

Review

Exosomal Functional Cargoes from Liquid Biopsy of Gastric Cancer: A Systematic Review of Studies With Potential Clinical Relevance

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Abstract. *Background/Aim:* Liquid biopsy (LB) is a promising non-invasive tool to detect cancer. Over the last few years, exosomes recruited from LB have attracted the attention of researchers for their involvement in cancer. We focused on the role of LB exosomes in gastric cancer (GC). *Materials and Methods:* We investigated the world literature on exosome-encapsulated functional biomarkers (non-coding RNAs and DNAs) taken from GC patients' LBs. Only the studies exploring serum, intraperitoneal fluid or gastric lavage were included. *Results:* As of 2022, fifty articles with an overall count of 3552 GC patients were investigated. Given the statistically significant associations with the clinicopathological categories of tumor depth, lymph node metastasis, staging class and tumor size, most exosome-mediated microRNAs, long non-coding RNAs and circular RNAs proved to exert a potentially important bioclinical role in terms of diagnosis, screening, prognosis and therapeutic targets. *Conclusion:* In the future, resorting to exosomal biomarkers taken from LB of affected patients could revolutionize the non-invasive fight against GC.

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Comparing the 2018 GLOBOCAN estimates of cancer incidence and mortality produced by the International Agency for Research on Cancer with the latter version edited in 2020, stomach cancer fell from fourth to fifth place of the most common types of cancer (but with increasing number of new cases from 1,033,101 to 1,089,103) and from the third place in 2018 to the fourth leading cause of global cancer deaths (causing 768,793 vs. 782,685 fatalities in 2018) (1, 2). Such epidemiologic ameliorations, although apparently minimal, are clinically of paramount importance, coming from decades of innumerable, sustained, and commendable efforts provided by the worldwide scientific community on all levels of research. Development of more precise systems of classification and prevention, innovative theories on metastatic routes, stronger indications to the type and timing of a multidisciplinary therapy strategy and standardization of surgical procedures (diagnosis, screening, therapy, and prognosis), in fact, have expanded the knowledge armamentarium and improved the survival chances (3-11). However, as of today, since most diagnoses are obtained at advanced stages, no standardized methods of non-invasive screening (alternative to gastroscopy) exist and its complex pathobiology is still far from being understood; gastric cancer (GC) keeps on being a fearsome disease with an ominous prognosis especially in the Western world. In fact, most GC cases continue to be detected at advanced phases of the disease when the prognosis is dismal (five-year survival rate of 10%) and the treatment options are limited (12). Although interesting, in terms of detection (especially for the early stages), the results of analyses of biomarkers taken from the sera of GC patients were of low specificity and sensitivity (this is particularly true for traditional markers such as pepsinogen, carcinoembryonic



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antigen and several carbohydrate antigens such as CA 19-9, Ca 72-4, Ca 125, Ca 24-2 and Ca 50), provisional (necessitating further corroboration by trial studies) or with limited applications (several circulating GC biomarkers are susceptible to endogenous degradation) (13-16). Such observations prompted researchers to look for novel and effective biological markers, generically termed as functional biomarkers, able to convey or regulate genetic information such as micro RNAs (miRNAs or miRs), long non-coding RNAs (lncRNAs), circular non-coding RNAs (circRNAs), or even DNAs (17-19). For the purposes of noninvasive recruitment useful to methods of screening, prognosis and prediction, the concept of liquid biopsy of GC was expanded. Therefore, in addition to plasma, ascites, or peritoneal lavage fluid (PLF), gastric juice (GJ) or lavage (GL) of patients became the new compartments to investigate as sources of traditional or new biomarkers (20). Intra-gastric fluid in particular, due to its closer vicinity with GC and for bypassing the metabolic functions of the liver, attracted the attention of scientific community because it is thought to be more specific than serum in view of its high levels of exfoliated malignant cells and tumor products (21-25). A further evolution in this field of research was the discovery that in body fluids, such cell-free (or circulating tumor) markers exist in at least three forms: unbound (single or double stranded nucleic acids), bound (assembled in lipoprotein macromolecules such as vitrosomes and NETosis) and encapsulated (in extracellular vesicles such as exosomes, microvesicles and apoptotic bodies) (26, 27). The study of genetic contents enclosed in exosomes derived from GC and taken from liquid biopsy represents a particular field of interest that begun only a few years ago but with already important and promising results. Herein, we offer a review on the clinical significance and possible implications of exosome-encapsulated functional biomarkers described so far by the world literature in the extracellular fluid compartments of GC patients.

Materials and Methods

We investigated the world literature written in the English language dealing with the exosome-encapsulated nucleic acids related to GC found in the liquid biopsy of affected patients. We consulted PubMed, Scopus, Science Direct, ResearchGate, Publons, Academia and Google Scholar as the main search engines. We used the following key-words and key-expressions: exosomal (exosome or exomic) DNA gastric cancer, exosomal miRNAs gastric cancer, exosomal lncRNAs gastric cancer, exosomal circRNAs gastric cancer, exosomes gastric cancer, serum exosomes gastric cancer, plasma exosomes gastric cancer, exosomes peritoneal lavage fluid, exosomes ascites, exosomes gastric juice, exosomes gastric lavage and exosomes gastric wash. Only prospective or retrospective works have been included but, in order to better assess the real clinical impact of exosomal molecular biomarkers, the following categories of articles were excluded from this review: studies on non-human subjects; studies not focused on at least one liquid biopsy

(biological fluids: blood, peritoneal lavage, gastric juice/lavage); studies fully devoid of patients' clinical features; studies dealing with exosomes derived from cultured cells only; past studies on the same markers (being analyzed more recently by updated researches); commentaries, editorials and letters to the editor. To improve the reporting quality of our systematic review, we resorted to a flow diagram following the PRISMA 2020 Explanation and Elaboration Document (28).

Results

The process and results of article selection for our systematic review were reproduced with a work flowchart according to the PRISMA 2020 V2 indications (Figure 1). After digging into the literature, the following findings were excluded from inclusion: 52 studies because they were conducted on cell lines only, fully *in vitro* or not including liquid biopsies (for example: only stomach tissues), 19 reviews, 2 letters to the editor and 7 former studies on exosomal biomarkers (we preferred to include more recent original reports). We thereby selected 50 studies dealing with functional contents encapsulated into exosomes derived from GC and isolated from liquid biopsy in GC patients. Almost the totality of the enrolled studies had a prospective nature; 37 works had an *in vitro* experimental part as well. As of 2022, no meta-analysis of studies on exosomal cargoes taken from liquid biopsy of GC exists. Twenty studies were on exosomal microribonucleic acids EmiRs (Table I) (29-48). Thirteen articles were on exosomal long non-coding ribonucleic acids ElncRNAs (Table II) (49-61). Fourteen studies were on exosomal circular ribonucleic acids EcircRNAs (Table III and Table IV) (61-74). Table V reviews the current publications on exosomal deoxyribonucleic acids EDNAs (76-78). Our review included 27 EmiRs (Table I and Table IV), 13 ElncRNAs (Table II), 14 EcircRNAs (Table III and Table IV) and 4 genomic EDNAs (Table V). Altogether, 3552 GC patients had been investigated with liquid biopsy (1,458 for EmiRs, 1,398 for ElncRNAs, 596 for EcircRNAs, 100 for EDNAs) (Table I, Table II, Table III, Table IV and Table V). Liquid biopsy mostly involved patients' sera (40 studies), followed by intra-gastric (GJ/GL) (6 studies) and intraperitoneal (PLF/ascites) (3 studies) compartments. Of the 2,999 GC patients investigated with liquid biopsy from serum (85.4% of total patients), 1239 were studied for EmiRs (41%), 1398 for lncRNAs (47%) and 362 for EcircRNAs (12%). Interestingly, all works on EDNAs investigated GJ samples (Table V). Exosomal cargoes were more frequently associated with an oncogenic rather than antioncogenic role: in fact, 12 out of 19 EmiR studies, 11 of 13 ElncRNAs papers and 9 out of 14 EcircRNAs publications dealt with oncogenic biomarkers. Conversely, studies on EDNAs focused more on tumor suppressor genes (Table V). When available, the pathologic pathways associated with each nucleic acid has been reported (Table I,

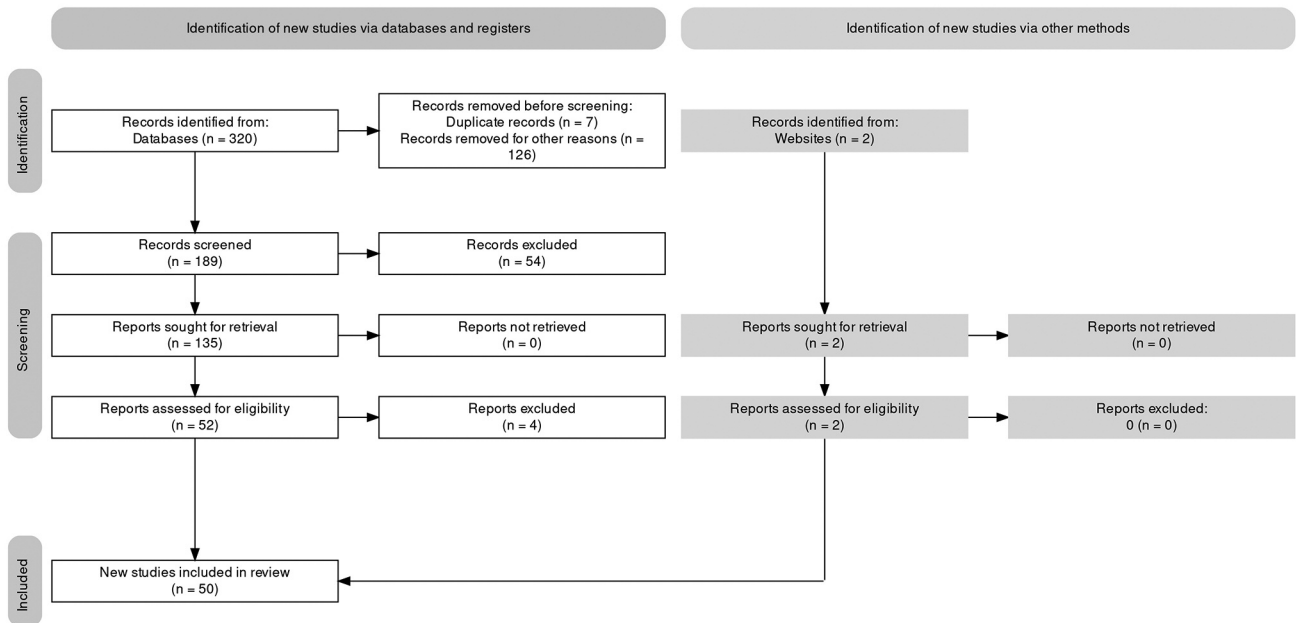


Figure 1. Flowchart of the study according to the PRISMA 2020 V2 indications.

Table II, Table III, Table IV and Table V). Associations between the up- or down-regulated expression of exosomal functional biomarkers and traditional clinicopathologic features of GC patients were clearly reported in 38 studies (76%). Staging class was the clinical parameter more often investigated (28 studies) and its association was statistically significant in 27 articles (96% of cases). Other relevant correlations were those with tumor depth (demonstrated in 9 out of 10 investigating studies, 90%), lymph node metastasis (13 of 14 exploring studies, 93%) and tumor size category (8 of 9 exploring studies, 89%). Most markers were also useful to diagnosis, screening and detection of recurrences and metastases with or without the combination of traditional soluble tumor antigens (Table I, Table II, Table III, Table IV and Table V). Moreover, in terms of survival, some exosomal nucleic acids resulted statistically significant independent factors of poor prognosis (32, 35, 38, 46, 47, 60, 62, 63, 65, 72). At last, some of these were identified as potential targets of therapy for their clinical role of chemosensitivity and chemoresistance (40, 51, 52, 68, 70) or the promotion effect on tumor microenvironment (19).

Discussion

Multicellular organisms can communicate either extra- or intra-cellularly, through direct interactions between cell surfaces (cell-cell contact) or transfer of functional molecules scavenged and secreted into extracellular vesicles (EVs) (79). EVs are small, spherical, membranous structures which

can be divided into three subgroups based on differences in biosynthesis and size: membrane-shedding EVs (also known as microparticles or microvesicles) (size of 50-3,000 nm), apoptosis-derived EVs (apoptotic bodies, 800-5,000 nm) and endosomal system-derived EVs (exosomes) which have the smallest diameter (40-100 nm) (79). The stability of the phospholipid bilayer of exosomes is a very important feature because, by conferring resistance to enzymatic degradation by RNase, it permits the preservation of such EVs in extracellular space and body fluids (blood, urine, saliva, breast milk, tears, cerebrospinal fluid, cervicovaginal lavage fluid, ascites and PLF, GJ and GL) for long periods of time as well as a safe long-distance conveyance of their content (29, 79). As observed in our review, exosomes contain several types of functional molecules such as mRNAs, DNAs and non-coding RNAs (miRNAs, lncRNAs, circRNAs) besides lipids, enzymes and proteins (Table I, Table II, Table III, Table IV and Table V) (29-78). Exosome-mediated intercellular communication can take place in four possible manners: stimulation after direct binding of EVs with cell surface ligands, release of receptors, deliver of functional proteins (pattern of particular importance in case of bacterial or viral infectious diseases) and transferal of genetic information (79). The latter has been the subject of this review. Through integration of oncoregulatory factors transported by tumor-derived exosomes (TEX), in fact, cancer cells can promote neoplastic initiation and progression by affecting proliferation, phenotype, functions and homeostasis of recipient cells (Table I, Table II, Table

Table I. Literature on exosomal microRNAs in liquid biopsy (serum or peritoneal lavage fluid), stomach tissue and cell lines from gastric cancer patients.

| Ref | Study type | Biomarker name | GC/Control Patients | Role | Serum expression* | Other fluid expression* | Pathologic associations | Mechanisms | Potential utility for GC |
|-----|------------|--|---------------------|------|-----------------------|---|---|--|---------------------------------------|
| 30 | R | miR-19b-3p, miR-106a-5p | 130/130 | O | Higher ($p<0.0001$) | Not studied | N ($p<0.01$), Stage ($p<0.05$) | Not declared | Diagnostic biomarkers |
| 31 | P, iv | miR-21, miR-1225-5p | 24/0 | O | Not studied | PLG (higher: $p=0.015$) | T4 ($p=0.027$, $p=0.008$) | p, PM (axis not studied) | Prognostic PM biomarkers |
| 32 | R | miR-29 family | 85 (33 PM+/52PM-) | TS | Not studied | PLG for miR-29 family (lower: $p<0.001$) | miR-29b-3p: bad OS ($p=0.014$), miR-29 fam: bad RFS ($p\leq 0.038$) | c, p, recurrence, and PM (axis not studied) | Prognostic PM biomarker; gene therapy |
| 33 | P | miR-552-5p | 30/15 | O | Higher ($p<0.05$) | iv (higher: $p<0.05$) | T ($p\leq 0.004$), N ($p\leq 0.011$), Stage ($p\leq 0.01$) | c, mi, EMT (via PTEN-TOB1axis), antiapoptosis (via caspase-3 axis), me | Prognosis, TT |
| 34 | R, iv | miR-195-5p, miR-211-5p | 88/88 | TS | Higher ($p<0.001$) | iv ($p=0.016$) | N ($p<0.01$), Stage ($p<0.05$) | Progression (axis not studied) | Diagno-prognostic biomarker |
| 35 | R, iv | miR-130b-3p, miR-15b-3p, miR-151a-3p, miR-1246 | 7/3 | O | Higher ($p<0.05$) | Urine (miR-1246 higher: $p<0.05$) | miR15b-3p: prognosis ($p<0.05$) miR-151a-3p: bad OS ($p<0.05$) | c,p,a (miR-15b-3p: DYNLT1/Caspase-3/-9 axis) | Diagno-prognostic biomarker, TT |
| 36 | R, iv | miR-10b-5p | 169/52 | O | Higher ($p<0.05$) | iv, GC tissue (higher: $p=0.016$) | N ($p=0.002$), Stage ($p=0.02$) | Proliferation (via PTEN), promotion (TGF β 1) | Diagnosis |
| 37 | P, iv | miR-122-5p | Not provided | TS | Lower ($p<0.05$) | iv (lower: $p<0.05$) | Not studied | Proliferation, me (via GIT1 expression) | Marker of c and progression |
| 38 | R, iv | miR-590-5p | 168/50 | TS | Lower ($p<0.05$) | Not studied | Lower in Stage 3/4 vs. Stage 1/2 ($p<0.05$); T, bad OS ($p<0.001$) | Invasion (axis not studied) | Diagnosis |
| 39 | R | miR-92a-3p | 131/122 | TS | Lower ($p<0.0001$) | Not available | N and Stage ($p<0.05$) | Proliferation, me | Diagnosis |
| 40 | P, iv | miR-374a-5p | 59/34 | O | Higher ($p<0.001$) | iv (higher: $p<0.05$) | Size ($p=0.01$); higher in oxaliplatin-resistance ($p<0.05$) | Chemoresistance (via Neurod1 expression) | Drug resistance appraisal, TT |
| 41 | P | miR-181b-5p | 92/73 | TS | Not studied | PLG (lower: $p<0.001$) | PM ($p<0.001$) | me (axis not studied) | MA diagnosis |
| 42 | P, iv | miR-1246 | 85/80 | O | Higher ($p<0.001$) | Not studied | Stage ($p<0.033$); M ($p<0.035$) | Not studied | Early diagnosis |
| 43 | P, iv | miR-1290 | 20/10 | O | Higher ($p<0.05$) | iv (higher: $p<0.05$) | Not studied | P (via NKD1 expression inhibition) | TT |
| 44 | P, iv | miR-135b | non-explicit | O | Higher ($p<0.05$) | iv, GC tissue (higher: $p<0.05$) | Not studied | Angiogenesis (via IL-8/FOXO1 axis) | TT (anti-VEGF drug) |
| 45 | P, iv | miR-107 | non-explicit | O | Higher ($p<0.01$) | iv, GC tissue (higher: $p<0.01$) | Not studied | P (via DICER1/PTEN/ARG1 axis) | TT |
| 46 | P | miR-23b | 232/20 | TS | Lower ($p<0.05$) | Not studied | T ($p=0.03$), Stage ($p<0.03$); Size ($p<0.02$); | Not studied | Prognosis and recurrence prediction |
| 47 | P, iv | miR-423-5p | 80/80 | O | Higher ($p<0.01$) | iv, GC tissue (higher: $p<0.01$) | N ($p=0.014$), poor OS ($p=0.039$) | p and mi via SUFU (TS) inhibition | Diagno-prognostic biomarker |
| 48 | P, iv | miR-221 | 40/20 | O | Higher ($p<0.05$) | iv (higher: $p<0.001$) | and DFS ($p=0.046$) Stage ($p=0.02$) | p, mi via PTEN/p27 | TT |

*Compared with control group (adjacent normal tissues/benign tissues/non-GC patients). R: Retrospective; GC: gastric cancer; iv: *in vitro/in vivo*; EMT: epithelial-mesenchymal transition); P: prospective; O: oncogene; MA: malignant ascites; PLF: peritoneal lavage fluid; p: progression; PM: peritoneal metastasis; TS: tumor suppressor; OS: overall survival; RFS: recurrence-free survival; c: carcinogenesis; AT: adipose tissue; mi: migration; me: metastasis; EMT: epithelial-mesenchymal transition; TT: therapeutic target; a: angiogenesis.

Table II. Literature on exosomal microRNAs in liquid biopsy (serum or peritoneal lavage fluid), stomach tissue and cell lines from gastric cancer patients.

| Ref | Study type | Biomarker name | Number of GC/Controls | Role | Serum expression* | Other tissue/fluid expression* | Pathologic associations | Mechanisms | Potential utility for GC |
|-----|------------|----------------------|-----------------------------|------|-----------------------|-----------------------------------|--|---|---------------------------------------|
| 49 | P, iv | ZFAS1 | 94/94 | O | Higher ($p<0.001$) | GC tissue (higher: $p<0.001$) | N ($p=0.008$), Stage ($p=0.034$) | Cell cycle progression, EMT progress, mig | Diagnostic biomarker, novel TT |
| 50 | R, iv | NR038975 | 86/47 | O | Higher ($p<0.001$) | GC tissue (higher: $p<0.001$) | T ($p=0.002$), N ($p=0.006$), Stage ($p=0.003$) | Proliferation, mig (via NF45/NF90 complex) | Diagnostic biomarker, novel TT (NF90) |
| 51 | R, iv | ENDOG-1:1 (lncFERO) | 112/104 | O | Higher ($p<0.01$) | Not declared | Not studied | Tumor ferroptosis inhibition (TS) (via SCD1/hnRNPA1) | Chemoresistance and recurrence |
| 52 | P, iv | CRNDE | 35/not explicit | O | Higher ($p<0.01$) | GC tissue (higher: $p<0.01$) | Not studied | p, invasion, drug resistance (via PTEN axis inactivation) | Cisplatin resistance reversion |
| 53 | R, iv | FRLnc1 | Serum: 60/60, tissue: 68/30 | O | Higher ($p<0.01$) | GC tissue (higher: $p<0.01$) | N ($p=0.004$), Stage ($p=0.009$) | proliferation, mig, invasion (via cyclin D1 mRNA) | Diagnosis, treatment |
| 54 | P, iv | X26nt | 16/16 | O | Higher ($p<0.01$) | iv, GC tissue (higher: $p<0.01$) | Not studied | angiogenesis (VE-cadherin expression) | Not declared |
| 55 | P, iv | H19 | 81/78 | O | Higher ($p<0.01$) | Not studied | Stage ($p=0.007$) | Not studied | Diagno-prognostic marker |
| 56 | P | MIAT | 109/98 | O | Higher ($p<0.001$) | Not studied | N ($p=0.0006$), Stage ($p<0.0001$) | Not studied | Prognostic marker |
| 57 | P | PCSK2-2:1 | 63/29 | TS | Lower ($p=0.006$) | Not studied | Size ($p=0.044$), Stage ($p=0.006$), LVI ($p=0.036$) | p | Diagnosis |
| 58 | P | lnc-GNAQ-6:1 | 43/27 | TS | Lower ($p=0.001$) | Not studied | all clinical features: $p>0.05$ | Not studied | Diagnosis |
| 59 | P, iv | lncUEGC1 | 51/60 | O | Higher ($p<0.0001$) | iv (higher: $p<0.01$) | Stages I-II ($p<0.0001$) | Not studied | EGC diagnosis |
| 60 | P, iv | HOTTIP | 126/120 | O | Higher ($p<0.001$) | iv (higher: $p<0.001$) | T ($p=0.029$), Stage ($p<0.001$), bad OS ($p<0.001$) | Not studied | Diagno-prognostic marker |
| 61 | P, iv | lncRNA1 (lncRNA-GC1) | 522/304 | O | Higher ($p<0.001$) | iv (higher: $p=0.002$) | G ($p<0.001$), Stage ($p<0.001$), Lauren ($p<0.001$) | p (axis not studied) | EGC diagnosis; follow-up |

*Compared with control group (adjacent normal tissues/benign tissues/non-GC patients). GC: Gastric cancer; O: oncogene; R: retrospective; iv: *in vivo/in vitro*; EMT: epithelial-mesenchymal transition; mig: migration; p: progression; TS: tumor suppressor; OS: overall survival.; c: carcinogenesis; EMT: epithelial-mesenchymal transition; TT: therapeutic target; LVI: lymphovascular invasion.

III, Table IV and Table V) (29-78). Tumor progression and metastasis are also facilitated by TEX with two other main mechanisms: on one hand this type of EVs can make tumor microenvironment (and its extracellular matrix) more favorable for secondary deposits with the release of specific integrins; on the other hand, they can suppress host innate and adaptive immune responses with the regulation of transforming growth factor- β , interleukin-6, prostaglandin E2 and other mediators (19, 79-81). With a total number of 50 studies and 3,552 patients, the important dimension reached by our review corroborates the pivotal role of soluble

exosomes for GC (Table I, Table II, Table III, Table IV and Table V). With the help of modern analytical techniques such as exosome precipitation kits, *in vitro* cell culture, quantitative reverse transcription-polymerase chain reaction, flow cytometry and many others, in fact, currently GC-derived exosomes can be easily isolated not only from tissues but also in several liquid compartments of affected patients such as blood, peritoneal lavage fluid/ascitis and gastric juice/gastric lavage (30-78). As already proven for other cancers, GC also uses exosomes as intercellular heralds to promote cell proliferation, progression, migration,

Table III. Literature on exosomal microRNAs in liquid biopsy (serum or peritoneal lavage fluid), stomach tissue and cell lines from gastric cancer patients.

| Ref | Study type | Biomarker name | Number of GC/Controls | Role | Serum expression* | Other tissue/fluid expression* | Pathologic associations | Mechanisms | Potential utility for GC |
|-----|------------|---------------------------|-----------------------|------|-----------------------|-------------------------------------|---|---|---------------------------------|
| 62 | P | circ_0001190 | 40/40 | TS | Lower ($p<0.05$) | GC tissue (lower: $p<0.05$) | Shorter OS ($p<0.05$) | via miR-586 (sponge)/SOSTDC1 (O) axis, angiogenesis | Prognostic biomarker |
| 63 | R, iv | circ_0001400 (circRELL1) | 64/64 | TS | Lower ($p=0.0025$) | iv, GC tissue (lower $p<0.001$) | G ($p=0.044$), T ($p=0.015$), N ($p=0.039$), Stage ($p=0.002$), bad OS ($p=0.009$), DFS ($p=0.004$) | via miR-637 (O) (sponge)/EPHB3 axis | Diagno-prognostic biomarker; TT |
| 64 | R, iv | circ_0005151 (circUBE2Q2) | 60/60 | O | Not studied | iv, GC tissue (higher: $p<0.01$) | N ($p=0.037$), Size ($p=0.018$) | c, mig, prog via miR-370-3p (sponge)/STAT3 axis | Prognostic factor; TT |
| 65 | R, iv | circ_0088300 | 60/60 | O | Higher ($p<0.01$) | iv, GC tissue (higher: $p<0.01$) | shorter OS ($p<0.01$) | c, prog via miR-1305 (sponge)/JAK/STAT axis | Diagno-prognostic biomarker |
| 66 | R, iv | circ_0044366 (circ29) | 10/0 | O | Higher ($p<0.01$) | iv | Not studied | c, prog, a (sponging miR-29a (TS)/VEGF) | TT |
| 67 | P, iv | circ-ITCH | 61/33 | TS | Lower ($p<0.05$) | iv, GC tissue (lower: $p<0.001$) | T ($p=0.021$) | me (via miR-199a-5p sponge/Khlot axis) | Diagnosis, therapy |
| 68 | P, iv | circ_0000260 | 27/27 | O | Higher ($p<0.01$) | GC tissue (higher: $p<0.001$) | Higher in cisplatin resistant group ($p<0.01$) | Cisplatin resistance (via miR-129-5p sponge/MMP11 axis) | Appraisal of CT resistance /TT |
| 69 | P, iv | circNHSL1 | 20/20 | O | Higher ($p<0.05$) | iv, GC tissue (higher: $p<0.05$) | N ($p=0.04$), Stage ($p=0.02$), M ($p=0.02$), Size ($p=0.006$) | Progression (via miR-149-5p sponge/YWHAZ axis) | TT |
| 70 | P, iv | circ-PVT1 | not available | O | Higher ($p<0.05$) | iv, GC tissue (higher: $p<0.05$) | Not studied | Progression (via miR-30a-5p/YAP1 axis) | Appraisal of CT resistance /TT |
| 71 | P, iv | circ_0000936 (circSHKBP1) | 224 (serum: 20) | O | Higher ($p<0.01$) | iv, GC tissue (higher: $p=0.0008$) | G ($p=0.001$), Stage ($p=0.027$), LVI ($p=0.036$), Size ($p=0.033$) | c,mig,prog,a (via miR-582-3p sponge/HUR/VEGF) | Diagno-prognostic marker, TT |
| 72 | P, iv | circ_0063526 (RanGAP1) | 97 (serum: 30) | O | Higher ($p<0.05$) | Higher ($p<0.05$) | N ($p=0.001$), Stage ($p=0.001$), Size ($p=0.016$), OS ($p=0.023$) | Invasion, me via miR-877-3p (sponge)/VEGFA | Diagno-prognostic marker |
| 73 | P, iv | circ_0032683 (circNEK9) | 30/30 | O | Higher ($p<0.0076$) | iv, GC tissue (higher: $p=0.0018$) | Stage ($p=0.0001$), Size ($p=0.0002$) | prog, invasion via miR-409-3p/ MAP7 axis | Follow-up |

*Compared with control group (adjacent normal tissues/benign tissues/non-GC patients). R: Retrospective; GC: gastric cancer; iv: *in vitro*; P: prospective; O: oncogene; prog: progression; TS: tumor suppressor; OS: overall survival; DFS: disease-free survival; c: carcinogenesis; EMT: epithelial-mesenchymal transition; mig: migration; a: angiogenesis; TT: therapeutic target; CT: chemotherapy. me: metastasis.

metastasis, neoangiogenesis and a favorable microenvironment for tumor growth and drug resistance (30-78). The leading and most commonly studied functional molecules encapsulated in GC-related exosomes are non-coding RNAs and DNAs. The former include EmiRs (or EmiRNAs), lncRNAs and circularRNAs. As elucidated by our review, the knowledge on the profile of exosomal non-coding RNAs is still limited since

it has been only a few years since the literature began dealing with these types of encapsulated biomarkers. EmiRs regulate tumor process with oncogenic or antioncogenic activity interacting with target messenger RNAs (mRNAs) and causing their degradation and translational repression (19, 30-48). Through the body fluids, as reported in our review, GC promotes an EV-mediated cell-to-cell pro-tumoral

Table IV. Literature on exosomal microRNAs in liquid biopsy (serum or peritoneal lavage fluid), stomach tissue and cell lines from gastric cancer patients.

| Ref | Study type | Biomarker name | Number of GC/Controls | Role | Intragastric expression* | Other tissue/fluid expression* | Pathologic associations | Mechanisms | Potential utility for GC |
|-----|------------|------------------|-----------------------|------|---------------------------|-----------------------------------|--|---|--------------------------|
| 74 | P | circ_000780 | 78/60 | TS | Lower ($p<0.001$) | GC tissue (lower: $p<0.001$) | T ($p=0.029$), LVI ($p=0.039$), Stage ($p=0.001$), Size ($p=0.02$) | Not studied (hypothesis of several miRNAs sponge) | EGC screening, prognosis |
| 75 | P | circ_0014717 | 96* | TS | Lower ($p<0.05$) | GC tissue (lower: $p<0.001$) | M ($p=0.048$), Stage ($p=0.037$), CEA ($p=0.001$), Ca 19.9 ($p=0.021$) | Not studied | GC screening |
| 19 | P, iv | miR16-5p, 191-5p | 18/0 | ? | Present (no p provided) | iv, GC tissue (higher: $p<0.01$) | Advanced stage (no p provided) | Microenvironment (fibroblasts recruitment) | diagnosis |

*Compared with control group (adjacent normal tissues/benign tissues or fluids/non-GC patients). GC: Gastric cancer; P: prospective; EGC: early gastric cancer; iv: *in vitro*; TS: tumor suppressor; LVI: lymphovascular invasion; ?: role not specified.

Table V. Literature on exosomal DNAs in the gastric juice samples from gastric cancer patients.

| Ref | Study type | Biomarker name | Number of GC/Controls | Role | Gastric juice expression* | Other tissue/fluid expression* | Pathologic associations | Mechanisms | Potential utility for GC |
|-----|------------|------------------------|-----------------------|-------|-----------------------------------|------------------------------------|---|--|--------------------------|
| 76 | P, iv | LINE1 gene, SOX17 gene | 20/0 | O, TS | Low methylation ($p=0.014$) | iv (low methylation: $p=0.013$) | Concordance of nuclear with exosomal methylations | DNA methylation | Non-invasive diagnosis |
| 77 | P, iv | BARHL2 gene | 70/32 | TS | Higher methylation ($p=0.0025$) | iv: high methylation ($p=0.002$) | BARHL2 protein silencing in EGC ($p=0.03$) | DNA methylation takes to loss of protein | EGC detection |
| 78 | P | miR-34b/c gene | 10/0 | TS | Higher methylation ($p=0.01$) | not studied | Lower miR-34 levels ($p=0.001$) | miR-34 modulation | GC diagnosis |

*Compared with control group (adjacent normal tissues/benign tissues/non-GC patients). GC: Gastric cancer; P: prospective; iv: *in vitro*; EGC: early gastric cancer.

communication enhancing the exosomal production of the oncogenic EmiRs (up-regulation of miR-19b-3p, miR-106a-5p, miR-552-5p, miR-195-5p, miR-211-5p, miR-130b-3p, miR-15b-3p, miR-151a-3p, miR-1246, miR-10b-5p, miR-374a-5p, miR-1246, miR-1290, miR-135b, miR-107, miR-423-5p and miR-221) or down-regulating the expression of those EmiRs functioning as tumor suppressors (miR-122-5p, miR-590-5p, miR-92a-3p and miR-23b) (Table I and Table IV). To potentiate its pro-tumoral efficacy, GC can also synergistically take advantage of ElncRNAs and EcircRNAs. Previously classified as competing endogenous RNAs (ceRNAs), such molecules can regulate gene expression through several interesting mechanisms including the sponging of miRNAs (49-75). Similarly to what was observed with EmiRs, in fact, according to their oncogenic

or antioncogenic activity, EceRNAs can show hyper- or hypo-expression in the liquid biopsies of GC patients (Table II, Table III and Table IV) (49-75). Our review also highlighted that the measurements of most reported exosomal non-coding RNAs (EmiRs, ElncRNAs and circRNAs) taken from serum, peritoneal lavage fluid/ascitis and GJ/GL of GC patients significantly correlated with the clinicopathological characteristics of an advanced disease such as tumor invasion depth (T3-T4), lymph node metastasis, late stage and larger size (Table I, Table II, Table III and Table IV). Furthermore, the dysregulated level of some exosomal nucleic acids was also identified as significant or independent factor of poor prognosis (32, 35, 38, 46, 47, 60, 62, 63, 65, 72). At last, we underscore the utility of investigating other non-blood liquid sources of

exosomal cargoes such as PLF/ascitis (31, 32, 41) and GJ/GL (19, 74, 75). In these samples, in fact, altered levels of EmiR-21, EmiR-1225-5p, EmiR-29b-3p, EmiR-181b-5p, EmiR-16-5p, EmiR-191-5p, Ecirc_000780 and Ecirc_0014717 correlated with peritoneal metastases, stage IV and shorter overall survival for GC patients (Table I and Table IV). All the clinical analyses herein displayed confirm soluble exosomes as bioclinical factors potentially useful to diagnosis, screening, prognosis, and target therapy of GC (30-78). Differently from non-coding ERNAs, EDNAs have been rarely addressed in the literature: in fact, only three studies have been published and only 4 exosomal genes (LINE1, SOX17, BARHL2 and miR-34b/c gene) have been examined so far (Table V) (76-78). Nevertheless, the study of these EDNAs appears extremely important and useful because it demonstrated that GC could modulate post-transcriptional expression accomplishing epigenetic gene silencing (*via* reversible methylation of DNA) not only in the primary cancer and metastatic foci but also in soluble exosomes and use such carriers with pro-tumoral and pro-metastatic intent (76-78).

Conclusion

Our review of the world literature on exosomal biomarkers isolated from liquid biopsy of GC patients demonstrates that future genetic and clinical investigations on this type of microbodies can revolutionize the strategies of diagnosis, screening, prognostic stratification, recurrence/metastasis prevention and treatment currently adopted against GC.

Conflicts of Interest

The Authors declare no conflicts of interest.

Authors' Contributions

All the Authors agreed with the content of the article. Dr. Virgilio conceived the research and wrote the manuscript. Dr. Virgilio, Dr. Montali, Dr. Annicchiarico and Dr. Salvemini reviewed the literature. Dr. Giarnieri, Dr. Montagnini and Dr. Villani verified the appropriateness of the articles to include in this review. Dr. Proietti and Dr. D'Urso reviewed the molecular pathways associated with the biomarkers included. Dr. Virgilio, Dr. Baldinu, Dr. Montali, and Dr. Annicchiarico reviewed the statistical analyses. Dr. Costi and Dr. Virgilio supervised the project.

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