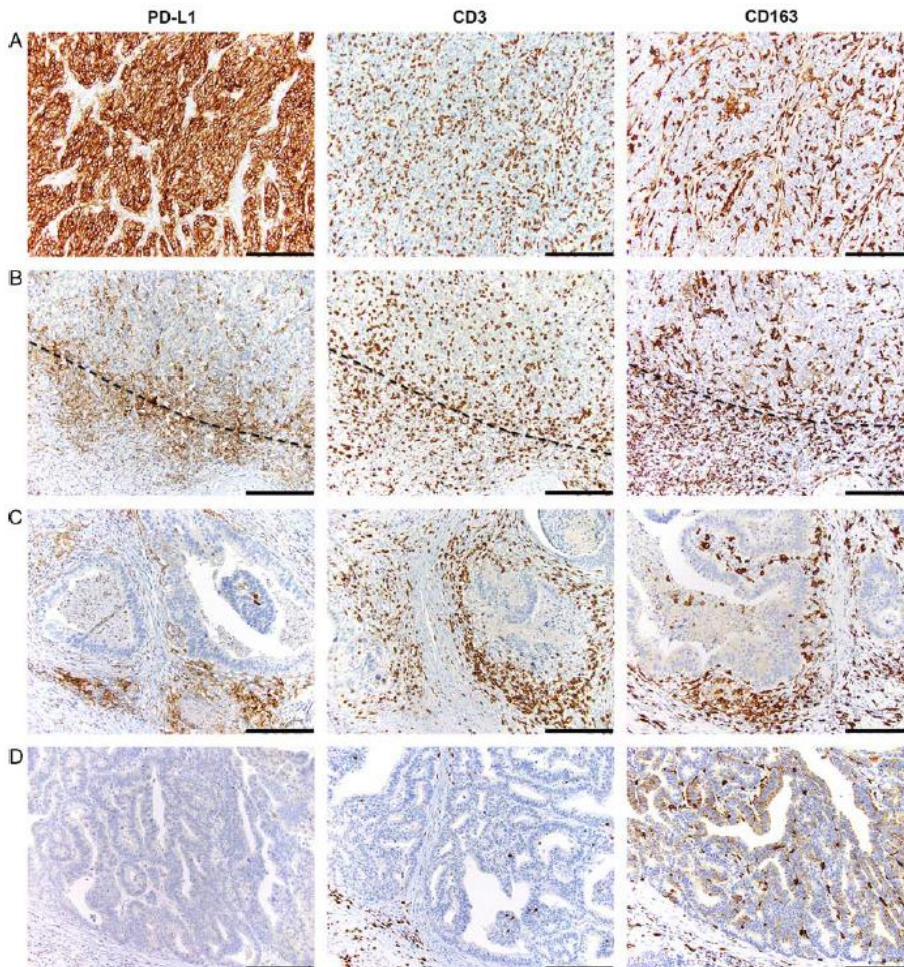


Fig. 3 A strong association was observed between programmed death ligand 1 (PD-L1) expression and high densities of CD3⁺, CD8⁺, and forkhead box P3 (FOXP3)-positive tumor-infiltrating

lymphocytes (TILs). Representative images of a case with a PD-L1 immunohistochemistry score 3+ on tumor cells and high densities of **b** CD3⁺, **c** CD8⁺, and **d** FOXP3⁺ TILs

Programmed Death-Ligand 1 Expression Is Common in Gastric Cancer Associated With Epstein-Barr Virus or Microsatellite Instability

Changqing Ma, MD, PhD,* Krishna Patel, MD,† Aatur D. Singhi, MD, PhD,*
Bing Ren, MD, PhD,* Benjamin Zhu, BA,* Fyza Shaikh, MD,† and Weijing Sun, MD†



A, Diffuse membranous PD-L1 staining in an MSI cancer.

B, Membranous PD-L1 staining at the invasive front in an MSI cancer. The dashed line in each photomicrograph indicates the invasive front of the tumor/tumor-stroma interface.

C, Membranous PD-L1 staining in immune infiltrates in an EBV/MSS cancer.

D, Negative/no PDL1 staining in tumor cells and immune infiltrates in an EBV/MSS cancer.



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TABLE 2. PD-L1 Expression and Tumor Immune Microenvironment Stratified by EBV and MSI Status

	All (N = 44)	EBV + (N = 7)	MSI (N = 16)	EBV – /MSS (N = 21)	<i>P</i>
Pattern of PD-L1 staining (n [%])					
Diffuse	10 (23)	4 (57)	5 (31)	1 (5)	< 0.001
Invasive front	14 (32)	2 (29)	9 (56)	3 (14)	
Immune infiltrates	8 (18)	1 (14)	0	7 (33)	
Negative	12 (27)	0	2 (13)	10 (48)	
Portion of cells in tumor with PD-L1 staining (n [%])					
0% (PD-L1 –)	12 (27)	0	2 (13)	10 (48)	0.013
> 0% (PD-L1 +)	32 (72)	7 (100)	14 (87)	11 (52)	
> 0, < 5%	16	2	5	9	
≥ 5%, < 10%	6	1	4	1	
≥ 10%, < 20%	3	1	2	0	
≥ 20%, < 30%	3	1	2	0	
≥ 30%, < 40%	1	1	0	0	
≥ 40%	3	1	1	1	
T cells at the invasive front (mean/high-power field [range])					
CD3	436 (112-865)	580 (265-865)	527 (149-780)	318 (112-654)	< 0.001
CD4	249 (51-516)	310 (164-516)	287 (51-489)	200 (52-514)	0.011
CD8	246 (35-640)	366 (129-512)	306 (63-640)	161 (35-338)	< 0.001
PD-1	97 (5-331)	137 (48-230)	127 (5-331)	60 (17-178)	0.002
CD4/CD8 ratio (n [%])					
CD4 ≥ CD8	29 (66)	3 (43)	8 (50)	18 (86)	0.028
CD4 < CD8	15 (34)	4 (57)	8 (50)	3 (14)	
Portion of immune cells expressing PD-1 (n [%])					
< 5%, > 0%	3 (7)	0	2 (13)	1 (5)	0.481
≥ 5%	41 (93)	7 (100)	14 (87)	20 (95)	



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0% (PD-L1 –)	12 (27)	0	2 (13)	10 (48)	0.013
> 0% (PD-L1 +)	32 (72)	7 (100)	14 (87)	11 (52)	
> 0, < 5%	16	2	5	9	
≥ 5%, < 10%	6	1	4	1	
≥ 10%, < 20%	3	1	2	0	
≥ 20%, < 30%	3	1	2	0	
≥ 30%, < 40%	1	1	0	0	
≥ 40%	3	1	1	1	
T cells at the invasive front (mean/high-power field [range])					
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CD4	249 (51-516)	310 (164-516)	287 (51-489)	200 (52-514)	0.011
CD8	246 (35-640)	366 (129-512)	306 (63-640)	161 (35-338)	< 0.001
PD-1	97 (5-331)	137 (48-230)	127 (5-331)	60 (17-178)	0.002
CD4/CD8 ratio (n [%])					
CD4 ≥ CD8	29 (66)	3 (43)	8 (50)	18 (86)	0.028
CD4 < CD8	15 (34)	4 (57)	8 (50)	3 (14)	
Portion of immune cells expressing PD-1 (n [%])					
< 5%, > 0%	3 (7)	0	2 (13)	1 (5)	0.481
≥ 5%	41 (93)	7 (100)	14 (87)	20 (95)	

EBV⁺ and MSI Gastric Cancers Harbor High PD-L1/PD-1 Expression and High CD8⁺ Intratumoral Lymphocytes



Medizinische Universität Graz


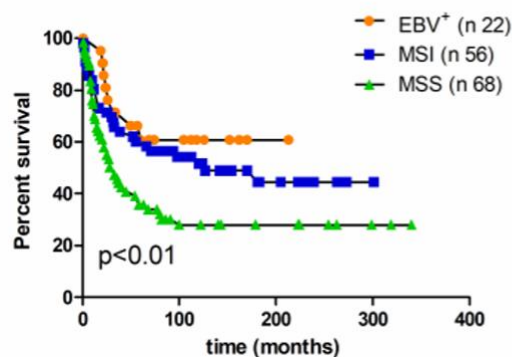
Simona De Rosa ¹, Nora Sahnane ² , Maria Grazia Tibiletti ¹, Francesca Magnoli ^{1,2},
Alessandro Vanoli ³, Fausto Sessa ^{1,2} and Anna Maria Chiaravalli ^{1,*}

Table 2. Immunophenotype of TILs and PD-L1 expression on tumor and immune cells.

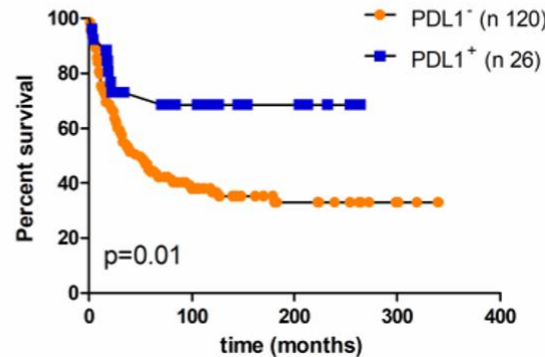
Feature	Total	EBV ⁺ Cases	MSI Cases	MSS/EBV ⁻ Cases	<i>p</i>
N. of cases	169	33	59	77	
PD-1 ⁺ cases	137 (81%)	30 (91%)	51 (86%)	56 (73%)	*
PD-1 ⁺ TILs Mean (range)	7 (0–74.6)	17.5 (0–74.6)	7 (0–35.3)	3.1 (0–26.7)	***
CD8 ⁺ TILs Mean (range)	28.9 (0–167.1)	64.2 (14.4–167.1)	23.1 (0–69.2)	15.8 (0–94.4)	*
PDL1 ⁺ TC cases	31 (18%)	15 (46%)	14 (24%)	2 (3%)	***
PDL1 ⁺ TC Mean % ^ (range)	25 (1–90)	33 (1–90)	18 (1–40)	17.5 (15–20)	**
PDL1 ⁺ IC cases	72 (42%)	31 (94%)	22 (37%)	19 (25%)	***
PDL1 ⁺ TI	31/72 (43%)	18/31 (58%)	12/22 (54%)	1/19 (5%)	***
PDL1 ⁺ IM	41/72 (57%)	13/31 (42%)	10/22 (46%)	18/19 (95%)	

Legend. TC, tumor cells; IC, immune cells; TI, tumor infiltrating pattern; IM, invasive margin * *p*-value < 0.05; ** *p*-value < 0.01; *** *p*-value < 0.001; ^ in positive cases.

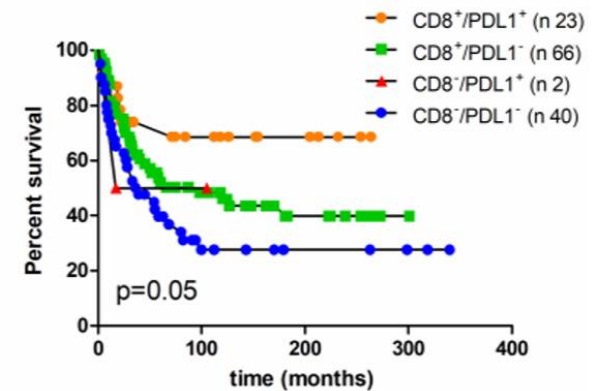
a) Type



b) PDL1 expression (all cases)



f) CD8 and PDL1





Intratumoral Immune Response to Gastric Cancer Varies by Molecular and Histologic Subtype

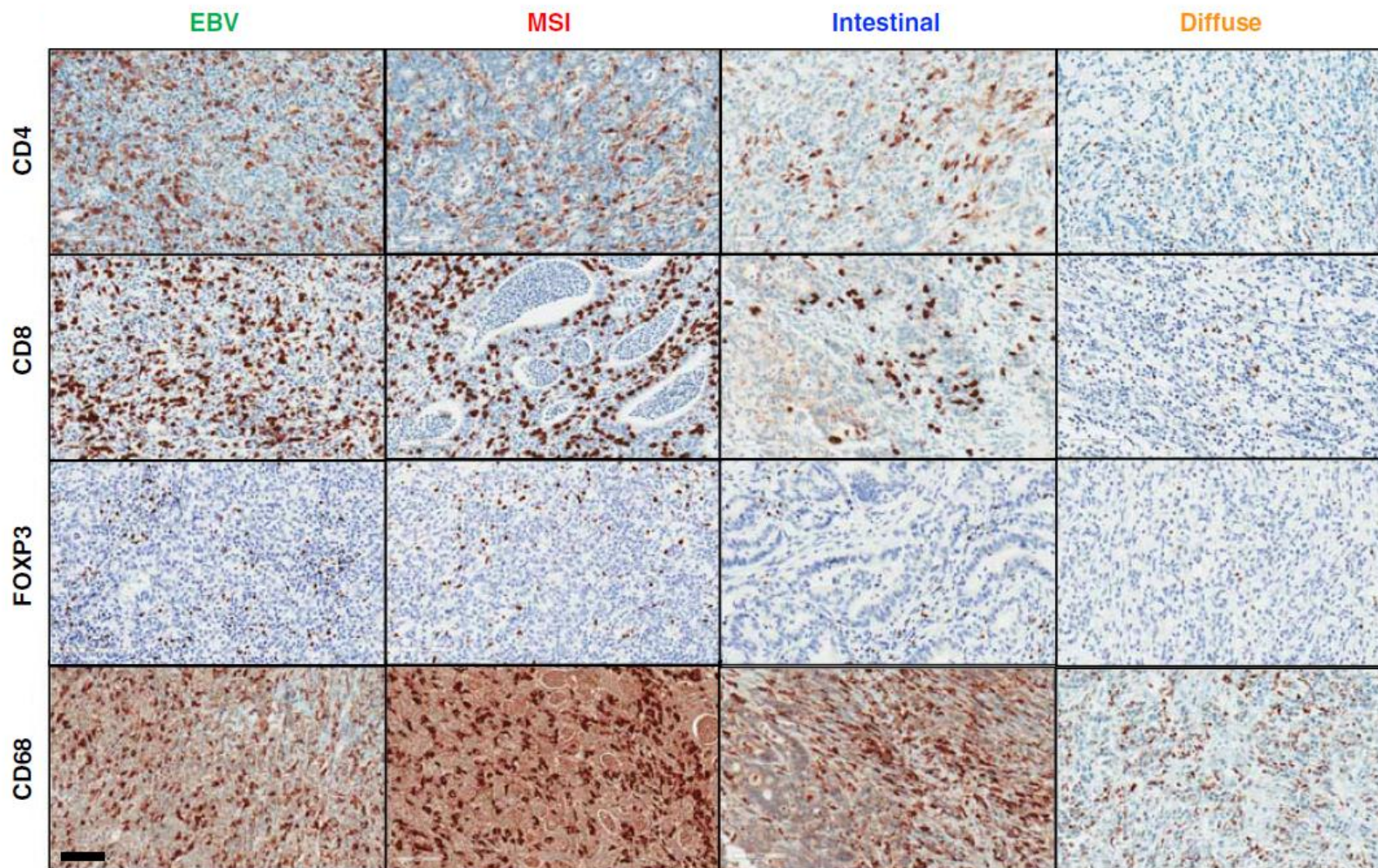
Teresa S. Kim, MD,* Edaise da Silva, PhD,† Daniel G. Coit, MD,‡
and Laura H. Tang, MD, PhD†

TABLE 1. Clinicopathologic Characteristics by Tumor Subtype

Characteristic	N (%)					P
	Total (43)	EBV (6)	MSI (11)	Intestinal (14)	Diffuse (12)	
Age (median [range]) (y)	68 (20-92)	72 (40-85)	74 (55-85)	78 (52-92)	48 (20-67)	<0.01
Sex						0.02
Male	24 (55.8)	5 (83.3)	5 (45.5)	11 (78.6)	3 (25.0)	
Female	19 (44.2)	1 (16.7)	6 (54.5)	3 (21.4)	9 (75.0)	
Tumor location						<0.01
Upper	2 (4.7)	1 (16.7)	0	0	1 (8.3)	
Middle	14 (32.6)	4 (66.7)	5 (45.5)	0	5 (41.7)	
Lower	25 (58.1)	1 (16.7)	6 (54.5)	14 (100)	4 (33.3)	
Entire	2 (4.7)	0	0	0	2 (16.7)	
<i>Helicobacter pylori</i> infection						0.03
Absent	32 (74.4)	2 (33.3)	7 (63.6)	12 (85.7)	11 (91.7)	
Present	11 (25.6)	4 (66.7)	4 (36.4)	2 (14.3)	1 (8.3)	
NLR (mean [range])	3.0 (1.1-6.8)	3.8 (2.0-5.6)	3.1 (1.2-6.8)	3.0 (1.3-4.8)	2.5 (1.1-4.1)	0.19
Tumor stage						0.39
T1	9 (20.9)	3 (50.0)	3 (27.3)	3 (21.4)	0	
T2	7 (16.3)	1 (16.7)	2 (18.2)	3 (21.4)	1 (8.3)	
T3	15 (34.9)	2 (33.3)	3 (27.3)	4 (28.6)	6 (50.0)	
T4	12 (27.9)	0	3 (27.3)	4 (28.6)	5 (41.7)	
Lymphovascular invasion						0.07
Absent	13 (30.2)	4 (66.7)	2 (18.2)	2 (14.3)	5 (41.7)	
Present	30 (69.8)	2 (33.3)	9 (81.8)	12 (85.7)	7 (58.3)	
Perineural invasion						0.01
Absent	17 (39.5)	3 (50.0)	7 (63.6)	7 (50.0)	0	
Present	26 (60.5)	3 (50.0)	4 (36.4)	7 (50.0)	12 (100.0)	
Nodal stage						0.45
N0	18 (41.9)	4 (66.7)	5 (45.5)	5 (35.7)	4 (33.3)	
N1	6 (14.0)	1 (16.7)	2 (18.2)	3 (21.4)	0	
N2	10 (23.3)	0	3 (27.3)	4 (28.6)	3 (25.0)	
N3	9 (20.9)	1 (16.7)	1 (9.1)	2 (14.3)	5 (41.7)	

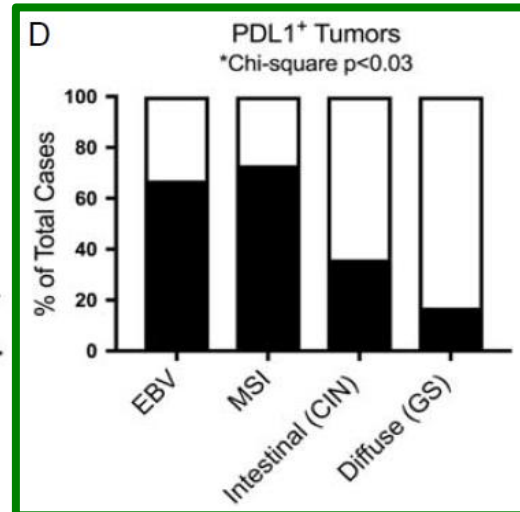
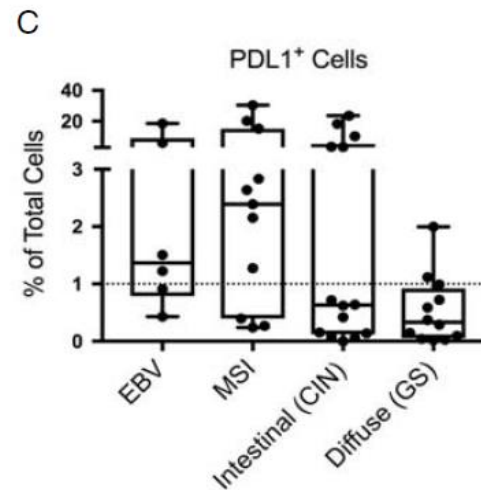
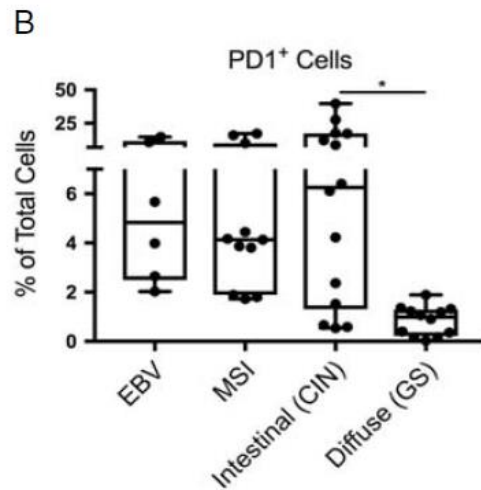
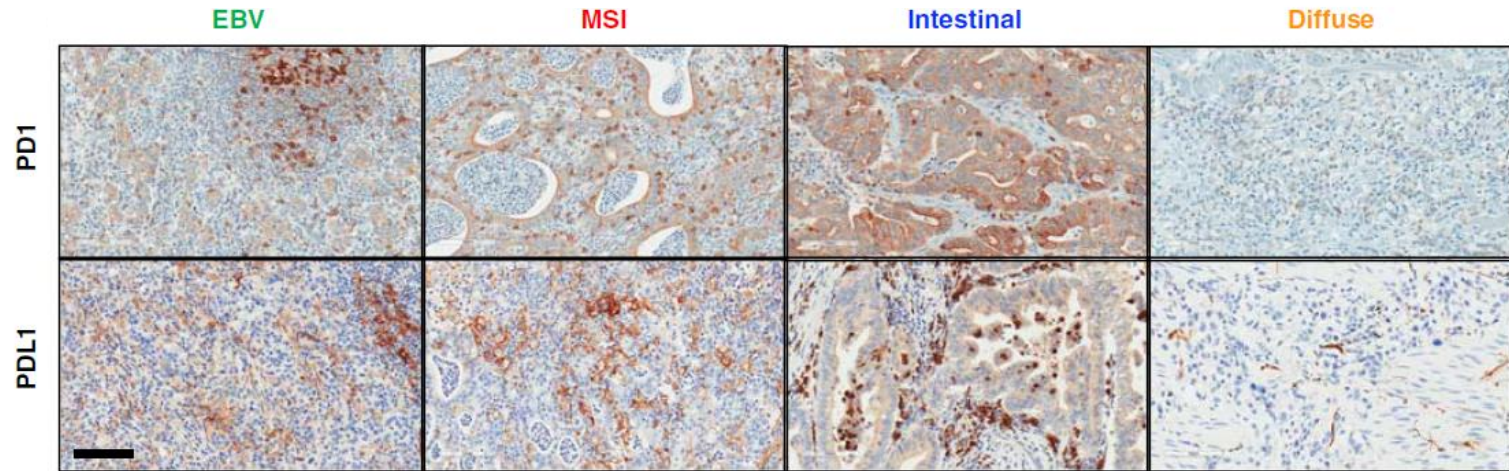
Intratumoral Immune Response to Gastric Cancer Varies by Molecular and Histologic Subtype

Teresa S. Kim, MD, Edaise da Silva, PhD,† Daniel G. Coit, MD,‡
and Laura H. Tan, MD PhD†*



Intratumoral Immune Response to Gastric Cancer Varies by Molecular and Histologic Subtype

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and Laura H. Tang, MD, PhD†



Clinical Utility of the Combined Positive Score for Programmed Death Ligand-1 Expression and the Approval of Pembrolizumab for Treatment of Gastric Cancer



Medizinische Universität Graz

Karina Kulangara, PhD; Nancy Zhang, MD; Ellie Corigliano, PhD; Lindsay Guerrero, MS; Stephanie Waldroup, BSc; Dipeshkumar Jaiswal, MS; Malinka Jansson, MS; Supriya Shah, PhD; Debra Hanks, MD; Jiangdian Wang, PhD; Jared Lunceford, PhD; Mary J. Savage, PhD; Jonathan Juco, MD; Kenneth Emancipator, MD

Scoring Methods

The CPS is given by summing the number of PD-L1–stained cells (tumor cells, lymphocytes, macrophages) and dividing the result by the total number of viable tumor cells, multiplied by 100, and is expressed by the following formula:

$$\text{CPS} = \frac{\text{No. PD-L1–stained cells (tumor cells, lymphocytes, macrophages)}}{\text{Total No. of viable tumor cells}} \times 100$$

Although theoretically that quantity can exceed 100, the maximum score is defined as 100. A minimum of 100 viable tumor cells must be present in the PD-L1–stained slide (sectioned tumor biopsy or resection tissue) for the specimen to be considered adequate for evaluation. Tumor cells must show partial or complete membrane staining ($\geq 1^+$) to be counted as “stained,” whereas immune cells are counted if there is any staining.

Clinical Utility of the Combined Positive Score for Programmed Death Ligand-1 Expression and the Approval of Pembrolizumab for Treatment of Gastric Cancer

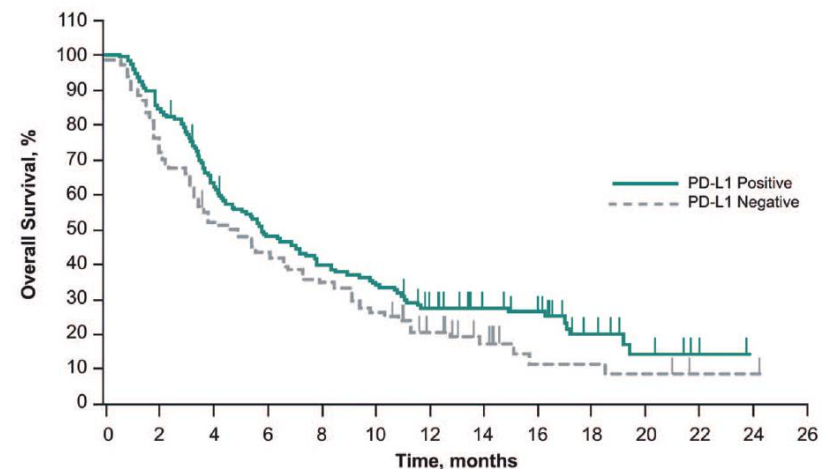
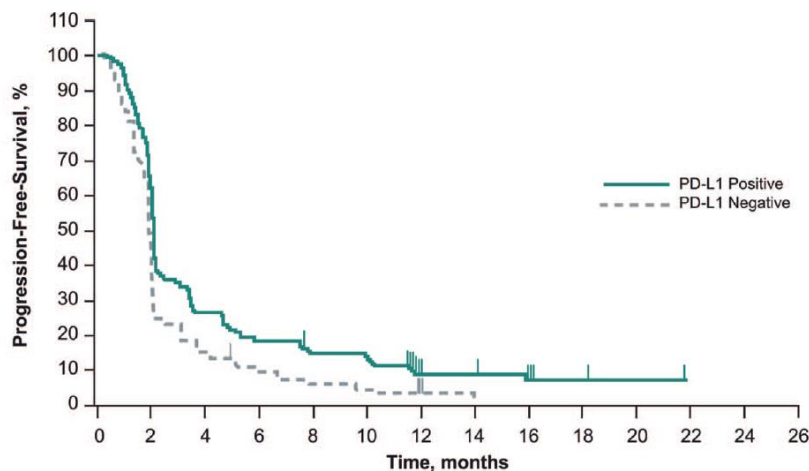


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Table 4. Objective Response Rate (ORR) From KEYNOTE-059 by Combined Positive Score (CPS) and Tumor Proportion Score (TPS; N = 257)

	Total (N = 257), No. (%)	Response	No Response	ORR, %	Odds Ratio
CPS ≥ 1	148 (57.6)	24	124	16.2	2.8
CPS < 1	109 (42.4)	7	102	6.4	
TPS ≥ 1	32 (12.5)	5	27	15.6	1.4
TPS < 1	225 (87.5)	26	199	11.6	



Meta-analysis of microsatellite instability in relation to clinicopathological characteristics and overall survival in gastric cancer

K. Polom^{1,6}, L. Marano², D. Marrelli¹, R. De Luca³, G. Roviello^{4,5}, V. Savelli¹, P. Tan⁷ and F. Roviello¹
















Reference	Relative weight (%)	Hazard ratio	Hazard ratio
An <i>et al.</i> ³⁰	6.42	1.26 (0.89, 1.78)	
Bae <i>et al.</i> ²⁵	5.49	1.80 (1.10, 2.94)	
Chuiaravalli <i>et al.</i> ⁵³	4.44	0.64 (0.33, 1.25)	
Cristescu <i>et al.</i> ⁴	6.16	0.58 (0.39, 0.86)	
Czopek <i>et al.</i> ⁵⁴	4.63	0.62 (0.33, 1.17)	
Falchetti <i>et al.</i> ⁵⁵	4.96	0.52 (0.29, 0.93)	
Fang <i>et al.</i> ³⁶	4.59	0.51 (0.27, 0.97)	
Gazvoda <i>et al.</i> ⁵⁶	2.32	0.53 (0.16, 1.73)	
Giampieri <i>et al.</i> ⁵⁷	6.14	0.24 (0.16, 0.36)	
Inada <i>et al.</i> ³⁷	5.31	0.74 (0.44, 1.25)	
Kim <i>et al.</i> ¹⁰	4.64	0.74 (0.39, 1.39)	
Kim <i>et al.</i> ⁵	3.35	0.56 (0.23, 1.36)	
Marrelli <i>et al.</i> ⁸	6.17	0.62 (0.42, 0.91)	
Oki <i>et al.</i> ¹⁴	4.89	1.06 (0.59, 1.91)	
Oliveira <i>et al.</i> ⁶⁰	5.31	0.62 (0.37, 1.04)	

Table 1 Summary of meta-analyses investigating relationship between microsatellite instability status and demographic and clinicopathological characteristics

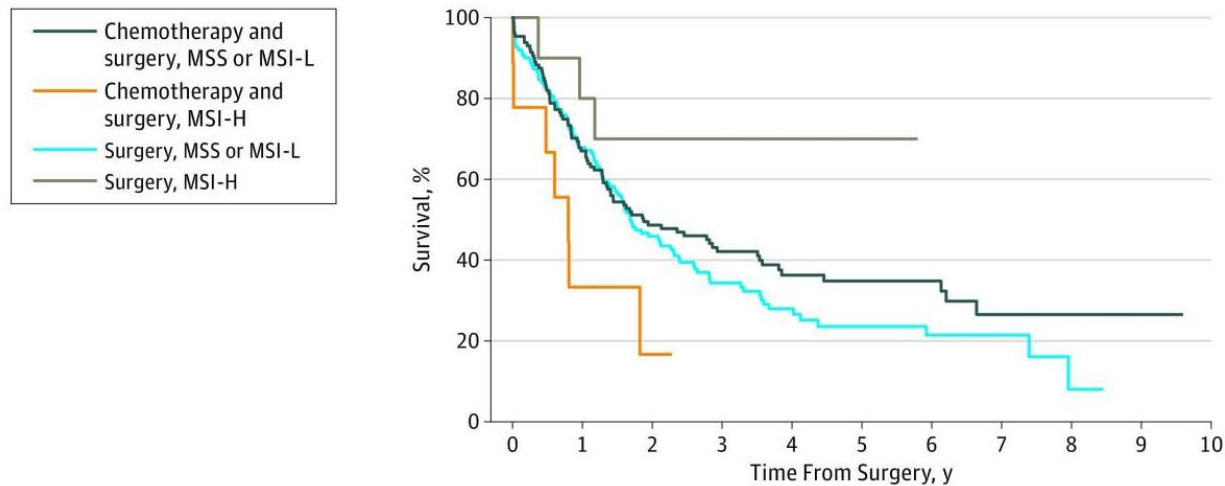
	No. of studies	Pooled odds ratio	P	Heterogeneity		Effect model
				I ² (%)	P	
Sex (F versus M)	35	1.57 (1.31, 1.89)	< 0.001	54.1	< 0.001	Random
Age (≥ 65 versus < 65 years)	48	1.58 (2.20, 1.13)	< 0.001	0	< 0.001	Fixed
Laurén classification (intestinal versus diffuse/mixed)	34	2.23 (1.94, 2.57)	< 0.001	29.9	0.05	Fixed
Tumour location (upper versus middle/lower)	36	0.38 (0.32, 0.44)	< 0.001	43.9	< 0.05	Fixed
Lymph node metastasis (yes versus no)	35	0.70 (0.57, 0.86)	< 0.001	61.0	< 0.001	Random
TNM stage (I–II versus III/IV)	8	1.77 (1.47, 2.13)	< 0.001	0	< 0.001	Fixed

Values in parentheses are 95 per cent confidence intervals.

Mismatch Repair Deficiency, Microsatellite Instability, and Survival

An Exploratory Analysis of the Medical Research Council Adjuvant Gastric Infusional Chemotherapy (MAGIC) Trial

Elizabeth C. Smyth, MB, BCh, MSc; Andrew Wotherspoon, MD; Clare Peckitt, MSc; David Gonzalez, PhD; Sanna Hulkki-Wilson, BSc, MSc; Zakaria Eltahir, PhD; Matteo Fassan, MD, PhD; Massimo Rugge, MD, FRCG; Nicola Valeri, MD, PhD; Alicia Okines, MD; Madeleine Hewish, MD, PhD; William Allum, MD; Sally Stenning, MSc; Matthew Nankivell, MSc; Ruth Langley, MD, PhD; David Cunningham, MD, FMedSci



Correlation of MMRD With MSI Status

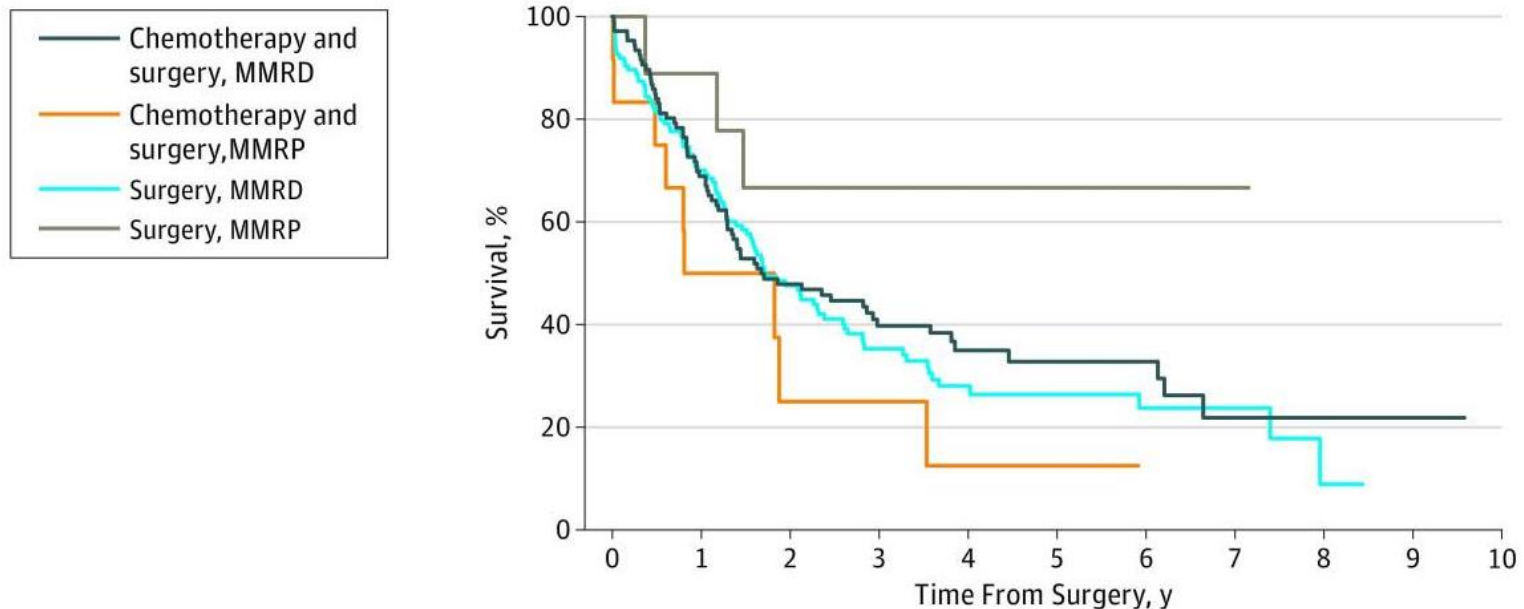
A total of 254 patients had MSI and MMR results available. Of these, 15 of 17 MSI-H tumors had MMRD detected. Thirteen of 15 MLH1-negative tumors (86.7%) with available MSI results had MSI-H tumors compared with 4 of 239 MLH1-positive tumors (1.7%). This finding results in a sensitivity of MLH1 deficiency testing for MSI prognosis of 76.5% (95% CI, 50.1%-93.2%) and a specificity of 99.2% (95% CI, 97.0%-99.9%). All patients with absent MSH2 and MSH6 had MSI-H tumors. Twelve of 16 patients (75.0%) with absent PMS2 and MSI results had MSI-H tumors compared with 4 of 236 patients (1.7%) with PMS2-positive tumors. Overall concordance between MSI-H and MMRD status was 97.6%.



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Conclusions and Relevance

In the MAGIC trial, MMRD and high MSI were associated with a positive prognostic effect in patients treated with surgery alone and a differentially negative prognostic effect in patients treated with chemotherapy. If independently validated, MSI or MMRD determined by preoperative biopsies could be used to select patients for perioperative chemotherapy.



Microsatellite Instability and Programmed Cell Death-Ligand 1 Expression in Stage II/III Gastric Cancer

Post Hoc Analysis of the CLASSIC Randomized Controlled study

Yoon Young Choi, MD,*† Hyunki Kim, MD, PhD,‡ Su-Jin Shin, MD, PhD,§ Ha Yan Kim, MS,¶
 Jinae Lee, PhD,¶ Han-Kwang Yang, MD, PhD,|| Woo Ho Kim, MD, PhD,** Young-Woo Kim, MD, PhD,††
 Myeong-Cherl Kook, MD, PhD,†† Young Kyu Park, MD, PhD,‡‡ Hyung-Ho Kim, MD, PhD,§§
 Hye Seung Lee, MD, PhD,¶¶ Kyung Hee Lee, MD, PhD,|||| Mi Jin Gu, MD, PhD,***
 Seung Ho Choi, MD, PhD,††† SoonWon Hong, MD, PhD,‡‡‡ Jong Won Kim, MD, PhD,§§§
 Woo Jin Hyung, MD, PhD,* Sung Hoon Noh, MD, PhD,*¶¶¶ and Jae-Ho Cheong, MD, PhD*†¶¶¶|||

TABLE 2. Associations Between Microsatellite Instability Status and Programmed Cell Death Ligand 1 Expression in Tumor Cells and Stromal Immune Cells

	MSI Status			sPD-L1 Status		
	MSS (n = 543)	MSI-H (n = 39)	P	Negative (n = 417)	Positive (n = 165)	P
tPD-L1 status						<0.001*
Negative (n = 566)	530 (97.6)				150 (90.9)	
Positive (n = 16)	13 (2.4)				15 (9.1)	
sPD-L1 status						
Negative (n = 417)	400 (73.7)					
Positive (n = 165)	143 (26.3)					

*Fisher exact test.

TABLE 3. Disease-free Survival Analyzed Using a Multivariable Cox Proportional-hazards Model

	HR (95% CI)	P
Treatment		<0.001
Surgery only	Reference	
Surgery + CTx	0.618 (0.472–0.809)	
Age, yr	1.016 (1.004–1.028)	0.009
Tumor grade		0.037
Intestinal	Reference	
Nonintestinal	1.385 (1.019–1.881)	
pTNM stage *		<0.001
II	Reference	
III	2.092 (1.568–2.79)	
MSI status		0.008
MSS	Reference	
MSI-H	0.301 (0.123–0.736)	
sPD-L1 status		0.044
Negative	Reference	
Positive	0.714 (0.514–0.991)	

CTx indicates adjuvant chemotherapy (capecitabine plus oxaliplatin).

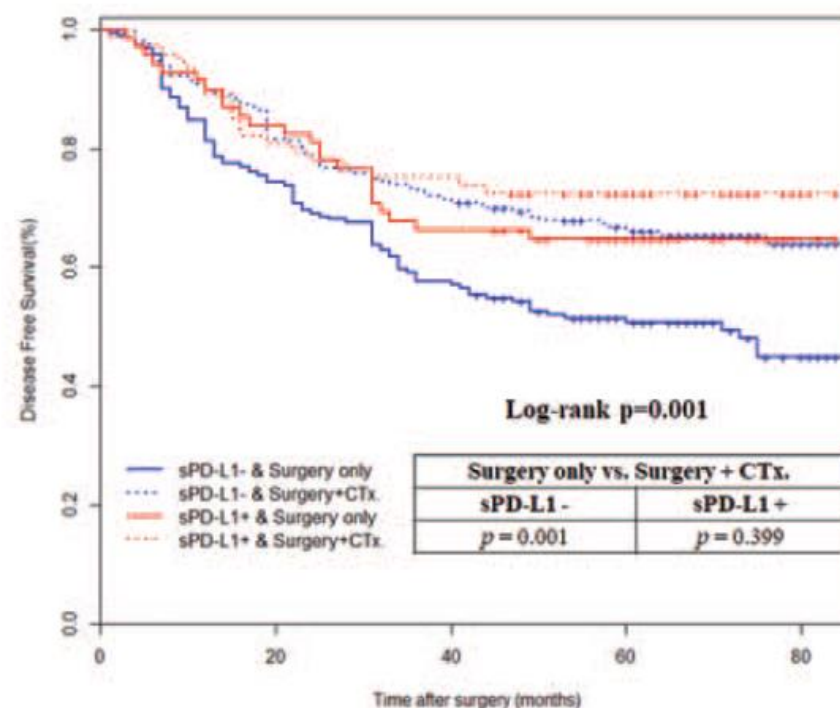
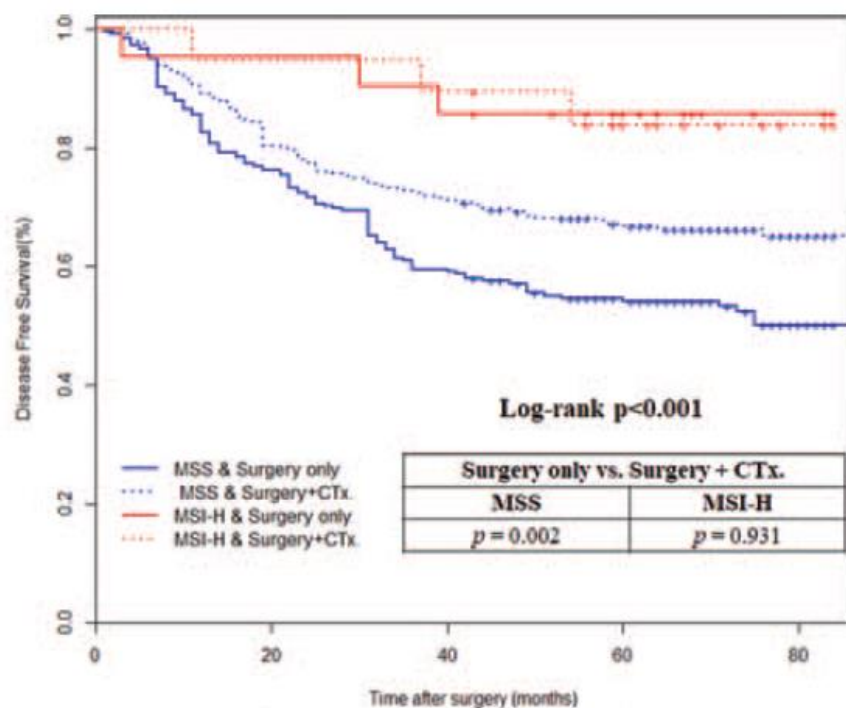
*According to TNM 6th edition.



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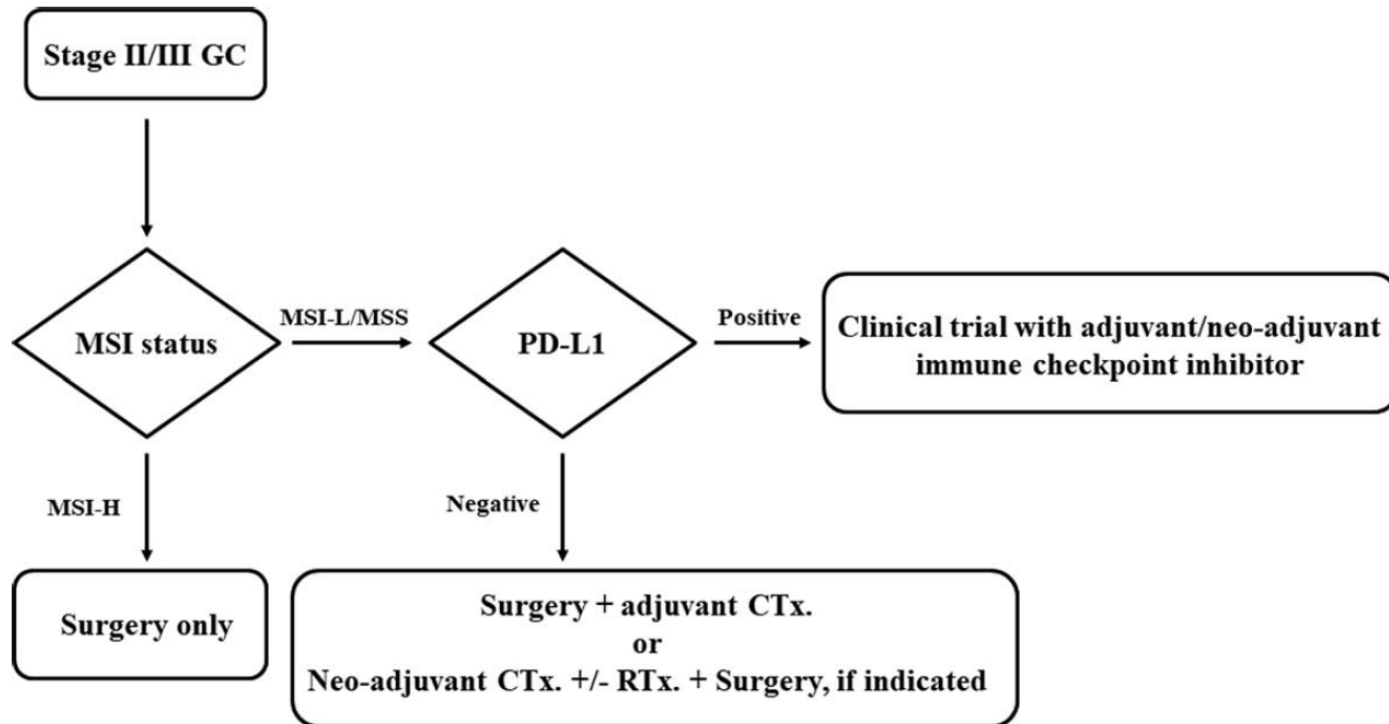


FIGURE 4. A suggested treatment algorithm for stage II/III gastric cancer according to MSI status and PD-L1 expression. CTx indicates chemotherapy; GC, gastric cancer; RTx, radiotherapy.

Agenda



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- Classification of gastric cancer
 - Histology
 - Molecular pathology
- Predictive pathology
 - HER2
 - PD-L1
 - Microsatellite instability
- **Sporadic vs hereditary gastric cancer**
- Take home messages

Gastric Cancer in Hereditary Cancer Syndromes

Syndrome	Genetic alteration
Lynch syndrome (HNPCC)	Mismatch repair genes (<i>MLH1</i> , <i>MSH2</i> , <i>MSH6</i> , <i>PMS2</i>)
Li-Fraumeni syndrome	<i>TP53</i>
Familial adenomatous polyposis (FAP)	<i>APC</i>
Hamartomatous polyposis syndromes	
▪ Peutz-Jeghers syndrome	▪ <i>STK1 (LKB1)</i>
▪ Juvenile polyposis	▪ <i>SMAD4 / BMPR1A</i>

Familial / Hereditary Gastric Cancer



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Syndrome	Genetic alteration
Hereditary Diffuse Gastric Cancer (HDGC)	<i>CDH1</i> (mainly)
Gastric Adenocarcinoma and Proximal Polyposis of the Stomach (GAPPS)	<i>APC</i> promoter
Familial Intestinal Gastric Cancer (FIGC)	Unknown

Hereditary Diffuse Gastric Cancer (HDGC)



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Hereditary Diffuse Gastric Cancer (HDGC)



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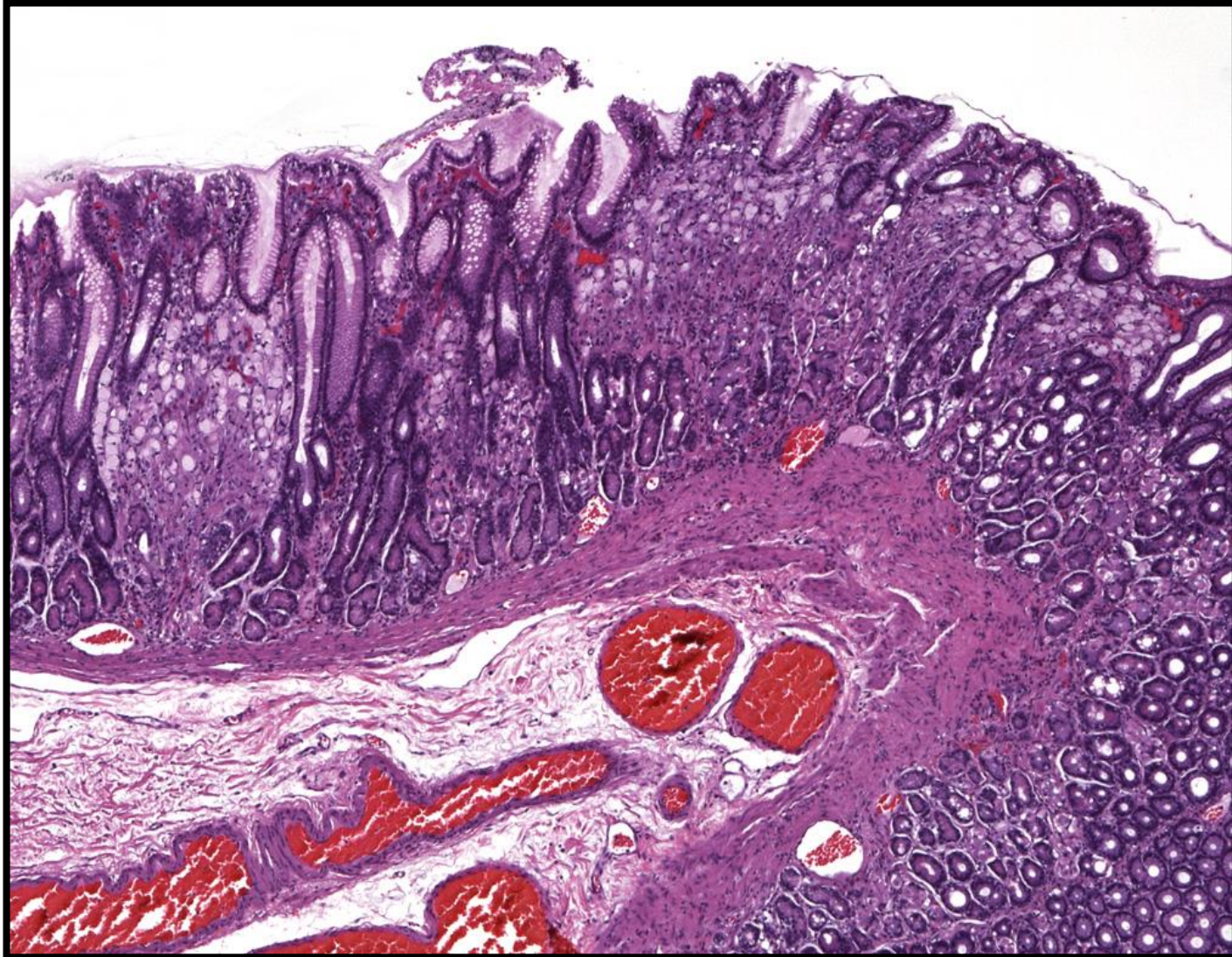


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Hereditary Diffuse Gastric Cancer (HDGC)



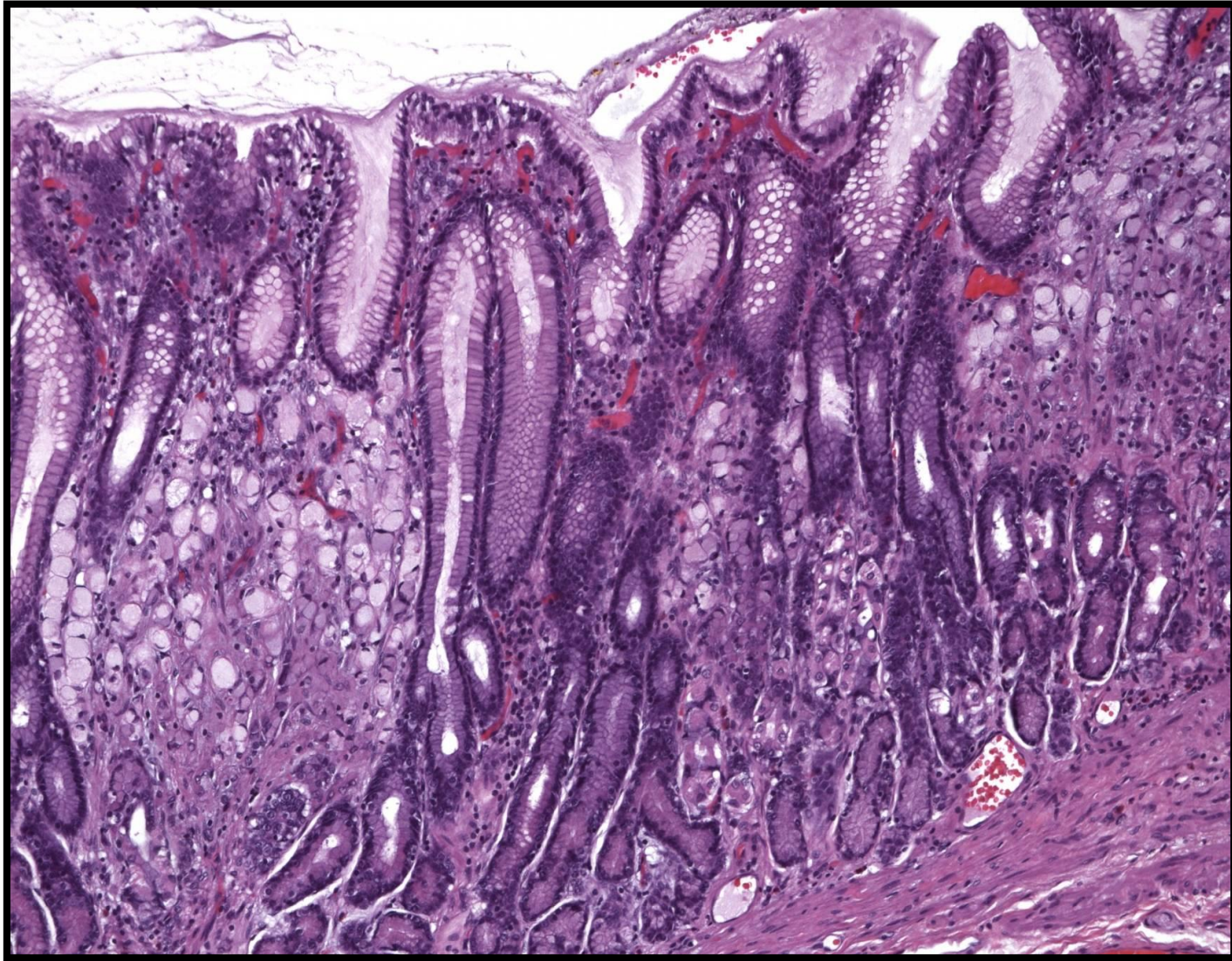
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Hereditary Diffuse Gastric Cancer (HDGC)



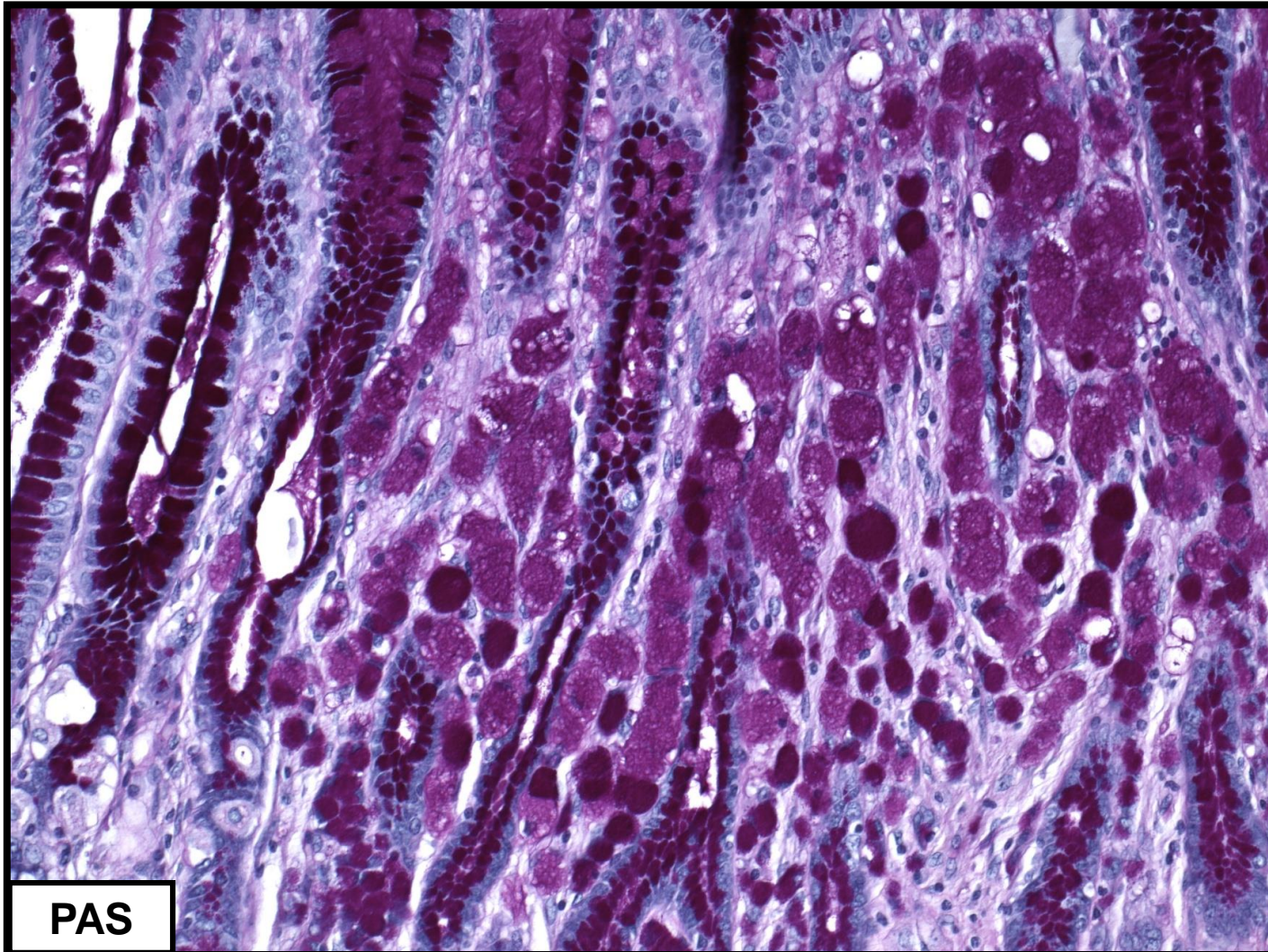
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Hereditary Diffuse Gastric Cancer (HDGC)



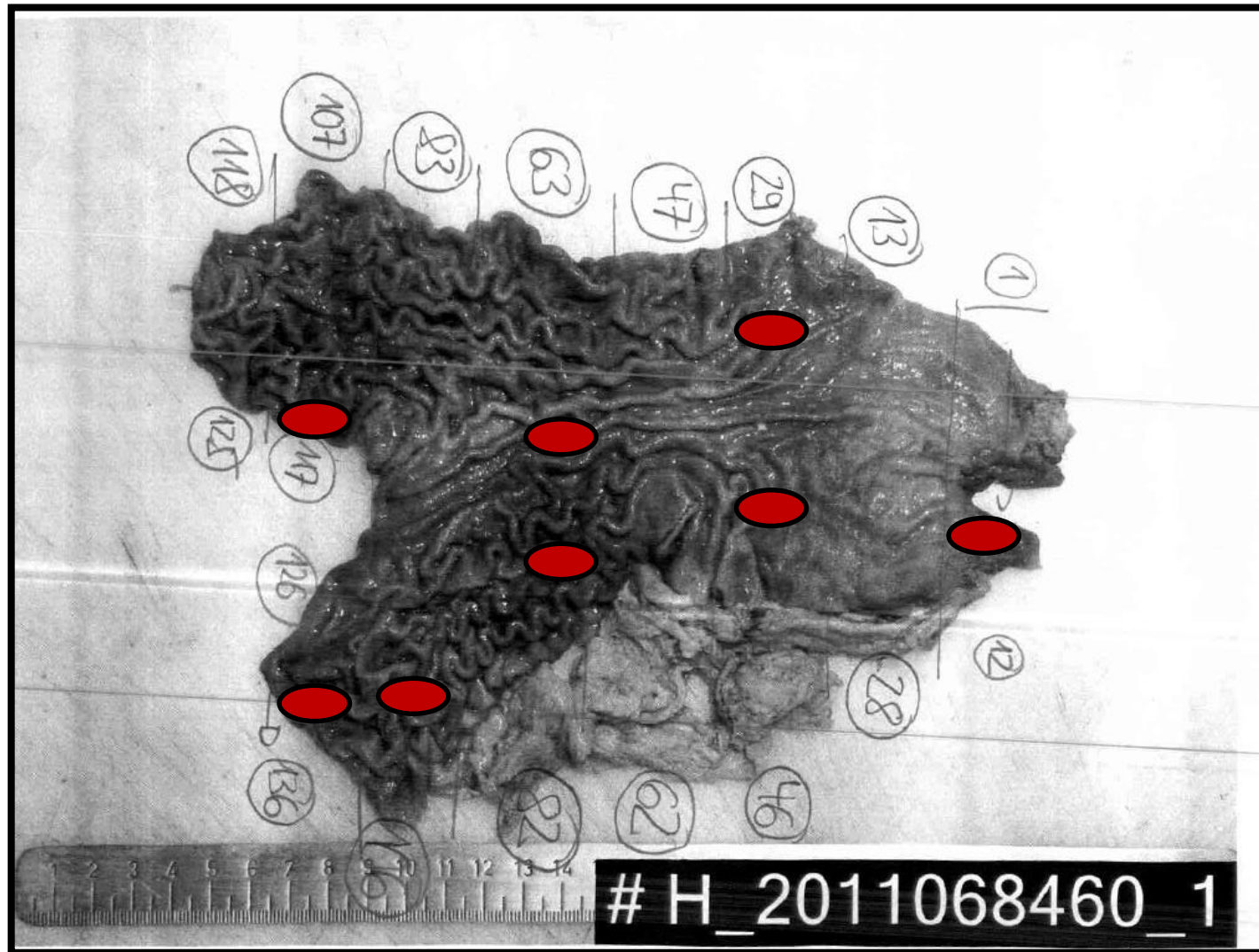
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Hereditary Diffuse Gastric Cancer (HDGC)



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HDGC Precursor Lesions



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Fig. 4.24 Pagetoid spread of signet-ring cells (arrow heads) representing Tis, and invasion of the lamina propria by a signet-ring cell (empty star), indicating T1a invasive intramucosal signet-ring cell carcinoma.

Pagetoid spread of signet-ring cells (pTis)

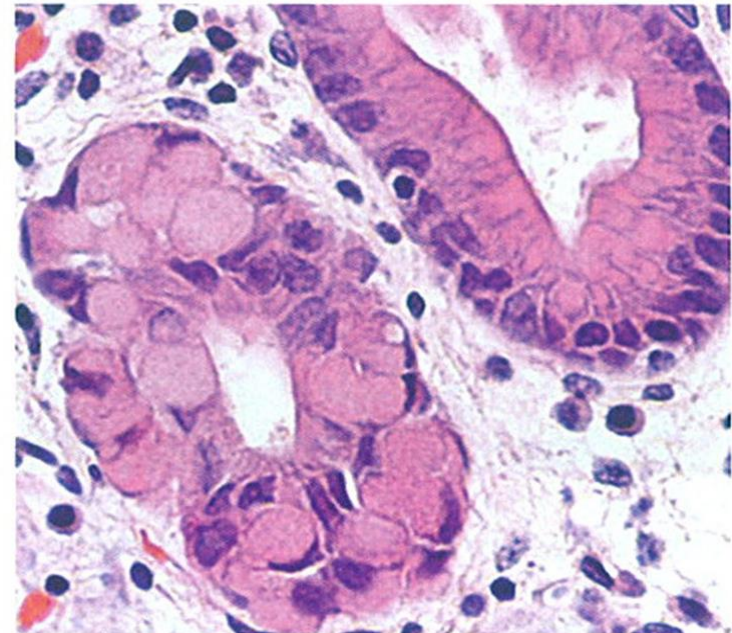


Fig. 4.23 Signet ring cell carcinoma *in situ* (Tis).

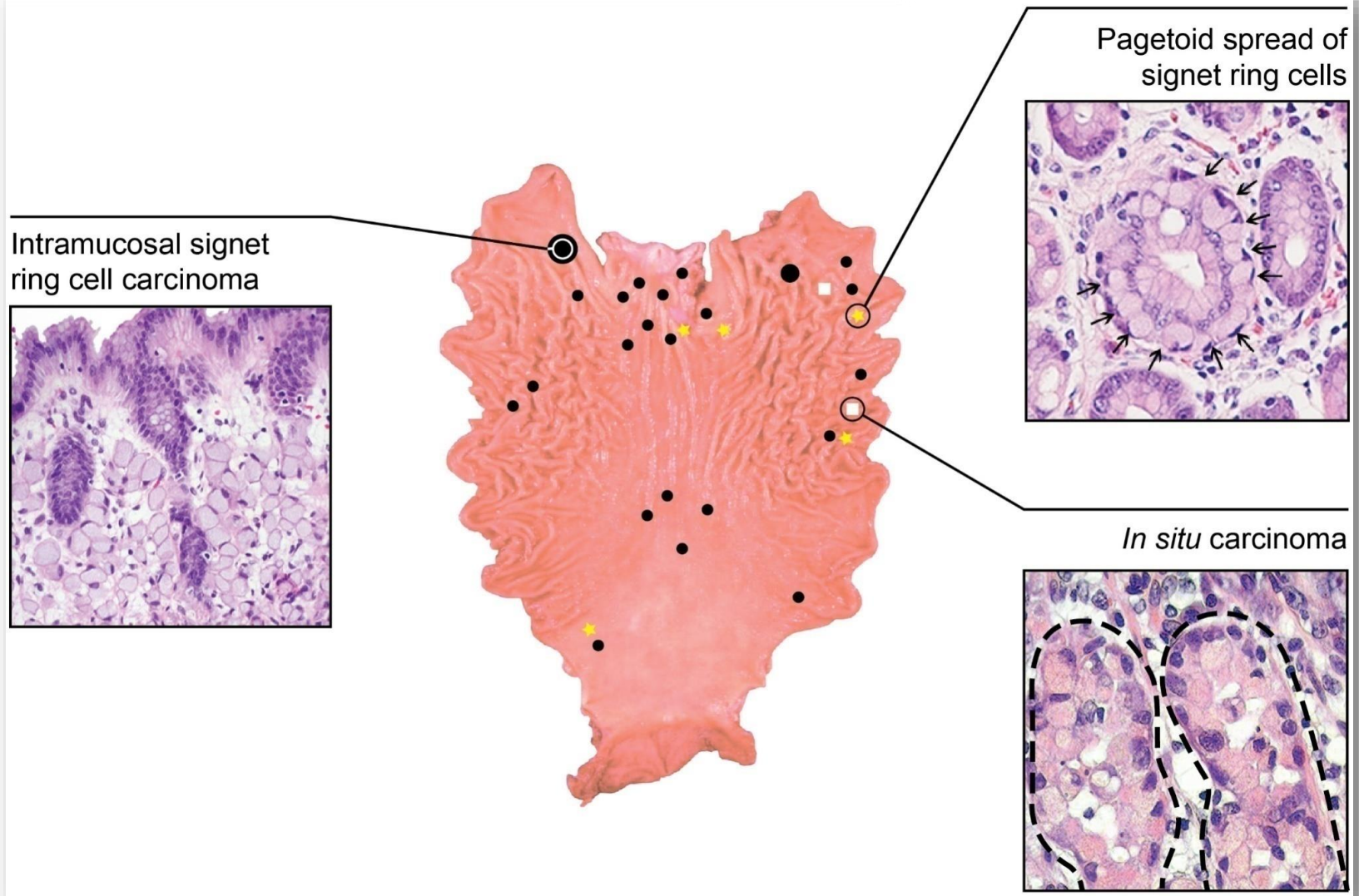
Signet-ring cell carcinoma in situ (pTis)

Familial gastric cancer: genetic susceptibility, pathology, and implications for management

Carla Oliveira*, Hugo Pinheiro*, Joana Figueiredo, Raquel Seruca, Fátima Carneiro



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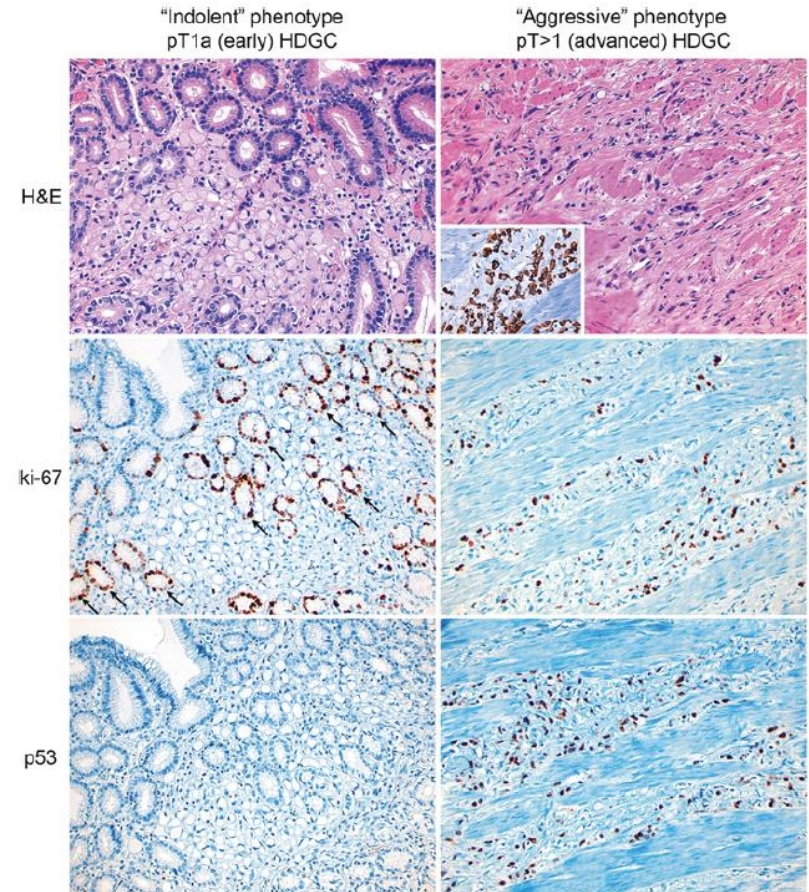
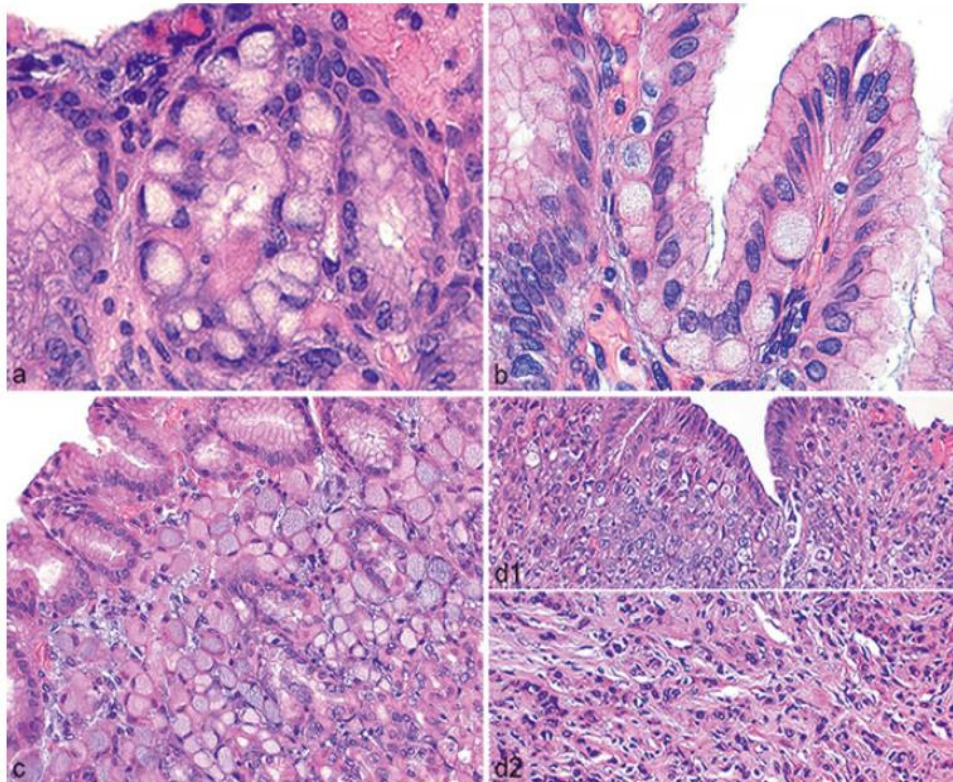


Histopathological, Molecular, and Genetic Profile of Hereditary Diffuse Gastric Cancer: Current Knowledge and Challenges for the Future

Rachel S. van der Post, Irene Gullo, Carla Oliveira, Laura H. Tang, Heike I. Grabsch, Maria O'Donovan, Rebecca C. Fitzgerald, Han van Krieken, and Fátima Carneiro



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Hereditary diffuse gastric cancer: updated clinical guidelines with an emphasis on germline *CDH1* mutation carriers

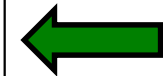
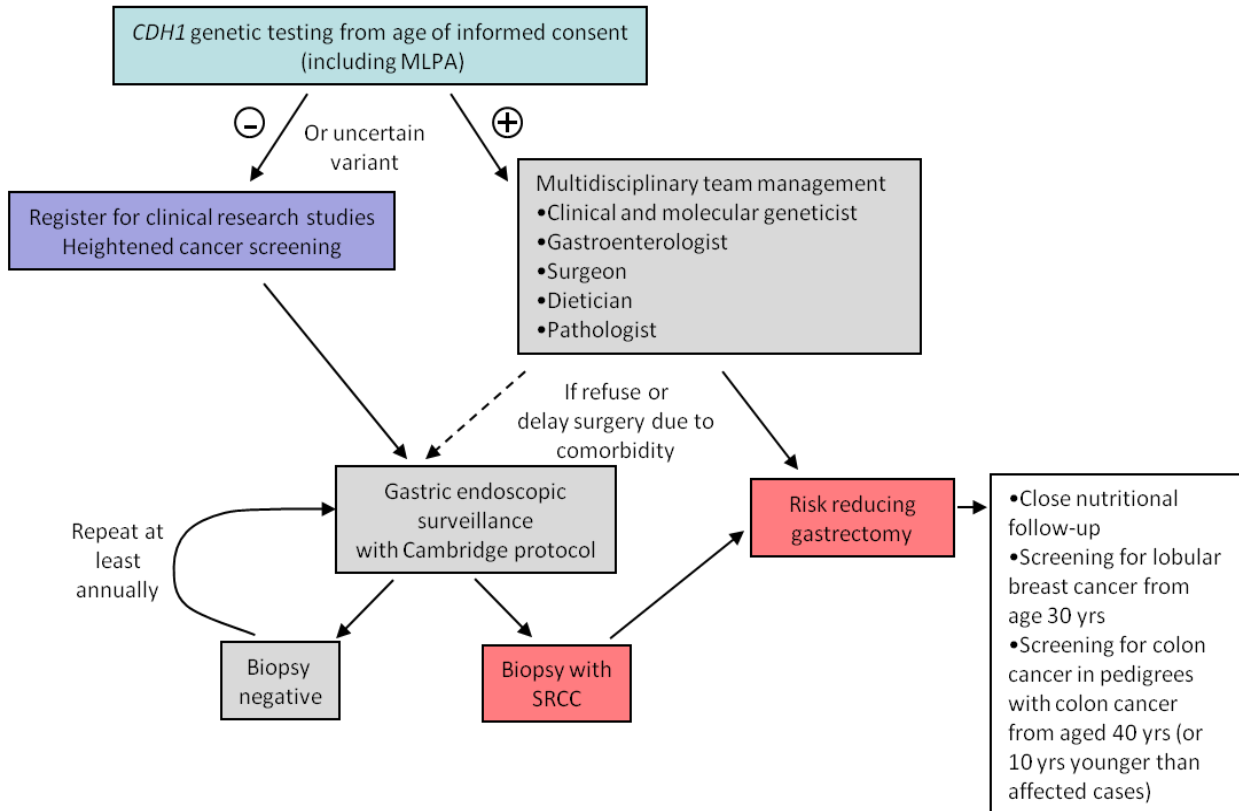


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<i>Established criteria*</i>
<ul style="list-style-type: none"> • 2 GC cases regardless of age, at least one confirmed DGC • One case of DGC <40 • Personal or family history of DGC and LBC, one diagnosed <50
<i>Families in whom testing could be considered*</i>
<ul style="list-style-type: none"> • Bilateral LBC or family history of 2 or more cases of LBC <50 • A personal or family history of cleft lip/palate in a patient with DGC • <i>In situ</i> signet ring cells and/or pagetoid spread of signet ring cells

*Including 1st and 2nd degree relatives

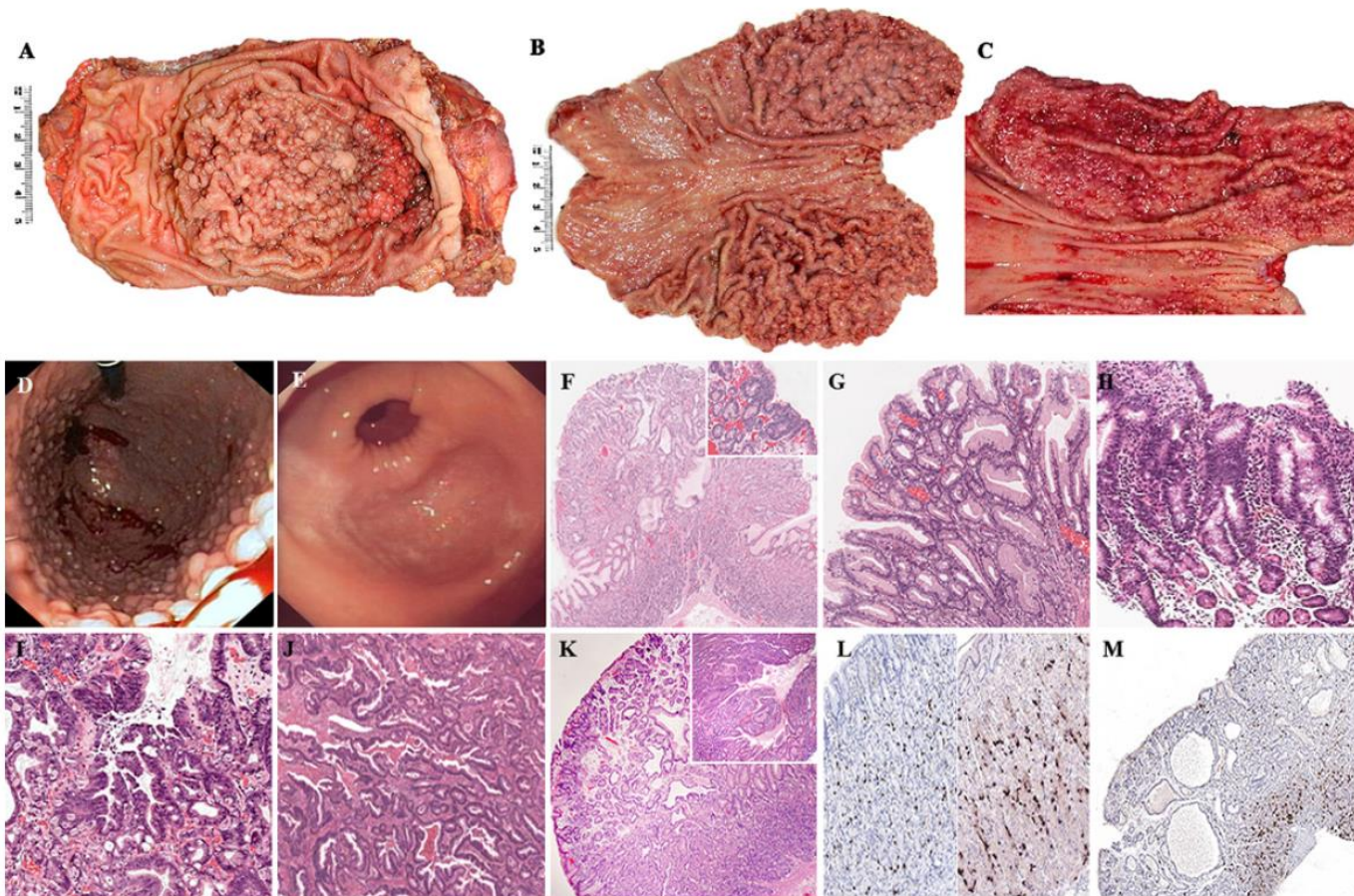


Gastric adenocarcinoma and proximal polyposis of the stomach (GAPPS): a new autosomal dominant syndrome



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D L Worthley,¹ K D Phillips,² N Wayte,³ K A Schrader,⁴ S Healey,⁵ P Kaurah,⁴
A Shulkes,⁶ F Grimpen,⁷ A Clouston,⁷ D Moore,⁸ D Cullen,⁹ D Ormonde,⁹
D Mounkley,¹⁰ X Wen,¹¹ N Lindor,¹² F Carneiro,¹¹ D G Huntsman,⁴
G Chenevix-Trench,⁵ G K Suthers^{2,13}





Point Mutations in Exon 1B of *APC* Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant

Jun Li,¹ Susan L. Woods,² Sue Healey,¹ Jonathan Beesley,¹ Xiaoqing Chen,¹ Jason S. Lee,¹ Haran Sivakumaran,¹ Nicci Wayte,¹ Katia Nones,¹ Joshua J. Waterfall,³ John Pearson,^{1,4} Anne-Marie Patch,¹ Janine Senz,⁵ Manuel A. Ferreira,¹ Pardeep Kaurah,⁶ Robertson Mackenzie,⁷ Alireza Heravi-Moussavi,⁸ Samantha Hansford,⁵ Tamsin R.M. Lannagan,² Amanda B. Spurdle,¹ Peter T. Simpson,^{9,10} Leonard da Silva,^{9,10} Sunil R. Lakhani,^{9,10,11} Andrew D. Clouston,^{12,13} Mark Bettington,^{10,13,14} Florian Grimpén,¹⁵ Rita A. Busuttil,^{16,17,18} Natasha Di Costanzo,¹⁶ Alex Boussioutas,^{16,17,18,19} Marie Jeanjean,²⁰ George Chong,²¹ Aurélie Fabre,^{22,23,24} Sylviane Olschwang,^{22,23,24} Geoffrey J. Faulkner,²⁵ Evangelos Bellos,^{4,26} Lachlan Coin,⁴ Kevin Rioux,²⁷ Oliver F. Bathe,^{28,29} Xiaogang Wen,^{30,31} Hilary C. Martin,³² Deborah W. Neklason,³³ Sean R. Davis,³ Robert L. Walker,³ Kathleen A. Calzone,³ Itzhak Avital,³⁴ Theo Heller,³⁵ Christopher Koh,³⁵ Marbin Pineda,³ Udo Rudloff,³⁶ Martha Quezado,³⁷ Pavel N. Pichurin,³⁸ Peter J. Hulick,³⁹

(Author list continued on next page)

Gastric adenocarcinoma and proximal polyposis of the stomach (GAPPS) is an autosomal-dominant cancer-predisposition syndrome with a significant risk of gastric, but not colorectal, adenocarcinoma. We mapped the gene to 5q22 and found loss of the wild-type allele on 5q in fundic gland polyps from affected individuals. Whole-exome and -genome sequencing failed to find causal mutations but, through Sanger sequencing, we identified point mutations in *APC* promoter 1B that co-segregated with disease in all six families. The mutations reduced binding of the YY1 transcription factor and impaired activity of the *APC* promoter 1B in luciferase assays. Analysis of blood and saliva from carriers showed allelic imbalance of *APC*, suggesting that these mutations lead to decreased allele-specific expression in vivo. Similar mutations in *APC* promoter 1B occur in rare families with familial adenomatous polyposis (FAP). Promoter 1A is methylated in GAPPS and sporadic FGPs and in normal stomach, which suggests that 1B transcripts are more important than 1A in gastric mucosa. This might explain why all known GAPPS-affected families carry promoter 1B point mutations but only rare FAP-affected families carry similar mutations, the colonic cells usually being protected by the expression of the 1A isoform. Gastric polyposis and cancer have been previously described in some FAP-affected individuals with large deletions around promoter 1B. Our finding that GAPPS is caused by point mutations in the same promoter suggests that families with mutations affecting the promoter 1B are at risk of gastric adenocarcinoma, regardless of whether or not colorectal polyps are present.

Neoplastic Lesions of Gastric Adenocarcinoma and Proximal Polyposis Syndrome (GAPPS) Are Gastric Phenotype



Medizinische Universität Graz

Willem B. de Boer, MBBS, FRCPA,* Hooi Ee, MBBS, FRACP, PhD,†
and Marian P. Kumarasinghe, MBBS, MD, FRCPA*

Fundic Gland Polyps (10/15 Patients)

Well developed FGP-like lesions, defined as “microcysts lined by fundic epithelium including oxyphilic cells,” were seen in 10 of 14 patients with polyposis (Fig. 2) but not in the biopsy of the 1 case of adenocarcinoma.

Hyperproliferative Aberrant Pits (12/15 Patients)

The most frequent pathology was disorganized proliferation of specialized/oxyntic glands high up in the mucosa involving the attenuated foveolar region around the gastric pits, forming a polypoid lesion (Figs. 3A, B). This imparted the appearance of upward migration of the tubular neck and the hyperproliferative nature was highlighted by heightened Ki-67 activity (Fig. 3C) giving the impression of an expanded proliferative zone. The surface epithelium was normal.

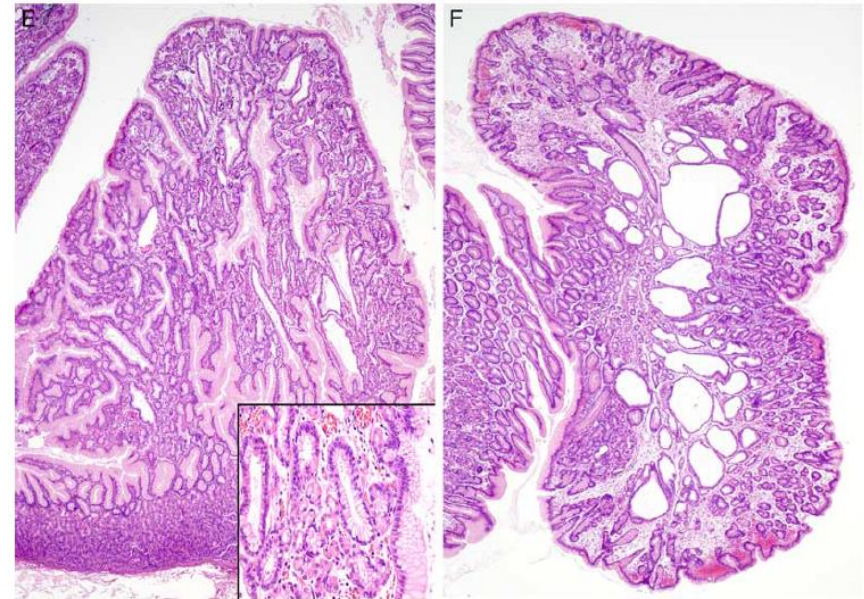


TABLE 2. Immunohistochemical Profile and Proliferation Index in Polypoid Lesions Associated With GAPPS

	Number	MUC2	MUC5AC	MUC6	CDX2	CD10	Beta Catenin	P53	Ki-67*
HPAP†	> 150	Negative	Positive	Positive deep	Variable positive	Negative	Negative	Positive	Increased
FGP‡	> 40	Negative	Positive	Negative	Variable positive	Negative	Negative	Negative	Normal
Adenoma	3	Negative	Positive	Positive focal	Variable positive	Negative	Negative	Variable positive	Increased
Dysplasia	7	Negative	Positive	Negative	Variable positive	Negative	Negative	Positive	Increased
Carcinoma	1	Negative	Positive	Negative	Variable positive	Negative	Negative	Positive	Increased

*Increased Ki-67 activity in the lesional area compared with the proliferative zone of the adjacent tubular neck region.

†Hyperproliferative aberrant pits.

‡Fundic gland polyps.

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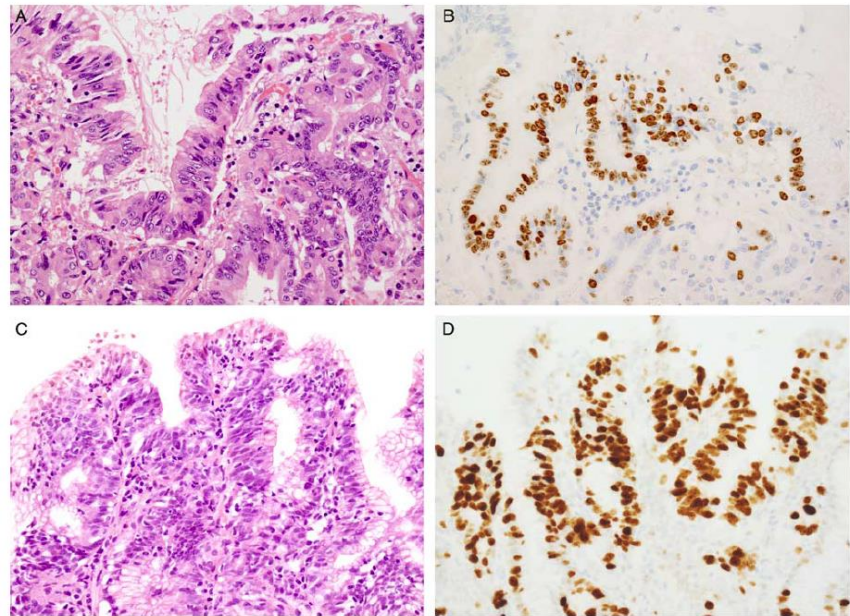


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Take Home Messages I

- **Poorly cohesive carcinoma (PCC)** comprises different phenotypes (signet-ring cell vs. PCC-NOS) with different molecular background and behaviour
- **Gastric carcinoma with lymphoid stroma** is related to EBV infection or microsatellite instability (MSI-H). Tumours harbour cytotoxic T-cells and often show PD-L1 positivity (compare below)
- Different types of clinically relevant **molecular subtypes** have been described (TCGA, ACRG etc). Assessment can be done by immunohistochemistry and *in situ* hybridization
- **HER2** assessment needs to be done following international Guidelines (Rüschoff et al.); select the best differentiated areas (intestinal morphology) for testing

Take Home Messages II

- EBV-positive or microsatellite instable (MSI-H) gastric cancers are potential candidates for **tumor immunotherapy** as they harbor the highest PDL-1 positivity rates
- Potential responders may also be identified among EBV-negative and MSS/MSI-L cancers (intestinal>diffuse): **PDL-1 assessment** needs to be done applying the CPS Score
- **Neoadjuvant chemotherapy** may have a negative effect on patients with MSI-H gastric cancer (post hoc analysis from MAGIC trial) → MMR/MSI testing on pretreatment biopsies
- Gastric cancer may occur within distinct **hereditary cancer syndromes** (e.g. Lynch syndrome, Peutz-Jeghers syndrome) and also distinct **hereditary gastric cancer syndromes**, including HDGC and GAPPS



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Thank you very much for your kind attention!

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