JOURNAL OF INONU LIVER TRANSPLANTATION INSTITUTE

DOI: 10.14744/jilti.2025.96646
J Inonu Liver Transpl Inst 2025;3(Suppl. 1): S63-S70

Review

Integration of Comprehensive Genomic Profiling into Clinical Settings for Gastrointestinal System Cancer Enhancing Diagnosis, Molecular Classification, and Therapeutic Precision

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Abstract

The advent of comprehensive genomic profiling (CGP) has revolutionized cancer diagnosis and personalized treatment and has become increasingly standard in oncology for advanced solid tumors. In gastrointestinal (GI) cancers, which include colorectal, gastric, pancreatic, esophageal, biliary tract cancers, and hepatocellular carcinomas, genomic insights have increasingly informed clinical decision-making. This review provides an overview of the current landscape of CGP integration into clinical practice for GI cancers, highlighting clinical applications, challenges, and future perspectives.

Keywords: Comprehensive genomic profiling, gastrointestinal cancers, liquid biopsy, molecular classification, precision medicine, targeted therapy

Please cite this article as "Akagunduz B, Sahin Y, Buyukdogan M, Yakicier MC. Integration of Comprehensive Genomic Profiling into Clinical Settings for Gastrointestinal System Cancer Enhancing Diagnosis, Molecular Classification, and Therapeutic Precision. J Inonu Liver Transpl Inst 2025;3(Suppl. 1): S63-S70".

Gastrointestinal cancers are among the leading causes of cancer-related morbidity and mortality globally. Traditional diagnostic approaches—relying on histopathology and imaging—fail to fully capture the molecular heterogeneity that influences tumor behavior and treatment response. The integration of comprehensive genomic profiling (CGP) via next-generation sequencing (NGS) and complementary techniques like immunohistochemistry (IHC) has transformed this landscape, enabling more precise tumor classification and personalized therap.[1]

In solid tumor analysis, CGP detects a broad spectrum of genetic alterations—including single nucleotide variants, insertions-deletions, copy number changes, gene fusions, and key signatures like microsatellite instability (MSI), tumor mutational burden (TMB), and homologous recombination deficiency (HRD). Liquid biopsy techniques, analyzing circulating tumor DNA (ctDNA), further enable non-invasive, real-time tumor profiling, monitoring resistance mechanisms, and detecting minimal residual disease.[2]

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By providing detailed molecular insights, CGP uncovers actionable mutations and molecular subtypes across GI cancers, thereby guiding targeted therapies and immunotherapies. Numerous studies report that molecular profiling identifies actionable mutations in over one-third of patients with solid tumors, leading to improved treatment outcomes and survival. Incorporating CGP and liquid biopsy into routine practice is now a pivotal step toward achieving true precision oncology, revolutionizing diagnosis, prognosis, and personalized management of GI cancers in many leading medical centers worldwide.[3,4]

Role of CGP in Colorectal Cancer Diagnosis, Classification and Managment

Vogelstein's multistep model of colorectal cancer (CRC) development elucidates how CRC evolves through a series of accumulating genetic alterations, transforming normal epithelium into invasive carcinoma.[5] This understanding of disease progression provides a crucial foundation for the therapeutic application of CGP. By identifying specific genetic mutations at various stages; such as APC, KRAS, BRAF, p53, or mismatch repair deficiencies, CGP enables clinicians to tailor targeted therapies and immunotherapies accordingly.

The model also helps in prognostication, as certain mutations like BRAF, TP53 or MSI status correlate with tumor aggressiveness, aiding risk stratification and treatment planning. Overall, integrating CGP into clinical practice based on the principles outlined by Vogelstein's model fosters personalized treatment approaches, improves outcomes, and guides the development of novel targeted interventions by highlighting critical molecular pathways involved in gastrointestinal cancers.[6]

The first predictive genomic biomarker incorporated into the standard of care for metastatic colorectal cancer (mCRC) was the KRAS gene; mutations in specific codons of KRAS were found to negate the effectiveness of anti-EGFR therapies such as cetuximab and panitumumab.[7] In addition to KRAS, the mutation statuses of NRAS and BRAF are also essential for guiding treatment decisions. Patients with wild-type (non-mutated) KRAS, NRAS and BRAF are considered suitable candidates for anti-EGFR therapies, as mutations in these genes confer resistance. However, additional resistance mechanisms—both primary (innate) and acquired—limit the benefits for many patients. Increasing evidence demonstrates that resistance arises from a complex network of molecular alterations that promote tumor growth independently of EGFR signaling. These include amplification of ERBB2 (HER2) and MET, activation of the PI3K and AKT pathways, extracellular domain mutations of EGFR, and rare kinase fusions. Moreover, the BRAF V600E mutation is associated with a poorer prognosis and often necessitates combination therapies or alternative treatment strategies to improve outcomes.[8, 9]

NCCN recommends testing for RET and NTRK1, 2, and 3 translocations; ERBB2 (HER2) amplification; as well as PIK3CA, BRAF V600E, and KRAS G12C mutations. Additionally, testing for microsatellite instability-high (MSI-H), tumor mutational burden-high (TMB-H), POLE, and POLD mutations is advised in patients with colorectal cancer.[10]

Circulating tumor DNA (ctDNA) testing has emerged as a revolutionary tool in the personalized management of colorectal cancer (CRC), offering a minimally invasive method to access tumor-specific genetic information through a simple blood draw.[11]

ctDNA testing can be broadly categorized into tumor-informed and tumor-agnostic approaches. This approach involves first performing comprehensive genomic profiling of the patient's tumor tissue to identify specific tumor mutations, structural variants, or alterations. Subsequently, personalized assays are designed targeting these known mutations to detect ctDNA in the patient's blood.[12]

Although still investigational, ctDNA has potential in screening high-risk populations for early detection of CRC. It can identify tumor-derived mutations before clinical symptoms or radiological evidence emerge, potentially enabling earlier intervention and improving outcomes.[13]

Monitoring ctDNA levels during therapy provides a dynamic measure of tumor burden. Decreasing ctDNA correlates with response, while rising levels may indicate treatment failure or progression, often before imaging detects changes. This real-time feedback allows for more timely adjustments to therapy.[14]

Postoperative ctDNA analysis can identify residual microscopic disease that may not be visible on imaging. The presence of ctDNA after surgical resection signifies a higher risk of recurrence, supporting decisions for adjuvant chemotherapy. Several studies have shown that ctDNA positivity post-surgery predicts relapse with high sensitivity and specificity.[15, 16]

During targeted treatments—for example, anti-EGFR therapy—ctDNA can detect emergent mutations (such as RAS or BRAF mutations) associated with resistance. Early detection of these mutations enables clinicians to modify treatment strategies before clinical progression occurs.[14, 16] Regular ctDNA testing during follow-up can detect molecular signs of recurrence months before radiological evidence appears, allowing for earlier intervention and potentially improved survival.[17]

In summary, ctDNA testing enhances the precision of CRC management by providing real-time, minimally invasive insights into tumor dynamics, resistance mechanisms, and residual disease. Its integration into clinical practice supports personalized treatment, timely decision-making, and improved patient outcomes.

Role of CGP in Gastric Cancer Diagnosis, Classification and Managment

Gastric cancer exhibits substantial molecular heterogeneity, which has important implications for prognosis and treatment. Different molecular subtypes demonstrate diverse genetic alterations, signaling pathway activations, and clinical behaviors.

Recent advances have led to the development of molecular classification systems based on genomic alterations identified through next generation sequencing (NGS) of gastric cancer samples. Notable among these are The Cancer Genome Atlas (TCGA) and Asian Cancer Research Group (ACRG) classifications, which categorize gastric cancers into distinct molecular subtypes:

Chromosomal instability (CIN): Characterized by aneuploidy, amplifications of receptor tyrosine kinases (e.g., HER2, EGFR), and TP53 mutations. These tumors often present with intestinal histology and respond to targeted therapies against HER2 or EGFR.

Genomically stable (GS): Frequently associated with diffuse histology and mutations affecting cell adhesion, such as CDH1 and RHOA mutations. These tumors tend to be more aggressive and less amenable to targeted therapy.

MSI-high: Marked by microsatellite instability and mismatch repair deficiency. These tumors tend to have a high mutational burden and are more likely to respond to immunotherapy.

Epstein-Barr virus (EBV)-positive: Characterized by frequent PIK3CA mutations, amplification of immune-related genes, and PD-L1 overexpression. These tumors may also benefit from immunotherapy.[18-20]

CGP provides the molecular signatures necessary for this classification, informing prognosis and guiding personalized therapy. The molecular insights derived from CGP have paved the way for targeted therapies, transforming gastric cancer management:

HER2 Amplification: Approximately 15-20% of gastric cancers overexpress HER2. CGP identifies HER2 gene amplifications or mutations, directing the use of HER2-targeted agents like trastuzumab, pertuzumab, and trastuzumab emtansine, which improve survival in HER2-positive tumors.

PIK3CA Mutations: Common in EBV-positive tumors, these mutations may be targeted through PI3K inhibitors, though clinical efficacy is under ongoing investigation.

FGFR2 Amplification: Several gastric tumors exhibit FGFR2 gene amplification. FGFR inhibitors are being evaluated in clinical trials as targeted options for these tumors.

MET Pathway Alterations: Amplifications or overexpression of MET are other potential targets, with some MET inhibitors in clinical trials or limited clinical use.

MSI-High Tumors and Immunotherapy: Tumors with high microsatellite instability or high tumor mutational burden (TMB) identified through CGP are more responsive to immune checkpoint inhibitors like pembrolizumab and nivolumab.

Claudin 18.2 (CLDN18.2) is gaining attention as an emerging marker because of its selective expression in gastric cancer cells. Novel therapeutic agents targeting CLDN18.2, such as monoclonal antibodies and bispecific constructs, are under development and showing promising clinical activity.

Other Emerging Targets: CGP continues to reveal novel alterations such as mutations in ERBB2 (HER2), MET, and other signaling pathways, expanding the repertoire of actionable targets.[20, 21]

The Role of Comprehensive Genomic Profiling in Esophageal and Esophagogastric Junction Cancers Diagnosis, Classification and Managment

Esophageal and esophagogastric cancers present significant clinical challenges due to their aggressive nature and late-stage diagnosis, with limited effective treatment options for advanced disease. Recent advances in high-throughput genomic technologies have transformed our understanding of their biology, offering new avenues for personalized medicine. CGP provides an invaluable tool to dissect tumor heterogeneity, refine diagnosis, classify tumors at a molecular level, and uncover actionable targets, all geared toward improving clinical outcomes.

Distinguishing between esophageal squamous cell carcinoma (ESCC) and esophageal adenocarcinoma (EAC) is crucial given their distinct clinical behaviors and therapeutic responses. CGP significantly improves diagnostic precision by revealing subtype-specific genetic signatures, especially in cases where histopathology is ambiguous or when metastatic lesions obscure primary classification. Next-generation sequencing (NGS) platforms analyze an extensive array of gene mutations, amplifications, deletions, and rearrangements, often uncovering clinically relevant alterations that confirm or refine the diagnosis of esophageal cancer subtypes.[22, 23]

While traditional classifications relied primarily on histological features, CGP delineates esophageal tumors into biologically and therapeutically relevant molecular subgroups:

EAC: Characterized by a higher frequency of mutations in KRAS and ERBB2 (HER2) amplification, alongside alterations in RAS/MEK/MAPK and TGF-β signaling pathways. These genomic signatures support targeted therapy approaches, such as HER2 inhibitors, and provide prognostic insights.[22, 23]

ESCC: Demonstrates a distinctive landscape with frequent alterations in PI3K/AKT/mTOR, NOTCH1, PTEN, FGFR1, and KEAP1/NRF2, alongside aberrant cell cycle regulation. Hierarchical clustering based on copy number alterations (CNAs) further stratifies ESCC into molecular subgroups, which correlate with clinical outcomes and guide personalized treatment decision-making.[22, 23]

This detailed molecular taxonomy offers prognostic utility and helps identify patients who might benefit from emerging targeted and immune-based therapies. The power of CGP lies in uncovering actionable genetic alterations:

HER2 Amplification: Present in a subset of EACs, HER2 overexpression can be targeted with trastuzumab or pertuzumab, offering survival benefits.

FGFR Alterations: FGFR2 gene amplifications and fusions are emerging targets, with several FGFR inhibitors under clinical evaluation.

EGFR and PI3K/AKT/mTOR Pathways: Amplifications and mutations in these pathways suggest potential for targeted inhibition, with ongoing trials testing relevant agents.

Emerging Targets in Immunotherapy: Alterations such as high tumor mutational burden (TMB) and PD-L1 expression, identified via CGP, identify patients who may respond to immune checkpoint blockade. Although less common than in other cancers, these biomarkers are gaining relevance in esophageal cancer.

NCCN currently recommends immunohistochemistry (IHC) for CLDN18.2 and/or molecular testing for HER2/ERBB2 status, microsatellite instability (MSI) or mismatch repair (MMR) deficiency, programmed death ligand-1 (PD-L1) expression, tumor mutational burden-high (TMB-H), neurotrophic tropomyosin-related kinase (NTRK) gene fusions, rearranged during transfection (RET) gene fusions, and BRAF V600E mutations in the clinical management of advanced esophageal and esophagogastric junction (EGJ) cancers. When tissue samples are limited or when patients are unable to undergo a traditional biopsy, testing with a validated next-generation sequencing (NGS) assay—performed in a CLIA-certified laboratory—may be considered to provide comprehensive molecular profiling. This approach allows for molecular insights that can guide targeted therapies and immunotherapy choices, especially in cases where obtaining sufficient tissue is challenging.[24]

As ongoing research continues to uncover novel targets and develop tailored therapies, integrating CGP into clinical practice will be pivotal in transforming esophageal cancer from a largely incurable disease to one amenable to precision medicine.

Role of CGP in Hepatocellular Carcinoma Diagnosis, Classification and Managment

Hepatocellular carcinoma (HCC) is characterized by diverse molecular alterations, including activation of oncogenic signaling pathways such as Wnt-TGFβ, PI3K-AKT-mTOR, RAS-MAPK, MET, IGF, and Wnt-β-catenin. Additionally, mutations in TP53 and the TERT promoter are commonly observed.[25]

Despite this molecular complexity, targeted therapies with proven differential benefit for specific molecularly defined HCC subgroups have yet to be developed or approved. Although numerous targetable genetic alterations have been identified in HCC patient samples, their overall prevalence remains relatively low compared to other cancers. While detecting these mutations can inform and guide targeted treatment strategies, their limited frequency means only a subset of HCC patients are likely to benefit from such therapies.[26]

While biomarkers like MSI, TMB, and HRD are important in cancer immunotherapy broadly, their roles in HCC are limited due to low prevalence, lack of standardized thresholds, and inconsistent predictive value. Notably, the emerging role of liquid biopsy—particularly circulating tumor DNA (ctDNA)—offers promising implications for early detection of hepatocellular carcinoma, especially in high-risk populations such as cirrhotic patients. Additionally, liquid biopsy techniques are showing potential in the early detection of recurrence post-liver transplantation, enabling minimally invasive, real-time monitoring of tumor dynamics and residual disease that may not be captured through conventional imaging. These innovations could revolutionize surveillance strategies, allowing for timely intervention and personalized management.[25,27]

According to recent NCCN guidelines, there is no established indication for routine molecular profiling in all HCC cases; however, it should be considered on a case-by-case basis. Clinical trials exploring molecular profiling and targeted therapies are strongly encouraged for this patient population. Tumor molecular testing may be warranted in cases with atypical histology, combined hepatocellular-cholangiocarcinoma (cHCC-CCA), unusual clinical presentations, or when enrolling in clinical trials.[28]

The Role of Comprehensive Genomic Profiling in Biliary Tract Cancer: Diagnosis, Molecular Classification, and Targeted Therapy

Biliary tract cancers (BTCs) represent a spectrum of malignancies arising from epithelial cells of the bile ducts, including cholangiocarcinoma (CCA) arising in the intrahepatic, perihilar or distal biliary tree, and gallbladder carcinoma. CGP is transforming the diagnosis, molecular classification, and targeted therapy of BTCs, including intrahepatic and extrahepatic cholangiocarcinoma as well as gallbladder cancer.

BTCs are rich in clinically actionable molecular alterations and CGP enables identification of specific genomic mutations and fusions (such as FGFR2, IDH1/2, ERBB2/HER2, BRAF, and KRAS), improving the accuracy of diagnosis and detection of rare but actionable alterations in BTC.[29] This molecular insight complements histologic and radiologic findings, especially in cases with ambiguous pathology or atypical clinical presentations. Approximately 40% of BTCs harbor potential druggable genetic alterations. For this reason, molecular analysis should be carried out before or during first-line treatment to timely establish the best therapeutic option for second or subsequent lines.[30]

The NCCN recommends biomarker testing in BTCs, including CGP with broad gene panels to identify actionable alterations such as IDH1/2, FGFR2, BRAF, HER2, MSI status, and tumor mutational burden (TMB). Testing is particularly advised for patients with unresectable, locally advanced, or metastatic disease to inform targeted therapy options and clinical trial enrollment.[31]

Because BTCs demonstrate high inter- and intra-tumoral heterogeneity with respect to tumor stroma content, appropriate FFPE block selection under the microscope is critical for reliable NGS analysis.[32] If a FFPE sample does not meet quality requirements for NGS, a tissue re-biopsy is recommended; if this is not feasible, then liquid biopsy–based NGS is recommended (Table 1).[31]

The Role of Comprehensive Genomic Profiling in Pancreatic Cancer: Diagnosis, Molecular Classification, and Targeted Therapy

Pancreatic cancer, especially pancreatic ductal adenocarcinoma (PDAC), is characterized by remarkable molecular heterogeneity that influences tumor progression, treatment response, and patient outcomes. Approximately 90% of PDAC cases harbor mutations in key driver genes, including KRAS, TP53, SMAD4, and CDKN2A. Although

Table 1. NCCN-recommended genes, incidence of therapeutic targets and targeted therapies in advanced biliary tract cancers

Recommended Molecular Testing	Anatomic Subsite				
	Frequency	Targeted Therapy	Gallbladder	Intrahepatic CCA	Extrahepatic CCA
NTRK gene fusion	X	X	X	<1%	Entrectinib, Larotrectinib, Repotrectinib
MSI-H/dMMR	X	X	X	1%–3%	Pembrolizumab
TMB-H	X	X	X	<5%	Nivolumab + Ipilimumab
BRAF V600E mutation	X	X	X	1%–5%	Dabrafenib + Trametinib
FGFR2 fusion or rearrangement	-	X	X	9%–15% of intrahepatic CCAs and rare in other subsites	Futibatinib, Pemigatinib Erdafitinib
IDH1 Mutation	-	X	X	10%–20% of intrahepatic CCAs and rare in other subsites	Ivosidenib
HER2 (ERBB2) overexpression and/or amplification	X	X	X	5%–20% of CCAs, 15%–30% of gallbladder cancer	Fam-trastuzumab deruxtecan-nxki Trastuzumab + pertuzumab Tucatinib + trastuzumab Zanidatamab-hrii
RET gene fusion	X	X	X	<1%	Pralsetinib Selpercatinib
KRAS G12C mutation	X	X	X	1%	Adagrasib

KRAS mutations are nearly ubiquitous and considered a hallmark of PDAC, alterations in TP53, SMAD4, and CDKN2A provide critical insights into tumor biology, aggressiveness, and prognosis.[33]

Currently, the standard-of-care approach for most patients with metastatic pancreatic cancer remains cytotoxic chemotherapy. However, for patients with metastatic pancreatic cancer, both germline and somatic sequencing should be performed in an expeditious manner as up to a quarter of patients with advanced pancreatic cancer might have a potentially actionable mutation and may be eligible for biomarker-directed therapies or clinical trials.[34,35]

Notably, it can identify rare but therapeutically relevant targets such as NTRK gene fusions, PIK3CA mutations, and microsatellite instability-high (MSI-H) status—findings that are increasingly pertinent for guiding targeted therapies or immunotherapy. For instance, tumors with MSI-H may respond favorably to immune checkpoint inhibitors, offering hope for a subset of patients. Furthermore, integrating CGP with other advanced diagnostic modalities, such as circulating tumor DNA (ctDNA) analysis, enhances early detection of tumor-derived genetic alterations, facilitates real-time monitoring of tumor burden, and provides insights into tumor evolution and resistance mechanisms over time.

Emerging molecular classifications of PDAC, derived from comprehensive genomic profiling (CGP) and transcriptomic data, have stratified tumors into distinct subtypes with important clinical implications:

Stable/KRAS-driven subtype: This is the predominant PDAC subtype, characterized by the presence of classic KRAS mutations, most commonly in codons G12D, G12V, and G12R. It generally exhibits relative genomic stability. Therapeutic options remain limited, except for the rare KRAS G12C mutation, which can be targeted with specific inhibitors. This subtype often displays a less invasive profile but has a variable prognosis.

Squamous or basal-like subtype: Marked by high rates of TP53 mutations and the loss of differentiation markers, this subtype is associated with aggressive tumor behavior, early metastasis, and poor survival outcomes. It aligns with features of epithelial-mesenchymal transition (EMT) and squamous differentiation, suggesting potential sensitivity to therapies targeting EMT pathways and basal-like features.

Immunogenic subtype: Defined by substantial immune cell infiltration, high tumor mutational burden (TMB), and in some cases, microsatellite instability-high (MSI-H), the immunogenic subtype exhibits the most promising therapeutic opportunities. These tumors may respond well to immune checkpoint inhibitors, highlighting the importance of molecular stratification for immunotherapy eligibility.

DNA damage repair deficient (DDR) subtype: This subtype includes tumors harboring deficiencies in homologous recombination repair mechanisms, often linked to mutations in BRCA1/2, PALB2, or other DNA repair genes. Such tumors tend to be more sensitive to platinum-based chemotherapy and PARP inhibitors, offering targeted options for this subgroup.

This molecular taxonomy aids in prognostic stratification and guides personalized therapy selection. However, the clinical implementation of these classifications is still evolving, with ongoing efforts to refine subtype definitions and integrate molecular profiles with treatment decision-making (Table 2).[36,37]

Table 2. Summary of NCCN-Recommended Genes, Diagnostic, and Molecular Testing for Gastrointestinal Cancers. Comprehensive genomic profiling tests

Type of GI Cancer	Genes to Test (according to NCCN)	Guideline-Required Tests	Recommended Tests
Colorectal Cancer	KRAS, NRAS, BRAF, MSI/MMR, HER2, PIK3CA, G12C, POLE, POLD	RAS (KRAS, NRAS) mutation testing before anti-EGFR therapy; MSI/MMR status; BRAF V600E	NGS panels covering RAS, BRAF, MSI, TMB, HER2; POLE/POLD mutation testing
Gastric Cancer	HER2, MSI, PD-L1, PIK3CA, TP53, FGFR2, ERBB2, CLDN18.2	HER2 testing (IHC/FISH); MSI testing; PD-L1 testing; PIK3CA mutations	NGS panels for MSI, TMB; HER2 amplification by FISH/IHC; PD-L1 expression
Pancreatic Cancer	BRCA1/2, KRAS, TP53, CDKN2A, MSI, NTRK, HER2	BRCA testing (for PARP inhibitors); MSI/MMR testing; NTRK fusion testing	Germline and somatic BRCA testing; NGS panels including MSI and NTRK
Esophageal Cancer	HER2, PD-L1, EGFR, MSI, TP53, CDKN2A	HER2 amplification; PD-L1 expression; MSI testing	IHC or FISH for HER2; MSI testing; NGS for PD-L1, EGFR mutations
Biliary Tract Cancer	IDH1/2, FGFR2, HER2, MSI, BRAF, KRAS, NTRK	IDH1/2 mutations; FGFR2 fusions; MSI status; HER2 amplification	NGS panels targeting FGFR, IDH, MSI; FISH/IHC for HER2
Hepatocellular Carcinoma	CTNNB1, TP53, TERT, MSI, NTRK, BRAF	TERT promoter mutations; MSI testing; NTRK fusion testing	NGS for TERT, TP53; MSI testing; NTRK fusion assays

Advancements in comprehensive genomic profiling (CGP) have profoundly transformed the landscape of gastrointestinal (GI) cancers, enabling more precise diagnosis, refined molecular classification, and tailored targeted therapies. Through detailed genomic and transcriptomic analysis, clinicians can now delineate distinct tumor subtypes with unique biological and clinical behaviors, guiding personalized treatment strategies that improve patient outcomes. The integration of CGP into routine clinical practice, supported by guidelines from organizations such as NCCN, facilitates identification of actionable mutations—such as HER2, FGFR2, IDH1/2, BRAF, and MSI-H—broadening therapeutic options beyond standard chemotherapies and embracing immunotherapy, targeted agents, and clinical trial inclusion.

Currently, certain cancers, such as HCCs, have limited applications for CGP. However, the landscape is evolving. In HCC, common mutations include TP53 and CTNNB1 (beta-catenin). Advances in targeted approaches, such as synthetic lethality strategies, may soon enable TP53 mutations to be exploited therapeutically—comparable to treatments targeting BRCA mutations. Additionally, oncogenic mutations like KRAS G12C, which can drive tumor growth, are increasingly recognized as potential therapeutic targets. As our understanding deepens and new targeted therapies emerge, CGP is expected to play a more significant role in the diagnosis and treatment planning of HCC, expanding its application in this challenging malignancy.

Despite these significant advances, challenges remain in fully translating molecular classifications into standard care, including issues related to tumor heterogeneity, sample availability, and evolving biomarker validation. Ongoing clinical trials and global sequencing initiatives continue to refine our understanding of disease subtypes, promising a future where molecular diagnostics are central to decision-making in GI oncology. Ultimately, harnessing CGP promises to not only improve survival rates but also herald an era of truly personalized medicine in the management of gastroenterological malignancies, transforming prognosis and quality of life for patients worldwide.

Disclosures

Authorship Contributions: Concept – B.A., M.C.Y.; Literature search – B.A., Y.S., M.B.; Writing – B.A., Y.S., M.B.; Critical review – M.C.Y.

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