



# *Review* **Current Applications of Liquid Biopsy in Gastrointestinal Cancer Disease—From Early Cancer Detection to Individualized Cancer Treatment**

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**Simple Summary:** Gastrointestinal (GI) cancers are a common cancer, affecting both men and women, normally diagnosed through tissue biopsies in combination with imaging techniques and standardized biomarkers leading to patient selection for local or systemic therapies. Liquid biopsies (LBs)—due to their non-invasive nature as well as low risk—are the current focus of cancer research and could be a promising tool for early cancer detection and treatment surveillance, thus leading to better patient outcomes. In this review, we provide an overview of different types of LBs enabling early detection and monitoring of GI cancers and their clinical application.

**Abstract:** Worldwide, gastrointestinal (GI) cancers account for a significant amount of cancer-related mortality. Tests that allow an early diagnosis could lead to an improvement in patient survival. Liquid biopsies (LBs) due to their non-invasive nature as well as low risk are the current focus of cancer research and could be a promising tool for early cancer detection. LB involves the sampling of any biological fluid (e.g., blood, urine, saliva) to enrich and analyze the tumor's biological material. LBs can detect tumor-associated components such as circulating tumor DNA (ctDNA), extracellular vesicles (EVs), and circulating tumor cells (CTCs). These components can reflect the status of the disease and can facilitate clinical decisions. LBs offer a unique and new way to assess cancers at all stages of treatment, from cancer screenings to prognosis to management of multidisciplinary therapies. In this review, we will provide insights into the current status of the various types of LBs enabling early detection and monitoring of GI cancers and their use in in vitro diagnostics.

**Keywords:** liquid biopsy; circulating tumor cells (CTCs); circulating tumor DNA (ctDNA); tumor exosomes; tumor-educated blood platelets (TEPs); organoids; gastrointestinal cancer

# **1. Introduction**

Gastrointestinal (GI) cancers are responsible for more cancer-related deaths than lung and breast cancer. Colorectal cancer (CRC) is the major type of GI cancer, with 1.9 million new cases diagnosed worldwide in 2020, making it after lung and breast cancer the third most common cancer of all organs. According to the International Agency for Research on Cancer, in the same year, 1.1 million new cases of gastric cancer, 900,000 new cases of liver cancer, 600,000 new cases of esophageal cancer, and 500,000 new cases of pancreatic cancer were diagnosed across the globe [\[1\]](#page-30-0).

Although the prognosis of many GI cancers has improved over the past decades [\[2](#page-30-1)[,3\]](#page-30-2), a late cancer diagnosis is still the leading reason for cancer-related deaths among all



**Citation:** David, P.; Mittelstädt, A.; Kouhestani, D.; Anthuber, A.; Kahlert, C.; Sohn, K.; Weber, G.F. Current Applications of Liquid Biopsy in Gastrointestinal Cancer Disease—From Early Cancer Detection to Individualized Cancer Treatment. *Cancers* **2023**, *15*, 1924. [https://doi.org/10.3390/](https://doi.org/10.3390/cancers15071924) [cancers15071924](https://doi.org/10.3390/cancers15071924)

Academic Editor: Fortunato Ciardiello

Received: 21 February 2023 Revised: 20 March 2023 Accepted: 21 March 2023 Published: 23 March 2023



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GI cancers [\[4\]](#page-31-0). Current research focuses therefore on improving early cancer diagnosis, possibly leading to better outcomes among all GI cancers [\[5](#page-31-1)[,6\]](#page-31-2). So far, endoscopic or CT-guided solid biopsies in combination with so-called serum-based tumor biomarkers are primary methods for the diagnosis of GI cancers [\[7\]](#page-31-3). Thereby, solid biopsies are considered the gold standard strategy capable of classifying tumors, identifying the mutational status, and providing prognostic information. However, these methods have some limitations, e.g., obtaining insufficient or inaccurate tissue samples possibly leading to false-positive or false-negative results. In addition, tissue biopsies might cause harm to the patient. However, recent studies suggest tissue biopsies taken from a single cancer nodule or single metastatic lesion may fail to represent the entire tumor heterogeneity within the patient, possibly being one of the main reasons for the failure of current targeted therapies [\[8](#page-31-4)[–13\]](#page-31-5). To date, several serum-based biomarkers such as carcinoembryonic antigen (CEA), carbohydrate antigen 19-9 (CA19-9), carbohydrate antigen 72-4 (CA72-4), carbohydrate antigen 125 (CA125), and alpha-feto protein (AFP) have been identified and widely used for diagnosis, prognosis, and monitoring of potential recurrence of GI cancers [\[14](#page-31-6)[,15\]](#page-31-7). Although, due to the limit of specificity and sensitivity most of these biomarkers are not useful for early cancer detection [\[16\]](#page-31-8). Therefore, LB emerged as a promising tool for early detection, treatment selection, and real-time prognosis.

In contrast to solid biopsy, LB is a minimally invasive approach enabling the real-time monitoring and early uncovering of alterations in cells or cell products shed from malignant lesions into the body fluids (Figure [1\)](#page-1-0). LB analysis can identify multiple heterogeneous resistance mechanisms in single patients compared to solid biopsy. Furthermore, LB facilitates the choice of the right treatment and observation of the treatment response. Due to the minimally invasive nature of LB, the resulting complications from obtaining solid biopsies could be prevented. A typical LB sample is taken from any biological fluid such as blood, saliva, cerebrospinal fluid, or urine. LB materials derived from peripheral blood have been investigated extensively. LB analysis from blood contains enrichment and isolation of CTCs, circulating blood platelets, ctDNA, and other tumor genetic material such as extracellular vesicles. As of today, several LB technologies have been approved by the United States Food and Drug Administration (FDA) for malignancies such as metastatic lung, breast, prostate, or colorectal cancer: CELLSEARCH CTC test using circulating tumor cells from Veridex, Guardant360 CDx, and FoundationOne Liquid CDx using circulating cell-free DNA (cfDNA) and next-generation sequencing to detect tumor-specific mutations.

<span id="page-1-0"></span>

**Figure 1.** Clinical application of liquid biopsy (LB) in gastrointestinal cancer (GICs). Circulating **Figure 1.** Clinical application of liquid biopsy (LB) in gastrointestinal cancer (GICs). Circulating tumor cells (CTCs), cell-free or circulating tumor DNA (cfDNA/ctDNA), tumor-educated platelets (TEP), exosomes, and RBCs in the blood of GICs patients can be used as potential biomarkers for LBs and their expression levels can be measured to determine the clinical status of GICs patients.

Due to the crucial role of LB markers, our main focus is on research findings and clinical applications in gastrointestinal cancers.

### **2. Overview of Different Methodologies and Their Current Clinical Application**

#### *2.1. Circulating Tumor Cells (CTCs)*

CTCs are tumor cells, shed from a primary tumor. They can enter the bloodstream or lymphatic system, potentially spreading into distant organs possibly leading to metastases [\[17,](#page-31-9)[18\]](#page-31-10). Nevertheless, only a minority of CTCs become solid metastatic lesions because of a complex sequence of events needed, i.e., the detachment from the primary tumor, migration through the circulating blood, immune escape, and survival. It remains unclear how the detachment process from the primary tumor tissue takes place. Evidence supports the involvement of epithelial to mesenchymal transition, by which transformed epithelial cells can acquire the ability to invade, resist apoptosis, and disseminate. This could be the main driver for the detachment of tumor cells from the primary tumor [\[19–](#page-31-11)[24\]](#page-31-12). Other reports hypothesize that cells split into different clusters [\[25\]](#page-31-13). It is noteworthy that gastrointestinal cancers compared to breast cancer have lower numbers of CTCs in peripheral blood due to portal vein circulations and a steady 'first-pass effect' in the liver [\[26\]](#page-31-14). Therefore, portal vein blood might be a unique sample site to isolate CTCs from gastrointestinal cancers. It has already been shown that the number of enriched CTCs from portal vein blood is higher than in the systemic circulation [\[27](#page-31-15)[,28\]](#page-31-16). Portal vein blood can be collected intraoperatively or even by endoscopic ultrasound (EUS)-guided sampling [\[29\]](#page-31-17).

In addition to the number of CTCs, the analysis of physical (size, density, and electric charge) and biological (cell surface expression) properties could play a crucial role in future clinical use [\[30\]](#page-31-18).

### 2.1.1. Isolation and Enrichment of CTCs

The isolation and enrichment of CTCs are technically challenging because of their low numbers and elimination by the body's immune system. The sensitivity of capture methods has improved in the last few years. First, based on cancer-specific characteristics, the cancer cells are separated from other blood components followed by enrichment procedures. There are two main techniques for isolating CTCs, one based on immunoaffinity properties, and the other based on biophysical properties. The immunoaffinity-based technology, including positive or negative selection assays, isolates CTCs with an antibody-immobilized inert surface combined with magnetic beads [\[31\]](#page-32-0) (Figure [2a](#page-3-0)). The epithelial cell adhesion molecule (EpCAM) is a commonly used cell surface marker for positive CTC selection and an immunomagnetic assay called CELLSEARCH®. To date, CELLSEARCH® is the only CTC technology that has gained FDA approval enabling the direct visualization and quantification of CTCs and the identification of living cells without the need for cell lysis. The functionality of CELLSEARCH<sup>®</sup> for the detection of CTCs in GI cancer was confirmed by different studies [\[32](#page-32-1)[,33\]](#page-32-2). In another approach, CTCs from blood samples of patients with CRC were pre-enriched through binding to VAR2CSA protein-coupled magnetic beads, and finally the colon-related mRNA transcripts USH1C and CKMT1A were detected by RT-qPCR [\[34\]](#page-32-3). Microfluidic chips as an immunoaffinity technology allow the selection of CTCs from small volumes of fluid under laminar flow, eliminating the need for sample processing. In a study by Lim et al. [\[35\]](#page-32-4), single CTCs and CTC clusters were captured on the membrane of a centrifugal microfluidic device, picked without fixation, and used for further molecular analysis. Researchers began to develop CTC isolation technologies based on the biophysical properties of CTCs to overcome the bias and narrow spectrum of immunoaffinity-based approaches for CTC isolation. These methods are characterized as label-free and isolate CTCs from the blood based on biophysical properties, such as density, size, deformability, and electrical charge [\[36\]](#page-32-5). In order to confirm that the enriched cells consist only of CTCs, the cells must undergo characterization. Currently, this is achieved by immunocytochemistry-based assays, including immunofluorescence and immunohistochemistry, and molecular approaches, including RT-qPCR, FISH, and

next-generation sequencing [\[37\]](#page-32-6). Using GILUPI Cell Collector (CC), a novel in vivo CTC detection device, researchers reported overcoming the limitations of small blood sample volumes. However, the clinical relevance of the CTCs detected was inferior to the CTCs identified by Cell Search [\[38\]](#page-32-7).

<span id="page-3-0"></span>

**Figure 2.** Techniques for detection of LB biomarkers in GICs. (a) Detection of CTCs, (b) detection of ctDNAs, (**c**) detection of tumor-educated platelets, and (**d**) detection of exosomes. ctDNAs, (**c**) detection of tumor-educated platelets, and (**d**) detection of exosomes.

# *2.2. Circulating Tumor DNA (ctDNA)*  2.1.2. Clinical Application/Relevance of CTCs

 $\frac{1}{2}$  group of  $\frac{1}{2}$  and  $\frac{1}{2}$  free cases the contract of  $\frac{1}{2}$  fragments in the contract plasma of  $\frac{1}{2}$  and  $\frac{1}{2$ localized colorectal cancer (CRC)  $[39,40]$  $[39,40]$ . In a series of 287 patients, a group demonstrated<br>that we construct CTC detection with  $\sim 2.1$  CTC (7.5 mJ, we can deduce in demonstrated  $\frac{1}{2}$  is not proper and  $\frac{1}{2}$  is the procedure of the anti-mediated to prognostic marker, whereas another group with 519 patients stated no association after prognosite marker, whereas another group with 515 patients salted ho association after<br>surgery [\[39](#page-32-8)[,41\]](#page-32-10). In high-risk CRC patients requiring adjuvant chemotherapy, CTC detection in the blood was correlated with worse outcomes  $[41–43]$  $[41–43]$ . A meta-analysis containing It which DNA fragments are related with which but below the plant of CTCs in the peripheral blood with 1847 patients (11 studies) indicated that the detection of CTCs in the peripheral blood with For patients (11 statutes) interested that the detection of ST est in the perspheral spock with CELLSEARCH® has predictive utility for patients with CRC [\[44\]](#page-32-12). VISNÚ-1, a multicentre, randomized phase III trial with 349 patients, indicated that the first-line FOLFOXIRIbevacizumab chemotherapy regimen significantly improved progression-free survival  $P_{\text{S}}$ ) in comparison to the FOLFOX-bevacizumab chemotherapy regimen in patients with metastatic CRC. This trial revealed that the CTC count might be a valuable non-invasive biomarker to aid in decision-making for patients undergoing intensive first-line therapy [\[45\]](#page-32-13). In a series of studies performed in metastatic CRC, patients with high baseline CTC count (≥3 CTCs/7.5 mL) could benefit from intensive chemotherapy regimens (four drugs), unlike patients with low CTC counts [\[44](#page-32-12),46-[48\]](#page-32-15). The PRODIGE 17 trial, conducted in 106 untreated .<br>patients with advanced gastric and esophageal cancer, reported that dynamic changes in CTC counts between baseline and 28 days after treatment were significantly associated with PFS and OS and could help in tailoring treatment regimens to each individual patient [\[49\]](#page-32-16). The above-mentioned findings might therefore help in the development of individualized treatment approaches in gastrointestinal canc[er](#page-4-0) patients. In Table 1, a broad application of CTCs and its clinical relevance in GICs is mentioned. Several studies have observed the prognostic value of CTCs for overall survival (OS) in that preoperative CTC detection with a  $> 1$  CTC/7.5 mL proved to be an independent

**Table 1.** Clinical relevance of CTCs in GICs.

<span id="page-4-0"></span>



### *2.2. Circulating Tumor DNA (ctDNA)*

A group of French scientists detected cfDNA fragments in the circulating plasma of patients with autoimmune disorders in 1948 [\[73\]](#page-33-18). Later it became clear that the release of cfDNA is not restricted to autoimmune disorders, but was also found amongst others in pregnant women [\[74\]](#page-33-19), septic patients [\[75\]](#page-34-0), people suffering from different types of cancers, and even in healthy individuals [\[76\]](#page-34-1). Numerous studies have been conducted to uncover the mechanisms by which DNA fragments are released from cells into the plasma or serum. Major mechanisms involve apoptosis, necrosis, phagocytosis, NETosis, or active secretion [\[77\]](#page-34-2). Basically, every cell and tissue type is able to release cfDNA into circulation. Consequently, based on cell and tissue-specific methylation patterns from comprehensive databases including the Cancer Genome Atlas (TCGA) an assignment of cfDNA to different origins became possible [\[78\]](#page-34-3). Accordingly, the major source of cfDNA in blood results from hematopoietic cells, followed by vascular endothelial cells (up to 10%). However, cfDNA from liver tissue can also frequently be detected at low levels in circulation (up to 1%) in healthy people [\[78\]](#page-34-3). CtDNA is a fraction of cfDNA that originates from primary tumors, metastases, or from CTCs. Additionally, some findings are suggestive of an active release of ctDNA from living tumor cells involving exosomes [\[79\]](#page-34-4). CtDNA is characterized by small 70–200 base pair fragments circulating freely within the blood [\[73\]](#page-33-18) showing a major fragment size of around 170 base pairs, which corresponds to nucleosomal fragments resulting from apoptosis [\[80\]](#page-34-5). The half-life of ctDNA is very short ranging from 15 min to 2.5 h before it is finally cleared by the liver and/or kidneys which is a prerequisite for a precise biomarker [\[81\]](#page-34-6). Concentrations of ctDNA in the blood of patients with a malignant tumor are significantly increased compared to healthy individuals [\[82\]](#page-34-7); however, levels of released ctDNA significantly vary between different tumor types and tumor stages. Furthermore, the match of cancer-specific alterations in the genome of solid tumors to those of ctDNA is a major discriminator between ctDNA and physiological cell-free DNA at steady state [\[83–](#page-34-8)[85\]](#page-34-9).

#### 2.2.1. Detection and Analysis of ctDNA

There are a number of technical challenges associated with the analysis of ctDNA. First, total cfDNA itself is present only at comparably low concentrations in the nanogram per ml range. Second, the fraction of ctDNA among total cfDNA in many cases is also relatively low. This becomes especially evident in the early stages of cancer development or for tumors that release only low amounts of DNA [\[76\]](#page-34-1). Therefore, an urgent need for enrichment approaches of ctDNA over total cfDNA still exists. In this context, it has been reported that ctDNA to some extent might be enriched in cfDNA fractions of smaller size (90–150 base pairs (bp)) separated from the major fraction of 170 bp fragments [\[86\]](#page-34-10) (Figure [2b](#page-3-0)). Although a tendency to higher ctDNA content in the 90–150 bp fraction could be found, enrichment factors of twofold in more than 95% of cases were still not satisfying [\[86\]](#page-34-10). In principle, a plethora of downstream analyses has been established for the diagnosis, prognosis, monitoring, and prediction of treatment response for all major cancer diseases. Among them are single nucleotide polymorphism (SNP) as well as copy number variation (CNV) analyses. When sufficient amounts of ctDNA templates (at least one genome equivalent per assay) are available in patient specimens, targeted assays based on PCR, for example, represent powerful approaches. Such PCR-based techniques which are characterized by high sensitivity showed the ability to identify relevant alterations in genes including RAS, HER2/NEU, BRAF, MET, BRCA2, APC, TP53, ALK, ROS1, PTEN, and NF1. However, when ctDNA content drops below one tumor genome equivalent per assay multi-target approaches become mandatory. Multi-gene panels are well established to similarly test for hundreds of targets. However, when it comes to early detection of cancer for screening purposes ctDNA contents of less than 0.01% represent a serious technical challenge to robustly assure high sensitivity and specificity. Cancer-specific methylomes in ctDNA were therefore proposed as a promising alternative [\[87\]](#page-34-11). In combination with next-generation sequencing (NGS), thousands of differential hyper-/hypo-methylated regions (DMRs) have been determined for a variety of cancers in addition to chromosomal and copy number changes or point mutations [\[88](#page-34-12)[,89\]](#page-34-13). Accordingly, complex signatures of DMRs, for

example, allow for early diagnosis with higher reliability. In general, it has been suggested that even for only as low as 0.01% ctDNA content prediction of cancer disease should be possible with 100–1000 DMRs when sequencing coverage of at least 100–1000x is given [\[87\]](#page-34-11).

#### 2.2.2. Clinical Application/Relevance of ctDNA

Analysis of tumor-linked genetic alterations and DNA methylation profiling has been recognized as a method for detecting potential biomarkers for disease diagnosis and prognosis [\[90\]](#page-34-14). In a study by Tam et al. [\[91\]](#page-34-15) the levels of TAC1 and SEPT9 methylation detected in postoperative sera of patients with CRC were independent predictors for tumor recurrence and unfavorable cancer-specific survival. Findings from several studies showed that high ctDNA levels combined with an increased number of mutations detected in the ctDNA were linked to poor survival and multi-site metastasis [\[92\]](#page-34-16). However, when the amount of ctDNA was <1 mutant template molecule per milliliter of plasma, tests fail to detect early-stage cancer [\[93\]](#page-34-17). Therefore, methylome analyses of cfDNA with thousands of cancer-specific DMRs might overcome such limitations. In 2019, the 'Galleri test' or the 'Galleri multicancer early detection (MCED) test' developed by GRAIL Inc. (Menlo Park, CA, USA) achieved Breakthrough Device designation. The Galleri test detects cancer- and tissue-specific alterations in the methylation patterns of cfDNA in a blood sample via NGS, which should allow early pan-cancer detection even for cancers with unknown primary. GRAIL's clinical trial includes three studies: the Circulating Cell-free Genome Atlas (CCGA) Study (Clinical Trial NCT02889978) [\[94\]](#page-34-18), the STRIVE Study (Clinical Trial NCT03085888), and the SUMMIT Study (Clinical Trial NCT03934866). In these studies including 2482 cancer patients covering approximately 50 different cancer types, sensitivities and specificities were tested by using a target hybridization capture approach for the analyses of 100,000 differentially methylated regions [\[95\]](#page-34-19). In a predefined subset of 12 cancer types which comprised roughly 63% of all US cancer cases average sensitivity was 67.3% accumulated for stage I–III at a very high specificity of 99.3% [\[95\]](#page-34-19). Sensitivity for all 50 cancer types accumulated for stage I–III dropped to 43.9% with 18% sensitivity for stage I and 43% in stage II. Remarkably, sensitivities for pancreatic cancer were significantly higher even at early stages with 63% and 83% in stage I and II, respectively. Although high specificities might predestine this test for negative prediction in screening approaches, moderate sensitivities still require improvements, especially for early diagnosis. Another FDA-approved LB-based test is Epi proColon<sup>®</sup> (Epigenomics AG, Berlin, Germany) targeting methylation changes used to screen for CRC. The test is based on a real-time PCR with a fluorescent hydrolysis probe and targets the methylation changes of the SEPT9 gene promoter in cfDNA isolated from plasma. To evaluate the clinical assessment, Epi proColon® was involved in a prospective multicenter study (Clinical Trial NCT00855348) [\[96](#page-34-20)[–98\]](#page-35-0).

A ctDNA-guided approach has been used by numerous clinical trials (DYNAMIC, CIRCULATE-Japan, CIRCULATE-trial, CIRCULATE-PRODIGE, and IMPROVE-IT2), all focused towards precise adjuvant therapy for stage II colon cancer patients [\[99](#page-35-1)[–103\]](#page-35-2). According to DYNMAIC-trial, a ctDNA-guided approach led to a reduction in the number of patients who received adjuvant therapy, and furthermore, ctDNA-positive patients appeared to benefit from adjuvant treatment. The other trials (CIRCULATE-trial, IMPROVE-IT2) mentioned above could help in decision-making before adjuvant treatment in stage II colon cancer. The outcome of these trials proposes that a survival benefit from adjuvant chemotherapy may be obtained in a well-defined subgroup of patients with stage II colon cancer—especially those with detectable ctDNA post-surgery. In the case of pancreatic cancer, ctDNA might be used as a marker for monitoring treatment efficacy and disease progression [\[104\]](#page-35-3). To prove the feasibility of a non-invasive detection in plasma, Liu et al. developed a pancreatic cancer detection assay (PANDA) for screening and validation of PDAC-specific DNA methylation in tissues and plasmas of PDAC patients [\[105\]](#page-35-4). In combination with age and CA19-9 plasma serum level, this assay showed encouraging results to discriminate PDAC plasma from non-malignant disease, showing its capability to be amended into a non-invasive diagnostics method for PDAC screening. In Table [2,](#page-8-0) a broad application of ctDNA/cfDNA and its clinical relevance in GICs is mentioned.

<span id="page-8-0"></span>

**Table 2.** Clinical relevance of ctDNA/cfDNA in GICs.



#### *2.3. Circulating Extracellular Vesicles (Tumor Exosomes)*

Exosomes are a subpopulation of extracellular vesicles (EVs), ranging in size from 30–150 nm. They are derived from the endosomal pathway via the formation of late endosomes or multivesicular bodies (MVBs). As an important mediator of intracellular communication, exosomes transmit various biological molecules including proteins, lipids, and nucleic acids over distances within the protection of a lipidic bilayer-enclosed structure. Nearly all types of cells and all body fluids contain exosomes [\[124,](#page-36-3)[125\]](#page-36-4). Cancer cells and other stromal cells in the tumor microenvironment (TME) also release exosomes and control tumor development through molecular exchanges mediated by exosomes [\[126](#page-36-5)[,127\]](#page-36-6). Circulating extracellular vesicles (cEVs) are implied to be more stable in comparison to serological proteins as the lipidic bilayers defend the content from proteases and other enzymes [\[128\]](#page-36-7).

## 2.3.1. Isolation of Tumor Exosomes

Exosomes can be isolated using various methodologies. Ultracentrifugation (UC) is the most widely used technique. Other techniques include differential centrifugation (DC), density gradient ultrafiltration (DG), size exclusion chromatography (SEC), precipitation, immunoaffinity capture based on the expression of endosomal surface proteins such as CD81, CD63, and CD9, and microfluidic-based assays [\[129\]](#page-36-8) (Figure [2d](#page-3-0)).

## 2.3.2. Clinical Application/Relevance of Tumor Exosomes

Exosomes demonstrate significant advantages over other sources of LBs. First, exosomes exist in almost all body fluids and are characterized by highly stable lipidic bilayers. Second, living cells secret exosomes. They thus contain biological information from the parental cells and are more representative than cell-free DNA secreted during necrosis or apoptosis [\[130\]](#page-36-9). Third, exosomes express specific proteins such as CD63, ALIX, TS101, and HSP70, 20 which can be used as markers to discriminate exosomes from other vesicles making their identification clear and simple [\[131\]](#page-36-10). Fourth, as exosomes can present specific surface proteins from parental cells or target cells, they can help in the prediction of organ-specific metastasis [\[132\]](#page-36-11). Fifth, compared to CTCs, they can be isolated using classic methods such as ultracentrifugation [\[133\]](#page-36-12).

Circulating exosomal PD-L1 was shown to contribute to immunosuppression, to reflect the immune status, and to better predict survival in patients with GICs, thereby making it a potential prognostic biomarker [\[134\]](#page-36-13). Additionally, EV proteins such as carcinoembryonic antigen-related cell adhesion molecules (CEACAMs), Tenascin C, Glypican-1, and ZIP-4 have been recognized as diagnostic biomarkers in GICs [\[135](#page-36-14)[–137\]](#page-36-15). The EV-Glypican-1 (GPC-1) derived from plasma has been described as a potential marker of early pancreatic ductal adenocarcinoma (PDAC) with higher diagnostic accuracy than CA19-9 [\[137\]](#page-36-15). A clinical trial (NCT03032913) performed by Etienne BUSCAIL involved 20 PDAC patients and 20 non-cancer patients, whose blood samples were collected to detect CTCs and GPC1+ exosomes for diagnostic accuracy assessment of CTCs and Onco-exosome Quantification. Very recently, Lin et al. presented the development of a signature of four EV-proteins—monocyte marker CD14, Serpin A4 (a regulator of angiogenesis), CFP (a positive regulator of the complement system), and LBP (lipopolysaccharide binding protein)—as prognostic biomarkers in colorectal liver metastases (CRLM). Thereby, they used matching pre- and post-operative serum samples of patients undergoing CRLM surgery and finally validated the discovered proteins in three independent cohorts. Additionally, they showed that EV-bound CXCL7 could serve as a biomarker of early response in CRML patients undergoing systemic chemotherapy [\[138\]](#page-36-16). Furthermore, three cancerspecific phospholipids were found in a study that analyzed 20 dysregulated phospholipids in pancreatic cancer compared to controls. Among them, LysoPC 22:0 was linked with tumor stage, whereas CA19-9 and CA242 were associated with tumor diameter and positive lymph node count [\[139\]](#page-36-17). Finally, diagnostic accuracy for WASF2, ARF6 mRNAs, SNORA74A, and SNORA25snoRNAs in circulating exosomes was greater than for CA19-9

in discriminating PC patients from controls [\[140\]](#page-36-18). Even though a limited number of studies on the application of exosome-based drug delivery vectors in the treatment of GICs exist, some of them report intriguing advancements in the field. Using an in vitro model Pascucci L. et al. demonstrated the role of exosomal-mesenchymal stromal cells (exo-MSCs) in the packaging and delivery of active drugs, suggesting a possible option of using the MSCs as a warehouse to develop drugs with a better specificity [\[141\]](#page-36-19). Another study showed the application of milk-derived exosomes for the oral delivery of PAC in early-stage and advanced-stage pancreatic and other cancers. It also evaluated the anti-tumor potency of the milk-derived exosomes loaded with PAC [\[142\]](#page-36-20). Furthermore, studies have verified the link between cancer-derived exosomes and the modulation of immune response in pancreatic cancer and have also indicated the application of these cargo carriers in targeting pancreatic cancer cells, whether as anti-tumor drugs and other molecules, such as RNAi against mutant KRAS [\[143\]](#page-36-21). More applications and the clinical relevance of exosomes are summarized in Table [3.](#page-12-0)

<span id="page-12-0"></span>

**Table 3.** Clinical relevance of Exosomes in GICs.



#### *2.4. Tumor-Educated Blood Platelets (TEPs)*

Platelets play a central role in blood coagulation and in the healing of wounds, and their relationship with cancer has been extensively investigated [\[156](#page-37-8)[–164\]](#page-37-9). There are two major studies that indicated the involvement of platelets during tumor progression. These studies contributed to the development of the concept of tumor-educated platelets (TEPs). The first study by Trousseau (1868) observed spontaneous coagulation being common in cancerous patients, stating that circulating platelets were affected by cancer [\[165\]](#page-37-10). The second study (Billroth T, 1877) described '' thrombi filled with specific tumor elements" as part of metastasis, pointing out a direct interaction of cancer cells and platelets [\[166,](#page-37-11)[167\]](#page-37-12). In recent years, several studies have focused on the impact of platelets during cancer progression, and some of them showed that platelet dysfunction and thrombotic disorders are important key factors in cancer development. By now it is well known that tumoreducated platelets (TEPs) are educated when they interact with the tumor cells in such a way as to lead to the detachment of biomolecules, such as proteins and RNA, tumor-specific splice events, and finally to megakaryocyte alteration [\[168\]](#page-37-13). Through this interaction, the RNA profile of blood platelets changes. This change has been used as an independent diagnostic marker for detecting TEPs in various solid tumors [\[169\]](#page-37-14). The RNA biomarkers of the directly transferred transcripts are EGFRvIII, PCA3, EML4-ALK, KRAS, EGFR, PIK3CA mutants, FOLH1, KLK2, KLK3, and NPY [\[170\]](#page-37-15). Here, we describe the isolation, detection, and clinical relevance of TEPsin GICs.

## 2.4.1. Isolation and Detection of Tumor-Educated Platelets

Tumor-educated platelets can be separated from peripheral blood by using a twostep centrifugation approach [\[171\]](#page-37-16). The first step separates the platelet-rich plasma (PRP) from the red blood and white blood cells, whereas the second centrifugation step yields the platelet pellet [\[172\]](#page-37-17). For the detection of the TEPs in the human plasma, the plasma pellets are dissolved in 1ml TRIZOL reagent. RNA is extracted from the plasma platelet pellet and the suboptimal quality of the platelet RNA is characterized by an absence of ribosomal 18S and 28S peaks and measured in a Bioanalyzer Picochip. Preferably, platelet mRNAs are measured by other methods, such as Fragment analyzer (Advanced Analytical Technologies, Ankeny, IA, USA) or Qubit Fluorometric Quantification (Thermo Fisher, Waltham, MA, USA) analysis (Figure [2c](#page-3-0)).

### 2.4.2. Clinical Application/Relevance of Tumor-Educated Blood Platelets

Platelet-related measures are considered important in anticipating long-term results in patients with GI cancer. A study distinguished 228 patients with localized and metastasized tumors from 55 healthy donors using the genetic profile of mRNA from TEPs. Additionally, mRNA sequencing of TEPs could accurately recognize MET or ERBB2-positive and mutant KRAS, EGFGR, or PIK3CA tumors. Moreover, TEPs have the ability to identify the location of primary tumors including colorectal cancer, non-small lung carcinoma, glioblastoma, pancreatic cancer, hepatobiliary cancer, and breast cancer [\[169\]](#page-37-14). Yang et al. showed that TIMP metallopeptidase inhibitor 1 (TIMP1) mRNA levels were higher in platelets from patients with CRC compared to those from healthy donors or patients with inflammatory bowel diseases, which could be another promising diagnostic signature [\[173\]](#page-38-0). A study in patients with hepatocellular carcinoma (HCC) conducted by Asghar et al. showed that the expression of TGF-β, NF-κβ, and VEGF was increased in TEPs of HCC patients compared to that from controls and thereby they suggested that these RNA based biomarkers could be used as a promising tool for early detection of HCC [\[174\]](#page-38-1). Furthermore, the alterations of platelet counts as a prognostic marker were studied in a clinical trial (NCT03717519) conducted by Corrado Pedrazzani. The study recruited 196 patients with synchronous colorectal liver metastases. In esophageal squamous cell carcinoma (ESCC), Ishibashi et al. performed a meta-analysis evaluating the prognostic values of platelet-related measures. The analysis revealed that a high platelet-to-lymphocyte ratio (PLR) was significantly correlated with poor OS [\[175\]](#page-38-2). A dual-center retrospective study performed by Yang et al. showed a standardized indicator of platelet counts was used to forecast the prognosis of 586 CRC patients by using a development-validation cohort. In the development cohort, postoperative platelet count and postoperative/preoperative platelet ratio (PPR) were independent predictors of prognosis in CRC patients. In the validation cohort, the platelet/lymphocyte ratio and PPR were used to test the OS of CRC patients and showed the largest AUC in reviewing 1-year and 3-year OS (AUC: 0.663 and 0.673) [\[176\]](#page-38-3). Based on the studies above, we summarize that PLR and PPR could serve as reliable and economic indicators to evaluate the prognosis of GI cancer. Interestingly, many new approaches have been utilized to explore the clinical relevance of TEPs in GICs. We have summarized some of them in Table [4](#page-15-0) below. TEPs have advantages over other blood-based sources due to their abundance in the blood, the ease with which they can be isolated, their high-quality RNA, and their ability to process RNA in response to foreign signals.

<span id="page-15-0"></span>**Table 4.** Clinical relevance of tumor-educated platelets in GICs.



# **3. Conclusions**

Due to the limitations of conventional tissue biopsies, there is an urgent need for new tumor biomarkers. As reviewed here, LBs have been well-evaluated and show promising results as an alternative clinical tool for the detection and treatment of gastrointestinal cancers, many of those currently being intensively investigated in various observational and interventional clinical trials (Tables [5](#page-16-0) and [6\)](#page-23-0). Multiple longitudinal biopsies allow for real-time monitoring of the tumor. This approach may facilitate the prediction of the possible treatment outcome and may help in choosing the optimal individualized therapeutic strategy. Therefore, the analysis of LB markers (TEPs, CTCs, ctDNA/cfDNA, and exosomes), in combination with modern imaging techniques and already existing protein markers might help to create an optimal clinical synergy that might be used as a standard procedure in the near future for early cancer detection and individualized cancer treatment.

<span id="page-16-0"></span>

**Table 5.** Observational study with ongoing clinical trials of LB in GICs.

**Liquid Biopsy Status Cancer Study Title Study Type Clinical Trial Identifier Estimated Enrollment Conditions Interventions Locations** CTC-7 CTC Recruiting Liver cancer The Role of Circulating Tumor Cells As Markers of Advanced Disease and Prognosis In HCC Observational NCT04800497 200 Hepatocellular Carcinoma, Recurrent Hepatocellular Carcinoma, Circulating Tumor Cell Procedure: hepatic resection 4 locations in Italy CTC-8 CTC Recruiting Colorectal cancer Sample Collection Study for the CellMax Life Circulating Tumor Cell and Circulating Tumor DNA Platforms for the Early Detection of Colorectal Cancer and Adenomas Observational NCT05127096 <sup>100</sup> Colorectal Cancer Screening Diagnostic test: FirstSight blood test Alabama, California, United **States** ctDNA-1 ctDNA Recruiting Gastric cancer Detection of ctDNA in the Diagnosis of Metastasis in Gastric Cancer Observational NCT05208372 200 Stomach Neoplasms, Metastasis Diagnostic test: ctDNA test Liaoning, China ctDNA-2 ctDNA Recruiting Gastric cancer ctDNA Screening in Advanced HER2 Positive Gastric Cancer Observational NCT04520295 <sup>100</sup> HER2-Positive Gastric Cancer Genetic: ctDNA screening Shanghai, China ctDNA-3 ctDNA Recruiting Gastric cancer Monitoring Minimal Residual Disease in Gastric Cancer by Liquid Biopsy Study Description Observational NCT05029869 <sup>100</sup> Gastric Cancer, ctDNA Diagnostic test: ctDNA Ho Chi Minh City, Vietnam ctDNA-4 ctDNA Recruiting Gastric cancer Potential Clinical Utilities of Circulating Tumor DNA in Advanced HER2 Negative Gastric Cancer Observational NCT05513144 <sup>30</sup> Gastric Cancer, ctDNA Jiangsu, China

![](_page_18_Picture_352.jpeg)

**Liquid Biopsy Status Cancer Study Title Study Type Clinical Trial Identifier Estimated Enrollment Conditions Interventions Locations** ctDNA-12 ctDNA Recruiting Liver cancer Tumor Cell and DNA Detection in the Blood, Urine and Bone Marrow of Patients with Solid Cancers Observational NCT02838836 120 Esophageal Cancer, Gastric Cancer, Pancreatic Cancer, Hepatocellular Cancer, Colorectal Cancer Procedure: study sample collection Missouri, United **States** ctDNA-13 ctDNA Recruiting Liver cancer Cohort Study of Patients with Hepatocellular Carcinoma and Circulating Tumor DNA Monitoring of Chemoembolization (Mona-Lisa) Observational NCT05390112 167 Circulating Tumor DNA Hepatocellular Carcinoma Non-resectable Biological: DNA Rouen, France ctDNA-14 ctDNA Recruiting Colorectal cancer Comparison of Diagnostic Sensitivity Between ctDNA Methylation and CEA in Colorectal Cancer Observational (Patient Registry) NCT05558436 712 Colorectal Cancer Diagnostic test: detection of ctDNA methylation Guangdong, China ctDNA-15 ctDNA Recruiting Colorectal cancer Role of Circulating Tumour DNA Testing in Assessing for Alterations of Primary Anti-EGFR Resistance in RAS/RAF Wild-type Metastatic Colorectal Cancer Patients Observational NCT05051592 40 Colorectal Cancer Singapore, Singapore ctDNA-16 ctDNA Recruiting Colorectal cancer Circulating Tumor DNA Analysis to Optimize Treatment for Patients with Colorectal Cancer Observational NCT03637686 1800 Colorectal Cancer 10 locations in Denmark ctDNA-17 ctDNA Recruiting Colorectal cancer Tracking Mutations in Cell Free Tumour DNA to Predict Relapse in Early Colorectal Cancer (TRACC) Observational NCT04050345 1000 Colorectal Cancer 36 locations in United Kingdom

![](_page_20_Picture_317.jpeg)

**Liquid Biopsy Status Cancer Study Title Study Type Clinical Trial Identifier Estimated Enrollment Conditions Interventions Locations** exo-1 Exosomes Recruiting Gastric cancer Use of Circulating Exosomal LncRNA-GC1 to Monitor Gastric Cancer Observational NCT05397548 700 Gastric Cancer Diagnostic test: measurement of levels of circulating exosomal lncRNA-GC1 Beijing, China exo-2 Exosomes Recruiting Pancreatic cancer Interrogation of Exosome-mediated Intercellular Signaling in Patients with Pancreatic Cancer Observational NCT02393703 111 Pancreatic Cancer, Benign Pancreatic Disease New York, United States exo-3 Exosomes Recruiting Pancreatic cancer New Biomarkers in Pancreatic Cancer Using EXPEL Concept **(PANEXPEL)** Observational NCT03791073 200 Oncology Montpellier, France exo-4 Exosomes Recruiting Pancreatic cancer A Pancreatic Cancer Screening Study in Hereditary High Risk Individuals Observational NCT03250078 <sup>100</sup> Pancreatic Neoplasms Diagnostic test: MRI/MRCP Connecticut, United States exo-5 Exosomes Recruiting Pancreatic A Study of Blood Based Biomarkers for Pancreas Observational NCT03334708 700 Pancreatic Cancer, Pancreatic Diseases, Pancreatitis, Diagnostic test: blood draw, diagnostic test: tumor tissue 13 locations in United

**Table 5.** *Cont.*

cancer

Adenocarcinoma

Pancreatic Cyst

collection, diagnostic test: cyst fluid

**States** 

(TEP)

**Liquid Biopsy Status Cancer Study Title Study Type Clinical Trial Identifier Estimated Enrollment Conditions Interventions Locations** exo-6 Exosomes Recruiting Liver cancer A Study of Imaging, Blood, and Tissue Samples to Guide Treatment of Colon Cancer and Related Liver Tumors Observational NCT03432806 <sup>80</sup> Colon Cancer, Liver Tumor Other: blood draws, procedure: colectomy or hepatectomy, diagnostic test: Fibroscan test New Jersey, New York, United States exo-7 Exosomes Recruiting Liver cancer Clinical Study for Combined Analysis of CTC and Exosomes on Predicting the Efficacy of Immunotherapy in Patients with Hepatocellular Carcinoma Observational NCT05575622 200 HCC Device: CTC PD-L1, exosomal PD-L1, and exosomal  $LAG-3$ detection Hubei, China TEP-1 Tumor educated Platelets (TEP) Recruiting Gastric cancer Project **CADENCE** (CAncer Detected Early caN be CurEd) Observational NCT05633342 15,000 Liver Cancer, Gastric Cancer, Colorectal Cancer, Esophageal Cancer, Pancreatic Cancer Singapore, Singapore TEP-2 Tumor educated Platelets (TEP) Not recruiting yet Pancreatic cancer ITGA2b and SELP Expression in Cancer Pancreas and Biliary Tract Cancer Observational (Patient Registry) NCT05493878 128 Pancreatic Cancer Diagnostic test: mRNA expression Assiut, Egypt TEP-3 Tumor educated Platelets Recruiting Pancreatic cancer Pre- and Post-operative TEG Indices in Patients with or without Adenocarcinoma Observational NCT05517811 400 Liver Cancer, Esophageal Cancer, Colorectal Cancer, Pancreas Cancer, Diagnostic test: TEG indices Colorado, United States

Undergoing Surgical Resection

**Table 5.** *Cont.*

Biliary Cancer

<span id="page-23-0"></span>![](_page_23_Picture_362.jpeg)

**Table 6.** Interventional study with ongoing clinical trials of LBs in GICs.

![](_page_24_Picture_396.jpeg)

![](_page_24_Picture_397.jpeg)

![](_page_25_Picture_368.jpeg)

![](_page_26_Picture_350.jpeg)

ctDNA-14 ctDNA

 $ctDNA-15$   $ctDNA$ 

Other: best practice, other:

![](_page_27_Picture_346.jpeg)

![](_page_27_Picture_347.jpeg)

![](_page_27_Picture_348.jpeg)

![](_page_28_Picture_373.jpeg)

![](_page_29_Picture_202.jpeg)

![](_page_29_Picture_203.jpeg)

**Author Contributions:** Conception and design: P.D., A.M., D.K. and G.F.W.; Collection and assembly of data: P.D., A.M., D.K., A.A. and G.F.W.; Methodology: P.D., A.M., D.K. and A.A.; Writing and editing: P.D., A.M., D.K., A.A., C.K., K.S. and G.F.W.; Administrative support: G.F.W.; Final approval of manuscript: All authors. All authors have read and agreed to the published version of the manuscript.

**Funding:** This research was funded by Das Bundesministerium für Bildung und Forschung (BMBF, 03INT506CA).

**Conflicts of Interest:** The authors declare no conflict of interest.

# **Abbreviations**

![](_page_30_Picture_219.jpeg)

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