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Extracellular vesicles and particles impact the systemic landscape of cancer

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Abstract

Intercellular cross talk between cancer cells and stromal and immune cells is essential for tumor progression and metastasis. Extracellular vesicles and particles (EVPs) are a heterogeneous class of secreted messengers that carry bioactive molecules and that have been shown to be crucial for this cell-cell communication. Here, we highlight the multifaceted roles of EVPs in cancer. Functionally, transfer of EVP cargo between cells influences tumor cell growth and invasion, alters immune cell composition and function, and contributes to stromal cell activation. These EVP-mediated changes impact local tumor progression, foster cultivation of pre-metastatic niches at distant organspecific sites, and mediate systemic effects of cancer. Furthermore, we discuss how exploiting the highly selective enrichment of molecules within EVPs has profound implications for advancing diagnostic and prognostic biomarker development and for improving therapy delivery in cancer patients. Altogether, these investigations into the role of EVPs in cancer have led to discoveries that hold great promise for improving cancer patient care and outcome.

Keywords biomarkers; cancer; extracellular vesicles and particles; metastasis; therapeutic deliverables

Subject Categories Cancer; Membrane & Trafficking

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Introduction

Extracellular vesicles (EVs), which constitute a heterogenous group of vesicles carrying various biomolecular materials that are secreted by most cells, have gained increasing attention due to their complex cargo and their ability to mediate long-distance communication in normal development and physiology, as well as in several pathophysiological conditions. The two major groups of EVs that have received intensive study include exosomes and microvesicles (MVs, also called ectosomes) (Cocucci & Meldolesi, 2015; Meldolesi, 2018; van Niel *et al*, 2018). MVs vary in size, ranging from 70 nm to almost 1 µm, and they are shed directly from the plasma membrane into the extracellular space. Exosomes form within the endosomal system prior to their secretion and are typically 50-150 nm in size. Further dissection of EVs has led to the recent discoveries of subcategories with different canonical EV markers and possibly of different cellular origins (Kowal et al, 2016), as well as of distinct subclasses with different sizes and cargo, named exosome small (Exo-S) and exosome large (Exo-L), and of a new non-membranous nanoparticle, named exomere (Zhang et al, 2018b). Thus, we refer to this collective secreted heterogeneous mixture consisting of MVs/ ectosomes, exosomes, and exomeres as extracellular vesicles and particles (EVPs). Throughout this review, we will use the term EVP, or we will use more specific nomenclature (e.g., MV, exosome, exomere) when subtype of EVPs are known for a particular study. For further discussion on appropriate use of EV terminology, we refer readers to a detailed description of this matter by Thery et al (2018).

While many physiological processes, including neurotransmission and immune signaling, are mediated by EVPs (Saliba et al, 2019; Zhou et al, 2020b), the role of EVPs in systemic aspects of human diseases, and in particular cancer, has attracted much attention. The inhibition of exosome production by cancer and stromal cells is invariably associated with reduced cancer growth and metastasis in a series of experimental studies (Bobrie et al, 2012; Peinado et al, 2012; Matsumoto et al, 2017; Richards et al, 2017), supporting the notion that exosome secretion is pivotal to cancer development. A considerable body of literature has shown the involvement of EVPs in all aspects of cancer progression, including host-microbiota interaction, carcinogenesis, metastasis establishment, and systemic effects of cancer on distant organs. EVPs are found in all bodily fluids, and their cargo signature can be used to predict cancer type at early stages and therapeutic responses (Hoshino et al, 2020; Shimada et al, 2021). The innate low toxicity and broad tissue distribution of EVPs also make them desirable and autologous carriers of chemotherapeutics, genetic material, or imaging agents.

In this review, we first present fundamental aspects of EVPs, particularly as they relate to cancer, including their heterogeneity, their mechanisms of biogenesis and uptake, and their diverse biomolecular cargoes. Next, we briefly cover key methods for the isolation and use of EVPs for experimental purposes. We will then discuss the multifaceted functional roles of EVPs during cancer (Figure 1), illustrating

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Diagram depicting the contribution of EVPs to different aspects of cancer initiation and progression, which is the subject of this review.

how EVPs from tumor, stroma, and immune cells in the tumor microenvironment organically orchestrate tumor growth and invasion, progression to metastatic disease, and systemic effects of cancer. Finally, we will examine the potential of EVPs as cancer biomarkers, therapeutic deliverables, and therapeutic/prognostic targets, highlighting their promises and limitations.

EVP heterogeneity and biogenesis

Complexity at the nanoscale level: EVP heterogeneity

EVPs represent a heterogeneous mixture of vesicles and particles that also vary in their biophysical properties, particularly with regard to size and density. Hence, characterization of the different subclasses is critical for understanding their contribution to cancer. By implementing asymmetric-flow field-flow fractionation (AF4) technology, Zhang *et al* (2018b) recently identified three distinct subpopulations of EVPs, named exosome small (Exo-S, 60–80 nm) and exosome large (Exo-L, 90–120 nm), alongside a newly discovered nanoparticle population, named exomere (<50 nm, with peak at ~ 35 nm), which lacks a membrane structure. In support, Zhang *et al* (2019e) also reported the isolation of exomeres from cultured cell lines using a modified ultracentrifugation strategy and demonstrated the transfer of functional exomere cargo to recipient cells. These novel nanoparticles were also found in human blood plasma by atomic force imaging (Bairamukov *et al*, 2020).

Exomeres exhibit a unique biomolecular composition compared to Exo-S and Exo-L. Specifically, they are more enriched in proteins involved in metabolic pathways, while Exo-S and Exo-L preferentially contain membrane proteins and signaling proteins. All three populations package DNA in a cell-type dependent manner, whereas RNA is generally more enriched in Exo-S and Exo-L across cell types. Exomeres contain less lipids than Exo-S and Exo-L and display a distinct composition profile of different lipid classes. Besides exomeres, Zhang et al (2021) recently reported additional non-membranous nanoparticles named supermeres, which were further isolated from EVs and exomere-depleted cell culture conditioned medial via ultracentrifugation. The protein and RNA composition of supermeres differ from Exo-S, Exo-L, and exomeres. Remarkably, the majority of extracellular RNA was found associated with supermeres rather than exosomes and exomeres. The biogenesis, molecular and structural organization, and functional mechanisms of supermeres remain to be determined. Furthermore, a recent study has reported that cytotoxic T cells release perforin and granzymes in stable particles named supramolecular attack particles (SMAPs), which represent another type of non-EV particle (Balint et al, 2020). The SMAPs are autonomously cytotoxic and ~ 120 nm in diameter, composed of a cytotoxic core and a shell of glycoproteins but lack a phospholipid membrane. More than 285 SMAP-associated proteins have been identified, including perforin and granzymes. A C-terminal fragment of thrombospondin-1 has been found in the shell structure and may contribute to the targeting specificity of SMAPs. Whether SMAPs function only through the immunological synapse or via other modes of action requires further investigation.

Other secreted vesicles with potentially more specialized functions have also been described. Recently, D'Acunzo *et al* (2021) reported the identification of mitovesicles, a new population of brain-derived double-membraned EVs of mitochondrial origin. These mitovesicles overlap in size and cosediment with exosomes, but they can be further separated from exosomes via a highresolution density gradient step. They contain a specific subset of mitochondrial constituents whose levels and cargo change during pathophysiological processes involving mitochondrial dysfunction, such as in Down Syndrome, but their mechanism of release is unknown. In addition, several studies have identified various types of larger, micro-sized vesicles. For example, adult neurons from *C. elegans* were found to extrude large vesicles called exophers (~ 4 μ m), which contain protein aggregates and organelles (Melentijevic *et al*, 2017). In migrating cells, an additional class of large vesicles (~ 1 μ m), named migrasomes, form at the tips and intersection of trailing edge retraction fibers and contain numerous smaller vesicles and cytosolic contents (Ma *et al*, 2015). Lastly, large oncosomes (0.5–10 μ m) carrying oncoproteins such as AKT1 are shed from the plasma membrane of cancer cells (Minciacchi *et al*, 2017).

New beginnings: biogenesis of endosome- and plasma membranederived EVPs

Exosome biogenesis begins with the formation of nano-sized intralumenal vesicles (ILVs) that are contained within endocytic compartments known as multivesicular endosomes or multivesicular bodies (MVBs) (Simons & Raposo, 2009; Gruenberg, 2020). ILVs form by inward budding of the endosome limiting membrane and detachment of the bud as a vesicle into the endosome lumen. MVBs traffic to the plasma membrane where they fuse and release the ILVs extracellularly as exosomes. By contrast, plasma-membrane-derived MVs form by direct budding of plasma membrane into the extracellular space (Sedgwick & D'Souza-Schorey, 2018; Clancy *et al*, 2021).

Intralumenal vesicle budding at multivesicular bodies

Pathways of ILV budding into MVBs during exosome biogenesis include those regulated by endosomal sorting complex required for transport (ESCRT) (Juan & Furthauer, 2018), by programmed cell death 6-interacting protein (also known as ALG-2-interacting protein X (Alix)) (Bissig & Gruenberg, 2014), and by lipids (Skotland *et al*, 2017b) (Figure 2A). These pathways have been studied in cancer cells, as well as non-cancer cell types that may be crucial microenvironmental regulators of tumor progression and metastasis.

The ESCRT pathway of ILV biogenesis involves a series of four main complexes, ESCRT-0, ESCRT-I, ESCRT-II, and ESCRT-III, which interact and assemble in an ordered, stepwise fashion on

Figure 2. EVP cargo, biogenesis, and uptake.

(A) EVP biogenesis occurs in MVB endosomes, giving rise to secreted exosomes, and at the plasma membrane, resulting in the generation of MVs, which are also termed ectosomes. Invagination of the endosome membrane leads to the formation of nanosized (50-150 nm) ILVs that are contained within the MVB lumen. ILV formation is regulated by various molecular processes at the MVB membrane that are each capable of capturing cargo and remodeling membranes for ILV generation and are also induced by upstream regulators. MVB trafficking is controlled by Rabs and SNARE-complexes for secretion of exosomes at the cell surface. MVS/ectosomes range in size from 50 nm to almost 1 µm. Their budding occurs at plasma membrane microdomains enriched for ESCRT proteins, like TSG101, which is recruited by ARRDC1 for MV formation, and MV biogenesis is also stimulated by ARF6. In cancer, molecular pathways involving RTKs/Rab31, SRC, ARF6/PLD2, Ral/PLD1, and mTOR/ PKM2 along with environmental and cellular factors related to hypoxia, pH, invasion, chemotherapy can all influence exosome biogenesis. Hypoxia and Rab22a promote MV formation in cancer cells. EVP uptake involves attachment of EVPs to extracellular matrix via adhesion molecules, such as integrins, on EVPs. Pathways of cellular uptake include endocytosis, macropinocytosis, and phagocytosis. Internalized EVPs traffic to the perinuclear area of recipient cells where they may fuse with lysosomes. (B) EVPs (including exomeres on the left and exosomes on the right) carry a variety of macromolecules, including proteins, nucleic acids, and lipids. Transmembrane proteins include adhesion molecules, like integrins, growth factor receptors, and tetraspanins, which are involved in biogenesis and which may also mediate adhesion. Cytosolic proteins such as actin, HSPs and other biogenesis factors are also commonly found in EVPs. Both dsDNA and ssDNA are found associated with EVPs. Doublestranded DNA is present both inside and on the surface of EVPs. Various RNAs, such as miRNAs, mRNAs, and other short and long noncoding RNAs, are carried by EVPs. Lipids, particularly cholesterol, phospholipids, ceramides, and sphingomyelin are enriched in EVPs. (C) Biogenesis and uptake factors functionally regulate in vivo cancer metastasis. Inhibition of Ral and Rab GTPases involved in biogenesis impairs metastasis. Blockade of exosomal integrins reduces exosome uptake and metastasis. HSP, heat shock protein; ILV, intralumenal vesicle; MVB, multivesicular body; MV, macrovesicle; RTK, receptor tyrosine kinases; dsDNA, double-stranded DNA; ssDNA, singlestranded DNA



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membranes (Hurley, 2015; Juan & Furthauer, 2018; Vietri *et al*, 2020). ESCRT-0, -I, and -II subunits possess ubiquitin binding domains for capture of ubiquitinated cargo, while ESCRT-I, -II, and -III promote membrane remodeling for ILV budding. The ATPase VPS4 interacts with ESCRT-III to support completion of ILV formation by promoting membrane scission, resulting in ILVs pinching off into MVB lumens. Importantly, depletion of multiple ESCRT protein subunits or VPS4 affects exosome biogenesis by altering exosome number, size, and protein composition to varying extents (Tamai *et al*, 2010; Baietti *et al*, 2012; Colombo *et al*, 2013; Jackson *et al*, 2017; Banfer *et al*, 2018).

Intraluminal vesicle biogenesis mediated by ESCRT-III is also induced by the ESCRT-associated protein Alix (Bissig & Gruenberg, 2014). Targeting of Alix to endosomes for ESCRT-III engagement occurs through multiple mechanisms that all have been shown to support exosome secretion in cancer cells. In MCF7 breast cancer cells, syntenin, a cytoplasmic adapter protein, recruits Alix to MVBs where interaction with ESCRT-III induces ILV formation (Baietti et al, 2012; Roucourt et al, 2015). Syntenin may be targeted to endosomes through activation of phospholipase D (PLD)2 by the GTPase ADP-ribosylation factor 6 (ARF6); PLD2, in turn, generates phosphatidic acid (PA) at the MVB limiting membrane to which syntenin can bind (Ghossoub et al, 2014). Generation of PA at endosomes can also occur via PLD1 activation by Ral GTPases to increase exosome biogenesis, and this function for Ral supports in vivo 4T1 mammary carcinoma metastasis (Ghoroghi et al, 2021). Localization of Alix to MVBs also occurs via association with the late endosome-specific lipid lysobisphosphatidic acid (LBPA) to support ESCRT-III-dependent ILV formation and exosome production in HeLa cells (Matsuo et al, 2004; Larios et al, 2020).

The lipid ceramide has also been implicated in exosome biogenesis (Skotland et al, 2017b; van Niel et al, 2018). Neutral sphingomyelinase 2 (nSMase2), which is the enzyme that generates ceramide from sphingomyelin at endosomes, increases ILV and exosome biogenesis (Trajkovic et al, 2008). This function of ceramide at MVBs may be enabled by multiple, additional pathways to enhance exosome biogenesis. The autophagy-related protein microtubule-associated protein 1A/1B-light chain 3 (LC3) may recruit FAN, an activator of nSMase (Adam-Klages et al, 1996), to endosome membranes where FAN could stimulate ceramidemediated ILV formation (Leidal et al, 2020). Moreover, activated Rab31 can augment exosome production and packaging of epidermal growth factor receptor (EGFR) into cancer cell-derived exosomes, and it was proposed that this occurs via the ceramide pathway of ILV production (Wei et al, 2021a), suggesting that it may be critical for cancer cell exosome biogenesis.

Trafficking and plasma membrane fusion of multivesicular bodies

The final stages of exosome biogenesis involve the trafficking of MVBs to the plasma membrane where they fuse and release ILVs as exosomes. Rab GTPase proteins, which are major regulators of intracellular membrane trafficking (Zhen & Stenmark, 2015), control the movement of MVBs toward the plasma membrane (Blanc & Vidal, 2018). Rab protein activity is regulated by GTPase-activating proteins (GAPs) (Zhen & Stenmark, 2015), and Rab-dependent pathways are further mediated by interaction with downstream effectors that are required for transport to and fusion of traveling vesicles with destination membranes (Fukuda, 2013). Alongside Rabs, these

Rab GAPs and effectors have also been implicated in exosome release (Figure 2A).

Rab27 and Rab35 are among the most recognized Rabs that influence MVB to plasma membrane trafficking for exosome secretion, and they also have functional roles in cancer. Rab27a and Rab27b associate with MVBs and mediate efficient release of exosomes by promoting targeting and docking of MVBs to the cell surface in HeLa cells (Ostrowski *et al*, 2010). The Rab27 effectors Slp4 and Slac2b also support exosome release (Ostrowski *et al*, 2010). Rab35 and its GAPs TBC1D10A, TBC1D10B, and TBC1D10C were also shown to regulate transport and fusion of MVBs with the plasma membrane in oligodendroglial cells (Hsu *et al*, 2010). Importantly, Rab27a and Rab35 are necessary for the secretion of exosomes from tumors *in vivo* (Bobrie *et al*, 2012; Peinado *et al*, 2012; Pucci *et al*, 2016). Rab11 (Savina *et al*, 2002) and Rab7 (Baietti *et al*, 2012) may also function in this final stage of exosome biogenesis.

Additional factors residing on the MVB membrane and at the cell periphery with direct roles in promoting fusion of membranes also control exosome secretion. These molecules include vesicle- and target-SNARES (v- and t-SNARES), which localize to the vesicle membrane and plasma membrane, respectively (Jahn & Scheller, 2006). The t-SNARE SNAP23 is phosphorylated and localizes to the intracellular face of the plasma membrane to promote exosome release in cancer cells (Wei *et al*, 2017b; Verweij *et al*, 2018; Yang *et al*, 2019b). Likewise, the v-SNAREs VAMP7 and Ykt6 are also implicated in exosome secretion by facilitating MVB-plasma membrane fusion in cancer cells (Fader *et al*, 2009; Gross *et al*, 2012; Sun *et al*, 2020a).

Biogenesis of endosome-derived EVPs in cancer cells

Although these pathways of exosome biogenesis have been extensively characterized, it remains uncertain which are crucial in cancer cells and if certain pathways are preferentially upregulated in cancer cells compared with non-transformed cells. As noted above, studies of some of these pathways have been conducted in cancer cell lines, and the functional roles of some biogenesis factors in mediating *in vivo* metastasis have been shown. However, more firmly establishing whether there are distinctions in mechanisms of exosome biogenesis pathways in cancer versus non-cancer cells and further illuminating how such pathways are triggered will uncover possible routes for safe therapeutic targeting of exosomes for cancer treatment.

Insight into such specificity is beginning to emerge. For instance, the tyrosine kinase SRC can enhance exosome secretion by stimulating ILV budding through phosphorylating syndecans and syntenin (Imjeti et al, 2017) and interacting with Alix (Hikita et al, 2019). Because SRC is overexpressed or exhibits increased activation by growth factor and integrin signaling in multiple cancers (Kim et al, 2009), it may potentiate the syntenin-Alix pathway of exosome biogenesis in cancer cells. Similarly, Rab31-dependent upregulation of ceramide-induced ILV formation may represent another cancer-cellspecific pathway of exosome biogenesis. Rab31 has been described to be overexpressed in cancer (Chua & Tang, 2015), and phosphorylation of Rab31 by various receptor tyrosine kinases often overactivated in cancer, such as EGFR, HER2, and MET, leads to abnormal activation of Rab31, which in turn could induce exosome biogenesis (Wei et al, 2021a). Overexpression or enhanced activation of other GTPases involved in exosome biogenesis, including ARF6 (Li et al,

2017d), Ral (Yan & Theodorescu, 2018), Rab27 (Li *et al*, 2018e), and Rab35 (Shaughnessy & Echard, 2018) in cancer cells has also been reported, indicating that pathways involving these factors may also be avenues by which exosome biogenesis is upregulated in cancer.

Microenvironmental and cellular stimuli frequently associated with cancer progression may also underlie tumor-cell-specific exosome production (Figure 2A). Notably, hypoxia, a common feature of the primary tumor microenvironment, has been shown to increase EVP production in various cancer types, including breast (King et al, 2012), lung (Hsu et al, 2017), prostate (Panigrahi et al, 2018), and ovarian cancer (Dorayappan et al, 2018) and melanoma (Park et al, 2019). Mechanistically, induction of HIF-1a supports enhanced EVP release during hypoxia in breast cancer cells (King et al, 2012), while hypoxia appears to enhance MVB biogenesis and release of endosome-derived exosomes in prostate cancer (Panigrahi et al, 2018) and ovarian cancer (Dorayappan et al, 2018). Additionally, alterations in pH associated with decreased extracellular and increased intracellular pH are prevalent in cancer cells (White et al, 2017), and augmented exosome biogenesis associated with changes in MVB biogenesis and transport has been observed when cancer cells are cultured in more acidic medium (Boussadia et al, 2018; Nakase et al, 2021). Impairment of lysosomal function can also promote exosome release and alter exosomal cargo by breast cancer cells (Latifkar et al, 2019). Progression of tumors to an invasive phenotype may similarly increase exosome biogenesis by supporting enhanced exosome secretion at sites of invadopodia, which are actin-rich cellular protrusions that degrade extracellular matrix (ECM) (Eddy et al, 2017). MVBs were shown to dock at invadopodia in a Rab27-dependent manner, and interfering with invadopodia reduced exosome secretion (Hoshino et al, 2013). MVB docking to the plasma membrane also relies on the actin-binding protein cortactin, which promotes invadopodia formation (Artym et al, 2006; Sinha et al, 2016). Further work is needed to better understand the extent to which tumorigenesis influences exosome biogenesis and has the exciting potential to uncover roles for additional cancerassociated phenotypes, such as altered metabolism, epithelial-tomesenchymal transition (EMT), ECM stiffness, stromal activation, and immune cell infiltration. It is noteworthy that many of these phenotypes are interconnected; hence, their ability to mediate exosome production may converge on common molecular mediators that would be attractive therapeutic targets.

Biogenesis of plasma-membrane-derived microvesicles

Biogenesis of plasma-membrane-derived MVs (also known as ectosomes) involves budding of the plasma membrane out into the extracellular space and release of the bud as a shed vesicle (Clancy *et al*, 2021) (Figure 2A). Initiation of MV formation begins with the establishment of plasma membrane domains rich in lipids such as cholesterol and ceramide (Sedgwick & D'Souza-Schorey, 2018). Additionally, discrete domains of the plasma membrane that are enriched with proteins involved in membrane reshaping, such as TSG101 and Vps4, have been associated with plasma membrane MV budding (Booth *et al*, 2006). Furthermore, targeting of TSG101 to the plasma membrane for MV biogenesis was demonstrated to occur via interaction with Arrestin Domain Containing 1 (ARRDC1) (Nabhan *et al*, 2012). Interestingly, ARRDC1 is distinctly localized to the plasma membrane and not the MVB, indicating that it may play a key role in dictating TSG101-dependent exosome versus MV formation. TSG101 may also facilitate cargo recruitment through protein–protein interactions as has been proposed for endosome-derived exosomes; indeed, TSG101 can regulate MV packaging of T cell receptors (Choudhuri *et al*, 2014). ARF6-induced actomyosin contractility promotes the final shedding step of plasma membrane blebs (Muralidharan-Chari *et al*, 2009).

In cancer cells, MV biogenesis is enhanced by hypoxia through an unclear mechanism involving upregulation of Rab22A (Wang *et al*, 2014). Protein targeting to MV in tumor cells has been linked to trafficking mediated by the SNARE protein vesicle-associated membrane protein 3 (VAMP3) (Clancy *et al*, 2015), and miRNA cargo can be directed to tumor MVs via an interaction between ARF6, a regulator of MV biogenesis, and Exportin-5, an RNA binding protein that mediates export of miRNA precursors out of the nucleus (Clancy *et al*, 2019). These studies have provided important insight into MV formation, but as with exosome biogenesis, further work is needed to understand mechanisms of MV biogenesis in cancer cells.

Biogenesis of exomeres

The biogenesis mechanisms of exomeres are still under investigation. While Exo-S and Exo-L are enriched in ESCRTs, Rabs, and SNARE-related proteins, indicating that biogenesis may involve MVB trafficking or plasma membrane budding, proteins associated with exosome and MV biogenesis were shown to be lacking in exomeres, suggesting that exomere biogenesis may rely on different, yet uncharacterized mechanisms (Zhang et al, 2018b, 2019e). Subcellular localization analysis of exomere-enriched proteins showed their specific association with endoplasmic reticulum and mitochondria, suggesting that their biogenesis may, at least partially, originate in these organelles. Enrichment in microtubuleassociated proteins in exomeres also implies the possibility of microtubule/cytoskeleton involvement in the secretion of exomeres. Furthermore, given the fact that exomere-specific proteins are involved in metabolic processes, cell metabolic status might dictate exomere production and release. Lastly, future investigations into lipid species selectively enriched in exomeres, such as triglyceride, ceramide, and cholesteryl ester, might provide further information on their biogenesis (Zhang et al, 2018b, 2019e).

Taking it all in: mechanisms of EVP uptake

Intercellular communication involving EVP uptake by recipient cells is essential for EVP-mediated cancer phenotypes. Therefore, understanding mechanisms of uptake may be key for identifying viable routes of therapeutic targeting of EVPs in cancer. In support, adjuvant treatment of mice with the drug reserpine, which was found to inhibit EVP uptake, appeared to eliminate lung metastasis of B16F10 melanoma cells (Ortiz *et al*, 2019), underscoring the potentially significant impact of targeting EVP uptake for cancer treatment.

The first step of EVP uptake involves attachment of vesicles to recipient cells. This binding can be mediated by surface molecules on EVPs. In particular, integrins and tetraspanins may regulate uptake either by directly promoting attachment to receptors on host cells or by supporting adhesion to cell-adjacent ECM, which enables uptake. For instance, B-cell-derived EVPs carrying integrins β_1 and β_2 can bind activated fibroblasts and also fibronectin and collagen-I (Clayton *et al*, 2004). Likewise, along with integrin α_4 or β_4 ,

tetraspanin 8 regulates differential uptake by numerous cell types, including endothelial cells, lung fibroblasts, and bone marrow cells, and in multiple organs, such as the lung, liver, spleen, and pancreas (Nazarenko *et al*, 2010; Rana *et al*, 2012). In cancer, this function of EVP integrins is critical for target cell selection and uptake in premetastatic niches; cancer cell EVPs can bind to laminin for uptake by fibroblasts and epithelial cells in the lungs or to fibronectin for uptake by Kupffer cells in the liver via integrin β 4 or β 5, respectively, and this ultimately determines metastatic organotropism (Hoshino *et al*, 2015).

Glycosylation of EVP surface proteins also influences EVP targeting and internalization. Increased glycosylation was shown to impede EVP uptake by ovarian cancer cells in vitro (Escrevente et al, 2011), and uptake of breast cancer cell EVPs by brain endothelial cells in vitro is also diminished by glycosylation (Nishida-Aoki et al, 2020). Interestingly, changes in certain glycosylation patterns alter in vivo biodistribution. Specifically, while removal of N-linked glycans did not appear to affect organ biodistribution of breast cancer cell EVPs, loss of O-linked glycans enhanced uptake by the lungs and brain without affecting uptake by the spleen and liver (Nishida-Aoki et al, 2020). Molecules on the surface of the receiving cell can also impact uptake of cancer cell EVPs. Cell surface 25hydroxycholesterol blocks EVP uptake (Ortiz et al, 2019), whereas heparan sulfate proteoglycans favor EVP uptake (Christianson et al, 2013). It would also be expected that additional integrin ligands or tetraspanin binding partners on host cells are required for uptake.

Methods employing fluorescent labeling of EVPs using lipophilic dyes and subsequent intracellular imaging of EVP fate in recipient cells have demonstrated that EVPs seem to be mainly internalized through regulated endocytosis, after which they enter the endocytic pathway and are trafficked to perinuclear late endosomes or lysosomes (Morelli et al, 2004; Tian et al, 2010, 2014a; Svensson et al, 2013; Costa Verdera et al, 2017). EVPs can also be taken up by macropinocytosis (Tian et al, 2014a; Nakase et al, 2015; Costa Verdera et al, 2017) and phagocytosis (Feng et al, 2010). Through these various modes of cellular uptake, EVPs would be expected to initially stay intact; hence, an outstanding question is how EVP cargoes are accessed by target cells. Backfusion of internalized EVPs with host endosomal membranes would facilitate liberation of intra-EVP cargoes and allow membrane-associated molecules to engage effectors by assuming the same orientation and topology relative to endosomal membranes as in donor cells. Direct monitoring and visualization of cargoes will be necessary to tease out these possibilities and more firmly corroborate direct and specific roles for EVP cargoes in eliciting changes in recipient cell phenotype.

Fully loaded: EVP cargo

EVP protein packaging

Packaging of particular proteins into EVPs functionally influences cancer progression and metastasis (Figure 2B). Most notably, EVP integrin profiles can distinguish cancers that metastasize to certain distant sites, and selective integrin packaging also plays a crucial role in dictating organ-specific uptake of EVPs and consequent premetastatic niche formation (Hoshino *et al*, 2015). EVPs derived from lung-tropic breast cancer cells package more $\alpha_6\beta_4$ and $\alpha_6\beta_1$ integrins than brain metastatic breast cancer cells or liver metastatic pancreatic cancer cells, whereas $\alpha_v\beta_5$ is more highly represented in EVPs from liver-tropic cells. Additionally, depletion of these integrins

impaired organotropic EVP uptake and reduced metastasis. Other EVP molecules, such as cell migration-inducing and hyaluronanbinding protein (CEMIP), are also associated with metastasis to particular organs. Brain metastatic breast cancer cells preferentially package CEMIP into EVPs, and EVP CEMIP functionally supports brain metastasis (Rodrigues *et al*, 2019). Although levels of cellular CEMIP protein are equivalent between lung-, bone-, and braintropic breast cancer cells, CEMIP was found markedly enriched in brain tropic cell-derived EVPs. Collectively, these studies illustrate the critical role of specific EVP protein packaging in determining metastatic fate. As a result, monitoring cancer patient EVPs for selectively packaged proteins, such as specific integrins or CEMIP, may aid in selection of therapies most effective in treating future metastases at specific organs.

The oncoprotein EGFR has been identified in EVPs derived from glioma cells, squamous cell carcinoma cells, lung cancer cells, and gastric cancer cells. Oncogenic activation of EGFR and increased expression of wild-type (WT) EGFR promote incorporation of EGFR into EVPs and allow for paracrine transfer of activated EGFR to less aggressive tumor cells and to endothelial cells to support tumor progression (Al-Nedawi et al, 2008, 2009). EGFR could only be detected in serum EVPs from gastric cancer patients compared with healthy donors and its levels increased with cancer stage (Qu et al, 2017). Moreover, EGFR⁺ EVPs promoted gastric cancer liver metastasis. Interestingly, Rab31 was shown to promote packaging of EGFR into exosomes via the ceramide pathway of ILV biogenesis. Activated EGFR can phosphorylate Rab31, which stimulates Rab31-dependent ILV formation and incorporation of EGFR into those ILVs (Wei et al, 2021a). Thus, although pathways of selective protein packaging into EVPs remain largely undefined, this study of EGFR packaging has begun to provide new insights into this process and may be blocked to inhibit EVP EGFR-mediated phenotypes. Another oncoprotein, MET, has also been shown to be selectively packaged into cancer cell EVPs. Comparison of MET levels between EVPs from metastatic B16F10 mouse melanoma cells and from the less aggressive B16F1 variant showed that increased MET correlated with metastatic ability, and EVP MET was responsible for promoting melanoma lung metastasis by favoring premetastatic niche conditioning, corroborating the functional importance of selective protein packaging in metastasis (Peinado et al, 2012).

In addition to these functional studies of particular EVP proteins, proteomic analysis of EVPs has been instrumental in defining the broad repertoire of nuclear, cytoplasmic, and membrane proteins incorporated into cancer EVPs. These studies have identified common proteins that tend to include defined EVP markers, such as molecules associated with biogenesis. Importantly, these investigations have substantiated the importance and prevalence of distinct protein packaging for cancer-associated EVPs, potentially making EVPs powerful tools for diagnosis and prognosis.

Analysis of EVPs from a panel of 60 cancer cell lines (NCI-60) representative of nine tissue types identified greater than 6,000 unique proteins across EVPs from all cell lines (Hurwitz *et al*, 2016). 213 common proteins were identified that include proteins, such as Rabs, that are expected regulators of biogenesis. This study also demonstrated that proteomes of EVPs from different cell lines but of the same cancer type cluster together, and further analysis of individual cancers showed that samples also cluster based on stage or aggressiveness of disease. These exclusive proteins may therefore

represent biomarkers for cancer type and prediction of disease state. These differences in proteins between EVPs generally reflected the varying levels of expression in the cells of origin, but this work also identified proteins that are preferentially enriched in certain EVPs even when similarly expressed between cell types, supportive of selective packaging.

A recent landmark study has reinforced the significance of EVP proteins as biomarkers through a large-scale analysis of hundreds of human patient-derived EVPs (Hoshino et al, 2020). This study aimed to identify EVP markers suitable for characterization of human patient EVPs, to establish whether cancer patient EVP proteomes are distinct from EVPs of healthy patients, and to determine if EVPs from patients with different types of cancer are distinct. Characterization of markers confirmed the presence of traditional EVP markers and also established new markers common to all samples. The conventional markers included HSP8 and Alix, which were also among the predominant ones found in the NCI-60 study of cancer cell lines (Hurwitz et al, 2016), indicating a refined panel including these along with the newly established markers may be optimal for characterization of EVPs from patients. Hoshino and colleagues also mined for proteins that may be associated with cancer EVPs and discovered that EVPs from tumor tissue explants carry distinct proteins compared to EVPs from non-tumor explants of the same tissue type. Furthermore, many of these proteins are significantly enriched in or exclusive to a particular cancer type, such as lung cancer or pancreatic cancer, but proteins common to different cancers were also identified in this tissue explant EVP analysis. Remarkably, these proteins were also observed to be enriched in EVPs from plasma of cancer patients compared to plasma-derived EVPs from healthy individuals. Thus, select EVP proteins can potentially serve as clinically tractable liquid biopsy tools to identify and diagnose cancer. Hoshino and colleagues further identified additional cancer-associated EVP proteins from other organ sources, such as immune organs, that are representative of systemic changes associated with cancer and therefore contribute to EVP proteome profiles which may help detect cancer via liquid biopsy.

Additional proteomic studies have more specifically focused on determining whether EVP proteomes may represent disease stage for types of cancer. For colon cancer, analysis of patient-derived primary colorectal cancer cells and paired lymph node metastatic cells revealed that EVPs from both cell types carry approximately 800 proteins each but, less than half are similarly abundant between the samples, demonstrating that the majority are selectively enriched and could be used as predictors of disease stage (Choi et al, 2012). Likewise, a larger analysis of seven human melanoma cell lines uncovered that EVPs from more aggressive or metastatic melanoma carry distinct molecules compared to EVPs from cell lines representative of less advanced disease (Lazar et al, 2015). Additionally, proteomic characterization of glioblastoma EVPs also showed that the enrichment of certain proteins is associated with tumor grade and aggressiveness (Mallawaaratchy et al, 2017). Furthermore, multiple reports detailing the proteome of breast cancer EVPs established specific EVP protein signatures based on metastatic ability (Gangoda et al, 2017), primary tumor molecular subtype (Rontogianni et al, 2019), and treatment status and recurrence (Vinik et al, 2020). Altogether, these studies have identified distinct proteins selectively packaged into EVPs, which may have prognostic and predictive value for cancer detection, progression, and therapeutic response.

EVP DNA and RNA cargo

DNA present in EVPs may be a valuable source of circulating tumor DNA for liquid biopsy biomarker analysis. Cancer cell derived EVPs contain a variety of DNA molecules, including genomic DNA (Balaj et al, 2011;Kahlert et al, 2014; Lázaro-Ibáñez et al, 2014; Thakur et al, 2014) and mitochondrial DNA (Guescini et al, 2010; Sansone et al, 2017). Genomic DNA represents the entire genome (Kahlert et al, 2014; Thakur et al, 2014) and may be single-stranded (Balaj et al, 2011) or double-stranded (Kahlert et al, 2014; Lázaro-Ibáñez et al, 2014; Thakur et al, 2014) (Figure 2B). Moreover, imaging (Maire et al, 2021) and biochemical analysis (Thakur et al, 2014) of EVP DNA showed that it is present both on the surface of and within EVPs. DNA sequencing has identified the presence of oncogenes in various cancer-derived EVPs, including amplified *c*-Myc in medulloblastoma EVPs (Balaj et al, 2011), mutant BRAF in melanoma EVPs, mutant EGFR in non-small-cell lung cancer EVPs (Thakur et al, 2014), mutant KRAS and p53 in pancreatic cancer EVPs (Kahlert et al, 2014), and mutant PTEN in prostate cancer EVPs (Lázaro-Ibáñez et al, 2014).

Mechanisms of EVP DNA incorporation remain understudied and obscure. The overall levels of DNA are higher in EVPs from cancer cells compared with normal fibroblasts (Balaj *et al*, 2011; Thakur *et al*, 2014), suggesting that tumorigenic phenotypes promote DNA packaging. Additionally, packaging of DNA into tumor-derived EVPs may be induced by several stimuli, including oncogenic *HRAS* transformation (Lee *et al*, 2014), chemotherapy (Ke *et al*, 2017; Kitai *et al*, 2017; Yokoi *et al*, 2019), and radiation therapy (Diamond *et al*, 2018). Recent work also suggested that secretion of DNA via EVPs is cytoprotective by alleviating cellular stress associated with accumulation of harmful cytoplasmic DNA and micronuclei (Takahashi *et al*, 2017; Yokoi *et al*, 2019). Hence, cancer-therapy-induced DNA damage may promote EVP DNA packaging. Molecularly, tetraspanins, which are abundant in EVPs, may control EVP DNA loading through interaction with histones and DNA (Yokoi *et al*, 2019).

EVPs also transport various mRNA and noncoding RNA species, and many of these RNAs are significantly enriched in EVPs compared with the cell of origin, indicating that active mechanisms drive their packaging. For example, some mRNAs that are present in EVPs from mast cells could not be detected in parent cells, while some miRNAs were more abundant in EVPs (Valadi *et al*, 2007). Similarly, diverse RNAs are more highly represented in tumor-derived EVPs compared to the tumor, including mRNAs in glioma cells (Skog *et al*, 2008), miRNAs in colorectal cancer cells (Cha *et al*, 2015), circular RNAs in liver cancer cells (Li *et al*, 2015c) and colon cancer cells (Dou *et al*, 2016), small nuclear RNAs in Lewis Lung Carcinoma (LCC) tumors (Liu *et al*, 2018).

Whether or not EVPs transfer sufficient amounts of RNA to elicit phenotypic changes in recipient cells has been debated. However, RNAs are enriched in EVPs from cancer patients, and EVP RNAs impact disease progression by promoting pre-metastatic niche formation and metastasis in mouse models (Xie *et al*, 2019; Möller & Lobb, 2020). Moreover, primary tumor cells may expose other cells in their immediate surroundings or at distant sites to a constant delivery of EVP-encapsulated RNA that may indeed be critical for cancer progression. Accordingly, the mechanisms governing EVP RNA sorting have garnered considerable attention. In cancer cells, EVP packaging may be modulated by activation of oncogenes, such as mutant KRAS, which alters loading of various RNA molecules into EVPs (Cha et al. 2015; Dou et al. 2016; Hinger et al. 2018), in part by regulating association of the miRNA-interacting protein Ago2 with MVBs (McKenzie et al, 2016). In addition, the nSMase2ceramide pathway was found to be dependent on 3' UGGA and 3' UUU motifs, which agrees with prior work describing an increased prevalence of 3'-end uridylated miRNA in EVPs compared with cells (Koppers-Lalic et al, 2014). The RBP hnRNPA2B1 promotes selective sorting of miRNA into EVPs by binding specific motifs (EXOmotifs) contained within those miRNAs (Villarroya-Beltri et al, 2013). Although it remains unclear how hnRNPA2B1 engages EVP biogenesis machinery, this study showed that hnRNPA2B1 associates with intracellular ceramide-rich MVB structures, suggesting that the nSMase2-ceramide pathway of exosome biogenesis may be involved. Moreover, this function of hnRNPA2B1 supports colorectal cancer liver metastasis (Zhao et al, 2020c) and bladder cancer lymphatic metastasis (Chen et al, 2019a) by regulating EVP sorting of tumor cell miRNA and long noncoding RNA, respectively. YBX1 is another RBP that mediates encapsulation of diverse small noncoding RNAs, including miRNA, tRNA, Y RNA, and Vault RNA, into EVPs (Shurtleff et al, 2016, 2017). Mechanistically, ubiquitination of YBX1, which supports interaction with TSG101 and consequent YBX1 secretion (Palicharla & Maddika, 2015), may further dictate loading of YBX1 and associated RNAs. Furthermore, secretion of EVP YBX1 was shown to be enhanced by EMT following HRASmediated transformation of epithelial cells (Tauro et al, 2013b), suggesting that YBX1-mediated packaging of miRNAs into EVPs may be augmented in cancer. Another recent study has identified an additional RBP-mediated pathway of RNA sorting that is anchored by the autophagy-related protein LC3 (Leidal et al, 2020). LC3 is targeted to MVB membranes and it interacts with the RBPs hnRNPK and SAFB. This interaction allows for capture and loading of small RNAs, namely snoRNAs and miRNAs, into exosomes. It remains unknown how this particular pathway may influence incorporation of RNA into cancer cell-derived EVPs. Autophagy is well recognized for being upregulated as a vital coping mechanism in normal and cancer cells in response to environmental stressors (Galluzzi et al, 2015). Therefore, the contribution of LC3 to classical autophagy versus exosomal loading may be fine-tuned to manage the homeostatic secretory and stress response needs of cells.

Overall, these studies of EVP RNA loading have provided considerable insight into selective packaging of bioactive molecules and may be key in guiding future interrogation of protein and DNA packaging. Such investigation could similarly be aimed at understanding how particular protein modifications influence packaging and how protein and DNA cargoes may interact with core biogenesis machineries.

EVP lipid content

Lipids represent an additional class of macromolecules that are packaged into EVPs (Figure 2B). They were first identified in EVPs from reticulocytes, which were reported to harbor cholesterol, sphingomyelin, and various phospholipids, including phosphatidylcholine, phosphatidylserine (PS), phosphatidylinositol, and phosphatidylethanolamine (Vidal *et al*, 1989). These lipids appeared mostly equivalently abundant in EVPs and cells, but subsequent studies of EVP lipid analysis have described an enrichment of lipids in EVP compared with cells, namely cholesterol, sphingomyelin, ceramide, and PS (Egea-Jimenez & Zimmermann, 2019). B cell EVPs have an increased abundance of cholesterol, sphingomyelin, and ganglioside GM3 compared with levels in cells, whereas multiple phospholipid species were less enriched in EVPs compared with cells (Wubbolts *et al*, 2003). This lipid profile of B cell EVPs was also shown to be associated with detergent resistance properties similar to lipid raft microdomains found within cellular membranes. Likewise, sphingomyelin was found to be the main lipid enriched in EVPs from both mast cells and dendritic cells, whereas cholesterol was not found to be enriched, and the phospholipids phosphatidylcholine and phosphatidylethanolamine were decreased or increased, respectively, in EVPs compared with cells (Laulagnier *et al*, 2004).

In cancer, similar trends of EVP lipid content appear to exist. A large-scale lipidomic analysis quantifying greater than 200 lipid species in EVPs from PC3 prostate cancer cells identified cholesterol, sphingomyelin, glycosphingolipids, such as ceramides, and PS as being more abundant in EVPs than cells, with other phospholipids generally lower in EVPs (Llorente et al, 2013). Furthermore, EVPs from urine of prostate cancer patients have higher levels of some lipids, namely ceramides, relative to urine-derived EVPs from healthy patients, suggesting that these lipids could serve as fluidbased biomarkers (Skotland et al, 2017a); however, in another study, ceramide levels were found to be decreased in urine EVPs from stage 2 benign prostate hyperplasia patients compared with urine EVPs from stage 3 prostate cancer patients (Clos-Garcia et al, 2018), complicating the potential use of this lipid for biomarker purposes. Additionally, EVPs from colorectal cancer cells, glioblastoma cells, and hepatocellular carcinoma cells also display an enrichment of cholesterol, sphingomyelin, and PS compared with cells (Lydic et al, 2015; Haraszti et al, 2016). These studies unveil common themes in EVP lipid content, and further work establishing mechanisms of lipid packaging and functional roles for EVPs lipids may enhance their biomarker and therapeutic potential.

Exomere cargo

Following their recent discovery, exomeres have been thoroughly characterized for their molecular composition (Zhang et al, 2018b, 2019e). Proteomics analysis revealed unique protein profiles of exomeres that are quite distinct from that of EVs. As expected, membrane-associated proteins are relatively low in exomeres, consistent with their lack of external membrane. Exomeres are instead enriched in metabolic enzymes and proteins involved in glycosylation, hypoxia, microtubule assembly, and coagulation. Gene Set Enrichment Analysis strikingly demonstrated that metabolic processes, including carbohydrate metabolism and protein synthesis, are selectively associated with exomere-specific proteins. These bioinformatic analyses suggest potential roles for exomeres in modulating the metabolism in the recipient cells. Furthermore, the biological activity of exomere protein cargo has been demonstrated by the functional work carried out by Zhang and collaborators, where they showed that exomeres-encapsulated β -galactoside $\alpha 2,6$ sialyltransferase 1 (ST6Gal-I) and amphiregulin (AREG) mediate hypersialyation of membrane proteins and activation of EGFR signaling, respectively, in the recipient cells (Zhang et al, 2019e).

Posttranslational modifications of proteins are critical for cell signaling. Via lectin blotting and glycomic MS analysis, our group further evaluated the N- glycan profiles of exomere and exosome subsets (Zhang *et al*, 2018b). The extent of N-glycosylation and the protein carriers present in exomeres were found different from that in Exo-S and Exo-L for the examined glycan species, including bisected and branched N-glycans, structures related to fucosylation (fucose-linked α -1,6) to GlcNAc or fucose-linked (α -1,3) to GlcNAc-related structures, and α -2,6-sialylated glycans. Instead, complex N-glycans with relatively high levels of sialylation are prevalent in all subsets. Glycomic studies further revealed differences in N-glycan composition and structures among exomeres, Exo-S, and Exo-L, as evidenced by detection of unique ions in exomeres specifically. Notably, the N-glycan profile of exomeres and exosomes is cell type-specific.

Interestingly, exomeres contain lipids, though their total lipid content is three to fivefold lower than EVs, which is consistent with the lack of an external membrane in exomeres (Zhang *et al*, 2018b, 2019e). Additionally, lipidomic analysis showed distinct lipid composition among exomere and EVs. Major structural components of the plasma membrane lipid bilayer, such as phospholipids, sphingomyelin, and sterols, ranked top in both exomeres and EVs. Compared with other lipid classes, relatively higher levels of triglycerides and ceramides and a higher ratio of esterified to unesterified cholesterol were observed in exomeres compared with EVs, suggesting that exomeres may serve as a major carrier to transport these metabolites to recipient cells.

Similar to EVs, nucleic acids have also been found as part of exomere cargo. DNA content of exomeres is comparable with that of EVs and display cell type-dependent patterns in their relative abundance (Zhang *et al*, 2018b, 2019e). As examined in a human pancreatic cancer cell line, DNA molecules carried by exomeres showed a slightly smaller size than those associated with EVs. In contrast to DNA, and regardless of cell type, exomeres contain less RNA and predominantly small RNAs (< 1,000 nucleotides). Interestingly, as examined in murine melanoma B16F10 cells, abundant small RNA peaks, likely composed of tRNAs, microRNAs, and other small RNAs, were detected in Exo-S and Exo-L, but not in exomeres (Zhang *et al*, 2018b).

Overall, the complex cargo of exomeres is starting to emerge, but questions remain regarding their packaging and regarding the biogenesis and biological functions of exomeres. Advanced, highresolution isolation platforms for single particle analysis and additional *in vivo* functional studies are desired to further investigate these aspects of exomeres biology.

Seeing is believing: isolation, labeling, and models for EVP studies Methods for EVP isolation

Technology has advanced significantly in the field of EVP study, leading to the development of various methodologies for EVP isolation in the past decade. Based on the fundamental principles for separating EVPs from other types of entities in biofluids, these methods can be grouped into two main categories: one exploits the size, density, and charge of EVPs, while the other uses affinity capture techniques, such as immuno-recognition of unique epitopes present on the EVP surface or specific ligand–receptor interaction.

The first category of EVP isolation and subtype separation methods includes differential ultracentrifugation (UC), density gradient, size exclusion chromatography (SEC), ultrafiltration (UF), anion exchange chromatography, and polymer precipitation (Thery *et al*, 2006; Merchant *et al*, 2010; Lasser *et al*, 2012; Tauro *et al*, 2012; Kim *et al*, 2016a). Additionally, AF4 has been successfully adapted to fractionate EVPs on the basis of hydrodynamic size. As we described (Zhang & Lyden, 2019), two perpendicular flows in a thin, flat, hollow channel with a semi-permissive bottom wall membrane allow for separation and elution of EVP subtypes at different time points. Several key advantages offered by the AF4 technique include high separation resolution (down to a few nanometers), the ability to separate EVPs across a large size range of a few nanometers to micrometers, and being label-free, gentle, rapid, and highly reproducible. However, due to the limited loading capacity, samples analyzed using AF4 usually need to be pre-processed by other methods (such as UC) to first enrich and concentrate EVPs. By employing this technique, we have reported successful separation of distinct subsets of EVs and identification of exomeres from multiple cell lines (Zhang et al, 2018b). Several studies have described isolation and analysis of plasma and urine EVPs utilizing AF4 after initial isolation steps, such as UC, UF, SEC, and immunoaffinity capture (Yang et al, 2017a; Oeyen et al, 2018; Kim et al, 2020; Multia et al, 2020; Wu et al, 2020a), though the yield and purity of EVPs isolated from these samples need to be compared with other methods in parallel.

The application of UF-based methods, such as dead-end filtration and tangent flow filtration, for EVP isolation has increased greatly in the past few years (Liangsupree et al, 2021). EXODUS (exosome detection via the ultrafast-isolation system) is a recently reported platform developed based on UF (Chen et al, 2021e). By enabling membrane vibration and generating transverse waves and acoustic streaming, EXODUS effectively limits the fouling effect and particle aggregation on the nanoporous membrane, thus increasing EVP isolation efficiency. Detailed characterization and comparison of EXODUS with other methods were conducted mainly on urine samples and showed superior performance in yield, purity, and speed. It can operate on a large range of sample volumes, from tens of microliters to hundreds of milliliters. Separating EVPs within different size ranges can be achieved by utilizing membranes with different pore sizes. In addition, the EXODUS workstation has the automatic operation feature, making it useful for high-throughput study. However, more extensive analysis is needed to determine the performance of EXODUS for the isolation of EVPs from plasma. A general limitation for size-based separation approaches, including EXODUS, is that it cannot separate EVPs from other types of molecular entities with similar sizes.

Wu *et al* (2017) described an acoustofluidic platform, which processes undiluted blood directly to isolate EVPs based on size. Two separation modules are integrated to first remove blood cells and platelets and subsequently separate EVPs from microparticles and other large bodies. The unique features of this approach include no requirement for blood pre-processing, being label-free and gentle, preservation of intact EVP morphology, flexibility to adjust the cutoff size for each separation module, and automation. However, as Wu and colleagues noted, the isolated samples may contain non-EV particles (i.e., exomeres) and aggregates with sizes similar to that of EVs, such as lipoprotein particles. Refining the device configuration to separate EVPs from lipoproteins based on their different acoustic contrast factors has been proposed.

Due to the net negative charge carried by EVPs, charge-based technologies, such as ion exchange and electrophoresis, have also been adapted to EVP isolation (Kim *et al*, 2016a; Kosanovic *et al*, 2017; Heath *et al*, 2018; Marczak *et al*, 2018; Chen *et al*, 2018a; Notarangelo *et al*, 2019; Kim & Shin, 2021). Ion exchange is a rapid and scalable approach, which can easily process samples in large volumes, an important application for large-scale preparation of

EVPs for therapeutic purposes. However, structural integrity and functionality of isolated EVPs have to be evaluated, especially in the case where buffers with extreme pH or high salt concentration have been used at the binding or elution steps. Analyzing complex samples, such as plasma, with charge-based techniques will be challenging, and combination with other methods will be necessary to increase the purity of isolated EVPs.

In the affinity-based category of EVP isolation methods, the most commonly utilized approach is immunoaffinity capture (IAC) by antibodies recognizing either general EV markers (such as tetraspanins CD9, CD81, and CD63) or membrane proteins that are unique to EVPs derived from specific cell types (such as EpCAM) (Tauro et al, 2013a; Kowal et al, 2016; Wang et al, 2016a; Zhao et al, 2016b; Brett et al, 2017; Ko et al, 2018; Sharma et al, 2018; Katsu et al, 2019; Lo et al, 2020). Both conventional immunoprecipitation and fluorescenceactivated cell sorting have been adapted for IAC of EVP subsets. Microfluidics coupling IAC with different fluidics designs represents a popular approach for positive or negative selection of EVP subsets in biofluids (Contreras-Naranjo et al, 2017; Wang et al, 2021b). The advantages of IAC include allowing isolation of select EVPs derived from a specific cell type and being a single-step, rapid, and flexible procedure. However, IAC approaches cannot separate EVP subsets that share the same targeting epitopes, and eluting EVPs from binding antibodies can be challenging, making IAC incompatible with functional studies that require intact EVPs.

Recent innovation in aptamers has made them promising alternatives to antibody-based probes for isolation of EVP subsets. Aptamers are chemically synthesized short RNA or single-stranded DNA molecules with unique 3D structures that bind their cognate targets with high specificity and affinity, comparable with antibodies (Sun et al, 2016). Remarkably, profiling of serum EVP surface proteins utilizing a panel of seven fluorescently labeled aptamers along with thermophoretic enrichment and linear discriminant analysis can successfully detect early stage cancers and classify cancer types with high specificity and sensitivity (Liu et al, 2019a). Liu and colleagues showed that this assay was superior to PSA levels for discrimination of prostate cancer from benign prostate enlargement and for recurrence assessment post-prostatectomy. Their study also indicated that the thermophoresis condition can be adjusted to further separate small EVPs from microparticles. A strategy for duplex detection of EpCAM and Her2 on a single EVP was further developed to improve the identification of breast cancer-derived EVPs by integrating hybridization chain reaction with dual DNA aptamer-mediated recognition of these two targets (Li et al, 2021c). Dong et al (2018) described a highly sensitive electrochemical method for detecting tumor-derived EVPs based on aptamer recognition-induced multi-DNA release and cyclic enzymatic amplification. Aptamer capturing can also be used for isolation of EVP subsets, and the captured EVPs can be nondestructively released via disruption of the aptamer 3D structure by incubating with complementary sequences or by restriction enzyme cleavage, allowing for preservation of EVP bioactivity (Zhang et al, 2019c).

Commercial kits have been developed based on the reversible binding of Tim4 protein to PS on the surface of EVPs. This affinity-based method is highly specific and calcium (Ca^{2+})-dependent (Miyanishi *et al*, 2007), facilitating release of intact EVPs by adding Ca^{2+} chelators (Nakai *et al*, 2016). This technique has been applied to various sample types and utilized for isolation and for

quantification by ELISA and flow cytometry. However, similar to other affinity-based approaches, this method cannot distinguish EVPs of different sizes. Moreover, for lipid-rich samples, such as plasma, it may be challenging to separate EVPs efficiently from other PS-containing particles. Strategies based on other separation principles may have to be included to improve the purity of isolated EVPs. To a lesser extent, lectin probes have been used to separate EVPs carrying characteristic glycans on their surface (Shimoda *et al*, 2019; Yamamoto *et al*, 2019; Jankovic *et al*, 2020). Heparin and peptides that exhibit specific affinity for canonical heat shock proteins have also been tested for EVP isolation (Ghosh *et al*, 2014; Balaj *et al*, 2015; Mao *et al*, 2019a).

Although many approaches for EVP isolation have been developed, different methods may result in enrichment of specific subsets of the heterogenous EVP population due to their unique separation principles. Therefore, caution should be exercised when determining the molecular composition and functional role of EVPs isolated by the various methods. The choice of method for EVP isolation depends on the sample complexity and quantity, and the required yield, purity, and bioactivity for downstream use. Technological advancements are still urgently needed for complex sample processing, high-throughput analysis, and large-scale preparation of highquality EVPs for therapeutic applications. Advancing our understanding of EVP biogenesis and the physical and molecular features of distinct EVP subpopulations is necessary to guide further methodology development for their isolation.

Tracking EVP biodistribution and uptake in vivo

Tracking the in vivo fate of cancer cell EVPs in mice is essential for understanding their contribution to tumor progression and metastasis. Mapping EVP organ biodistribution and cellular uptake has primarily been accomplished by injecting mice with EVPs purified from in vitro cell lines. The administration of exogenous EVPs has the drawback of not fully recapitulating the endogenous release of tumor EVPs in mice. However, because tumors secrete additional factors, such as soluble proteins, it has the distinct and critical advantage of allowing for the study of EVP-specific phenotypes in vivo. Visualizing these injected EVPs has relied mainly on labeling them prior to injection using fluorescent lipophilic dyes that can be detected ex vivo in whole organs or in tissue sections. These dyes have multiple advantages. They are available as different fluorochromes, providing flexibility for signal readout and combined immunofluorescence-based analysis of cell type-specific EVP uptake. Their use also does not require any prior knowledge of EVP biomolecule content, as they will label all lipid-containing particles isolated by conventional EVP purification procedures. Finally, they can label EVPs isolated from samples, such as patient-derived specimens, for which genetic-mediated tagging of EVPs may not be feasible. However, limitations of the dyes include formation of aggregates that could lead to signal artifacts and fluorescent signal half-lives that may not completely reflect the biological fate and turnover of circulating EVPs. Nevertheless, this approach combined with functional validation of EVP-mediated phenotypes has been crucial for unraveling key aspects of cancer progression and metastasis (Peinado et al, 2012; Costa-Silva et al, 2015; Hoshino et al, 2015; Rodrigues et al, 2019).

There remains a pressing need for imaging and tracking of EVPs secreted endogenously by tumors *in vivo* to functionally connect

EVP biodistribution with EVP-mediated phenotypes. Limited studies have made use of cancer cell lines stably expressing genetic reporters, allowing implanted cells to release tagged EVPs that can be traced. These reporters are typically fusion proteins that consist of a signal generating protein to visualize EVPs and an EVP targeting sequence to ensure EVP packaging of the fusion protein. In particular, expression of GFP or luciferase targeted to EVPs through fusion to CD63 or lipid anchoring domains has been used to track EVPs secreted by tumors in mice. Orthotopic mammary tumors were shown to secrete GFP-CD63 EVPs into the surrounding microenvironment, where they are taken up by stromal cells (Suetsugu et al, 2013). Spontaneous metastasis of these cells was associated with EVP uptake in the lungs and the presence of GFP⁺ circulating EVPs in blood. Similarly, CD63-GFP EVPs secreted by melanoma in vivo were observed to be taken up by macrophages in tumor-draining lymph nodes (Pucci et al, 2016). Genetically stable expression of membrane-bound, EVP-targeted Gaussia luciferase was also used to show that melanoma tumors secrete EVPs that reach distant tissues by measuring luciferase activity in harvested organs. Fusion of GFP to a palmitoylation signal also targets GFP to EVPs and allows for tracing of EVPs within the tumor microenvironment of thymoma tumors in mice (Lai et al, 2015). Likewise, fusion of the high intensity luciferase NanoLuc (Nluc) to CD63 enabled in vivo detection of EVPs secreted by subcutaneous colon cancer xenograft tumors in the stomach and intestine (Hikita et al, 2018). Multiple other luciferase-based fusion proteins have been developed, but their ability to mark EVPs in vivo has only been investigated in the context of exogenous administration of luciferase⁺ EVPs from cultured cells (Takahashi et al, 2013; Lai et al, 2014; Wang et al, 2020c). Overall, these studies using fluorescent and bioluminescent reporters demonstrate how tumor-derived EVPs communicate with their local and distant environments, providing support for endogenous secretion of tumor EVPs in mediating metastasis.

In addition to tracing EVPs in vivo, tracking delivery of specific EVP cargo remains a considerable challenge. Gain- and loss-offunction approaches have been crucial in defining the importance of various cargoes in mediating EVP-dependent phenotypes, but understanding whether cargoes are active in recipient cells in vivo will establish direct links between EVP molecules and the observed phenotypes. Studies exploiting the packaging of Cre mRNA into EVPs have made headway into addressing this question. In this approach, tumor cells expressing a Cre transgene package Cre mRNA into EVPs; in vivo injection of these tumor cells into Cre-reporter mice allows for visualization of host cells that acquire EVP Cre mRNA. Intracranial injection of Cre⁺ glioma cells into Cre-reporter mice showed that Cre mRNA is delivered mainly to CD45⁺ leukocytes and also to neurons, microglia, and endothelial cells (Ridder et al, 2015). Similarly, Lewis lung carcinoma cells also deliver exosomal Cre mRNA primarily to CD45⁺ leukocytes when injected intravenously or subcutaneously, and Cre mRNA can be detected in serum EVPs of tumorbearing mice (Ridder et al, 2015). This same approach has been used to demonstrate that B16 melanoma tumor EVPs can deliver Cre mRNA to the lymph nodes, lungs, and spleen and that aggressive breast cancer cells can deliver mRNA to less aggressive breast cancer cells in vivo (Zomer et al, 2015). These proof-of-principle studies have been valuable in tracking uptake and transfer of endogenous EVPs and EVP molecules, but more consistent implementation of similar approaches combined with functional analysis is needed.

EVP Functions

Under construction: pre-cancer origins Chronic inflammation

Prolonged or chronic inflammatory conditions associated with immune infiltration and cytokine release precede the development of various cancers, including colorectal and liver cancer (Greten & Grivennikov, 2019). Immune cells are a major source of circulating EVPs in this context. For instance, the concentration of monocytederived and T-cell-derived EVPs is increased in the serum of patients with systemic lupus erythematosus and correlates with activation of monocytes, neutrophils, B cells, and CD4⁺ lymphocytes (Lopez et al, 2020). T-cell-derived EVPs were found significantly enriched in tRNA fragments in comparison to releasing cells (Chiou et al, 2018). This selective packaging was proposed to be a mechanism for disposing of tRNAs that inhibit T cell ability to home to lymph nodes, become activated, and produce cytokines. Myeloid-derived suppressor cells (MDSCs), which expand during chronic infectious and inflammatory diseases (Gabrilovich & Nagaraj, 2009), are also major producers of EVPs. For example, MDSC-derived EVPs from individuals with late chronic sepsis or human immunodeficiency virus (HIV) or hepatitis C virus (HCV) infections are involved in priming naïve myeloid cells for differentiation into immunosuppressive MDSCs and in inhibiting T cell activation via transfer of the long noncoding RNA transcript HOTAIRM1 (Wang et al, 2018b; Alkhateeb et al, 2020; Thakuri et al, 2020).

Among other inflammatory conditions, chronic pancreatitis is associated with release of circulating EVPs enriched in proinflammatory miRNAs and proteins that may foster systemic disease. These EVPs home to distant organs, such as the liver, lungs, and intestines, and induce pyroptosis of alveolar macrophages and polarization macrophages to an inflammatory phenotype associated with release of cytokines such as IL-1β, IL-6, and CCL-2, leading to vascular leakage and exacerbating lung injury (Bonjoch et al, 2016; Jimenez-Alesanco et al, 2019; Wu et al, 2020f). EVPs were also found to be associated with the onset of inflammatory bowel diseases (IBDs), such as colitis and Crohn's disease, which predispose to the development of colorectal cancer (CRC) (Stidham & Higgins, 2018; Guan, 2019). In an experimental model of dextran sulfate sodium (DSS)-induced colitis, circulating EVPs expressing a series of acute-phase proteins and lncRNA NEAT1-induced polarization of macrophages toward a pro-inflammatory phenotype (Wong et al, 2016; Liu et al, 2018c). EVPs from the colon of mice with colitis were found to express proteins associated with cell proliferation (e.g., epithelial growth factor receptor, EGFR) and induce fibroblast proliferation via EGFR-ERK signaling, suggesting that EVPs produced during IBD development may directly lead to CRC onset (Hasegawa et al, 2020).

Similar to a wound that does not heal, fibrotic diseases are associated with the chronic differentiation and accumulation of myofibroblasts and excessive deposition of ECM components such as collagen I and lead to a higher risk of organ failure, morbidity, and progression to malignancy (Distler *et al*, 2019). EVPs have a central role in the development of lung fibrosis. EVPs from macrophages promote the proliferation of pulmonary interstitial fibroblasts via miR-328 transfer, aggravating fibrosis (Yao *et al*, 2019). Instead, EVPs from pulmonary fibroblasts suppress the differentiation of neighboring myofibroblasts by delivering anti-fibrotic prostaglandin (PG)E₂ (Lacy et al, 2019). EVPs are also involved in the etiology of liver fibrosis, where hepatic stellate cells (HSCs) proliferate and differentiate into pro-tumorigenic myofibroblasts. EVPs derived from HSCs, hepatocytes, and inflammatory macrophages in fibrotic livers induce HSC proliferation, migration, and metabolic switch via their protein and miRNA cargo, promoting progression of liver fibrosis (Wang et al, 2015; Seo et al, 2016; Chen et al, 2018b, 2019b, 2020c; Wan et al, 2019; Gao et al, 2020a; Zhang et al, 2020f). In HSCs, the deregulation of autophagy pathways, such as the PDGF/SHP2/mTOR and TRIB3/SQSTM1 pathways, allows for an increased release of EVPs with fibrogenic properties (Gao et al, 2020a; Zhang et al, 2020f). Conversely, NK cell-derived EVPs decrease TGF-B1-dependent HSC activation, proliferation, and autophagy (Wang et al, 2020g, 2020h). Finally, in diabetes or cardiac dysfunction, EVPs derived from macrophages, cardiomyocytes, CD4⁺ T cells, and endothelial progenitor cells promote a fibrogenic response in cardiac fibroblasts, leading to myocardial fibrosis (Ke et al, 2017; Nie et al, 2018; Cai et al, 2020; Govindappa et al, 2020).

Mutations in oncogenes and tumor suppressors

Oncogenes are drivers of cancer initiation, progression, and metastasis, and numerous studies have started to unravel how they promote cancer progression by regulating biogenesis and secretion of EVPs that contribute to the establishment of tumor-supportive microenvironments.

Kras is one of the most frequently mutated oncogenes in many cancers, including pancreatic, colon, and lung cancers (Prior et al, 2012). Using isogenic CRC cell lines that differ only in Kras mutation status, Higginbotham and collaborators have pioneered studies aimed at understanding how Kras exerts non-cell autonomous effects via EVPs and reported that activated mutant Kras controls the molecular composition and functions of EVPs. For example, elevated levels of amphiregulin (AREG), KRAS, EGFR, Src family kinases, and integrins were detected in Kras mutant EVPs (Higginbotham et al, 2011; Demory Beckler et al, 2013; Clark et al, 2016). In vitro functional studies consistently showed that EVPs derived from Kras mutant cells, but not from Kras-WT cells, can enhance invasion and 3D growth of non-transformed Kras-WT cells (Higginbotham et al, 2011; Demory Beckler et al, 2013), implying that mutant Kras can alter the signals mediated via EVPs and confer a growth advantage for surrounding WT cells. Kras mutant cells also package functional GLUT1 in EVPs, which in turn regulates the balance between glycolysis and oxidative phosphorylation in recipient cells and within intestinal adenomas in vivo (Zhang et al, 2018c). Another report indicated that Rab13 is not only specifically recruited to EVPs but also required for the secretion of EVPs from Kras mutant cells, whereas Rab13 depletion has no effect on the EVP production in Kras-WT cells, indicating that tumor cells with overactivated Kras employ distinct EVP biogenesis mechanisms (Hinger et al, 2020). An important unanswered question is how mutant Kras regulates EVP cargo sorting. RNA profiling analyses showed a Kras-dependent selective exporting of miRNAs and long RNAs (mRNAs and ncRNAs) (Cha et al, 2015; Hinger et al, 2018), although the molecular mechanism is unknown. Together, these studies suggest that specific Kras mutant-dependent EVP cargoes may serve as potential biomarkers for cancer detection and as therapeutic targets.

Oncogenic Hras also exerts paracrine activities by altering EVP production and cargo composition. For example, Hras-transformed MDCK cells release EVPs enriched in proteases, integrins, VEGFassociated proteins, and the master transcriptional regulator YBX1 (Tauro et al, 2013b). These EVPs induced angiogenesis, indicating that EVP-mediated communication between tumor cells and endothelial cells commences during early stages in the metastatic cascade (Gopal et al, 2016). Fibroblasts expressing constitutively active Hras-V12 undergo senescence and release EVPs with distinct lipid signatures enriched in hydroxylated sphingomyelin, lyso- and ether-linked phospholipids, and sulfatides (Buratta et al, 2017). Lee and colleagues showed that in transformed rat intestinal epithelial cells oncogenic Hras stimulates release of EVPs containing chromatin-associated double-stranded DNA fragments covering the entire host genome, including full-length Hras (Lee et al, 2014). EVPs containing oncogenic Hras DNA stimulated endothelial cell proliferation and migration and also increased p53 levels, phosphorylated yH2AX, and micronuclei formation, which are all reminiscent of a genotoxic stress response.

EGFR, which has a pivotal role in the pathogenesis of many human cancers, is also incorporated into EVPs (Al-Nedawi et al, 2008, 2009; Skog et al, 2008) and is involved in regulating EVP biogenesis and EVP-mediated signaling pathways. Constitutively active EGFR (EGFRvIII) is frequently detected in glioblastoma multiforme and reported to alter the expression of EVP-regulating genes and EVP properties, including their protein composition (Choi et al, 2018). For instance, pro-invasive proteins (CD44, basigin, and CD151) were shown to be associated with EVPs of EGFRvIII-expressing glioma cells, whereas EVP markers (CD81 and CD82) were downregulated in EVPs of EGFRvIII-negative cells. Increased EVP uptake by EGFRvIII-positive glioma cells was also observed. EGFR and p53 mutations are common genetic alterations in NSCLC. Transformation of normal human bronchial epithelial cells by p53 knockdown and overexpression of EGFR L858R promotes secretion of EVPs enriched in proteins involved in E2F and Myc pathways, which may induce proliferative and migratory phenotypes in recipient cells (Lobb et al, 2017). In head and neck cancer cells, EGFR overexpression coupled with E-cadherin blockade led to loss of EGFR and tissue factor (TF) from the plasma membrane, coinciding with a surge in emission of EVPs containing both receptors. These EVPs transferred TF to cultured endothelial cells, rendering them highly pro-coagulant (Garnier et al, 2012). Thus, EVPs might have a role in connecting aberrant EGFR signaling in cancer cells with dysregulated coagulation, a key process in malignant cancer progression.

Specific *p53* mutations have oncogenic functions and promote tumor progression and metastasis (Olive *et al*, 2004; Hingorani *et al*, 2005; Morton *et al*, 2010; Freed-Pastor & Prives, 2012; Cooks *et al*, 2013; Zhu *et al*, 2015). Recent studies demonstrated that cells expressing such oncogenic *p53* mutants (*Mutp53*) can utilize EVPs to reprogram recipient tumor cells, fibroblasts, and tumor-associated macrophages. For instance, NSCLC expressing oncogenic *p53R273H* and *p53R175H* mutants produce EVPs that promote invasion and migration of other tumor cells (Novo *et al*, 2018). This process requires the ability of *Mutp53* to control the levels of EVP podocalyxin, a sialomucin linked to cancer aggressiveness, and to increase Rab-coupling protein (RCP)-dependent integrin trafficking in target cells. EVPs from *Mutp53*-expressing tumor cells promote integrin recycling to the plasma membrane of fibroblasts and

influence their ECM deposition and remodeling, generating a supportive microenvironment for tumor initiation and cell invasion. In agreement, Ju and colleagues demonstrated that Mutp53s can activate stromal fibroblasts in colon cancer, a process dependent on transfer of specific EVP-associated miRNAs (Ju et al, 2019). In addition, colon cancer cells expressing Mutp53 promote the differentiation of a distinctive, tumor-supportive macrophage subpopulation via EVPs carrying miR-1246. Co-injection of tumor cells with these reprogrammed macrophages resulted in larger primary tumors and increased liver and lung metastatic burden (Cooks et al, 2018). Furthermore, *p53* null and especially DNA contact *Mutp53* (*p53R273H*) enhance Hsp90a secretion by cancer cells via RCP adaptor (Zhang et al, 2020c). Notably, administration of Hsp90a monoclonal antibody attenuated lung and liver metastases in mice carrying p53R270H (equivalent to R273H in humans) or p53-null tumors. Taken together, these studies provide evidence that oncogenic p53 mutants influence the tumor microenvironment via an EVPmediated, paracrine fashion to promote malignancy, and that different Mutp53s utilize distinct mechanisms to regulate EVP-transmitted oncogenic functions.

Besides oncogenes, *Apc* mutation increases EVP secretion via activation of Wnt pathway when introduced into WT small intestinal organoids (Szvicsek *et al*, 2019). Since *Apc* mutation is an early event in intestinal and colorectal tumorigenesis, this evidence implicates tumor-derived EVPs at an early stage of tumor development. A newly discovered role of the tumor suppressor *Lkb1* in EVP biogenesis and release was also described (Zhang *et al*, 2018a). Restoration of *Lkb1* expression in lung cancer cells enhanced EVP secretion, and EVPs from *Lkb1*-expressing cells promoted recipient cell migration by downregulating expression of migration-suppressing miRNAs and EVP secretion. Lastly, in rhabdomyosarcoma, PAX3-FOXO1 fusion drives the alteration of myoblast EVP content, particularly miR-486-5p, which mediates fibroblast migration and invasion (Ghamloush *et al*, 2019).

In conclusion, oncogenes take part in the biogenesis and secretion of EVPs, instruct selective packaging of EVP cargo molecules, act as active cargo themselves, and influence the uptake of EVPs and multiple signaling pathways in recipient cells. Crosstalk mediated by tumor-derived EVPs, occurring at local or distant sites, contributes to key aspects of tumorigenesis and metastasis, such as immunosuppression, ECM organization, angiogenesis, and vasculature remodeling. Future studies incorporating multi-omics characterization of EVP composition and genetic manipulation of key DNA components will be critical for further understanding the contribution of oncogenes to EVP biogenesis and cargo packaging. This knowledge will guide the development of novel therapeutic strategies that target EVPs for cancer intervention.

Metabolic reprogramming

Metabolic rewiring is one of the first steps of transformation that supports the higher nutrient demands of cancer cells (Fendt *et al*, 2020). It has been recognized that metabolic reprogramming during cancer initiation is both the cause and consequence of EVP excretion.

The metabolome of EVPs is relatively understudied compared with proteome and transcriptome, but recent studies identified an array of metabolites in EVPs, such as amino acids, organic acids, sugars and their conjugates, nucleotides and nucleosides, cyclic alcohols, carnitines, aromatic compounds, and vitamins (Altadill et al, 2016; Zhao et al, 2016a; Puhka et al, 2017; Clos-Garcia et al, 2018; Luo et al. 2018; Zebrowska et al. 2019). Additionally, a diverse set of metabolic enzymes has been documented in EVPs derived from various sources. For example, glucose deprivation in cardiomyocytes increases the synthesis and release of EVPs loaded with functional glucose transporters and glycolytic enzymes, which in turn potentiate glucose uptake of recipient endothelial cells (Garcia et al, 2016). Similarly, human prostate-derived EVPs carry functional glycolytic enzymes that produce ATP when supplied with substrates (Ronquist et al, 2013). Furthermore, neural stem/progenitor cell-derived EVPs harbor the catalytically active asparaginaselike protein 1 (Asrgl1) enzyme capable of increasing glutamate, GABA, and aspartate while decreasing asparagine in cell culture media (Iraci et al, 2017). Similarly, arginase-1 activity is associated with hepatocyte-derived EVPs and induces a significant change in arginine metabolites in serum (Royo et al, 2017), suggesting that EVPs are capable of modifying their metabolic environment before being internalized by target cells.

EVPs can also mediate the exchange of regulators of metabolic signaling pathways under a broad range of pathophysiological conditions, such as altered glucose metabolism and inflammation, which are predisposing factors for cancer initiation. Pancreatic β cells are a major source of EVPs with metabolic reprogramming potential, particularly in patients with type 2 diabetes (Li et al, 2020a). Increased glucose levels stimulate pancreatic β cell release of EVPs enriched in lncRNA-p3134, which promotes insulin secretion and suppresses cell death from glucotoxicity (Ruan et al, 2018). Similarly, miR-29 packaged in β cell EVPs stimulates chemotaxis and activation of pro-inflammatory macrophages via induction of IL-12, IL-6, and IL-1β. Consequently, systemic inflammation promotes insulin insensitivity, leading to predisposition to type 2 diabetes (Sun et al, 2021c). In addition, EVPs from serum of diabetic patients are enriched in miR-20-5b and are taken up by skeletal muscle cells, which in turn increase their glycogen synthesis via AKTIP/STAT3 regulation (Katayama et al, 2019).

A recent study by Goulielmaki and colleagues revealed a novel EVP-based link between DNA damage, metabolic disorders, and inflammation (Goulielmaki *et al*, 2020). Using an engineered mouse model carrying an ERCC1-XPF DNA repair defect ($Er1^{F/-}$), the authors showed that persistent DNA damage accumulation in $Er1^{F/-}$ tissue-infiltrating macrophages triggers cytoplasmic stress and increases EVP biogenesis. These EVPs, which were also detected in $Er1^{F/-}$ animal sera, promoted glucose uptake in recipient pancreatic cells and hepatocytes by upregulating glucose transporters, such as *GLUT1*, and enhanced glucose tolerance in WT mice. Future studies are necessary to identify the specific EVP cargoes that mediate such metabolic reprogramming in recipient cells.

EVPs have also been implicated in the etiology of obesityinduced insulin resistance, a known risk factor for cancer development (Kahn *et al*, 2006; Romeo *et al*, 2012; Johnson & Olefsky, 2013; Barazzoni *et al*, 2018). EVPs from adipocytes, especially those from obese mice, are enriched in enzymes and substrates of fatty acid oxidation and increase the motility of tumor cells (Lazar *et al*, 2016; Clement *et al*, 2020). In obesity and under lipolytic stimuli, adipocytes release EVPs enriched in aP2 (also called fatty acid binding protein 4), which can affect glucose and lipid metabolism in target cells and is involved in diabetes, fatty liver disease, and cancer (Ertunc *et al*, 2015). Furthermore, chronic inflammation and accumulation of proinflammatory macrophages, particularly in the adipose tissue and liver, are hallmarks of obesity and have been previously linked to obesity-induced insulin resistance and cancer (Romeo et al, 2012; Li et al, 2015a, 2016; Lackey & Olefsky, 2016; Kita et al, 2019). Recent work by Ying and colleagues uncovered a new function for adipose tissue macrophages (ATMs), whereby they systemically modulate insulin action via EVPs (Ying et al, 2017). The authors reported that treating lean mice with EVPs derived from obese mice ATMs led to glucose intolerance and insulin resistance, whereas treating obese mice with EVPs derived from lean mice ATMs led to improved glucose tolerance and insulin sensitivity. MiR-155 contained in ATM EVPs from obese mice emerged as a key factor regulating these processes in the liver, adipose tissue, and muscle, likely via downregulating GLUT4. In a similar fashion, EVPs derived from HSCs in fibrotic livers reprogram glucose metabolism in neighboring HSCs, Kupffer cells, and sinusoidal endothelial cells and induce a shift from oxidative phosphorylation to aerobic glycolysis, which has been associated with tumor development (Wan et al, 2019). Lastly, EVPs derived from adipocytes undergoing endoplasmic reticulum stress cause glucose and lipid metabolic changes in hepatocytes, leading to nonalcoholic hepatic steatosis, fibrosis, and inflammation (Gu et al, 2021).

Collectively, these studies demonstrate that EVPs are key players in metabolic reprogramming at local and systemic levels in different physiological and pathological conditions and may thus provide therapeutic targets to maintain metabolic homeostasis and prevent cancer initiation. In addition, metabolome studies on EVPs derived from different body fluids will identify biomarker candidates for disease detection and monitoring.

Parasites, viruses, and microbiota

EVPs have emerged as essential routes of bilateral communication between hosts and organisms (i.e., parasites, viruses, and bacteria) that govern cancer pathogenesis. Common parasites, such as Plasmodium species, Leishmania species, and Toxoplasmas gondii, produce EVs enriched in parasite antigens and nucleic acids that stimulate the host immune response and parasite survival and induce EVP release by host stromal cells (Wu et al, 2018; Liang et al, 2019). For example, macrophages stimulated with Plasmodium berghei, Leishmania, or T. gondii EVs overexpress CD40 ligand and release IL-8, IL-12, IFN- γ , and TNF- α (Couper *et al*, 2010; Silverman et al, 2010; Dlugonska & Gatkowska, 2016), inducing a protective immunity for infections and, potentially, cancer initiation. Similarly, EVs from Schistosoma mansoni are internalized by endothelial cells and induce a phenotype consistent with endothelial activation, thrombosis, and immune cell recruitment (Kifle et al, 2020).

EVPs have a central role in viral infections. Epstein-Barr virus (EBV)-infected B cells release EVPs containing the small viral RNA EBER1 and activate an anti-viral immune response in recipient plasmacytoid DCs (Baglio *et al*, 2016). Interestingly, cells may also employ EVPs as a means to excrete viral DNA from cells (Takahashi *et al*, 2017). Human papilloma virus (HPV)-infected cancer cells (e.g., HeLa cells) transfer long noncoding RNAs (lncRNAs) to uninfected cervical cells and affect their metabolism and viability (Hewson *et al*, 2016). EVPs from HVC-infected hepatocytes activate TGF- β 1 expression in HSCs via miR-19a/miR-192 shuttling, inducing their activation and expression of fibrogenic markers (Devhare *et al*, *a*).

2017; Kim *et al*, 2019b). HIV-infected $CD4^+$ T cells release EVPs enriched in pro-hypoxic and pro-inflammatory mediators (Duette *et al*, 2018). Furthermore, lymphatic endothelial cells infected with Kaposi's sarcoma-associated herpesvirus (KSHV) release viral miRNA-enriched EVPs that mediate metabolic reprogramming of non-infected vascular and lymphatic cells, thereby increasing aerobic glycolysis, propensity to KSHV infection, angiogenesis, and migration, potentially promoting sarcoma development (Yogev *et al*, 2017). Finally, latent membrane protein 1 (LMP1) encoded by EBV-infected cells is packaged into EVPs and induces activation of normal fibroblasts to cancer-associated fibroblasts (CAFs) via regulation of the NF-kB pathway and glucose metabolism (Wu *et al*, 2020d).

Bacteria, including gut microbiota, are an important source of EVs. As bacteria are deficient in canonical EV secretion systems, these vesicles originate from outer membrane budding and are thus indicated as outer membrane vesicles (OMVs) (Shen et al, 2012). Other mechanisms of EV release have been characterized but are less studied (Chronopoulos & Kalluri, 2020). Despite differences in secretion pathways of eukaryotes and prokaryotes, OMVs range from 20 to 100 nm in diameter, are similar to eukaryotic EVs and exomeres, and have the ability to communicate with the host immune system. Beneficial bacteria strains, such as Bacteroides fragilis, release OMVs enriched in surface bacterial capsular polysaccharides, which orchestrate an immune-suppressive response involving Tregs, T cells, and DCs. Importantly, adoptive transfer of OMV-stimulated DCs protects mice from DSS-induced colitis (Shen et al, 2012). Similarly, OMVs from Bacteroides acidifaciens and Akkermansia muciniphila strains provide a protective effect against colitis-associated weight loss, inflammatory cell infiltration, and cytokine release by colon epithelial cells, ultimately ameliorating the severity of IBD (Kang et al, 2013; Patten et al, 2017; Ashrafian et al, 2019), as well as reducing gut permeability in type 2 diabetes (Chelakkot et al, 2018). Conversely, strains of probiotic and commensal Escherichia coli produce LPS-expressing OMVs that induce secretion of pro-inflammatory and immunomodulatory cytokines, such as IL-10, IL-8, and TNF- α , by peripheral blood mononuclear cells and intestinal epithelial cells (Ellis & Kuehn, 2010; Fabrega et al, 2016; Patten et al, 2017; Canas et al, 2018). As a result, OMV-associated LPS was detected at significantly higher levels in the plasma of patients with IBD and chemotherapyinduced intestinal mucositis in comparison to healthy controls and is a potential biomarker of intestinal barrier dysfunction (Tulkens et al, 2020). The composition of gut microbiome and corresponding OMVs dramatically changes upon colitis or IBD development in mice and humans, with a striking reduction in numbers of OMVs from less immune-activating strains of Bacteroides acidifaciens and Akkermansia muciniphila strains (Kang et al, 2013) and a change of OMV content toward inducing oxidative stress (Zhang et al, 2018e). Hence, inflammatory gut syndromes are associated with the release of bacterial OMVs that might exacerbate advancement of malignant disease. More indirectly, myeloid DCs exposed to Helicobacter pylori release EVs that express bacterial components and elicit systemic immune reactions, such as CD4⁺ T cell activation, explaining skin eruptions in H. pylori-infected patients (Ito et al, 2018).

Host and dietary EVPs can affect the gut microbiota. Common gut bacteria strains (e.g., *Fusobacterium nucleatum* and *Escherichia* coli) internalize EVPs from different host cells, including adipose and gut epithelial cells. These EVPs increase the proliferation rate and gene expression profile of gut bacteria, which may be involved in initiating the development of pre-cancerous conditions, such as colitis (Liu et al, 2016b; Yu et al, 2019b). EVPs from dietary sources elicit different microbiota responses. To illustrate, EVPs from edible plants, such as ginger root, are preferentially taken up by Lactobacillaceae and promote their production of IL-22, thereby providing protection against gut permeability and colitis (Teng et al, 2018). On the other hand, milk-derived EVPs are preferentially internalized in Escherichia coli and Lactoplantibacillus plantarum and are enriched in miRNAs that influence bacterial expression of genes involved in adhesion and invasion (Yu et al, 2019b). Viable Fusobacterium nucleatum has been found in primary and distant metastatic sites of CRC patients and mouse xenografts, where it supports tumor growth and progression (Bullman et al, 2017). Hence, host-microbiota-diet interplay via EVPs may facilitate bacterial colonization of distant organs, possibly promoting cancer initiation and progression.

Build it up: cancer promotion

Cancer stem cells

A small fraction of pluripotent and mostly quiescent tumor cells named cancer stem cells (CSCs) have been shown to be responsible for tumor initiation. The resistance of CSCs to conventional chemotherapy and their ability to propagate largely account for the high rates of therapeutic failure and recurrence in primary and metastatic tumors (Batlle & Clevers, 2017). Cancer-associated EVPs play a central role in maintaining CSC pluripotency, similarly to how embryonic stem cells maintain their pluripotency via EVPmediated intercellular communication (Hur *et al*, 2020) (Figure 3). Chen and colleagues were the first to demonstrate that culture media from several mouse tumor cell lines promoted the differentiation of mouse induced pluripotent cells into cancer initiating cells in vivo (Chen et al, 2012). Further, it was determined that cancerderived EVPs activate expression of core stemness drivers Nanog and Oct3/4 in mouse induced pluripotent cells, conferring on them properties of self-renewal and plasticity (Yan et al, 2014b; Calle et al, 2016). Interestingly, EVPs from breast cancer and serous carcinoma contain the mRNA and protein of Nanog and other stemness drivers, and their levels correlate with poor overall survival (Rodriguez et al, 2015; Sherman-Samis et al, 2019). These mRNAs, however, may not be responsible for promotion of pluripotency. Instead, fibronectin exposed on the surface of cancer-associated EVPs may be responsible for CSC maintenance (Hur et al, 2020). CAFs are a major source of EVPs promoting CSC maintenance and chemoresistance by inducing the de-differentiation of cancer cells and the activation of stemness expression pathways, such as Wnt/ β -catenin pathway, via EVP-associated mRNAs, miRNA, and lncRNAs (Hu *et al*, 2015, 2019b; Ren *et al*, 2018; Rodrigues *et al*, 2018; Wang *et al*, 2019c; Liu *et al*, 2020a).

In turn, CSC-derived EVPs support tumor progression through multiple pathways. For instance, pancreatic cancer CSCs induce a distinct transcriptomic change, including activation of EGF/VEGF and EMT pathways, in non-CSCs cancer cells, rendering them apoptosis-resistant, invasive, proliferative, and metastatic. Importantly, this reprogramming depends on the activation of EVPinduced cellular signaling rather than on direct transfer of mRNAs/ miRNAs (Wang *et al*, 2019d). Angiogenesis is also supported by CSCs EVPs, with lncRNA H19 and miR-26a being central players (Conigliaro *et al*, 2015; Wang *et al*, 2019e). Finally, CSC EVPs promote the differentiation of normal fibroblasts into CAFs (Zhang *et al*, 2020a).

Thus, a growing body of evidence suggests that cancerassociated EVPs, both cancer cell- and stroma-derived, drive the dynamic balance between induction, maintenance, and differentiation of CSCs, which in turn promote tumor progression via EVPmediated communication.

Tumor growth

The importance of EVPs in sustaining tumor growth and tumor cell proliferation is demonstrated by the observation that treatment with GW4869, an inhibitor of ceramide-mediated biogenesis, or knockout of Rab27a slows tumor growth in vivo (Bobrie et al, 2012; Matsumoto et al, 2017; Matsumoto et al, 2017; Richards et al, 2017). In contrast, exposure of cancer cell lines, such as pancreatic cancer, lung adenocarcinoma, and breast cancer cells, to endogenous EVPs or EVPs from more invasive cell lines promotes growth and cell cycle progression and inhibits apoptosis of cancer cells (Qu et al, 2009; Harada et al, 2017; Xie et al, 2020a; Shen et al, 2021). Pathway analysis has shown enrichment of proliferative pathways in cancer-derived EVPs (Shi et al, 2020a). Several EVP cargos, including miRNAs, circRNA, and enzymes, such as lysyl oxidase-like 4, have been found responsible for this proliferation-promoting effect (Chen et al, 2014; Zhang et al, 2018f; Li et al, 2019d; Luan et al, 2020; Xie et al, 2020a; Wang et al, 2020d). Moreover, numerous growth factors are selectively packaged in cancer cell line- and patient-derived EVPs (Hoshino et al, 2020) (Figure 3).

Host-derived EVPs also play a prominent role in tumor growth, and CAF-derived EVPs in particular enhance proliferation of cancer cells (Zhao *et al*, 2016a, 2020a; Zhou *et al*, 2021b). Notably, CAFs obtained from breast cancer biopsies, but not fibroblasts from adjacent tissue, release EVPs that induce breast cancer cell proliferation

Figure 3. EVPs promote multiple aspects of cancer growth.

The growth of primary tumors is positively impacted by EVPs released by tumor cells and other cells in the tumor microenvironment, including stroma cells (fibroblasts, MSCs, and adipocytes) and immune cells (TAMs, DCs, T lymphocytes, NK cells, and neutrophils). These EVPs influence tumor cells directly by promoting tumor formation and progression via different means, including maintaining CSC pluripotency, promoting tumor cell proliferation, inducing tumor cell EMT and invasion, and altering tumor metabolic demands. Additionally, cancer cell-derived EVPs generate a favorable microenvironment permissive for local tumor expansion by promoting angiogenesis and vascular remodeling, and modulating immune functions towards a pro-tumorigenic and immunosuppressive phenotype. Finally, tumor- and stroma-derived EVPs have a central role in inducing cancer resistance to chemotherapy and radiation therapy. Several EVP cargoes have been found responsible for these pro-tumorigenic roles, including nucleic acids (mRNAs, miRNAs, lncRNAs, circRNAs, DNAs), proteins, enzymes, surface receptors and lipids. TAM, tumor-associated macro-phage; DC, dendritic cell; NK, Natural Killer; MSC, mesenchymal stem cell; CSC, cancer stem cell.



Figure 3.

via transfer of LINC00355 and miR-500a-5p (Yan *et al*, 2020; Chen *et al*, 2021a). Metabolic reprogramming of cancer cells might be another major feature of CAF-derived EVPs, as highlighted by the observation that CAF EVPs promote growth of pancreatic cancer cells by reducing mitochondrial respiration and enhancing glucose and glutamine metabolism via their cargo of amino acids, lipids, and other metabolic intermediates (Zhao *et al*, 2016a). Additionally, CAF EVPs also have a major role in driving chemoresistance, as reviewed below.

Recent evidence shows that innervation of the tumor mass, a process defined as axonogenesis, promotes growth and metastasis of different cancer types, such as head and neck and prostate cancer. Madeo and colleagues recently discovered that blood EVPs from patients with head and neck cancer and from several oropharyngeal squamous cancer cell lines induce neurite outgrowth *in vitro* and *in vivo*, an effect that depends on exosomal ephrin-B and that is abrogated by Rab27a/b knockout (Madeo *et al*, 2018).

EMT, migration, and invasion

The phenotypic plasticity of cells is a physiological aspect of embryo development that has been adopted by tumor cells for enhanced motility and immune evasion that facilitates local and distant invasion (Brabletz et al, 2021). Higher motility and ability to undergo EMT can be transferred in an autocrine and paracrine manner via EVP cargo (Figure 3). For example, EVPs from highly metastatic cell lines can transfer EMT properties to lowly metastatic cell lines by regulating MAPK/ERK, PTEN/Akt/Snail, Ras and mTOR signaling, with miRNA shuttling playing a prominent role (Wang et al, 2016b; Chen et al, 2018c, 2020d; He et al, 2019b; Yang et al, 2020a; Sun et al, 2021a). Similarly, CAFderived EVPs induce EMT, migration, and ultimately metastasis of various cancer types, including castration-resistant prostate cancer, ovarian cancer, and breast cancer (Li et al, 2017e; Novo et al, 2018; Wang et al, 2020a). Upregulation of E-cadherin, vimentin, N-cadherin, ZEB1, Snail, Slug, Twist1, and MMPs, and activation of PTEN/PI3K/AKT/\beta-catenin and EGFR/ERK pathways in cells taking up CAF EVPs are all major drivers of tumor cell EMT (Li et al, 2017e; Novo et al, 2018; Wang et al, 2020a; Yang et al, 2020b; Zhang et al, 2020h). Further, intratumoral fibroblasts interacting with interferon-stimulated gene responsive (ISG-R) breast cancer cells undergo NOTCH1-MYC activation and produce EVPs that, similar to viruses, are enriched in 5'-triphosphate RNAs and induce an anti-viral response in breast cancer cells, promoting pulmonary metastasis (Nabet et al, 2017). This signaling requires activation of the RIG-I receptor in cancer cells by unshielded RN7SL1 RNA in stromal EVPs (Wang et al, 2010; Nabet et al, 2017). In hypoxic tumors, bone-marrow-derived mesenchymal stem cells (MSCs) promote EMT and invasion of lung cancer cells via transfer of different miRNAs and activation of STAT3 signaling (Zhang et al, 2019g). CSC-derived EVPs can also promote EMT of neighboring differentiated cancer cells in clear cell renal cell carcinoma (CCRCC) patients by inducing activation of PTEN-dependent EMT gene expression and, consequently, promoting pulmonary metastasis of CCRCC cells. EVPs from CSCs isolated from metastatic CCRCC patients were particularly potent drivers of tumor growth and lung metastasis (Wang et al, 2019a), suggesting the existence of functional changes in CSCs EVP cargoes in advanced disease.

EVP-induced EMT program may also result in increased cell migration, although the two processes can be independent of one another (He et al, 2019c; Schelch et al, 2021). Direct autocrine and paracrine shuttling of EVP cargo, including tetraspanins, promotes in vitro migration of cancer cells (Pace et al, 2019; Matsumoto et al, 2020; Huang et al, 2020c). EVPs mediate in vivo communication between highly invasive MDA-MB-231 and less invasive T47D breast cancer cell lines to facilitate cancer cell motility, invasiveness, and metastatic potential (Zomer et al, 2015). Further, Luga and colleagues have shown that EVPs from fibroblast-like L cells activate Wnt11-dependent planar cell polarity signaling in cancer cells and promote the formation of protrusive invadopodia (Luga et al, 2012). Among other EVP factors, TGF- β is a central regulator of EMT and cell migration and has been detected in EVPs from cancer cells and CAFs, but not in EVPs from other cancer-associated cells, underscoring the importance of cancer cell and fibroblast communication in EMT and migration (Webber et al, 2010; Wang et al, 2016b; Li et al, 2017e; Ringuette Goulet et al, 2018; Batlle & Massague, 2019; Ferguson Bennit et al, 2021). In response, cells stimulated by TGF-B release a second wave of EVPs that induce MMP-2 expression in neighboring cancer cells, further expanding the migratory potential (Wu et al, 2018). Other evidence suggests that EVPs from tumorassociated macrophages (TAMs) contribute to tumor cell invasion via shuttling ApoE and activation of the PI3K/Akt pathway in tumor cells, partially explaining the association between TAM density and poor prognosis (Zheng et al, 2018b; Lan et al, 2019). Interestingly, Fas ligand (FasL)⁺ EVPs from activated CD8⁺ T cells promote MMP-9 expression and motility of tumor cells in vitro and lung invasion in vivo, while surprisingly lacking pro-apoptotic ability via Fas-FasL engagement (Cai et al, 2012). This suggests that in "hot tumors," cancer cells exploit the EVP cargo of cytotoxic T cells to their advantage, hijacking the tumor-suppressive role of T cell activation.

Angiogenesis

Cancer-derived EVPs induce significant changes in the endothelial cell compartment associated with angiogenic switch (Figure 3). As vascular beds are the gateway for dissemination, the pro-angiogenic properties of EVPs correlate with metastatic potential and poor prognosis (Zhou *et al*, 2014; Maji *et al*, 2017; Tang *et al*, 2018a).

Several EVP cargoes mediate a pro-angiogenic effect. EVPs derived from glioblastoma cells support tube formation of brain endothelial cells via transfer of pro-angiogenic IL-6, IL-8, VEGF, and TIMP-1/2 selectively packaged in these EVPs (Skog et al, 2008). Likewise, pro-angiogenic angiopoietin 2 (ANGPT2) was found expressed in HCC-derived EVPs and was internalized and recycled by endothelial cells (Xie et al, 2020a). mRNAs of pro-angiogenic cytokines, such as CXCL1, 2 and 8, are enriched in EVPs from melanoma cell lines but not normal melanocyte cultures (Bardi et al, 2019). Similarly, the cell adhesion molecule E-cadherin is released by ovarian cancer cells into conditioned medium and patientderived ascites via EVPs and induces vascularization in vitro and in vivo (Tang et al, 2018a). EVPs from HCC cell lines promote growth, migration, and differentiation of HSCs into functional α -SMA⁺ CAFs, via transfer of miR-21 and activation PTEN/PDK1/AKT pathway, which in turn supports release of pro-angiogenic factors and HCC tumor growth in vivo (Zhou et al, 2018). Interestingly, inflamed perivascular adipose tissue in obese mice releases EVPs enriched in miR-221-3p, which promote vascular remodeling by

inducing proliferation and migration of vascular smooth cells (Mao et al. 2019b). The same miRNA was found to target thrombospondin-2 (THBS2) in endothelial cells and increase endothelial cell migration, tube formation, and sprouting in cervical squamous cell carcinoma (Wu et al, 2019c). Several other EVPassociated miRNAs and circRNAs increase angiogenesis and endothelial barrier permeability (Bao et al, 2018; Zeng et al, 2018; Yang et al, 2018a; Li et al, 2018b; He et al, 2019a; Du et al, 2020b; Huang et al, 2020d). These results are substantiated by preclinical models in which education with miRNA-enriched cancer-derived EVPs increased tumor microvessel density and intratumoral VEGF levels, promoting tumor growth (Zeng et al, 2018; Xie et al, 2020b). The release of EVPs with pro-angiogenic properties is significantly affected by microenvironmental factors, such as nutrient availability and oxygen levels. EVPs from cancer cells under hypoxia or aerobic glycolysis have a more potent effect on tube formation and tumor vascularization in vivo than normoxic EVPs, due to the enrichment of pro-angiogenic mRNA, miRNA, and VEGF cargo (Umezu et al, 2014; Mao et al, 2019b; Zhang et al, 2020d). Among others, the activation of PTEN/AKT/VEGFA, beta-catenin, NF-kB, Tie2, and EPHB2/STAT3 signaling pathways was observed in endothelial cells exposed to cancer-derived EVPs (Tang et al, 2018a; Sato et al, 2019; He et al, 2019a; Xie et al, 2020a; Song et al, 2021).

It is interesting to note that also HUVEC-derived EVPs reduce expression of tight junction proteins in neighboring endothelial cells via endoplasmic reticulum stress response and increase vascular permeability and metastasis *in vivo* (Lin *et al*, 2020), but the signaling controlling the release and cargo of EVPs from tumor-associated endothelial cells needs to be further investigated.

Immune modulation

Immune cells are primary targets of cancer cell-derived EVPs in mouse models, especially in the lungs and liver, with neutrophils and myeloid cells being the most avid takers (Hoshino *et al*, 2015; Ridder *et al*, 2015; Zomer *et al*, 2015; Wen *et al*, 2016). On the one hand, intratumoral release of EVPs correlates with immune cell recruitment. Infiltration of neutrophils in orthotopic 4T1 murine breast carcinoma tumors was dramatically reduced by Rab27a knockdown in tumor cells (Bobrie *et al*, 2012). MMP3/9 and chemoattractant G-CSF were found enriched in these EVs, supporting neutrophil recruitment and tumor growth, but this effect might also be due to neutrophil differentiation from bone marrow precursor cells via other factors contained in EVs (Bobrie *et al*, 2012).

On the other hand, cancer-derived EVPs induce modulation of immune functions, predominantly with pro-tumorigenic consequences. While M1 and M2 macrophage phenotypes have been characterized *in vitro* and in mice, macrophage polarization is less dichotomous in humans. In general, tumor-associated macrophages (TAMs) can be found in a classic pro-inflammatory Th1/M1-like and tumor suppressive phenotype, or an alternative antiinflammatory M2-like phenotype that has been associated with increased cancer invasiveness, motility, and metastasis (Noy & Pollard, 2014; Laviron & Boissonnas, 2019). Several lines of evidence indicate that cancer-cell-derived EVPs induce polarization of TAMs toward an M2-like tumor-promoting phenotype. CRC cell lines exposed to CXCL12, a cytokine found in the CRC microenvironment, produce EVPs enriched in different miRNAs that induce the activation of PTEN/PI3K/Akt signaling pathway in TAMs, shifting them toward an M2 phenotype. Polarized macrophages then support tumor cell EMT, endothelial cell tube formation, and progression to liver metastatic CRC in vivo (Wang et al, 2020c). CRC tumor cellderived EVPs reprogram macrophages to release MCP-1 and TNF and to undergo cytoskeleton rearrangement and protrusion formation (Chen et al, 2016b). In the brain, glioma cells shed EVPs that induce activation of astrocytes, ultimately promoting glioma growth (Gao et al, 2020b). EVPs enriched in miR-1246 from p53-mutant CRC cells stimulate the enrichment of polarized TAMs in tumors that correlate with poor prognosis (Cooks et al, 2018). Other EVP miRNA cargos were found responsible for eliciting macrophage protumorigenic activation and causing intratumoral infiltration (Casadei et al, 2017; Hsieh et al, 2018; Chen et al, 2018d; Kwon et al, 2020; Zhao et al, 2020c). Similarly, T cells respond to miR-415-enriched EVPs from gastric cancer cells by undergoing mTOR activation and differentiation into Th17 cells, promoting tumor infiltration (Liu et al, 2018a). Circular RNA circPACRGL, expressed in CRC-derived EVPs, serves as a sponge for miR-142-3p and miR-506-3p in cancer cells, resulting in upregulation and release of TGF- β 1, and induction of phenotypic switch from N1 to N2 neutrophils (Shang et al, 2020). N2 neutrophils have been found to promote tumor growth and progression elsewhere (Fridlender *et al*, 2009).

Cancer-derived EVPs are also a significant source of secreted PD-L1 in the tumor microenvironment, making them major regulators of immune checkpoints. NSCLC, glioblastoma, prostate, and CRC cell lines all release $\mbox{PD-L1}^{\scriptscriptstyle +}$ EVPs that block T cell activation and expansion in vitro and in lymph nodes in vivo (Ricklefs et al, 2018; Poggio et al, 2019; Kim et al, 2019a). The subsequent reduction of intratumoral CD8/CD4 ration and T cell exhaustion promote tumor growth. This evidence is further supported by the observation that Rab27a- or nSMase-KO cell lines grow slower than their WT counterparts in immunocompetent mice, but to a similar extent in T cell deficient mice (Poggio et al, 2019). PD-L1 exposure on EVPs also prevents the activation of an immune memory response against tumor cells (Poggio et al, 2019). EVPs might also transfer expression of PD-L1 to other cells (Ricklefs et al, 2018; Yin et al, 2020; Liang et al, 2020b). For example, cancer cell-derived EVPs induce PD-L1 expression in DCs and decreases their antigen presenting and CD8⁺ T cell priming activity, supporting the generation of a tumorpermissive microenvironment and resistance to immunotherapy. DC cell dysfunction is induced by lipid accumulation and fatty acid oxidation in DCs as a result of EVP fatty acid transfer (Yin et al, 2020). Of note, PD-L1 expression in plasma EVPs associates with disease progression in different types of cancer (Theodoraki et al, 2018; Li et al, 2019a). Other inhibitory immune checkpoints, such as B7-H3, were also found expressed on cancer-derived EVPs, although less well studied compared with PD-L1 (Purvis et al, 2020).

Conversely, EVPs derived from immune cells themselves have both tumor-supportive and tumor-suppressive properties, depending on the cell source. NK cell-derived EVPs directly caused tumor cell cytotoxicity via shuttling of FasL, perforin, and NKG2D, and reduced tumor growth and metastasis in murine models of glioblastoma and melanoma (Lugini *et al*, 2012; Shoae-Hassani *et al*, 2017; Zhu *et al*, 2017, 2018b), suggesting that NK EVP-driven cytotoxicity might be a source of tumor control. The microenvironmental cues and factors leading to release of NK cell EVPs remain unclear. Most TAM-derived EVPs do not share the immunosuppressive phenotype of the parental cells and, instead, are endowed with an immunomodulatory phenotype that induce T cell activation and expansion, ultimately promoting tumor cell cytotoxicity. In addition, lipids and several proteins involved in lipid metabolism were represented in TAM-derived EVPs and induced the production of thromboxane (TXA₂), but not other pro-inflammatory eicosanoids such as PGE₂, by tumor cells (Cianciaruso et al, 2019). PDAC-associated TAMs release EVPs enriched in miR-501-3p that instead induce migration and apoptosis resistance of pancreatic cancer cells via TGF-β pathway, angiogenesis, as well as primary tumor growth and metastasis in vivo (Yin et al, 2019). Furthermore, EVPs from HCCassociated CD206⁺ M2-like TAMs are induced a migratory phenotype in HCC cells, partially explaining the association between TAM infiltration and risk of metastasis in HCC patient. This effect relies on different mechanisms, including the transfer of exosomal $\alpha_M \beta_2$ to HCC cells leading to increased endothelial cell adhesion, as well as increased MMP-9 activity in HCC cells that promotes their invasion of distant sites (Wu et al, 2020b). Finally, EVPs from exhausted CD8⁺ T cells in human HCC further promote the exhaustion of naive $CD8^+$ T cells, supporting immune evasion (Wang *et al*, 2019b).

In conclusion, cancer-associated immune cells are both the source and recipient of EVPs, with different immune modulating properties. Cancer-derived EVPs preferentially induce polarization of immune cells toward a tumor-promoting phenotype and prevent infiltration and activation of anti-tumor lymphocytes, generating an immunosuppressive and permissive microenvironment. In turn, immune-derived EVPs have shown both anti- and pro-tumorigenic functions, highlighting the different contribution of immune cellderived EVPs in the progression of a range of tumor types.

Cancer cell metabolic plasticity

Reprogrammed energy metabolism is a hallmark of cancer (Hanahan & Weinberg, 2011). Cancer-derived EVPs from culture or patient biofluids are particularly rich in mediators of metabolic reprogramming, including purine metabolites, glycolytic, and gluconeogenic enzymes, which confer higher invasive phenotype to recipient cells (Ronquist et al, 2016; Zhang et al, 2017c; Ludwig et al, 2020) (Figure 3). In NSCLC, EVP-associated lncRNAs and circRNAs potentiate glucose uptake and lactate production, which are the main forms of energy sustaining cancer growth (Ding et al, 2020; Chen et al, 2021b). Our lab has determined that the distribution of metabolic mediators in different EVP subgroups is not equal. Instead, metabolic enzymes involved in glycolysis and mTOR signaling are specifically enriched in exomeres derived from different types of cancer cells (Zhang et al, 2018b, 2019e). These exomeres primarily target the liver in animal models, supporting the hypothesis that tumorderived exomeres can systemically influence metabolism of cancer patients (Zhang et al, 2018b).

Besides intrinsic regulation of tumor cell metabolism, several studies have highlighted the importance of EVP-mediated metabolic crosstalk between cells in the tumor microenvironment as another tier of cancer metabolism regulation. Mast cell-derived EVPs are particularly rich in regulators of eicosanoid metabolism, which is involved in DC maturation, inflammation, cell growth, angiogenesis, and thrombosis (Subra *et al*, 2010; Cianciaruso *et al*, 2019; Mizuno *et al*, 2019). Similarly, cancer-associated adipocytes (CAAs) promote tumor progression via storage of energy molecules, cytokines, and growth factors and are associated with poor prognosis (Park *et al*, 2014). In order to reprogram adipocytes into CAAs, breast

cancer cells shuttle EVP miRNAs involved in alteration of adipocyte homeostasis (Wu *et al*, 2019b). In turn, CAAs promote extensive metabolic remodeling in tumor cells, including increased glucose and fatty acid uptake and support an aggressive phenotype (Wu *et al*, 2019b). In HCC, adipocyte-derived EVPs reduce DNA damage and promote cell cycle progression via USP7/Cyclin A2 (Zhang *et al*, 2019a). Adipocyte EVPs can also transfer fatty acids and stimulate fatty acid oxidation in melanoma cells, a process increased by obesity (Clement *et al*, 2020). These transferred fatty acids fuel fatty acid oxidation, which subsequently redistributes mitochondria to membrane protrusions of migrating cells and increases their migration capability.

The conversion of normal fibroblasts into tumor-promoting CAFs relies on metabolic reprogramming, in part induced by cancer cell-derived EVPs and their miRNAs. Breast-cancer-secreted, EVPencapsulated miR-105 activates Myc signaling in CAFs, which reprograms their metabolism in favor of glycolysis and glutaminolysis and allows secretion of glucose- and glutamine-derived metabolites to fuel adjacent tumor cells. In addition, by consuming metabolic byproducts and promoting extracellular acidification, EVPreprogrammed CAFs generate a nutrient-rich and permissive microenvironment that promotes tumor cell growth and migration (Yan et al, 2018b). Breast-cancer-derived EVPs carry high levels of miR-122, which suppresses glucose uptake by lung fibroblasts and brain astrocytes in the pre-metastatic niche, thereby increasing the nutrient availability for tumor cells and facilitating metastasis (Fong et al, 2015). Additionally, in CAFs, glycolysis is favored to oxidative phosphorylation in response to EVP-associated integrin β_4^+ and miRNAs, potentially providing lactate and pyruvate as means of energy for breast and melanoma tumor cells (Pavlides et al, 2009; Shu et al, 2018; Sung et al, 2020). Instead, EVPs from colorectal cancer cells lead to metabolic reprogramming of fibroblast by upregulating proteins required for glycogen metabolism, amino acid biosynthesis, and transporters for glucose, lactate, and amino acids (Rai et al, 2019). The functional contribution of such metabolic transformation to tumor progression needs to be evaluated. In return, EVPs released by CAFs increase glucose uptake and glycolysis and inhibit mitochondrial oxidative phosphorylation in prostate cancer cells (Zhao et al, 2016a). Metabolomic characterization of CAF EVPs revealed high levels of different amino acids, fatty acids, and TCA-cycle intermediates, which can be readily utilized by host cells. Importantly, the authors provided evidence that CAF-derived EVPs can supply metabolites to cancer cells and rescue their proliferation and growth under nutrient deprivation.

These studies collectively suggest that distinct types of metabolic interactions between tumor and stroma exist to facilitate tumor progression, and this may depend on tumor type, stage, and the metabolic conditions provided by the tumor microenvironment.

Intervention, radiation, and chemotherapy

A growing body of evidence suggests that standard of care treatment, such as surgery, radiation therapy, and chemotherapy, is associated with a surge in circulating EVPs that may come from tumor or stromal cells that survive treatment (Figure 3). Both therapy-induced metabolic changes and selection of cells with altered EVP release might be potential underlying mechanisms. Surgery is associated with a change in EVPs levels and cargo in the bodily fluids of cancer patients (Campanella *et al*, 2015; Butz *et al*, 2016; Rodriguez Zorrilla *et al*, 2019). The levels of CD63⁺ EVPs were found to return to normal days after tumor resection, but high EVPs count immediately after surgery was predictive of poor overall survival in oral squamous cell carcinoma patients (Rodriguez Zorrilla *et al*, 2019).

Treatment of different cancer cells with sublethal doses of common chemotherapeutics, such as rapamycin, doxorubicin, cisplatin, panabinostat, bortezomib, carfilzomib, or melphalan, increases the release of EVPs, often called chemoexosomes, and changes their protein and miRNA cargo (Bandari et al, 2018; Samuel et al, 2018; Tubita et al, 2019; Wills et al, 2021; Li et al, 2021d). Different protein cargo was also identified in EVPs from irradiated cancer cells (Mutschelknaus et al, 2017; Abramowicz et al, 2019; Mo et al, 2020). EVPs released upon radiation therapy can affect multiple components of the tumor microenvironment. EVPs from irradiated lung cancer, head and neck cancer, and ovarian cancer cells stimulate tumor cell motility, migration, and proliferation (Mutschelknaus et al, 2017; Samuel et al, 2018; Mo et al, 2020; Wang et al, 2020b). Several mechanisms have been characterized, including packaging of angiopoietin-like 4 in EVPs (Mo et al, 2020), EVP enrichment of metabolic enzymes, such as ALDOA and ALDH3A1 (Wang et al, 2020b), induction of the AKT and p38/JNK signaling pathway (Mutschelknaus et al, 2017; Samuel et al, 2018), and transfer of EVP ECM-degrading heparanase in recipient cells (Bandari et al, 2018). Additionally, these EVPs increase angiogenesis via VEGF-B upregulation in endothelial cells (Mo et al, 2020), as well as stimulate macrophage migration and secretion of TNF-α, ultimately promoting tumor growth (Bandari et al, 2018).

Drug resistance can also be transmitted via EVPs, and thus EVPmediated communication might represent an additional mechanism of expansion of therapy-resistant subclones and cell competition, as described in detail by Parker and colleagues in this Cancer Reviews series (Parker et al, 2021). Gemcitabine-resistant NSCLC cells transfer resistance to parental cells via shuttling of EVP miR-222-3p, which targets suppressor of cytokine signaling 3 (SOCS3) followed by activation of JAK/STAT signaling. As expected, levels of miR-222-3p in serum EVPs from NSCLC patients negatively correlated with response to gemcitabine treatment and higher levels identified patients with no response and progressive disease (Wei et al, 2017a). EVPs from adriamycin-resistant breast cancer cells transmit resistance to sensitive cells via transfer of GSTP1 and Hsp70, the latter of which reprograms the energy metabolism of recipient cells toward reduced mitochondria respiration and increased glycolysis (Yang et al, 2017c; Hu et al, 2021). Levels of GSTP1 mRNA were higher in serum EVPs from chemo-resistant breast cancer patients in comparison to patients who achieve complete response (Yang et al, 2017c). EVPs from hypoxic ovarian cancer cells propagate cisplatin resistance by decreasing dsDNA damage and increasing survival (Dorayappan et al, 2018). MDA-MB-231 cells treated with different microtubule stabilizers release survivin-enriched EVPs that promote survival of adjacent tumor cells and fibroblasts (Kreger et al, 2016). EVP-encapsulated miR-155 from chemoresistant cells confers resistance to recipient sensitive cells in breast cancer, oral squamous carcinoma, and PDAC (Mikamori et al, 2017; Santos et al, 2018; Kirave et al, 2020). Finally, EVPs from glioblastoma cells harboring the PTPRZ1-MET fusion mutation mediate the horizontal transfer of chemoresistance to temozolomide in vitro and in patients (Zeng et al, 2017).

Multiple reports point to CAFs, which are innately chemoresistant (Richards et al. 2017), as a main source of EVPs promoting chemoresistance. EVPs from normal skin fibroblasts exposed to radiation therapy were found enriched in hyaluronic acid, which promotes different aspects of cancer progression (Zare et al, 2020). Additionally, EVPs from CAFs derived from CRC tissue, but not normal fibroblasts from control colorectal mucosa, induce resistance of cancer cells to 5-FU/L-OHP chemotherapy, and promote metastasis via transfer of miR-92-3p, which activates Wnt/β -catenin pathway and inhibits mitochondrial apoptosis in recipient cells (Bandari et al, 2018; Hu et al, 2019a). Similarly, cultured CAFs induce resistance of bladder cancer cells to paclitaxel and doxorubicin via EVPmediated miR-148-3p and downregulation of PTEN (Shan et al, 2021). Lastly, EVPs from CAFs exposed to gemcitabine promote proliferation and chemoresistance of PDAC cells and orthotopic tumors via transfer of miR-146a and Snail mRNA (Richards et al, 2017).

Our current knowledge on the mechanisms of EVP release relies on experiments performed on untreated cancer cells. The evidence summarized here suggests that the amount and cargo of EVPs are affected by chemo- and radiotherapy on both tumor, immune and stromal cell components, but further research is needed to understand the effect of clinical intervention on EVP biogenesis and release.

Creating a favorable soil: pre-metastatic niches

EVPs from different cell and tissue sources have the "innate" tendency to distribute to pre-metastatic sites, such as lungs, liver, bone marrow, and brain, that reflect the organotropism of the releasing cells (Peinado et al, 2012; Hoshino et al, 2015; Yoshida et al, 2019). Peinado and colleagues have shown that the protein content of EVPs correlates with their metastatic potential (Peinado et al, 2012). Building on this, integrin expression was found to be a major pattern of EVPs orchestrating the formation of pre-metastatic niches at future sites of organotropic metastasis (Hoshino et al, 2015; Yoshida et al, 2019). EVP organotropism has important functional consequences, such as promoting metastatic seeding of the distant site by allowing formation of pre-metastatic niches (Figure 3). This is demonstrated by the observation that inhibition of exosome exocytosis via Rab27a-KO is sufficient to reduce the likelihood of distant metastasis in a plethora of models, including mammary carcinoma cells (Bobrie et al, 2012; Zhang et al, 2015b) and melanoma cells (Peinado et al, 2012; Guo et al, 2019a). It remains to be determined if inhibition of exomere release affects metastasis similarly. Due to their ability to selectively deliver their cargo at specific distant sites, EVPs might as well be the first and foremost messengers preparing a "congenial soil" for the "seed."

Gateways to colonization: vascular leakiness and angiogenesis

The continuity of the endothelial lining of the blood and lymphatic system represents an important barrier to improper extravasation of immune cells and tumor cells and to potentially harmful therapeutics at distant sites. Peinado and colleagues were the first to show that murine melanoma B16F10-derived EVPs, but not EVPs from non-metastatic Melan-A cell line, increased lung vascular permeability, an initial step in pre-metastatic niche formation. This promoted the rate and extent of spontaneous lung and bone metastasis, while minimally affecting tumor growth (Peinado *et al*, 2012). Further, EVPs from highly brain-invasive breast cancer cells increased

permeability of the blood–brain barrier (BBB) and promoted brain metastasis of less invasive cells (Tominaga *et al*, 2015). Rodrigues and colleagues more recently confirmed this finding showing that brain-tropic EVPs are taken up by CD31⁺Glut1⁺ brain endothelial cells and increased leakiness in brain capillaries (Rodrigues *et al*, 2019).

Endothelial cell junctions are a major target of cancer-derived EVPs. miR-105 and miR-181 are restricted to EVPs from highly metastatic breast cancer cell lines, suppress expression of tight junction proteins, such as zona occludens (ZO)-1, and dysregulate localization of N-cadherin and actin in microvascular endothelial cells, leading to endothelial barrier disruption, cancer cell transendothelial migration, and lung and brain metastasis (Zhou et al, 2014; Tominaga et al, 2015). Functional miR-105⁺ EVPs were also detected in the serum of patients with stage II and III breast cancer and correlate with risk of metastasis (Zhou et al, 2014). Similarly, highly invasive variants of hepatocellular carcinoma cell lines, but not nonmetastatic variants, release EVPs that reduce expression of VEcadherin and ZO-1 in endothelial cells, leading to endothelial permeability and tumor cell transendothelial migration (Fang et al, 2018; Yokota et al, 2021). These EVPs were found enriched in different miRNAs, some of which associate with lower disease-free survival and higher frequency of distant metastasis in HCC patients (Fang et al, 2018; Yokota et al, 2021). Other miRNAs were found highly expressed in EVPs from breast cancer, CRC, hepatoma, and ovarian cancer cells and patient plasma, and were shown to compromise the integrity of endothelial cell junctions via downregulation of VEcadherin, ZO-1, and Claudin-5, and silencing of KLF2/4, factors controlling transcription of VEGF and junction proteins, ultimately promoting metastasis to both livers and lungs (Di Modica et al, 2017; Fang et al, 2018; Zeng et al, 2018; Lin et al, 2020). More recent evidence has shown that tubulin tyrosine ligase like 4 (TTLL4) expressed in EVPs from breast cancer cell lines MDA-MB-231 and MDA-MB-468 contributes to EVP biogenesis, endothelial cell permeability, and tumor cell adhesion to endothelial cells (Arnold et al, 2020). Along the same lines, MDA-MB-231-derived EVPs are enriched in nucleoside diphosphate kinase (NDPK) A and B in comparison to their non-tumorigenic counterpart (HME1) and activate P2Y1 receptor signaling in lung microvascular cells, inducing cell migration and decreased junctional β-catenin. This resulted in increased vascular leakiness and pulmonary metastasis, an effect that could be prevented by P2Y1 inhibitors (Duan et al, 2021). Finally, Yoshida and colleagues showed that EVPs isolated from high-grade bladder cancer cells are carriers of tyrosine kinases, such as ErbB2 and CRK, and, in addition to promoting proliferation of tumor cells locally, stimulate FAK/AKT signaling, migration, and proliferation of endothelial cells, and promote lung metastasis in EVP-educated mice (Yoshida et al, 2019).

A fertile soil for metastasis might also be "prepared" by EVPs at local or distant lymph nodes. Melanoma-derived EVPs promote angiogenesis and chemotaxis in sentinel lymph nodes, facilitating tumor cell infiltration at later stages of disease (Hood *et al*, 2011). These findings were corroborated recently by other groups showing that EVP-associated lncRNAs, miRNA, and CXCL4 promote lymph node remodeling and lymphatic metastasis in cancer types prone to this route of dissemination, such as breast cancer, cervical squamous carcinoma, and CRC (Li *et al*, 2018c; Zhou *et al*, 2019a; Chen *et al*, 2020a). A direct effect of EVPs on tube formation of lymphatic

Immune cell and bone marrow cell recruitment

Tissue-resident immunity is typically refractory to tumor cell colonization, but the accumulation of bone-derived immune cells or the activation of resident immune cells at distant sites generates an immune suppressive environment that allows for metastatic dissemination and outgrowth (Kaplan et al, 2005; Murgai et al, 2017; Kaczanowska et al, 2021). In the liver niche, Pan02 EVPs harboring migration inhibitory factor (MIF) educate hepatic Kupffer cells to release TGF-B, which induces differentiation of HSCs and deposition of fibronectin. the recruitment of bone marrow-derived cells (BMDCs), including macrophages and neutrophils, to fibronectinrich microenvironments ultimately supports metastasis formation (Costa-Silva et al, 2015). These findings were recently corroborated by the observation that EVPs from KPC murine pancreatic cancer cells promote enrichment of macrophages in the liver niche. However, these EVPs could not rescue the reduction of myeloid cell infiltration in livers of mice engrafted with Rab27a-deficient KPC cells, suggesting that Rab27a has autologous functions in pre-metastatic niche formation in addition to EVP-mediated mechanisms (Kren et al, 2020). Several PDAC EVP cargo proteins, such as MET, ADAM9, S100A4, LGALS3, and integrins β_4 and β_5 , are involved in immune modulation and cell recruitment, while EGFR, CLDN1, CAV1, and SDC1 are associated with angiogenesis, innate immune response, and cell migration in the pre-metastatic liver (Emmanouilidi et al, 2019). Gastric cancer-derived EVPs overexpress epithelial growth factor receptor (EGFR) in both murine models and patients, especially at advanced stage of disease. By upregulating hepatocyte growth factor (HGF) in the liver microenvironment, these EGFR⁺ EVPs act as a chemoattractant to tumor cells expressing c-MET, the HGF receptor (Zhang et al, 2017b). Interestingly, EBV infection in the liver has been correlated with release of EVPs enriched in LMP1, which promotes expression of pre-metastatic markers S100A8, fibronectin, and VEGFR1 in liver and lungs (Wu et al, 2020d).

Comparable changes to the immune profile of pre-metastatic lungs have been observed in response to EVPs from lung-tropic cancer types such as breast cancer and melanoma. Bobrie and collaborators showed that murine breast carcinoma tumors promote infiltration of neutrophils into pre-metastatic lungs (Bobrie et al, 2012). Similarly, murine breast cancer E0771 and 4T1-derived EVPs induce an immunosuppressive pre-metastatic niche in lungs and liver of naïve mice, with increased granulocytic and myeloid MDSCs and, as a consequence, reduced infiltration of CD8⁺ T and NK cells (Wen et al, 2016). The tumor-suppressive activity of NK cells and CD4⁺/CD8⁺ T cells was also directly suppressed by EVPs (Wen et al, 2016). EVPs from invasive breast cancer cell lines are enriched for Annexin II and prime macrophage activation at distant sites, including the brain and lungs, via activation of MAPK, NF-kB, and STAT3 signaling, leading to the release of pro-inflammatory IL-6 and TNFa (Maji et al, 2017). Enrichment in insulin-like growth factor 2 mRNA binding protein 1 (IGF2BP1) has been observed in EVPs from melanoma cell lines and increased the deposition of fibronectin as well as recruitment of CD45⁺ cells in lungs, further promoting lung cancer metastasis (Ghoshal et al, 2019).

Recruitment of immune cells to lungs can also happen via education of other stroma cells, especially fibroblasts. Hoshino and colleagues have shown that lung-tropic EVPs expressing integrin $\alpha_6\beta_4$ upregulated pro-inflammatory S100 proteins in lung fibroblasts (Hoshino et al, 2015), which function as damage-associated molecular pattern (DAMP) molecules for the migration and activation of macrophages, neutrophils, and DCs (Xia et al, 2017). Similarly, EVPs from Lewis lung carcinoma cells (LLC) are mainly engulfed by pulmonary fibroblasts and activate their NF-kB signaling via miR-3473b transfer. In response, fibroblasts release proinflammatory cytokines, such as IL-6, CCL-2, and CCL-5, and drive recruitment of B cells, promoting pulmonary colonization (Du et al, 2020a). Moreover, EVPs produced upon direct interaction between breast cancer cells and fibroblasts in the primary tumor induce activation of distant myeloid and DC immune cells in the spleen (Nabet et al, 2017) and might thus be involved in the generation of premetastatic niches.

While our knowledge of pre-metastatic niches in the lungs and liver has exponentially grown in the last decade, we know very little about other pre-metastatic sites. EVPs from the metastatic melanoma cell line B16F10 educate BMDCs and increase the production of c-Kit⁺Tie2⁺ precursor cells. This effect is due to the horizontal transfer of oncogenic MET, which induces S6 and ERK phosphorylation in BMDCs and promotes the mobilization of vasculogenic and hematopoietic BMDC precursor cells from the bone marrow to future metastatic sites. When transplanted into lethally irradiated naïve mice, MET⁺ EVP-educated BMDCs promote primary tumor growth as well as metastasis to multiple organ sites, including distant lymph nodes and brain (Peinado *et al*, 2012).

The brain has been known for a long time to be a sanctuary site for cancer metastasis, where tumor cells are protected from chemotherapy and immune surveillance. The mechanisms leading to preparation of a favorable soil for tumor dissemination are not yet fully understood. By employing an organotypic brain slice culture system, Rodrigues and colleagues have shown that brain tissue preconditioned with EVPs from brain tropic breast cancer cell, but not from their parental counterpart, is more receptive to tumor cell colonization (Rodrigues et al, 2019). CEMIP, which was found restricted to brain-tropic EVPs, was the culprit of brain preconditioning by inducing transcriptional changes in brain endothelial cells consistent with altered morphogenesis, junction formation, and vascular permeability. The clinical implication of these findings is illustrated by the observation that CEMIP levels were much higher in brain metastasis tissue and their EVPs than adjacent and distant tissues and correlated with shorter survival (Rodrigues et al, 2019).

Finally, the contribution of neutrophil extracellular traps (NETs), which have been detected at primary and distant sites in a series of cancers, to pre-metastatic niche formation is still lacking (Yang *et al*, 2015a; Tohme *et al*, 2016). In a seminal paper, Park and colleagues have shown that tumor-driven NET formation in the lung vasculature is an essential step for breast cancer metastasis (Park *et al*, 2016). Recently, Leal and colleagues have determined that breast cancer cell–derived EVPs induce NET formation *in vitro* and in mice (Leal *et al*, 2017), but the underlying mechanisms are not yet known. Further research might unveil the role of EVP-induced NETs in the establishment of pre-metastatic niches at different sites.

Metabolic reprogramming

Similar to their role within the tumor microenvironment, cancerderived EVPs promote the metabolic reprogramming of stromal and immune cells at distant sites prior to tumor cell colonization. For example, prostate-cancer-derived EVPs transfer functional pyruvate kinase M2 (PKM2) to bone marrow fibroblasts, where it drives HIF- 1α -dependent production of CXCL12 and stimulates tumor cell proliferation via the CXCL12:CXCR4 axis (Dai *et al*, 2019). Furthermore, melanoma-derived EVPs and their miR-155 and miR-210 cargo promote glycolysis and inhibit oxidative phosphorylation in fibroblasts, inducing extracellular acidification that has been previously associated with pre-metastatic niche formation (Shu *et al*, 2018).

Looking at immune cells, CD11b⁺ cells in the bone marrow take up EVPs from Pan02 murine pancreatic cancer cells and shift toward a tumor permissive phenotype. In particular, Pan02 EVPs induced significant transcriptional changes in bone marrow monocytes/macrophages, consistent decreased differentiation, increased polarization towards a tumor-suppressive M1-like phenotype, and upregulation of immunoglobulins (Ig) genes, which have been implicated in inflammation, immune cell recruitment, and activation (Maia *et al*, 2020). The role of EVPs in inducing macrophage polarization is reverted in hypoxic conditions, where tumor-derived EVPs instead steer macrophage differentiation toward an M2-like protumorigenic phenotype, with increased oxidative phosphorylation and suppressed mTOR pathways (Park et al, 2019). Finally, education with prostate-cancer-derived EVPs induces NF-kB signaling and versican (VCAN) expression in myeloid cells and drives osteoclast proliferation and differentiation to a bone resorption phenotype. These effects lead to increased metastatic colonization of bones via tumor cell adhesion to VCAN-rich bone marrow niche (Henrich et al, 2020). Interestingly, prostate cancer-derived EVPs do not affect tumor cells directly, further supporting the idea that longdistance changes in the pre-metastatic stromal and immune compartments are essential for tumor cell seeding and metastasis (Dai et al, 2019).

ECM remodeling

A prerequisite for pre-metastatic niche establishment is the formation of a remodeled ECM backbone that allows for improved tumor cell and immune infiltration and provides sufficient tissue stiffness for tumor cell invasion (Kai *et al*, 2019). Considering the distinct integrin expression profile of tumor cells and their EVPs with different organ tropism, ECM alteration at the distant sites might also direct tissue homing. Thus, by altering ECM of distant organs, tumor-derived EVPs might achieve both increased and directional colonization.

Fibroblasts in the lungs and HSCs in the liver are major orchestrators of ECM composition. Fibroblasts educated with EVPs from p53 mutant lung and pancreatic cancer cells produce an ECM mesh that is dramatically different in structure, binding, and composition to fibroblasts educated with EVPs from p53 competent cells. In particular, fibrillar collagen in educated lungs appeared to have a more punctate and less organized structure, reminiscent of the unstructured vasculature of tumors. EVP sialomucin podocalyxin was found responsible for these changes (Novo *et al*, 2018). Similar fibroblast activation was observed in correlation with enhanced pulmonary metastasis in animal models, suggesting that Mutp53s potentially drive this phenomenon via EVPs. In support of this observation, Capaci and colleagues recently showed in a breast cancer model that Mutp53s induce Golgi tubule vesiculation and alter the secretome of tumor cells, ultimately enhancing tumor growth and metastatic colonization via ECM remodeling (Capaci *et al*, 2020). Though the contribution of EVPs in this process was not investigated, it is reasonable to speculate that EVPs as a major component of the secretome play an important role here.

Education of the pre-metastatic liver with pancreatic cancer cellderived EVPs induces activation of HSCs via Kupffer cell-derived TGF-B, allowing for a 10-fold increase in fibronectin and collagen I deposition and repressing the deposition of vitronectin and tenascin C (Costa-Silva et al, 2015; Xie et al, 2021). Activation of IGF-1/ PI3K/AKT pathways has been reported in PDAC EVP-educated HSCs (Xie et al, 2021). HSC activation was also observed in LLC tumorbearing mice, where EVPs from myeloid BMDCs drive their production of collagen I, promoting recruitment of granulocytic MDSCs and cancer cell adhesion and extravasation. Enrichment of miR-92a in BMDC-derived EVPs, which decreases expression and phosphorylation of SMAD7 in HSCs, was responsible for their metastatic niche-promoting activity. miR-92a-enriched EVPs were also found in the serum of lung cancer patients and induce a similar reprogramming of HSCs (Hsu et al, 2020). The mechanism through which primary lung cancer cells influence BMDCs to release pro-metastatic EVPs is still unknown. Intratumor hypoxia might increase the ECM remodeling properties of EVPs, as shown by evidence that EVPs from hypoxic PC-3 cells caused MMP-dependent deposition of fibronectin and collagen IV at various pre-metastatic sites (Deep et al, 2020).

In the bone niche, bone formation and resorption are the main ECM remodeling events. Certain cancers, such as prostate cancer, take advantage of osteoblast proliferation or activation and ECM mineralization to metastasize to bones, while other cancers, such as breast, lung, and kidney cancer, favor increased osteoclast activity. The EVP miRNA profiles of cancer cell lines inducing either phenotype are dramatically different. In particular, miR-940 and -1260a were found enriched in EVPs from cells promoting osteoblastic lesions and were associated with osteoblast differentiation and osteogenesis (Hashimoto *et al*, 2018). In the pre-metastatic bone, miR-375⁺ prostate-cancer-derived EVPs directly promote formation of calcium nodules in osteoblasts, leading to ECM mineralization (Li *et al*, 2019e).

EVPs can be themselves carriers of ECM proteins and remodeling enzymes. Laminin, collagens, and cathepsin hydrolases were detected (Hood *et al*, 2011; Latifkar *et al*, 2019). In clinical settings, EVPs from pancreatic duct fluid, plasma, and tumor tissue of PDAC patients were enriched in tenascin C, laminin subunits, THBS1/2 and versican, consistent with the alteration of ECM composition in PDAC and pre-metastatic liver (Zheng *et al*, 2018a; Hoshino *et al*, 2020).

Induction of pre-metastatic niche by chemotherapy

Chemotherapy has been found associated with a higher risk of metastatic disease in preclinical models and in patients that do not achieve complete response (Liedtke *et al*, 2008; Volk-Draper *et al*, 2014; Karagiannis *et al*, 2017; Keklikoglou *et al*, 2019; D'Alterio *et al*, 2020). It is believed that therapy-induced tissue damage mimics early events associated with the establishment of pre-metastatic niches, including release of cytokines, chemokines, and EVPs (Rataiczak et al. 2013). Doxorubicin treatment induces the overexpression of the pro-inflammatory glycoprotein PTX3 in MDA-MB-231derived EVPs, which then establishes a favorable pulmonary premetastatic niche for both highly metastatic and poorly metastatic TNBC cell lines (Wills et al, 2021). Similarly, mouse education with EVPs from paclitaxel-treated breast cancer cells or from tumors of paclitaxel- or doxorubicin-treated MMTV-PyMT mice increases lung colonization. These EVPs were found to be enriched in annexin A6 (ANXA6), which induces release of CCL2 by endothelial cells, promoting the recruitment and expansion of Ly6C⁺CCR2⁺ monocytes in the pre-metastatic lungs. ANXA6-positive EVPs were also found in the plasma of breast cancer patients undergoing neoadjuvant chemotherapy (Keklikoglou et al, 2019). Furthermore, EVPs derived from rapamycin-treated HCT116 cells are enriched in miRNAs that can functionally decrease expression of histone genes in lung fibroblasts, reprogramming them toward decreased DNA packaging and chromatin assembly. This epigenetic reprogramming might reduce the ability of fibroblasts to differentiate into myofibroblasts in premetastatic sites (Tubita et al, 2019).

Not only chemotherapy itself, but also resistance to chemotherapy alters the amount and cargo of circulating EVPs, shifting it to a pre-metastatic niche promoting one. To illustrate, ovarian cancer patients have higher serum concentration of EVPs in comparison to cisplatin sensitive patients, potentially due to intra-tumor hypoxic conditions (Dorayappan et al, 2018). Moreover, temozolomideresistant glioblastoma cells selectively package lncRNA HOTAIR into their EVPs, which propagate chemoresistance and, potentially, metastatic ability of tumor cells (Yuan et al, 2020). Conversely, EVPs from doxorubicin- and panabinostat-resistant cells are enriched in Bcl2-associated athanogene 6 (BAG6), which induces transcriptomic changes in pre-metastatic lungs consistent with reduced recruitment and activation of pro-metastatic neutrophils and increased accumulation of Ly6C^{low} anti-tumor patrolling monocytes. As a result, education with BAG6-expressing EVPs reduced lung metastasis (Schuldner et al, 2019).

Determining the right destination: organotropic metastasis

Over the years, different theories have been proposed to explain the selective metastatic distribution of different cancer types. By proposing the "anatomical and mechanical" theory in 1858, Virchow and others speculated that metastatic tropism relied on the physical arrest of tumor cells in the vasculature of distant organs, and that circulatory patterns drive organ distribution (Ewing, 1928; Virchow, 1989). This theory could not explain the selective colonization of organs with similar blood supply and was then challenged by the famous "seed and soil" theory by the British surgeon Stephen Paget (Paget, 1989). Many experimental evidences have supported this theory by showing that the genetic makeup of tumor cells, the structural and molecular properties of the distant niches and the interaction of tumor cells with the metastatic microenvironment all drive metastasis organotropism (Gao et al, 2019). Recent evidence has added to this paradigm showing that distant sites are not always intrinsically receptive to tumor cells, but are rather remotely educated by primary tumor-derived soluble factors and EVPs. In a seminal paper, Hoshino and colleagues have shown that EVPs share the same organ distribution pattern of the secreting cells and that EVP integrins are major determinants of this selective homing (Hoshino

et al, 2015). In more details, integrins $\alpha_6\beta_4$ and $\alpha_6\beta_1$ were abundant in lung tropic EVPs, while integrin $\alpha_v\beta_5$ was found enriched in livertropic EVPs. Similarly, Rodrigues and colleagues identified exosomal CEMIP as driver of brain metastatic colonization (Rodrigues *et al*, 2019). Other evidence has shown that in the complex ecosystem of the tumor microenvironment specific subpopulations of EVPs have different organotropism. For example, among all circulating EVPs in CCRCC patients, CSC-derived CD103⁺ EVPs specifically home to primary tumors and pre-metastatic lungs, while CD103⁻ EVPs lack this selectivity (Wang *et al*, 2019a).

As reviewed in the previous sections, organotropic EVPs set the stage for tumor cell colonization by inducing vascular remodeling and inflammation in the pre-metastatic niche (Peinado et al, 2012; Hoshino et al, 2015; Rodrigues et al, 2019). For example, lungtropic EVPs drive the colonization of the lungs by bone-tropic tumor cells, showing for the first time that tumor-derived EVPs can redirect the organotropic pattern of tumor cells and allow dissemination of tumor cells with poor intrinsic metastatic potential (Hoshino et al, 2015). At the same time, pre-education of mice with B16F10-derived EVPs allows their seeding not only to lungs, but also to contralateral lymph nodes, brain, and mesentery (Peinado et al, 2012). This evidence adds a new layer of complexity to the seed and soil theory, suggesting that the "congenial soil" is actively prepared by EVPs with selective organotropism. EVPs can define the pattern of organ distribution regardless of the innate organotropism of tumor cells, suggesting that intrinsic tumor features might not be sufficient prognostic markers of metastasis site. Instead, the levels of integrin β_4 , integrin α_v , and CEMIP were found significantly higher in plasma EVPs of patients with lung, liver, and brain metastasis, respectively (Hoshino et al, 2015; Rodrigues et al, 2019). Together, these reports indicate that EVP markers are both drivers and bona fide predictors of organotropic metastasis.

A new life: metastatic colonization

The survival and outgrowth of tumor cells that have infiltrated a distant organ are critical bottlenecks in the metastatic cascade. Once in the parenchyma of a distant organ, tumor cells have to face a dramatic reduction in nutrient availability, as well as withstand an inhospitable and immune-reactive microenvironment, resulting in only a few tumor cells being able to expand to a macrometastatic status. The establishment of a pre-metastatic niche partially overcomes this limitation by manipulating distant tissues and allowing for better survival of colonizing immune cells. Our knowledge of early stages of metastatic outgrowth is still limited, but it appears that tumor cell- or stroma-derived signaling is essential to clinically manifest metastasis. Similar to EVPs derived from primary tumor cells, those derived from metastatic cells themselves may shape the metastatic niche to allow survival and overt growth or, alternatively, maintain a temporary dormancy status leading to metastatic latency.

Metastasis-initiating cells

Of the millions of tumor cells shed by a primary tumor per day, only a few metastasis-initiating cells (MICs) will proceed to form macrometastasis. Although the features, emergence, and selection of these metastatic progenitor cells are not fully understood, some MIC traits are starting to emerge more clearly. Ganesh and colleagues have shown that L1CAM expression in CRC epithelial cells triggers the tissue regenerative, chemoresistant, and disseminating abilities of MICs (Ganesh *et al*, 2020). They showed that L1CAM mediates the interaction of MICs with laminin-rich ECMs, such as in EVP-educated pre-metastatic lungs (Hoshino *et al*, 2015; Ganesh *et al*, 2020). L1CAM was detected in B16F10 Exo-Ls (Zhang *et al*, 2018b), supporting the notion that EVPs from primary tumors may directly influence the emergence and metastatic spreading of MICs. Likewise, thrombospondin and collagen-interacting CD36, a *bona fide* marker and driver of the MIC phenotype (Pascual *et al*, 2017), are ubiquitous markers of human EVPs, both from non-tumor and tumor tissue sources (Hoshino *et al*, 2020).

It is also possible that tumor- or stroma-derived EVPs may alter the expression profile of a proportion of CTCs, either before or after intravasation, transforming them into MICs. In breast cancer patients, circulating tumor cells (CTCs) with bone-metastasisinitiating potential were found to express CD44, CD47, and MET (Baccelli *et al*, 2013). Fibroblasts are a major source of CD47⁺ EVPs that can horizontally transfer CD47 to tumor cells, where it helps evade immune surveillance in the blood circulation and at distant organs (Kamerkar *et al*, 2017). In addition, EVPs from highly metastatic melanoma cell lines increase the expression of CD44 and MET in bone marrow progenitor cells, suggesting a similar transfer from breast cancer cells (Peinado *et al*, 2012).

Interestingly, the cargo of EVPs from metastatic sites can differ dramatically from the EVPs from primary sites. In a murine model of CRC, EVPs from metastasis-bearing livers were found enriched in tumor-suppressive miRNAs (e.g., miR-19 and miR-193a) and depleted of oncogenic miRNAs (e.g., miR-21) in comparison to EVPs from primary colon tumor tissue. Teng and colleagues found that this difference relies on differential packaging of miRNA, whereby tumor suppressive miRNAs are actively shed by MICs and their progenitor cells via overexpression of miR-binding major vault protein (MVP). As a consequence, human CRCs, which are poor in tumor suppressive miRNAs and rich in MVP, have a higher risk of metastasis (Teng *et al*, 2017). Understanding the mechanisms that lead to selection or adaptation of MICs with a different EVPs packaging profile will help identify how metastases initiate and progress.

Metastatic microenvironment

In the secondary site, co-option of the metastatic microenvironment allows MICs to either maintain dormancy or sustain growth. Metastasis-associated fibroblasts (MAFs) play a central role in promoting MIC outgrowth. Pein and colleagues have shown that, early in dissemination, factors such as IL-1 α and IL-1 β derived from micrometastatic lesions trigger the transition of lung fibroblasts into activated and pro-inflammatory MAFs, which promote progression to macrometastasis via CXCL9/10 secretion (Pein et al, 2020). Similar cancer cell-derived factors were detected in EVPs from ovarian cancer patients (Bretz et al, 2013) and lung-tropic EVPs were found to induce activation of fibroblasts (Hoshino et al, 2015). Although direct evidence is still missing, a growing body of work has revealed a direct effect of cancer cell-derived EVPs in the metabolic reprogramming of fibroblasts at primary and distant sites and suggests that EVP-associated factors may be involved in inducing MAF differentiation.

In the bone niche, osteolytic activity of osteoclasts promotes release of growth factors and nutrients that support the initial division of tumor cells (Esposito *et al*, 2018). EVPs from prostate cancer MICs are rich in RANK ligand (RANKL) and EVPs from NSCLC cells promote osteocyte expression of RANKL (Taverna *et al*, 2017), a potent inducer of macrophage differentiation into osteoclasts (Shiao *et al*, 2016). Prostate cancer cell–derived EVPs induce osteoblast differentiation directly (Itoh *et al*, 2012; Inder *et al*, 2014; Ye *et al*, 2017; Hashimoto *et al*, 2018; Li *et al*, 2019e; Borel *et al*, 2020), while both breast cancer cell– and lung cancer cell–derived EVPs promote osteoclast differentiation (Taverna *et al*, 2017; Xu *et al*, 2018b; Tiedemann *et al*, 2019; Guo *et al*, 2019b; Loftus *et al*, 2020), reflecting the osteoblastic and osteoclastic metastatic niches induced by these different types of cancer.

EVPs also contribute to metastasis initiation and sustained growth in the brain. Conditioned medium of brain metastasis cells containing factors, such as EGF, TGF-a, and MIF, the latter of which has been previously detected in EVPs from breast and pancreatic cancer cells (Costa-Silva et al, 2015), stimulates STAT3 activation in astrocytes to support the initial steps of MIC growth. The hypothesis that cancer-derived EVPs may be major drivers of astrocyte activation, even at pre-metastatic stages, is supported by the observation that EVPs from brain-tropic MDA-MB-231 cells are actively taken up by astrocytes, albeit in lower amounts than by endothelial cells and microglia (Rodrigues et al, 2019). In response, astrocyte-derived EVPs induce PTEN loss in cancer cells locally by shuttling miR-19a to MICs. As a result, NF-κB phosphorvlation and CCL2 secretion by cancer cells promote infiltration of CCR2⁺ myeloid cells in the brain metastases, further supporting metastasis growth and reducing survival (Zhang et al, 2015b). In addition, reactive astrocytes promote outgrowth of brain metastatic nodules via recruitment of Iba1⁺ microglia and reduction of $CD8^+$ T cell anti-tumor response (Priego *et al*, 2018). In a similar manner, VEGF-A, TIMP-1, and the ECM proteins collagen and tenascin-C, all of which are found in the conditioned medium of reactive astrocytes and of patient brain metastasis explants, dampen CD8⁺ T cell activation (Priego et al, 2018; Hoshino et al, 2020).

The angiogenic switch is an essential event to sustain metastatic outgrowth and exit from dormancy and relies on local release of growth factors and recruitment of endothelial progenitor cells from the bone marrow (Gao et al, 2008). In primary tumors, EVPs are prime carriers of pro-angiogenic factors, such as miRNAs, VEGF-A, and IL-6 (Skog et al, 2008; Umezu et al, 2014; Mao et al, 2019b; Zhang et al, 2020d), or induce their synthesis by endothelial cells (Tang et al, 2018a; Sato et al, 2019; He et al, 2019a; Xie et al, 2020a; Song et al, 2021). Moreover, EVPs from primary and potentially secondary melanoma tumors influence the expression of MET oncoproteins in vasculogenic c-Kit⁺Tie2⁺ bone marrow precursors, inducing the activation of a signaling pathway involved in cell motility. Indeed, the numbers of CD45⁻c-Kit⁺/TIE2^{+/low} progenitor cells with increased MET activation were the highest in the blood of patients with Stage IV metastatic melanoma, suggesting that MICderived EVPs may be involved in sustained angiogenesis in the metastatic niche (Peinado et al, 2012).

In conclusion, EVP cargo has potential roles in the bilateral tumor–microenvironment interplay at metastatic sites, with the lethal consequence of metastatic progression. Functional experiments will need to be conducted to understand the change in EVP release between cancer cells in the primary tumor and MICs as well as to fully puzzle out their role in metastatic growth.

Tumor cell dormancy

As discussed above, the metastasis microenvironment is a key determinant of MIC fate. MICs undergo metastatic dormancy via entry into a proliferative quiescence or failure to sustain proliferation due to tissue-resident immunity, lack of angiogenesis, or nutrient deficiency (Goddard et al, 2018). Both direct and indirect evidences suggest that EVPs contribute to maintaining or awakening dormant tumor cells, particularly in breast cancer, where bone metastasis is a main cause of minimal residual disease and relapse. Ono and colleagues have shown that EVPs from human bone marrow MSCs induce dormancy and cell cycle arrest and impair tumor growth in vivo by targeting cell-cycle-related genes via exosomal miR-23b (Ono et al, 2014). Noticeably, breast cancer cells with high miR-23b levels and MSCs were found in close contact in the bone marrow of patients with breast cancer. More recently, Bliss and colleagues confirmed that miR-222/-223 encapsulated in EVPs from cancereducated MSCs, and to a lesser extent naïve MSCs, promotes cell cycle arrest and decreases chemosensitivity of breast cancer cells (Bliss et al, 2016). EVPs from bone marrow stromal cells, in particular macrophages polarized toward an M2-like phenotype, maintain quiescence of breast cancer cells (Lim et al, 2011; Walker et al, 2019), while pro-inflammatory macrophages tend to awaken dormant cells by activating NF- κB pathway and cell cycle progression (Walker et al, 2019). Sansone and colleagues have shown that, in hormonal therapy-resistant breast cancer, mitochondrial genes packaged into CAF-derived EVPs may be responsible for inducing oxidative phosphorylation in breast cancer CSCs, provoking the tumor cells to exit from dormancy and consequently fostering the recurrence of metastatic cancer (Sansone et al, 2017). The perivascular niche is a sanctuary for tumor cell quiescence at the metastatic site (Ghajar et al, 2013; Ghajar, 2015), with endothelial-derived thrombospondin-1 as a main inducer of breast cancer dormancy and TGF-β1 and periostin inducing exit from senescence. All of these factors have been recently characterized in human cancer cellderived EVPs (Hoshino et al, 2020). Similarly, a seminal paper by Lawson and colleagues reported that breast cancer cells from earlystage metastasis harbor a dormant-like expression signature with a high expression of quiescence-associated genes, such as CDKN1B, CHEK1, TGFBR3, and TGFB2, while progression to macrometastatic disease is accompanied by expression of genes involved in dormancy escape, such as MYC, CDK2, and MMP-1 (Lawson et al, 2015). It is tempting to speculate that EVPs from the primary tumor may be involved in the exit from dormancy, as suggested by the evidence that human cancer-associated EVPs are enriched in MYC targets, CDK2, and MMPs (Hoshino et al, 2015; Rodrigues et al, 2019). Similarly, TGF-B has cytostatic effects and has been directly linked to induction of dormancy in tumor cells (Massague & Ganesh, 2021). Both TGF- β and proteins involved in TGF- β signaling have also been found in various cancer cell-derived EVPs (Webber et al, 2010; Wang et al, 2016b; Li et al, 2017e; Ringuette Goulet et al, 2018; Batlle & Massague, 2019; Ferguson Bennit et al, 2021; Hoshino et al, 2020). Anti-mitogenic DKK is packaged into cancer cell-derived EVPs, particularly those that display organotropisms to the brain, bone, and lung, major sites of tumor cell dormancy (Lim et al, 2012; Faict et al, 2018; Gan et al, 2020). Finally, NETs have been associated with the tumor cell exit from dormancy via proteolysis of extracellular laminin in the metastatic lung niche, which activates intracellular integrin $\alpha_3\beta_1$ signaling in cancer cells (Albrengues

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et al, 2018). By inducing NET formation (Leal *et al*, 2017), cancer cell-derived EVPs may prepare an environment that is permissive for dormancy evasion and metastatic progression.

Whether inhibiting or promoting exit from dormancy is better for targeting dormant cells is still under debate (Ghajar, 2015), our current knowledge indicates that EVPs may drive tumor cell dormancy in both directions, but further experiments are needed to address their contribution in different types of cancer and metastatic niches.

Within circulating distances: EVPs as mediators of the systemic effects of cancer

Due to their ability to signal at a long-range distance, cancerassociated EVPs mediate the most systemic and deadly aspects of cancer. It has been estimated that tumor-derived EVPs represent up to 10% of the total EVPs found in plasma of cancer patients (Fraser *et al*, 2019). Moreover, Hoshino and colleagues have shown that among cancer-associated EVPs in plasma, approximately 50% are from the primary tumor and its tumor microenvironment, whereas other cancer-associated EVPs are produced by distant organ sites, such as the liver and immune organs (Hoshino *et al*, 2020). This evidence indicates that EVP-mediated signaling in cancer is rarely the product of a single site, but rather is an orchestrated, multiorgan process.

Thrombosis

Cancer patients have a higher risk of being affected by a hypercoagulable state, with deep vein thrombosis and pulmonary embolism being the most frequent and lethal complications (Caine *et al*, 2002). Preliminary evidence suggests that tumor-derived EVPs may induce systemic thrombosis. Breast cancer cell-derived EVPs directly interact with platelets and induce their activation and subsequent aggregation (Gomes et al, 2017). Interestingly, the pro-thrombotic effect of EVPs correlates with the metastatic potential of the releasing cells (Gomes et al, 2017). Moreover, induction of thrombosis in mice by EVPs from murine 4T1 breast cancer cells is associated with the formation of NETs (Leal et al, 2017), which have been previously implicated in cancer-associated thrombosis (Thalin et al, 2019). Despite this evidence, our knowledge of the factors leading to EVP-induced thrombosis is still lacking. EVPs from a variety of cancer cell lines and tumor tissues express coagulation factors, such as factor X, thrombospondin, and collagens (Zhang et al, 2018b; Hoshino et al, 2020). PS, a membrane lipid that supports the assembly of coagulation factor complexes during the coagulation cascade, is preferentially exposed on the outer leaflet of the tumor cell membrane and found in a range of EVPs, including tumor and immune cell-derived EVPs (Utsugi et al, 1991; Tripisciano et al, 2017; Zhang et al, 2018b; Skotland et al, 2019). Furthermore, several breast cancer cell lines release EVPs carrying TF, a major initiator of the coagulation cascade (Garnier et al, 2012; Gomes et al, 2017; Leal et al, 2017; Tawil et al, 2021). TF seems to be preferentially associated with Exo-L and EVPs from highly invasive cancer cell lines (Gomes et al, 2017; Zhang et al, 2018b). Neoadjuvant and adjuvant therapies can increase the ratio of TF/TF pathway inhibitor in plasma EVPs of patients with breast cancer, partially explaining the link between chemotherapy and thrombosis (Aharon et al, 2017). TF-expressing EVPs directly induce platelet activation and blood clotting ex vivo and can transfer TF to endothelial cells, increasing their pro-coagulant activity (Garnier et al, 2012; Gomes et al, 2017; Iyer et al, 2021; Tawil et al, 2021). However, this effect was not observed in patients as demonstrated by the evidence that TF is not present in EVPs from a wide range of cancers and tissues, not even in cancer types associated with the highest risk of thrombosis, such as pancreatic cancer and lung cancer (Hoshino *et al*, 2020). These observations suggest the existence of TF-independent pathways of EVP-induced thrombosis. Further research is needed to address this important but understudied field of cancer research.

Cancer cells are likely not the only source of pro-thrombotic EVPs. For example, TAM-derived EVPs are enriched in enzymes and lipid substrates of TXA2 synthesis pathway, which is a major activator of platelet aggregation (Cianciaruso et al, 2019), suggesting that they contribute to immuno-thrombosis similar to their parent cells. Furthermore, activated platelets are a major source of blood EVPs, which can be taken up by several cell types, including other platelets, vascular smooth muscle cells, and endothelial cells (Heijnen et al, 1999; Srikanthan et al, 2014; Tan et al, 2016; Li et al, 2017c). Platelet-derived EVPs are enriched in TF and PS and lead to the generation of thrombin in vesicle-free plasma. This effect was inhibited by incubation with PS-blocking Annexin V, but not with anti-TF antibody (Tripisciano et al, 2017), further supporting the notion that TF might not be the main pro-coagulant factor in EVPs. The release of EVPs by cancer-educated platelets, the protein expression profile of platelet-derived EVPs, and the role of plateletderived EVPs in cancer still need to be determined.

Immune dysregulation

DAMPs include a broad range of factors that are released by damaged or activated cells and that interact with pattern recognition receptors (PRRs) on immune cells to achieve their activation and defense response. Just like a wound that does not heal, primary and metastatic tumors release large amounts of EVPs enriched in different DAMPs. Among other DAMPs, dsDNA detected on the surface of cancer cell-derived EVPs is a potent inducer of immune responses, including inflammatory responses and type-I interferon signaling (Thakur et al, 2014; Lou & Pickering, 2018; Wang et al, 2018c; Maire et al, 2021). EVP DNA may induce systemic activation of STING in DCs, eliciting an anti-tumor response via DC activation and CD8⁺ T-cell infiltration, but also may induce the release of proinflammatory cytokines by innate immune cells (Hernandez et al, 2016; Sharma & Johnson, 2020). The release of EVP-associated DNA by CRC tumors during the course of irinotecan therapy and its uptake by intestinal macrophages and DCs, followed by activation of the AIM2 inflammasome, may partially explain the intestinal damage associated with chemotherapy (Lian et al, 2017). Similar responses may be achieved by extracellular DNA produced during the process of NETosis in response to cancer-derived EVPs (Leal et al, 2017). DAMP proteins, such as versican and galectin 9, have also been found to be expressed in EVPs from pancreatic and lung cancer tissue, but not in EVPs from adjacent or distant tissues (Hoshino et al, 2020). These molecules can trigger secretion of proand anti-inflammatory cytokines by distant immune cells and promote systemic inflammation and evasion from T cell anti-tumor activity (Wight et al, 2020; Yang et al, 2021d).

Cachexia

Cancer-associated cachexia is a systemic disorder associated with body weight loss and unbalanced energy expenditure, which cannot be reversed via nutritional intervention (Argiles *et al*, 2018; Baracos *et al*, 2018). Inflammation and metabolic alterations in the skeletal muscle, liver, gut, and adipose tissues together contribute to the pathology of this paraneoplastic disorder. EVPs may be important mediators in the communication between different organs in cachexia, as suggested by evidence that EVPs from CRC, gastric cancer, and pancreatic cancer cells induce weight loss and muscle atrophy in mice (Argiles *et al*, 2018; Zhang *et al*, 2019b; Di *et al*, 2021). The role of EVPs in cancer-induced cachexia is further supported by the finding that mice harboring tumors and treated with GW4869 or mice injected with Rab27 knockdown tumors did not develop muscle wasting (Zhang *et al*, 2017a; Qiu *et al*, 2020a).

The metabolic changes occurring in both adipose tissue and muscle are affected by cancer-derived EVPs. To illustrate, white adipose tissue (WAT) browning is induced by EVPs from colon cancer and gastric cancer cell lines both in vitro and in mice, and it can be reversed by inhibiting exosome release via GW4869 (Zhang et al, 2019b; Di et al, 2021). These functions were driven by EVP cargo of miR-146-5p and ciRS-133, which regulate genes involved in oxygen and glucose consumption, differentiation, and transcriptomic changes consistent with WAT browning (Zhang et al, 2019b; Di et al, 2021). In gastric cancer patients, EVP ciRS-133 was found enriched more than 120 folds in comparison to healthy controls and was an independent biomarker of brown adipose tissue mass and body fat percentage (Zhang et al, 2019b). Lipolysis and adipogenesis by adipose tissue-derived MSCs (hAD-MSCs) are also perturbed in patients with cachexia. Pancreatic cancer EVPs, including those from patient blood, activate lipolysis of subcutaneous adipocytes via transfer of the hormone adrenomedullin early on during cancer progression (Sagar et al, 2016). Lipolysis and cachexia induced by LLCderived exosomes were suppressed by GW4869 in vitro and in vivo (Hu et al, 2018), while A549 lung cancer cell-derived EVPs activate TGF-β signaling in hAD-MSCs, reducing adipogenic differentiation and thus contributing to adipose tissue loss (Wang et al, 2017c).

Another aspect of cancer-associated cachexia known to be affected by EVPs is muscle wasting, associated with degradation of myofibrillar proteins and changes in muscle metabolism (Fearon *et al*, 2012). The transfer of EVP miRNAs from oral squamous carcinoma cells induces endoplasmic reticulum stress in recipient muscle cells, resulting in myotube atrophy and apoptosis (Qiu *et al*, 2020a). Moreover, EVP-associated Hsp70/90 released by a range of cachexic tumor types induces myotube catabolism and muscle wasting via TLR4/p38 MAPK signaling in muscle cells (Zhang *et al*, 2017a). Muscle-derived stem cells are also affected by cancer-derived EVPs, such as in the case of osteosarcoma-derived EVPs that induce Notch signaling in MDSCs, leading to decreased myogenesis and muscle atrophy (Mu *et al*, 2016).

Organ failure

Secondary organ failure is a major cause of death in cancer patients and is linked to systemic tumor-derived factors and to tissue injury upon surgery, chemotherapy, or radiotherapy. Acute liver failure is a common condition in patients at advanced stages of cancer and can develop in the absence of malignant invasion of the liver (Smith & James, 1998), suggesting the involvement of distant signaling via cytokines and EVPs. Hepatic failure can develop following microemboli, which can be directly induced by tumor-derived EVPs (Gomes *et al*, 2017; Leal *et al*, 2017), or might be induced by the infiltration of immune cells in the liver in response to EVP inflammatory and chemoattractant mediators, such as DAMPs (Hoshino *et al*, 2020; Wu *et al*, 2010). Cardiovascular failure is another major aspect of cancer at late stage. By inducing thromboembolism, EVPs may contribute to the most fatal aspects of cardiovascular failure. Evidence also shows that, in patients under immune checkpoint blockade therapy, EVPs from PD-1 inhibitor-treated macrophages induce cardiac senescence in cardiomyocytes and may partially explain the cardiovascular adverse events of immunotherapy (Xia *et al*, 2020). The expression profile of serum EVPs from heart failure patients after transplant differs from patients with no organ rejection, in particular in terms of proteins involved in inflammation and immunity (Kennel *et al*, 2018), further pointing to a role for EVPs in the etiology of immune-driven cardiac complications.

EVPs as promising nanotools in oncology

EVPs hold tremendous potential as prognostic and deliverable tools for the clinical management of cancer. Three major lines of research are actively pursued and will be the subject of this section. First of all, the involvement of EVPs in cancer progression and in response to clinical intervention is reflected in altered EVP levels or EVP cargoes in blood and tissues of cancer patients. These EVPs collectively form a reservoir of biomarkers to be mined for early cancer detection, treatment monitoring, and prognosis of disease development. Secondly, endogenous and engineered EVPs have been explored as delivery vehicles for various types of therapeutics and imaging reagents in animal models. They hold greater potential than conventional nanoparticles such as liposomes due to their low immunogenicity and toxicity, unique targeting specificity, which can be further engineered by expressing specific surface features, and capability to deliver a variety of therapeutics ranging from drugs, nucleic acids, to immune adjuvants and imaging molecules. Lastly, we will review the research effort on targeting the EVP production and uptake for cancer management. Given the fact that EVPs mediate the intercellular communication in many fundamental physiological processes, understanding how to target the production and uptake of EVPs specifically involved in cancer progression will be critical in this line of research.

Cancer diagnostic and prognostic biomarkers Tissue-derived biomarkers

The use of tissue biopsies to analyze the production and content of EVPs is an important tool in the discovery of cancer biomarkers. Tumor tissue-derived EVPs in fact have protein expression profiles that are distinct from adjacent and distant tissues and thus can be utilized for cancer diagnosis (Figure 4). In the case of pancreatic cancer, pro-inflammatory mediators, such as S100A13 and periostin, were exclusively found in tumor-tissue-derived EVPs (Hoshino *et al*, 2020). Several ubiquitous tissue-derived EVP proteins (e.g., thrombospondin and versican) could be used to discriminate tumor tissue versus non-tumor tissues with 90% sensitivity and 94% specificity, while other EVP proteins could discriminate between different tumor types (Hoshino *et al*, 2020). Among them, EVPs from pancreatic cancer tissues were particularly enriched in factors involved in coagulation and EMT, while lung cancer tissues produced EVPs enriched in RNA processing proteins, which suggests selective

packaging or different microenvironmental sources of EVPs in these two cancer types.

The profile of tissue-derived EVPs is directly related to the composition of circulating EVPs. By analyzing the proteome of tissueand plasma-derived EVPs of pancreatic and lung cancer patients, Hoshino and collaborators demonstrated that several protein markers were present in both tissue-derived and plasma-derived EVPs and that they were selective for the cancer cell of origin (Hoshino et al, 2020). In contrast, other proteins were only present in plasma EVPs. In pancreatic cancer, many proteins restricted to immune cell lineages were found exclusively expressed in plasma EVPs, suggesting systemic immune dysregulation. EVP size distribution can also potentially distinguish EVPs derived from tumor cells and other cells or organs. In NSCLC, pulmonary vein EVPs were smaller than EVPs from peripheral veins and were associated with a higher risk of relapse and shorter overall survival (Navarro et al, 2019). It could be speculated that, during lung cancer progression, tumor-derived EVPs become enriched in smaller particles, such as exomeres, with metabolism-reprogramming and tumor-promoting properties. These findings further underscore the heterogeneity of cell and organ sources that contribute to the pool of circulating EVPs.

Liquid biopsies

The use of EVPs from bodily fluids as predictive markers of cancer, cancer type, and stage of disease is of particular importance in the absence of tissue biopsies and for large-scale screening of the general population, providing that the latest Minimal Information for Studies of Extracellular Vesicles (MISEV) guidelines are met for EVP preparation, analysis, and reporting (Thery et al, 2018). The use of EVPs as biomarkers might overcome some limitations associated with CTCs, including their very low concentration (Pantel & Alix-Panabieres, 2019). To illustrate, 1 milliliter of plasma from glioblastoma patients contains more than 10 billion circulating EVPs and it has been estimated that at least 1 billion of them are cancer cellderived EVPs (Fraser et al, 2019). The high persistence of EVPs in blood is probably due to the fact that they may evade clearance by patrolling NK cells and phagocytes in the circulation and thus may represent a more stable picture of homeostasis. Moreover, EVP cargo reflects the contents of the cell of origin, including surface markers and oncogenes, thus allowing to capture the phenotypic heterogeneity and invasive potential of the primary tumor and aiding in the estimation of metastatic risk. In contrast, no more than 17% of CTCs in peripheral blood have a phenotype consistent with MICs (Lawson et al, 2015), suggesting that liquid biopsies based on CTCs may largely miss patients at high risk of metastasis. On a technical note, EVPs are stable and retain functional activity if stored frozen for several months and can thus be used in retrospective studies (Mendt et al, 2018). Finally, prognostic EVP markers may be more potent than cancer- and CTC-derived biomarkers. Melo and colleagues showed that EVP glypican-1 could be used to distinguish samples from healthy controls and from patients with pancreatic pre-cancerous lesions, allowing for early detection, which is not achievable with the current CA19-9 PDAC biomarker (Melo *et al*, 2015). Thus, EVPs can be utilized as bona fide liquid biopsies for cancer diagnosis and prognosis.

Many studies have highlighted the association between EVPbased liquid biopsies and disease. Various EVP cargos, including RNAs (miRNAs, mRNAs, lncRNAs, circRNAs, and tsRNAs), DNA, proteins, enzymes, glycoproteins (Ko et al, 2018; Chen et al, 2020g), and lipids (Skotland et al, 2017a), are dysregulated in bodily fluids of cancer patients, as summarized in Figure 4. Other parameters found to be associated with cancer diagnosis and poor prognosis include increased EVP mRNA or protein (Peinado et al, 2012; Dijkstra et al, 2014), increased absolute EVP numbers (Kharmate et al, 2016; Galbo et al, 2017; Navarro et al, 2019; Moloney et al, 2020), and EVP size (Navarro et al, 2019). Notably, RNA editing in originating cells was also reflected by EVP cargo. Nigita and colleagues have shown that the edited forms of three miRNAs, miR-381-3p, miR-589-3p, and miR-411-5p were dysregulated in EVPs from patients with lung cancer, despite no changes in their rate of editing (Nigita et al, 2018). Hoshino and colleagues have recently characterized the complete proteomic profile of EVPs from plasma samples of 16 different cancer types and identified predictive proteins, mainly immunoglobulins, overrepresented or downregulated in cancer-associated EVPs that could discriminate cancer versus non-cancer or different types of cancers with more than 95% sensitivity and 90% specificity (Hoshino et al, 2020). This large study has provided evidence of the feasibility and potential use of liquid biopsy markers for the early diagnosis of cancer of unknown origin, which might have applications in the large-scale screening of the general population (Figure 5).

Sequential tumor stages are also associated with specific EVP markers. To illustrate, stage III and stage IV melanoma patient EVPs had increasing amounts of tumor cell markers TYRP2 and prometastatic MET/pMET, and patients with stage IV disease had EVPs with high levels of VLA-4 and HSP70, supporting the value of these markers for the diagnosis and prognosis of melanoma (Peinado *et al*, 2012). In PDAC patient samples, EVP markers, such as S100A13, periostin, and basigin, could differentiate between various PDAC stages and distinguish between PDAC and chronic pancreatitis with high specificity and selectivity (Jiao *et al*, 2019; Hoshino *et al*, 2020; Yu *et al*, 2020; Huang *et al*, 2020a). For example, MIF has been found to be present at significantly higher levels in EVPs from patients with PDAC and in mouse models of pancreatic intraepithelial neoplasia (PanIN) and PDAC relative to healthy controls (Costa-Silva *et al*, 2015). Preliminary evidence suggests that

Figure 4. EVPs contribute to organotropism and pmn formation.

(A) Several EVP surface receptors drive organotropism to different metastatic sites. EVP integrins $\alpha_6\beta_4$ and $\alpha_6\beta_1$ drive lung tropism, integrin β_5 drive liver tropism, and CEMIP drives brain tropism. The determinants of EVP bone tropism are yet not known. The tissue-specific uptake of EVPs promotes pre-metastatic niche formation and defines organotropism of disseminating tumor cells. (B) EVP uptake by stroma and immune cells at distant sites induces the generation of a favorable pre-metastatic niches, highly receptive for tumor cell seeding and outgrowth. Endothelial and lymphatic cell proliferation and vascular permeability, recruitment of BMDCs, activation of resident immune cells, remodeling of ECM, and metabolic reprogramming of fibroblasts and immune cells are the major phenotypical changes associated with pre-metastatic niche formation. EVPs released by the primary tumor after chemotherapy and radiotherapy are also involved in pre-metastatic niche formation. CEMIP, Cell migration-inducing and hyaluronan-binding protein; ECM, extracellular matrix.



Figure 4.

metastatic progression could be predicted by EVP markers in osteosarcoma (Wang *et al*, 2020f), gastric cancer (Ohzawa *et al*, 2020), CRC (Teng *et al*, 2017), oral squamous cell carcinoma (Li *et al*, 2019c), and PDAC (Melo *et al*, 2015). Larger studies are needed to determine the ability of EVP markers to predict the onset of metastatic disease or diagnose occult metastasis.

Interestingly, mutated oncogenes have also been detected in plasma of cancer patients. EGFRvIII, the mutant form of EGFR, was detected in tumor samples and plasma EVPs from glioblastoma patients (Skog et al, 2008; Fraser et al, 2019). KRAS^{G12D} and TP53^{R273H} mutated DNAs were specifically detected in EVPs from the plasma of patients with chronic pancreatitis and PDAC, suggesting early onset of these mutations in the pancreatic microenvironment (Yang et al, 2017b). Similarly, mutant KRAS mRNA (either the KRAS^{G12D} or KRAS^{G12V} variant) was found in serum EVPs of patients with PDAC, but interestingly they were restricted to cancer cellderived EVPs expressing glypican-1. Using c-Met expression in plasma EVPs, Lux and colleagues were able to diagnose PDAC with a sensitivity of 72.4% and specificity of 89.5% (Lux et al, 2019). Thus, EVP DNA has the potential to provide clinical information on the mutational status of the tumor cell of origin and help drive personalized therapy. Mutated genes or proteins, however, may not be good targets to predict cancer incidence, as they are not detected in EVPs from healthy individuals (Yang et al, 2017b).

Measures of therapeutic responses

Therapeutic intervention changes the profile of circulating EVPs (see Build it up: Cancer promotion). Overall, levels of EVPs markers are decreased significantly in gastric and breast cancer patients after surgery, suggesting that they are mostly cancer-derived (Tang et al, 2019a; Zheng et al, 2020a). Similarly, Gumireddy and colleagues showed that levels of AKAP4⁺ EVPs decrease after NSCLC resection but undergo a surge later only in patients experiencing recurrence (Gumireddy et al, 2015). After chemotherapy, patients with progressive disease had higher levels of expression of EVP markers than patients with partial or complete responses in CRC (Yang et al, 2018b), breast cancer (Aharon et al, 2017; Tang et al, 2019a), lung cancer (Yuwen et al, 2017, 2019; Ma et al, 2019b; Zhao et al, 2020d), rectal cancer (Kral et al, 2018), prostate cancer (Khan et al, 2012), ovarian cancer (Yang et al, 2019a), and rhabdomyosarcoma (Ghamloush et al, 2019). Similarly, circulating EVP numbers and size increase in patients with CRC and breast cancer after chemotherapy (Aharon et al, 2017; Bar-Sela et al, 2020). EVP miRNAs and proteins were also found to be dysregulated in relation to radiotherapy response in several cancer types, including glioma (Li et al, 2020f), esophageal squamous cell carcinoma (Luo et al, 2019; Chen et al, 2021c), NSCLC (Dinh et al, 2016), and brain metastasis (Chen et al, 2021d). Importantly, EVPs may be used as liquid biopsies to determine the feasibility and efficacy of immunotherapy. Not only does blood EVP PD-L1 reflect PD-L1 and CD8⁺ T cell infiltration in tumors, but the EVP PD-L1 and miRNA signature in plasma is also informative with respect to PD-L1 expression and efficacy of immunotherapy, especially in NSCLC, allowing for the selection of patients most likely to benefit from checkpoint blockade inhibitors (Katakura *et al*, 2020; Peng *et al*, 2020; Shimada *et al*, 2021).

In conclusion, there is emerging evidence that EVP profiles change in response to therapeutic interventions, with more pronounced alterations in protein and RNA/miRNA levels in response to chemotherapy and radiation therapy. We could speculate that this effect is due to either induction of transcriptomic changes in treated cells (tumor adaptation) or a Darwinian selection of resistant clones, and thus EVP cargo might provide information of tumor evolution over the course of therapy (Vendramin et al, 2021). Although the exact nature, cause, and applicability of this expression change need to be further determined, we could hypothesize that EVPs might be employed as liquid biopsies to measure therapeutic readouts that cannot currently be assessed by conventional imaging methods, such as presence of occult residual disease or minimal (< 10%) tumor shrinkage (Martens et al, 2014). Additionally, circulating EVPs might offer early response prediction within days from treatment onset, instead of at the end of the therapy cycle, allowing for faster determination of therapeutic strategies and treatment plan adjustments.

Therapeutic delivery strategies

Advances in nanotechnology have led to the engineering of a new generation of therapeutics-loaded nanomaterials with improved stability, tissue penetration, and intracellular targeting compared to traditional agents (Mitchell et al, 2021). Despite the potential of engineered nanoparticles to become a new frontier of precision medicine, some limitations, including clearance, toxicity, and nonspecific distribution, still remain. As a natural vehicle for proteins, lipids, and nucleic acids, EVPs present a few advantages over other delivery nanotools. First, EVPs are endowed with very low immunogenicity and can deliver cargoes to various cell types at distant sites without prior clearance by innate immune cells (Lai et al, 2014). EVP size may matter in this regard, as EVPs are in an optimal size range to avoid rapid excretion by the kidneys, while being sufficiently small to avoid opsonization and immune cell recognition (Mitchell et al, 2021). The presence of the "self" marker CD47 and the exposure of negatively charged lipids (e.g., PS) and proteins on EVP surfaces may also explain the resistance to phagocytosis (Kamerkar et al, 2017; Zhang et al, 2018b).

Further, EVPs have a broad tissue biodistribution, including most hematopoietic organs (i.e., liver, spleen, bone marrow, lymph nodes), lungs, and kidneys (Lai *et al*, 2014; Hoshino *et al*, 2015; Zhang *et al*, 2018b). Exomeres preferentially localize to the liver (Zhang *et al*, 2018b), but their mechanism of tissue homing needs to be further investigated. High accumulation in the liver and spleen has also been observed with engineered nanoparticles (Mitchell *et al*, 2021). EVPs can cross the blood–brain barrier after intranasal

Figure 5. EVPs serve as biomarkers in cancer.

List of the most recent EVP cargoes found dysregulated in bodily fluids or tissue biopsies in different cancer types. Only EVP biomarkers significantly correlating with clinicopathological parameters (such as overall survival or relapse-free survival) are shown. Parameters correlating with therapeutic response are indicated. Arrows denote upregulated or downregulated markers.

HEAD AND NECK SQUAMOUS CELI	/ORAL L CARCINOMA
Proteins P↑ CD44v3+ P↑ CD16 P↑ PF4V1/F13A1/ ApoA1	Theodoraki <i>et al</i> , 2020 Hofmann <i>et al</i> , 2020 Li <i>et al</i> , 2019c
mRNAs P↑EGFRvIII	Manda et al, 2018
LUNG CANCER	
miRNAs	
 ● T miR-92b-3p ● ● ↑ miR-323-3p 	Li et al, 2021 Janpipatkul et al, 2021
 ● P↑ miR-1468-3p ● P↑ miR-5189-5p 	
◆ P↑ miR-6513-5p	Y
TP↑ SUV39H2	Xu et al, 2021
P↑ miR-1290 TP↑ miR-342-5p	Wu et al, 2020g Han et al. 2020
TP↑ miR-574-5p	Chen et al. 2020b
◆TP miR-200b	Katakura et al, 2020
 ● P↑ miR-1273a ● P↑ miR-320d 	Zhao <i>et al,</i> 2020e Peng <i>et al,</i> 2020
 P↑ miR-320c P↑ hsa-miR-320b 	•
 P↑miR-425-3p 	Yuwen et al, 2019
 ● P↑ miR-32 ●↑ ED-miR-381-3p 	Xu et al, 2019b Nigita et al, 2018
P↑ED-miR-589-3p P↑ED-miR-411-5p	
P↑ miR-451	Kanaoka et al, 2018
 P1 miR-146a-5p P1 miR-222-3p 	Wei et al, 2017a
P↑ miR-4257 P↑ miR-23b-3p	Dejima <i>et al,</i> 2017 Liu <i>et al,</i> 2017a
P↑ miR-10b-5p	,,
 P↑ miR-29a-3p/ miR-150-5p 	Dinh <i>et al</i> , 2016
IncRNAs P↑TBILA	Tao et al. 2020b
P1 AGAP2-AS1	Tong of al. 2019
P↑ MALAT-1	Zhang et al, 2019
circRNAs P↑ circRNA-102481 P↑ circ-SATB2	Yang <i>et al,</i> 2021 Zhang <i>et al,</i> 2020b
mRNAs ♦TP↑PD-L1	Shimada e <i>t al,</i> 2021 Yang e <i>t al,</i> 2021c
Proteins	Shimada at al. 2001
VIP PD-EI	Yang et al, 2021c
P↓GAS5 TP↑ADAM10sa	Li et al, 2019b Yoneyama et al, 2018
P↑LBP P↑NY-FSO-1	Wang et al, 2018d Sandfeld-Paulsen et al.
P↑ CD151	2016a Sandfeld-Paulsen <i>et al</i> , 2016b
P1 CD171	20100
 P↑ Tetraspanin 8 P↑ AKAP4 	Gumireddy et al, 2015
BREAST CANCER	
TP↑miR-21-5p	Liu <i>et al,</i> 2021c
P↑miR-363-5p P↑miR-7641	Wang et al, 2021f Shen et al, 2021
P↑miR-423-5p	Liu et al, 2021a
P ↑ miR-223 P ↑ miR-1246	Jang et al, 2021a
P↑miR-206 P↑miR-24	
P↑miR-373	
P ↑ miR-6875	
P↑miR-202 P↑miR-219B	
P↓miR-17-5p	Lv et al, 2020b
U 1 miR-21	Ando <i>et al</i> , 2019
P↓miR-223-3p	roshikawa et al, 2018
	Zhong et al., 2020
circRNAs	lin st st 20001b
Proteins	Liu et al, 20210
P1 Del-1	Lee et al, 2021 Kanpan et al, 2016
P1 MFN2	Nailliall et al, 2016
 ● ↑ CD144 ● ↑ CD62E 	Aharon et al, 2017
♦ P↑TF/TFPI ratio	

NEUROBLASTON	IA
miRNAs	l an et al. 2020
P1 miR-210 P1 miR-301a	Lan <i>et al</i> , 2020
IncRNAs	Tan et al. 2018
Proteins	141101 49, 2010
P↑ CD9/GFAP/SVN TP↑ EGFRvIII	l Galbo <i>et al,</i> 2017 Manda <i>et al,</i> 2018
ESOPHAGEAL CA	NCER
miRNAs ♦ P↑ miR-340-5p	Chen <i>et al,</i> 2021c
 ● ↓ miR-339-5p ● ↑ miB-93-5p 	Luo <i>et al,</i> 2019 Liu <i>et al.</i> 2018b
P↑miR-21	Tanaka <i>et al</i> , 2013
IncRNAs	2010
P↑ UCA1	Zhu <i>et al,</i> 2020
COLORECTAL CA	NCER
miRNAs	Han et al. 2021
P↑miR-16	Tiali et al, 2021
P↑miR-21	
P↑miR-122	Sun et al, 2020b
P↑ circ-133	Yang et al, 2020c
TP↑miR-1539	Cui et al, 2020c
◆ TP ↑ miR-199a/b-3p	Baek et al, 2020
◆ TP ↑ miR-199a-5p	
P↑miR-320d	Tang et al, 2019c
P↓miR-92b ◆ P↑miB-125b	Min et al, 2019 Yagi et al. 2019
P↑miR-146a	Cheng et al, 2019
P↓miR-486-5p P↑miR-181a-5p	Bjornetro et al, 2019
P↑miR-30d-5p	
P↑miR-25-3p	Zeng et al, 2018
P↑miR-92a-3p	10 81 81, 2010
 P↑miR-17/92 clust P↑miR 5490 50 	er Kral et al, 2018
P↑miR-6803-5p	Yan et al, 2018a
P↓miR-638	Yan et al, 2017
TP1 miR-125a-3p	Tsukamoto et al. 2017
Pt GPC1	Listal 2017b
1 di Ol	Liela, 2017D
P↑miR-96-5p P↑miR-149	Li et al, 20170
P↑miR-96-5p P↑miR-149 P↓miR-4772-3p	Liu <i>et al</i> , 2016a
P↑miR-96-5p P↑miR-149 P↓miR-149 P↓miR-4772-3p P↑miR-19a	Liu <i>et al,</i> 2016a Matsumura <i>et al,</i> 2015
P↑miR-96-5p P↑miR-149 P↓miR-4772-3p P↑miR-19a IncRNAs P↓HOTTIP P↓CRIDE_b	Liu <i>et al</i> , 2016a Matsumura <i>et al</i> , 2015 Oehme <i>et al</i> , 2019
P↑miR-96-5p P↑miR-149 P↓miR-149 P↓miR-19a IncRNAs P↓HOTTIP P↑CRNDE-h circCRNAs	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c
P † miR-96-5p P † miR-149 P ↓ miR-149 P ↓ miR-19a IncRNAs P ↓ HOTTIP P ↑ CRNDE-h circRNAs P ↑ circ-0004771	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020
P↑miR-96-5p P↑miR-149 P↑miR-172-3p P↑miR-172-3p P↑miR-19a IncRNAs P↓HOTTIP P↑CRNDE-h circRNAs P↑crc-0004771 Proteins P↑FGA	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020 Zheng et al, 2020b
P↑miR-96-5p P↑miR-96-5p P↑miR-149 P↑miR-172-3p P↑miR-19a IncRNAs P↓CNDEP P↑CRNDE-h circRNAs P↑CRNDE-h circRNAs P↑CRO04771 Proteins P↑FGA P↓CPC1 P↑GA	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020 Zheng et al, 2020b Li et al, 2017a
P↑miR-96-5p P↑miR-149 P↓miR-149 P↓miR-172-3p P↑miR-19a IncRNAs P↓HOTTIP P↑CRNDE-h CirCRNAs P↑circ-0004771 Proteins P↑CGA P↓GPC1 P↑CPNE3	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020 Zheng et al, 2020b Li et al, 2017a Bar-Sela et al, 2020 Sun et al, 2020
P↑miR-36-5p P↑miR-36-5p P↑miR-149 P↓miR-172-3p P↑miR-19a IncRNAs P↓HOTTIP P↑CRNDE-h circRNAs P↑circ-0004771 Proteins P↑FGA P↓GPC1 P↑CPNE3	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020 Zheng et al, 2020b Li et al, 2017a Bar-Sela et al, 2020 Sun et al, 2019a
P↑ miR-36-5p P↑ miR-149 P↓ miR-142 P↓ miR-4772-3p P↑ miR-19a IncRNAs P↓ HOTTIP P↑ CRNDE-h circRNAs P↓ GPC1 P↑ tega P↓ CPNE3	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020 Zheng et al, 2020 Liet al, 2017a Bar-Sela et al, 2020 Sun et al, 2019a
P↑ miR-36-5p P↑ miR-36-5p P↑ miR-36-5p P↑ miR-149 P↓ miR-472-3p P↑ miR-4772-3p P↑ miR-19a IncRNAs P↓ HOTTIP P↑ cre-0004771 Proteins P↑ fciR-0004771	Liu et al, 2016 Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016 Pan et al, 2020 Zheng et al, 2020 Liu et al, 2020 Sun et al, 2020 Sun et al, 2021 IAN CANCER Zhou et al, 2021
P↑miR-36-5p P↑miR-36-5p P↑miR-149 P↑miR-172-3p P↑miR-19a IncRNAs P↑CRNDE-h circRNAs P↑CRNDE-h circRNAs P↑CRD4 P↑CRD4 P↑CPC1 P↑Angiostatin P↑CPNE3 CERVICAL/OVAR miRNAs P↑miR-3468-5p P↑miR-3468-5p P↑miR-3468-5p	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020 Zheng et al, 2020b Li et al, 2020b Li et al, 2020b Sun et al, 2020 JAN CANCER Zhou et al, 2021a Maetal, 2019a
P↑miR-36-5p P↑miR-36-5p P↑miR-143 P↑miR-172-3p P↑miR-19a IncRNAs P↑CRNDE-h circRNAs P↑CRNDE-h circRNAs P↑CRD2+ CERVICAL/OVAR miRNAs P↑miR-3468-5p P↑miR-3468-5p P↑miR-3468-5p P↑miR-3468-5p P↑miR-3468-5p P↑miR-3468-5p P↑miR-3468-5p	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020 Zheng et al, 2020b Li et al, 2017a Bar-Sela et al, 2020s IAN CANCER Zhou et al, 2021a Maeda et al, 2020 Maet al, 2019a
P † miR-36-5p P † miR-36-5p P † miR-142 P ↓ miR-4772-3p P f miR-172-3p P t miR-19a IncRNAs P ↓ CRNDE-h circRNAs P ↑ CRNE3 CERVICAL/OVAR miR-1468-5p P ↑ miR-34a T ↑ ↑ miR-34a T ↑ ↑ miR-31a-3p T ↑ miR-31a-3p P ↑ miR-34a T ↑ ↑ miR-31a P ↑ miR-34a	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020 Zheng et al, 2020b Li et al, 2020b Li et al, 2020b Sun et al, 2020b IAN CANCER Zhou et al, 2021a Maeda et al, 2020 Ma et al, 2019a
P t miR-36-5p P t miR-149 P J miR-148-772-3p P t miR-172-3p P t miR-172-3p P t miR-172-3p P t miR-172-3p P t miR-3p P t cRNAs P t cRNDE-h circRNAs P t circ-0004771 Proteins P t circ-0004771 Proteins P t GA P t CRNE P t concount P t CRNE P t Angiostatin P t CRNE3 P t miR-34a P t miR-34a TP t miR-34a TP t miR-35a TP t miR-37a TP t miR-34a TP t miR-34a	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020 Zheng et al, 2020b Li et al, 2017a Bar-Sela et al, 2020 Sun et al, 2019a IAN CANCER Zhou et al, 2021a Maeda et al, 2020 Ma et al, 2019a
P † miR-149 P ↓ miR-149 P ↓ miR-148-772-39 P † miR-172-39 P f miR-172-39 P t cRNDE-h circRNAs P t circ-0004771 Proteins P t fGA P & Angiostatin P t CPNE3 CERVICAL/OVAR miRNAs P † miR-1468-5p P † miR-34a T P † miR-34a T P † miR-310 P † miR-151a-39 T P † miR-151a-39 P † miR-2100 P † miR-210 P † miR-2020	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020 Zheng et al, 2020b Liet al, 2017a Bar-Sela et al, 2020 Sun et al, 2019a IAN CANCER Zhou et al, 2021a Maeda et al, 2020 Ma et al, 2019a
P † miR-36-5p P † miR-36-5p P † miR-149 P ↓ miR-4772-3p P † miR-172-3p P † miR-172-3p P t miR-172-3p P t miR-172-3p P t miR-172-3p P t cRNDE-h circRNAs P t circ-0004771 Proteins P t fGA P t QPC1 P t Angiostatin P t CPNE3 CERVICAL/OVAR miRNAs P t miR-1468-5p P t miR-31a-3p T t miR-31a-3p T t miR-31a-3p P t miR-32 P t miR-32 P t miR-310 P t miR-31-45a P t miR-31-3p P t miR-31-3p P t miR-31-30	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020 Zheng et al, 2020 Li et al, 2017a Bar-Sela et al, 2020 Sun et al, 2020 Sun et al, 2021a Maeda et al, 2020 Ma et al, 2019a Kim et al, 2019c Yang et al, 2019
P † miR-36-5p P † miR-36-5p P † miR-149 P † miR-19a IncRNAs P ↓ HOTTIP P † CRNDE-h circRNAs P ↑ crNDE-h circRNAs P ↑ crCN04771 Proteins P ↑ crCN04771 P ↑	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020 Zheng et al, 2020 Liet al, 2017a Bar-Sela et al, 2020 Sun et al, 2019a IAN CANCER Zhou et al, 2021a Maeda et al, 2020 Ma et al, 2019c Yang et al, 2019c Yang et al, 2019a
P t miR-36-5p P t miR-149 P t miR-148 P t miR-372-3p P t miR-172-3p P t miR-172-3p P t miR-172-3p P t miR-172-3p P t cRNDE-h circRNAs P t circ-0004771 Proteins P t fGA P d GPC1 P t Angiostatin P t CPNE3 CERVICAL/OVAR miRNAs P t miR-1468-5p P t miR-34a TP t miR-31a TP t miR-31a P t miR-34a TP t miR-31a P t miR-3210 P t miR-33p P t miR-33p P t miR-337 P t miR-307 P t miR-3107 P t miR-3107 P t miR-3107 P t miR-314-3p P t miR-314-3p P t miR-324-3p P t miR-39a-5p	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020 Zheng et al, 2020b Liet al, 2017a Bar-Sela et al, 2020 Sun et al, 2019a IAN CANCER Zhou et al, 2021a Maeda et al, 2020 Ma et al, 2019c Yang et al, 2019a Su et al, 2019a Yang et al, 2019a Yang et al, 2019a
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P † miR-36-5p P † miR-143 P † miR-144-772-3p P † miR-19a IncRNAs P ↓ HOTTIP P ↑ CRNDE-h circRNAs P ↑ CRNDE-h circRNAs P ↑ CRNDE-h circRNAs P ↑ CRNDE-h circRNAs P ↑ CRNDE-h circRNAs P ↑ CRNDE-h CERVICAL/OVAR miRNAs P ↑ miR-3468-5p P ↑ miR-346	Liu et al, 2016 Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2010 Pan et al, 2010 Zheng et al, 2020 Li et al, 2020 Li et al, 2020 Sun et al, 2020 Ma et al, 2019a Xim et al, 2019a Kim et al, 2019a Yang et al, 2019a Yang et al, 2019a Yang et al, 2019a Yang et al, 2019a Guo et al, 2020 Oiu et al, 2020
P † miR-36-5p P † miR-36-5p P † miR-143 P † miR-4772-3p P † miR-4772-3p P † miR-19a IncRNAs P † cRNDE-h circRNAs P † crc-0004771 Proteins P ↑ cRNDE-h circRNAs P ↑ anglostatin P ↑ CPNE3 CERVICAL/OVAR miRNAs P ↑ miR-3468-5p P ↑ miR-375 P ↑ miR-375 P ↑ miR-375 P ↑ miR-375 P ↑ miR-375 P ↑ miR-398-5p IncRNAs P ↑ EXOC7 P ↑ aHIF Bertation	Liu et al, 2016 Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016 Pan et al, 2010 Zheng et al, 2020 Li et al, 2020 Li et al, 2020 Bar-Sela et al, 2020 Sun et al, 2019a IAN CANCER Zhou et al, 2021a Maeda et al, 2020 Ma et al, 2019a Kim et al, 2019a Su et al, 2019a Su et al, 2019a Su et al, 2019a Su et al, 2019a Guo et al, 2020b Qiu et al, 2018 Tang et al, 2019b
P † miR-36-5p P † miR-36-5p P † miR-143 P ↓ miR-4772-3p P ↑ miR-19a IncRNAs P ↓ HOTTIP P ↑ CRNDE-h circRNAs P ↑ CRNDE-h circRNAs P ↑ CRNDE-h CERVICAL/OVAR miRNAs P ↑ miR-1468-5p P ↑ miR-3468-5p P ↑ miR-3468-5p P ↑ miR-3468-5p P ↑ miR-3468-5p P ↑ miR-310 P ↑ miR-310 P ↑ miR-310 P ↑ miR-310 P ↑ miR-321-3p P ↑ miR-345 P ↑ miR-345 P ↑ miR-345 P ↑ miR-345 P ↑ miR-345 P ↑ miR-345 P ↑ miR-375 P ↑ miR-375 P ↑ miR-39a-5p IncRNAs P ↑ EXOC7 P ↑ MALAT1 TP ↑ aHIF Proteins P ↑ CAV-1	Liu et al, 2016 Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016 Pan et al, 2020 Zheng et al, 2020b Li et al, 2020b Li et al, 2020b Sun et al, 2020b Ma et al, 2019a Kim et al, 2021a Maeda et al, 2020 Ma et al, 2019a Kim et al, 2019a Su et al, 2019 Yang et al, 2019 Guo et al, 2020b Guo et al, 2020b Guo et al, 2020b Yang et al, 2019b
P † miR-149 P ↓ miR-36-5p P ↓ miR-149 P ↓ miR-1472-3p P ↑ cRNAs P ↓ HOTTIP P ↑ CRNDE-h circRNAs P ↑ cRNDE-h circRNAs P ↑ crc-0004771 Proteins P ↑ crc-0004771 Proteins P ↑ cRNA P ↓ GPC1 P ↑ cRNAs P ↑ aniR-1468-5p P ↑ miR-1468-5p P ↑ miR-214-3p P ↑ miR-214-3p P ↑ miR-214-3p P ↑ miR-214-3p P ↑ miR-214-3p P ↑ miR-375 P ↑ miR-375 P ↑ miR-214-3p P ↑ miR-375 P ↑ miR-214-3p P ↑ miR-375 P ↑ miR-214-3p P ↑ miR-375 P ↑ miR-214-3p P ↑ miR-375 P ↑ miR-3107 P ↑ m	Liu et al, 2016 Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016 Pan et al, 2020 Zheng et al, 2020 Li et al, 2020 Li et al, 2020 Bar-Sela et al, 2020 Sun et al, 2019a IAN CANCER Zhou et al, 2021 Maeda et al, 2020 Ma et al, 2019a Kim et al, 2019c Yang et al, 2019a Su et al, 2019a Su et al, 2019a Guo et al, 2019a Guo et al, 2020b Oiu et al, 2020b
P↑miR-36-5p P↑miR-36-5p P↑miR-149 P↓miR-4772-3p P↑miR-19a IncRNAs P↓CRNDE-h circRNAs P↑CRNDE-h circRNAs P↑CRNE3 CERVICAL/OVAR miRNAs P↑CPNE3 CERVICAL/OVAR miRNAS P↑CPNE3 CERVICAL/OVAR miRNAS P↑CPNE3 CERVICAL/OVAR miRNAS P↑CPNE3 CERVICAL/OVAR miRNAS P↑CPNE3 CERVICAL/OVAR miRNAS P↑CPNE3 P↑CAL25 P↑CAL25 P↑CAL25 P↑EGFR P↑ERC	Liu et al, 2016a Matsumura et al, 2019 Liu et al, 2019 Liu et al, 2010 Pan et al, 2020 Zheng et al, 2020b Li et al, 2017a Bar-Sela et al, 2020 Sun et al, 2020b TAN CANCER Zhou et al, 2021a Maeda et al, 2020 Ma et al, 2019a Kim et al, 2019a Yang et al, 2019b Yang et al, 2020b Qiu et al
P † miR-36-5p P † miR-36-5p P † miR-143 P † miR-19a IncRNAs P ↓ HOTTIP P † CRNDE-h circRNAs P ↑ crNDE-h circRNAs P ↑ crCNCAL P ↑ crCNCAL	Liu et al, 2016a Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016c Pan et al, 2020 Zheng et al, 2020b Li et al, 2017a Bar-Sela et al, 2020 Sun et al, 2020b Maeda et al, 2020 Maet al, 2019a Kim et al, 2019a Yang et al, 2019a Yang et al, 2019a Guo et al, 2020b Giu et al, 2020b Giu et al, 2020b Giu et al, 2020b Giu et al, 2020b Chen et al, 2020b Chen et al, 2020b Chen et al, 2020b Chen et al, 2020b
P † miR-36-5p P † miR-36-5p P † miR-143 P ↓ miR-4772-3p P † miR-19a IncRNAs P ↓ HOTTIP P ↑ CRNDE-h circRNAs P ↑ CRNDE-h CERVICAL/OVAR miRNAs P ↑ miR-3468-5p P ↑	Liu et al, 2016 Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2010 Pan et al, 2010 Zheng et al, 2020 Li et al, 2020 Li et al, 2020 Sun et al, 2020 Ma et al, 2020 Ma et al, 2019a Kim et al, 2019a Yang et al, 2019a Yang et al, 2019a Guo et al, 2019a Yang et al, 2019a Yang et al, 2019a Yang et al, 2019a Yang et al, 2019b Yang et al, 2020 Oliu et al, 2020 Oliu et al, 2020 Yang et al, 2020 Oliu et al, 2020 Oliu et al, 2020 Chang et al, 2020 Chang et al, 2019d
P † miR-36-5p P † miR-36-5p P † miR-143 P ↓ miR-4772-3p P ↑ miR-19a IncRNAs P ↓ HOTTIP P ↑ CRNDE-h circRNAs P ↑ CRNDE-h circRNAs P ↑ CRNDE-h CERVICAL/OVAR miRNAs P ↑ miR-3468-5p P ↑ miR-348-5p P ↑ miR-348-5p P ↑ miR-348-5p P ↑	Liu et al, 2016 Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016 Pan et al, 2010 Zheng et al, 2020 Li et al, 2020 Li et al, 2020b Li et al, 2017a Bar-Sela et al, 2020 Sun et al, 2019a IAN CANCER Zhou et al, 2021a Maeda et al, 2020 Ma et al, 2019a Kim et al, 2019a Su et al, 2019a Su et al, 2019a Su et al, 2019a Su et al, 2019a Guo et al, 2020b Oliu et al, 2018 Tang et al, 2019 Yang et al, 2020b Chen et al, 2020b Chen et al, 2020b Chen et al, 2020b
P † miR-36-5p P † miR-36-5p P † miR-143 P ↓ miR-4772-3p P ↑ miR-19a IncRNAs P ↓ HOTTIP P ↑ CRNDE-h circRNAs P ↑ CRNDE-h circRNAs P ↑ CRNDE-h circRNAs P ↑ CRNDE-h CERVICAL/OVAR miRNAs P ↑ miR-3468-5p P ↑ miR-3468-5p P ↑ miR-3468-5p P ↑ miR-3468-5p P ↑ miR-3168-5p P ↑ miR-316	Liu et al, 2016 Matsumura et al, 2015 Oehme et al, 2019 Liu et al, 2016 Pan et al, 2020 Zheng et al, 2020b Li et al, 2020b Li et al, 2020b Sun et al, 2020b Ma et al, 2019a Xinn et al, 2021a Maeda et al, 2020 Ma et al, 2019a Xinn et al, 2019a Yang et al, 2019a Su et al, 2019a Su et al, 2019a Su et al, 2019a Su et al, 2019a Guo et al, 2020b Oiu et al, 2020b Chen et al, 2020b
P † miR-36-5p P † miR-36-5p P † miR-149 P ↓ miR-4772-3p P ↑ miR-19a IncRNAs P ↓ HOTTIP P ↑ CRNDE-h circRNAs P ↑ CRNDE-h circRNAs P ↑ CRNDE-h circRNAs P ↑ CRNDE-h CERVICAL/OVAR miRNAs P ↑ miR-1468-5p P ↑ miR-214-3p P ↑ miR-214-3p	Liu et al, 2016a Matsumura et al, 2019 Liu et al, 2010 Pan et al, 2019 Liu et al, 2016c Pan et al, 2020 Li et al, 2020b Li et al, 2020b Li et al, 2020b Ma et al, 2019a IAN CANCER Zhou et al, 2021a Maeda et al, 2020 Ma et al, 2019a Kim et al, 2019a Su et al, 2019a Su et al, 2019a Su et al, 2019a Guo et al, 2020b Giu et al, 2018 Tang et al, 2019b Yang et al, 2019b Yang et al, 2019b Yang et al, 2020b Chen et al, 2020b Chen et al, 2020b Chen et al, 2020b Chen et al, 2019d

LIVER CANCER/	
HEPATOCELLUL	AR CARCINOMA
miRNAs	
PTmiR-18a	Huang et al, 2021
P↑miR-221	
P ↑ miR-638	Yokota et al, 2021b
DemiD 105h	Shi et al, 2018
PT MIR-1250	Liu et al. 2017b
P ↓miR-320d	Li et al, 2020e
P ↑ miR-10b-5p	Cho et al, 2020
♦ P↑miR-92b	Nakano et al, 2019
P1miR-224 P1miR-93	Xue et al. 2018
Proteins	,
P↑ULBP1	Easom et al, 2020
IncRNAs	
P T CRNDE	Wang et al, 2021e
P↑ENST00000440	688 1
P↑ENST00000457	302.2
circRNAs	
P ↑ circ-0028861	Wang et al, 2021h
P↑circ-0006602	Guo et al, 2021
P↑circ-0051443	Chen et al, 2020f
mRNAs	Vu at al. 2010-
	Au el al, 2018a
CASTRIC CANOF	. D
GASTRIC CANCE	R
miRNAs	Zhong of al. 0001
P ↑ mirB-10b-5p	Zheng et al, 2021 Zhang et al, 2020g
P↑miR-101-3p	
P1 miR-143-5p	
P↑miR-1246	Shi et al, 2020b
F TmiR-21-5p	Unzawa et al, 2020a
F 1 miR-92a-3p	
F ↑miR-342-3p	
F ↓ miR-29s	Ohzawa et al, 2020b
P↓miR-21	Soeda et al, 2019
P↓miR-92a	li et el 0010
P T miR-374a-5p P T miR-23b	JI et al, 2019 Kumata et al. 2018
P↑miR-19b/	Wang et al. 2017b
miR-106a	3 /
Proteins	
	Sun et al, 2021b
P T CEBPA-AST P T Dicer	Plao et al, 2020 Okuda et al, 2020
TP J GCP3	Rahbari et al, 2019
IncRNAs	
P↑CCAT1	Xiao et al, 2021
◆ TP ↑ MIAT	Xu et al, 2020
PTH19 PLONAD 6:1	∠nou <i>et al,</i> 2020a
	Lietai, 20200
	Zhend et al 2020a
P ↓ PCSK2-2:1	Cai et al, 2020a
PTSLC2A12-10:1 P↓PCSK2-2:1 P↑UEGC1	Cai et al, 2020a Cai et al, 2019 Lin et al, 2018
PTSL02A12-10:1 P↓PCSK2-2:1 P↑UEGC1 TP↑ZFAS1	Cai et al, 2020a Cai et al, 2019 Lin et al, 2018 Pan et al, 2017
PTSLC2A12-10:1 P↓PCSK2-2:1 P↑UEGC1 TP↑ZFAS1 P↑LINC00152	Cai <i>et al</i> , 2020a Cai <i>et al</i> , 2019 Lin <i>et al</i> , 2018 Pan <i>et al</i> , 2017 Li <i>et al</i> , 2015b
PT5LC2A12-10:1 P V PCSK2-2:1 P V UEGC1 TP 1 ZFAS1 P 1 LINC00152 circRNAs TP 1 circSUKEP1	Zineng et al, 2020a Cai et al, 2019 Lin et al, 2018 Pan et al, 2017 Li et al, 2015b
P T SLC2A12-10:1 P ↓ PCSK2-2:1 P ↑ UEGC1 TP ↑ ZFAS1 P ↑ LINC00152 circRNAs TP ↑ circSHKBP1 TP ↓ circ 0065149	Cheng et al, 2020a Cai et al, 2019 Lin et al, 2018 Pan et al, 2017 Li et al, 2015b Xie et al, 2020b Shao et al. 2020
P ↑ 5LC2A12-10:1 P ↓ PCSK2-2:1 P ↑ UEGC1 TP ↑ ZFAS1 P ↑ LINC00152 circRNAs TP ↑ circSHKBP1 TP ↓ circ_0065149 P ↑ circ-KIAA1244	Cherg et al, 2020a Cai et al, 2019 Lin et al, 2018 Pan et al, 2017 Li et al, 2015b Xie et al, 2020b Shao et al, 2020 Tang et al, 2018b
P + DC2A12-10:1 P ↓ PC5K2-2:1 P ↑ UEGC1 TP ↑ ZFAS1 P ↑ LINC00152 circRNAs TP ↑ circSHKBP1 TP ↓ circ_0065149 P ↑ circ-KIAA1244	Zneng et al., 2020a Cai et al., 2019 Lin et al., 2018 Pan et al., 2017 Li et al., 2015b Xie et al., 2020b Shao et al., 2020b Tang et al., 2018b
P ↓ PC3K22-21 P ↓ PC3K2-21 P ↑ UEGC1 T ↑ ZFAS1 P ↑ LINC00152 circRNAs T P ↓ circSHKBP1 T P ↓ circ.0065149 P ↓ circ.NIAS1244 PANCREATIC CA	Zneng et al, 2020a Cal et al, 2019 Lin et al, 2018 Pan et al, 2017 Li et al, 2015b Xie et al, 2020b Shao et al, 2020b Shao et al, 2020b Tang et al, 2018b
P ↓ PCSK2-2:1 P ↓ PCSK2-2:1 P ↑ UEGC1 P ↑ 2FAS1 P ↑ LINC00152 circRNAs TP ↑ circSHKBP1 TP ↓ circ_0065149 P ↑ circ-KIAA1244 PANCREATIC CA miRNAs	Zneng et al, 2020a Cai et al, 2019 Lin et al, 2018 Pan et al, 2017 Li et al, 2017 Li et al, 2015b Xie et al, 2020b Shao et al, 2020 Tang et al, 2018b
P + JCC2A12-10:1 P + JCSK2-2:1 P ↑ UEGC1 TP ↑ ZFAS1 P ↑ LINC00152 circRNAs TP ↑ circSHKBP1 TP ↓ circ_0065149 P ↑ circ_KIAA1244 PANCREATIC CA miRNAs P ↓ miR-19b D ↓ miR-19b	Zneng et al, 2020a Cai et al, 2019 Lin et al, 2018 Pan et al, 2017 Li et al, 2015b Xie et al, 2010b Shao et al, 2020b Shao et al, 2020b NCER Wang et al, 2021d Diard et al, 2021d
P → FGLU2A12-10:1 P ↓ PC6K2-2:1 P ↑ UE6C1 TP ↑ ZFAS1 P ↑ LINC00152 circRNAs TP ↑ circSHKBP1 TP ↓ circ-KIAA1244 PANCREATIC CA miRNAs P ↓ miR-19b TP ↑ miR-483-3p P ↑ miR-1296-3p	Zneng et al, 2020a Cai et al, 2019 Lin et al, 2018 Pan et al, 2017 Li et al, 2015b Xie et al, 2020b Shao et al, 2020 Tang et al, 2018b NCER Wang et al, 2021d Shao et al, 2021d Shao et al, 2021d Shao et al, 2021
P + F3LU2A12-10:1 P + PC8K2-2:1 P ↑ UEGC1 T ↑ ZFAS1 P ↑ LINC00152 circRNAs T P ↑ circSHKBP1 T P ↓ circ_0065149 P ↑ circ-KIAA1244 PANCREATIC CA miRNAs P ↓ mIR-19b T ↑ mIR-1286-3p P ↑ mIR-21	Zneng et al, 2020a Cai et al, 2019 Lin et al, 2018 Pan et al, 2017 Li et al, 2015b Xie et al, 2020b Shao et al, 2020 Tang et al, 2018b NCER Wang et al, 2021d Shao et al, 2021d Shao et al, 2021d Wang et al, 2021d Wang et al, 2021a Wu et al, 2020c
P ↓ FGLU2A12-10:1 P ↓ PCSK2-2:1 P ↑ UEGC1 T ↑ ZFAS1 P ↑ LINC00152 circRNAs T P ↑ circSHKBP1 T P ↓ circ_0065149 P ↑ circ-KIAA1244 PANCREATIC CA miRNAs P ↓ miR-19b T ↑ miR-183-3p P ↑ miR-210 P ↑ miR-210	Zneng et al, 2020a Cai et al, 2019 Lin et al, 2018 Pan et al, 2017 Li et al, 2015b Xie et al, 2020b Shao et al, 2020 Tang et al, 2018b NCER Wang et al, 2021d Wang et al, 2021a Wang et al, 2021a Wu et al, 2020c
P + JC22A12-10:1 P ↓ PC5K2-2:1 P ↑ UEGC1 TP ↑ ZFAS1 P ↑ LINC00152 circRNAs TP ↑ circSHKBP1 TP ↓ circ_0055149 P ↑ circ-KIAA1244 PANCREATIC CA miRNAs P ↓ miR-19b TP ↑ miR-483-3p P ↑ miR-1226-3p P ↑ miR-210 U ↑ miR-210 U ↑ miR-3940-5p/	Zneng et al, 2020a Cai et al, 2019 Lin et al, 2018 Pan et al, 2017b Li et al, 2015b Xie et al, 2020b Shao et al, 2020 Tang et al, 2018b NCER Wang et al, 2021d Shao et al, 2021 Wang et al, 2021d Shao et al, 2021 Wang et al, 2021a Wu et al, 2020c Yoshikawa et al, 2020
P + DC3K2-2:1 P + DC3K2-2:1 P ↑ UEGC1 T + ZFAS1 P ↑ LINC00152 circRNAs T + circSHKBP1 T + circSHKBP1	Zneng et al, 2020a Cal et al, 2019 Lin et al, 2018 Pan et al, 2017 Li et al, 2015b Xie et al, 2020b Shao et al, 2020 Tang et al, 2021d Shao et al, 2021d Data et al, 2021a Wu et al, 2020c Yoshikawa et al, 2020
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Tao et al, 2019

Lipids P↑LysoPC 22:0 P↑PC (P-14:0/22:2) P↑PE (16:0/18:1)

miRNAS P↓mir-92a-1-5p P↑mir-149-3p P↑mir-149-3p P↑mir-424-3p P↑miR-210 P↑miR-210 P↑miR-1233 P↑miR-126-3p U↑miR-126-3p U↑miR-34b-5p Proteins Xiao *et al,* 2020 Song et al, 2020 Zhang et al, 2018e

P↑miR-1233 P↑miR-224 U↑miR-126-3p U↑miR-449a <i>or</i> U↑miR-34b-5p	Fujii e <i>t al,</i> 2017 Butz et al, 2016		
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P↑GGT1	Horie et al, 2020		
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U TKRT17	
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PTmiR-181a-5p PTmiR-423-3n	Wang et al, 2021g Guo et al, 2020a
U ↑miR-151a-5p	Fredsoe et al, 2019
U ↑miR-204-5p	
U ↑miR-222-3p	
U ↑miR-331-3p	
P ↑ miR-1290	Huang et al, 2015
P ↑ miR-375	
mRNAs	Was stal 0000
U TGAIA2	W00 et al, 2020
U TMPRSS2-ERG	1
Proteins	
P↑PKM2	Dai et al, 2019
P T Claudin-3	vvorst et al, 2017 Bijnsdorn et al, 2013
◆TP↑Survivin	Khan et al, 2012
Lipids	
U ↑Phosphatidyl-	Skotland et al, 2017b
serine/lactosyl-	
Ceramide	
U ↑PCA3	Kohaar et al, 2020
U ↑PCGEM1	
OTHER CANCERS	5
OSTEOSARCOM	A
P↑PD-L1/	Wang et al, 2020f
N-cadherin	
LEUKEMIA	
P↑miR-10b	Fang et al, 2020
THYROID CANCE	ER
P↑miR-145	Boufragech et al, 2014
P↑miR-130a-3p	Yin et al, 2021
MELANOMA	
P↑miR-143	
P TmiR-221	Husna et al, 2021
CHOLANGIOCAR	CINOMA
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inhalation (Zhuang *et al*, 2011; Haney *et al*, 2015), with some limitations, however, due to dosing variability (Mitchell *et al*, 2021). Importantly, brain homing can be achieved after intracardiac delivery of EVPs from brain-tropic cells, which preferentially localize to endothelial cells and microglia (Hoshino *et al*, 2015; Rodrigues *et al*, 2019), indicating a permeability of the blood–brain barrier to EVPs that has not yet been observed with engineered nanoparticles (Mitchell *et al*, 2021). Thus, EVPs could be particularly useful as delivery systems for organs with low-permeability physical barriers, such as the central nervous system and the gastrointestinal tract.

Finally, non-engineered nanoparticle drug carriers become concentrated preferentially at certain sites, such as the spleen and liver, by virtue of an enhanced permeability and retention effect of the vasculature as well as phagocyte accumulation (Schroeder *et al*, 2011; Mitchell *et al*, 2021). In contrast, EVPs have an innate organ distribution, with integrins being major determinants of their tropism (Hoshino *et al*, 2015). Furthermore, these EVP surface integrins and receptors achieve activation of intracellular signaling cascades with potential therapeutic applications (Costa-Silva *et al*, 2015; Hoshino *et al*, 2015; Rodrigues *et al*, 2019).

Altogether, this growing evidence suggests that endogenous or engineered EVPs represent promising delivery tools for precision medicine in oncology.

Endogenous EVPs as therapeutic tools

Despite their distinctive tissue homing, cancer cell-derived EVPs are not desirable therapeutic or delivery tools due to their systemic effects on oncogenesis, pre-metastatic niche establishment, and thrombosis. EVPs from other cell sources have been evaluated and have shown endogenous functions.

MSCs have often been used as a source of therapeutic EVPs due to their self-renewal and multipotent properties (Gabrilovich & Nagaraj, 2009). Moreover, MSC-derived EVPs can mimic the regenerative and immunosuppressive properties of MSCs, but with increased tissue permeability due to their smaller size. A growing body of literature shows promising therapeutic properties of endogenous cargo of adipose-, bone marrow-, or umbilical cord-derived EVPs from MSCs in ischemic stroke (Xin et al, 2013; Chen et al, 2016a; Huang et al, 2020b; Li et al, 2020b; Zhao et al, 2020e), diabetic retinopathy (Safwat et al, 2018; Gu et al, 2020), Alzheimer's Disease (Wendeln et al, 2018; Feng et al, 2020), and arthritis (Wu et al, 2020e). EVPs derived from MSCs ameliorate the severity of IBD in mice by reducing infiltration of macrophages in colon tissue and decreasing their expression of pro-inflammatory mediators, such as TNF- α , IL-1 β , and IL-7 (Mao *et al*, 2017; Ma *et al*, 2019c). MSC-derived EVPs prevent development of pulmonary complications, such as bronchopulmonary dysplasia (Willis et al, 2020). MSC-derived EVPs can also prevent liver fibrosis by reactivating HSC autophagy (Qu et al, 2017) and suppressing HSC activation and collagen deposition (Lou et al, 2017). While a beneficial effect of MSC-derived EVPs has been identified in these pre-cancerous conditions, multiple findings have shown a deleterious effect of these EVPs on cancer progression. In particular, MSC-derived EVPs from different sources, including cancer-associated MSCs, bone marrow aspirates, and adipose tissue, were found to promote cancer cell proliferation (Roccaro et al, 2013), increase tumor growth in mice (Roccaro *et al*, 2013; Vallabhaneni *et al*, 2015), suppress CD4⁺ T cell proliferation (Cheng et al, 2020), promote EMT and migration (Lin *et al*, 2013; Gu *et al*, 2016), support ECM remodeling (Yang *et al*, 2015b), potentiate angiogenesis (Zhang *et al*, 2015a), and sustain chemoresistance (Ji *et al*, 2015). Conversely, studies on glioma have reported anti-tumor effects of MSC-derived EVPs, such as a reduction of tumor cell proliferation and migration (Lee *et al*, 2013; Xu *et al*, 2019a). The nature of this dichotomy is not known. Roccaro and colleagues proposed that pro-tumorigenic properties could be restricted to tumor-educated MSCs, while normal MSCs mainly have anti-tumorigenic effects (Roccaro *et al*, 2013). Nevertheless, MSC-derived EVPs, especially from autologous sources, may not be an ideal candidate for cancer treatment.

Another main issue with MSC-derived EVP isolation is that MSCs have limited self-renewal capacity and undergo senescence within a few passages in culture. EVPs from senescent MSCs might have deleterious properties, including cancer induction (Severino et al, 2013). Different approaches have been employed to avoid MSC senescence and improve EVP manufacturing, including MSC immortalization via lentiviral MYC transduction (Chen et al, 2011), exposure to hypoxia (Gonzalez-King et al, 2017; Zhu et al, 2018a), and small-molecule inhibitors treatment with (Wang et al. 2020e). Despite successfully increasing EVP release, some of these approaches were shown to alter the cargo and functional effect of MSC-derived EVP and thus strategies to improve EVP manufacturing need to be further evaluated. Among them, the embryonic cell line HEK293T has been tested for safety and efficacy in preclinical experiments (Liang et al, 2020a), but the role of their endogenous cargo still needs to be elucidated. Similarly, reticulocytes have been used to produce EVPs with low immunogenicity as scaffolds for drug and magnetic particle loading (Blanc et al, 2005; Qi et al, 2016). Finally, Pan and colleagues have shown high purity and yield of urinary EVPs for autologous delivery, with more than 3 mg of EVPs per half liter of urine (Pan et al, 2020).

Immune cells may be another valuable source of EVPs for cancer management, mainly due to their endogenous anti-inflammatory and anti-tumor properties, but their applicability entirely depends on the immune cell source. EVPs from bone marrow-derived macrophages reduce hematopoiesis in atherosclerotic mice (Cianciaruso et al, 2019) and promote an anti-tumor T cell response (Bouchareychas et al, 2020) via their cargo of miRNAs and lipid biosynthesis enzymes. On the contrary, EVPs from M2-polarized macrophages mediate resistance to cisplatin and apoptosis of gastric cancer cells via miR-21 delivery and activation of the PI3K/AKT signaling pathway (Zheng et al, 2017) and thus may not be an ideal tool for biomolecule delivery. EVPs from Treg cells reduced DSS-induced IBD in mice by decreased apoptosis of intestinal epithelial cells through miR-195a-3p transfer (Liao et al, 2020). EVPs from NK cells also have high potential as therapeutic tools, as they share the same tumor cytotoxic properties of the producing cells (Lugini *et al*, 2012; Shoae-Hassani et al, 2017; Zhu et al, 2017, 2018b). Other advantages of NK cell-derived EVPs also include their selective uptake by tumor cells, but not by other resting PBMCs, and their selective homing to tumors in vivo (Lugini et al, 2012; Zhu et al, 2018b). To overcome the low availability of NK cell EVPs, Zhu and colleagues designed a novel protocol with a higher efficiency of isolation of NK EVP mimetics. Finally, further information on the immune properties of EVPs has been gained by studies on DC-derived exosomes (Dex). Zitvogel and colleagues were the first to show that Dex from immature DCs expresses MHC-I and MHC-II complexes and that,

when mature DCs are exposed to tumor-specific antigens, their EVPs can halt tumor growth *in vivo* by inducing CD8⁺ T cell activation and immunize the host after a single injection, alone or in conjunction with adjuvants (Zitvogel et al, 1998; Chaput et al, 2004). Remarkably, Dex immunization was more effective at controlling tumor progression than DC adoptive transfer (Zitvogel et al, 1998). Further work by Thery and colleagues and other groups elucidated that Dex can activate CD4⁺ and CD8⁺ T cells in vivo via autocrine and paracrine mechanisms, with potential innate anti-tumor effects. First, Dex from mature DCs, and to a lesser extent immature DCs, are taken up by other DCs, especially the $CD8\alpha^{-}$ subtype, and B cells to present EVPs markers on their MHCs and engage CD4⁺ T cell activation into effector T cells (Thery et al, 2002; Segura et al, 2005a). Further, MHCs on Dex taken up by DCs work directly as adjuvant for their antigen-presenting activity (Thery et al, 2002). Moreover, Dex themselves present peptides to T cells to induce T cell activation and proliferation, a process also dependent on Dex expression of ICAM-1 and B7.2 surface proteins (Hwang et al, 2003; Segura et al, 2005a,b). Lastly, Dex can also prime NK cells via their cargo of IL-15 α and NKG2D ligand, thus eliciting an anti-tumor immune response (Viaud et al, 2009). Several clinical trials using DC-derived EVPs as cancer vaccines have been designed, with increasing levels of T cell responses due to improved Dex manufacturing (Lamparski et al, 2002; Escudier et al, 2005; Viaud et al, 2011; Damo et al, 2015).

Finally, EVPs from dietary sources hold great promise as natural nanoparticles for treatment and delivery. EVPs containing RNA (miRNA, mRNA, and lncRNA) and proteins are found in the whey fraction of human and animal milk (Izumi et al, 2015; van Herwijnen et al, 2016; Zeng et al, 2019). Milk EVPs are resistant to gastric, bile, and pancreatic juices, thus contributing to a major portion of nucleic acids in blood cells and tissues (Baier et al, 2014; Zeng et al, 2019; Wu et al, 2019a), and are well tolerated in vivo upon oral administration (Arntz et al, 2015; Somiya et al, 2018; Stremmel et al, 2020). Cow milk may represent the most available and costeffective source of EVPs. A number of studies have provided evidence that bovine milk-derived EVPs are taken up by cecal microbiota and intestinal cells, where they reduce oxidative stress, and by immune cells, including human PBMCs (Arntz et al, 2015; Somiya et al, 2018; Zhou et al, 2019b; Wang et al, 2021c). The endogenous cargo of milk-derived EVPs was shown to have immunoregulatory properties by reducing systemic inflammation and preventing the onset of arthritis and IBD (Arntz et al, 2015; Wu et al, 2019a; Stremmel et al, 2020). Importantly, milk EVPs were found to induce activation of NK cells and CD8⁺ T cells directly (Komine-Aizawa et al, 2020), suggesting that these EVPs may directly mediate anti-tumor immune responses. The uptake of EVPs from bovine raw milk was also observed for several cancer cell lines, including leukemia (Izumi et al, 2015), colon carcinoma (Wolf et al, 2015), and ovarian cancer cells (Benmoussa et al, 2020), although further investigations are necessary to determine the effect of the endogenous cargo of milk EVPs on cancer progression.

Similar to all other eukaryotes, plant cells are endowed with MVBs and can release exosome-like vesicles (An *et al*, 2007). EVPs have been successfully isolated from the juice of edible plants, such as carrots, ginger root, grapes, and citrus fruits, including grapefruit, clementine, and lemon, and contain a cargo of RNAs and proteins (Mu *et al*, 2014; Baldini *et al*, 2018; Stanly *et al*, 2019). Lemon

juice-derived EVPs have distinctive antioxidant properties on MSCs due to their naturally occurring cargo of citrate, vitamin C, small RNAs, and protein transporters (Baldini *et al*, 2018). Although surface proteins might be altered at low pH in the stomach and intestine, Mu and colleagues showed active uptake of plant-derived EVPs in intestinal macrophages and stem cells (Mu *et al*, 2014). In particular, ginger-derived EVPs induce the synthesis of immunomodulatory IL-10 and IL-6 and promote activation of macrophage Nrf2 and intestinal Wnt/TCF4 pathways, inducing an anti-inflammatory response in the gut. Although the nature and function of protein and nucleic acid cargo in plant-derived EVPs need further elucidation, they may represent the new frontier of inter-species deliverables with beneficial innate properties.

Engineered EVPs

Exogenous EVP cargo allows for tissue distribution and cellular uptake that is not achievable by naturally occurring EVPs or by unshielded therapeutic agents, making engineered EVPs ideal carriers for cancer therapeutic and imaging agents. Different EVP engineering workflows have been devised for this objective. Autologous EVPs may represent the best approach to ensure increased targeting (Liu *et al*, 2019d), high biocompatibility, and low toxicity, but other types of EVPs also may be valid alternatives in terms of availability, cost-effectiveness, and endogenous beneficial properties.

Genetic engineering of EVP-releasing cells allows for enhanced targeting and bioactive properties of EVPs. Lysosome-associated membrane glycoprotein 2 (Lamp2) is highly packaged into EV membranes and has been used as part of an expression construct for the introduction of targeting moieties on EVs. Alvarez-Erviti and colleagues were the first group to report the generation of autologous Dexs engineered to express a fusion construct between the extracellular N-terminus of Lamp2 and peptides binding specific acetylcholine receptors in the brain and muscle of mice. These EVs were found to selectively home to these tissues in vitro and in vivo (Alvarez-Erviti et al, 2011). Along the same lines, EVPs expressing CD63-Apo-A1 were found to have increased uptake in liver cancer cells via interaction of Apo-A1 with their scavenger class B type 1 receptor (Liang et al, 2018), while expression of lipotropic peptide-TNF-a vectors in EVP-producing cells allows anchorage of TNF-a to the EVP membrane (Zhuang et al, 2020). Through a similar approach, other groups have engineered EVPs to express several targeting molecules: RGD peptides specific for $\alpha_V \beta_3$ integrin on breast cancer and gastric cancer cells (Tian et al, 2014b; Xin et al, 2021; Gong et al, 2019); Her2-binding antibody mimetics and designed ankyrin repeated proteins (DARPins) to target Her2⁺ colorectal and breast cancer cells, respectively (Gomari et al, 2018; Limoni et al, 2019; Liang et al, 2020a); aminoethylanisamide, a ligand for sigma receptors in NSCLC (Choi et al, 2018); folic acid that recognizes folate receptors expressed on tumor cells (Pi et al, 2018; Li et al, 2018f; Feng et al, 2021), and tumor MUC-1-interacting 5TR1 aptamer (Schindler et al, 2019; Bagheri et al, 2020). These EVPs showed better uptake by cancer cells in vitro and accumulation in tumors in mice, were well tolerated in vivo, and did not cause any organ toxicity or hematological or histopathological abnormalities (Liang *et al*, 2020a).

EVPs can also be directly decorated with molecules not incorporated into their membranes. For example, allowing cells to produce EVPs in the presence of azide-choline drives the incorporation of azide groups on membrane lipids of the EVP surface, followed by conjugation with antibodies for targeted delivery (Nie *et al.* 2020). This approach results in the local release of antibodies at low pH conditions, such as in the acidic tumor microenvironment. EVPs can be conjugated with PEGylated antibodies for direct cancer antigen targeting, such as in the case of antibodies against somatostatin receptor 2 on neuroendocrine tumor cells (Si et al, 2020). Similarly, EVPs can be coated with Fe₃O₄ superparamagnetic nanoparticles coupled with antibodies against A33 antigen, expressed in more than 95% of CRC biopsies (Li et al, 2018d). Other engineered EVP products have been reported. Morishita and colleagues successfully achieved the synthesis of EV particles expressing a fusion product of exosome-specific lactadherin bound to extracellular streptavidin (Morishita et al, 2016), which works as a platform for EV coating with biotinylated DNAs, RNAs, and proteins. Astutely, Pi and colleagues devised a workflow to decorate EVPs with nucleic acids, peptides, or naturally occurring vitamins. Their innovative method makes use of the arrow-shaped motor packaging RNA (pRNA) of the bacteriophage phi29 (pRNA-3WJ), engineered to display cancerselective ligands, such as folate, selective for folate receptor on cancer cells, and RNA aptamers of prostate-specific membrane antigen (PSMA) and EGFR. Additionally, cholesterol conjugation to different extremities of the arrow-shaped pRNA-3WJ allows for different conformations of RNA loading on EVP membranes or partial internalization in the EVP lumen (Pi et al, 2018).

Most intravenously injected tumor cell-derived EVPs are quickly cleared by macrophages, especially in the liver and spleen (Imai *et al*, 2015). To overcome this, genetic engineering of donor cells or direct EVP manipulation can be employed to improve their circulation half-life. In this regard, the expression of the "do not eat me" signal CD47 on EVPs results in better tumor distribution and lower clearance by circulating myeloid cells (Kamerkar *et al*, 2017; Mendt *et al*, 2018; Lv *et al*, 2020a). Kim and colleagues incorporated PEG into EVPs as a method to decrease immunogenicity and blood clearance and to add vector moieties to EVPs altogether (Choi *et al*, 2018).

The targeting ability of EVPs has also been achieved by coupling them with magnetic nanoparticles, such as superparamagnetic iron oxide nanoparticles, and driving their tumor infiltration via application of a local magnetic field (Li *et al*, 2018d; Zhuang *et al*, 2020). Through a different approach, Qi and colleagues employed the presence of transferrin receptors on the surface of reticulocyte-derived EVs, which are produced during maturation of reticulocytes into erythrocytes, to achieve EV coating with superparamagnetic magnetite colloidal nanocrystal clusters (SMCNCs). These SMCNCcoupled EVs could be directed to hepatoma tumors in mice upon application of a mild magnetic field (Qi *et al*, 2016). Similarly, EVPs loaded with sinoporphyrin sodium could be induced to accumulate in tumors via guided ultrasound (Liu *et al*, 2019d).

EVPs as therapeutic carriers

EVPs are naturally occurring carriers of functional genetic information and are endowed with low toxicity and broad tissue distribution *in vivo*. EVPs show more than 30 times higher cell uptake than other vectors, such as nanoparticles or liposomes (Kim *et al*, 2016b; Pan *et al*, 2020). Moreover, EVPs are resistant to harsh environmental conditions, such as low pH in gastric juices and shear stress in the blood, and it is thus conceivable that they can be employed as delivery vehicles for drugs, nucleic acids, and imaging agents in cancer patients. EVPs hold particularly great promise as delivery vehicles for anti-cancer drugs, especially for compounds with low solubility. Because of their targeted delivery and their ability to cross most physical barriers in the body, EVP-encapsulated drugs have the potential to improve localized treatments while minimizing side effects from off-target delivery, which is the main limitation of cancer chemotherapy (Hadla et al, 2016; Schindler et al, 2019). EVP-loaded chemotherapeutics also have a stronger cytotoxic effect than free drugs (Saari et al, 2015), providing room for reduced clinical doses. Drug loading has been achieved by incubation and cocentrifugation of EVPs with drugs, leading to passive surface binding, EVP permeabilization, or EVP sonication or electroporation in the presence of soluble drugs, which achieves drug loading inside the EVP membrane (Tian et al, 2014b; Saari et al, 2015; Kim et al, 2016b; Liang et al, 2020a). Based on these approaches, EVPs from various cancer or macrophage cell lines have been successfully loaded with drugs, including doxorubicin (Hadla et al, 2016; Schindler et al, 2019; Wei et al, 2019; Bagheri et al, 2020; Tian et al, 2014b; Qi et al, 2016; Kim et al, 2016b; Gomari et al, 2018, 2019; Gong et al, 2019), paclitaxel (Saari et al, 2015; Kim et al, 2016b; Choi et al, 2018; Schindler et al, 2019; Bagheri et al, 2020; Zhang et al, 2020c), 5-fluorouracil (Liang et al, 2020a), erastin (Yu et al, 2019a), aspirin (Tran et al, 2019), cisplatin (Li et al, 2020c; Zhang et al, 2020e), romidepsin (Si et al, 2020), cabazitaxel (Qiu et al, 2020b), and atorvastatin (Nooshabadi et al, 2020). EVP-bound drugs were shown to be released into the cell cytoplasm after EVP endocytosis and caused cancer cell death, with higher efficiency and lower doses than drugs alone (Saari et al, 2015; Kim et al, 2016b; Gomari et al, 2019; Yu et al, 2019a). Growth of primary tumors and lung metastasis in mice was found to be reduced in response to EVPs loaded with doxorubicin (Tian et al, 2014b; Qi et al, 2016; Gong et al, 2019; Schindler et al, 2019; Bagheri et al, 2020) and paclitaxel (Kim et al, 2016b; Choi et al, 2018), respectively. Importantly, EVPs could be loaded with drug payloads that would be too toxic in their free form but caused no side effects if selectively delivered to tumors (Si et al, 2020). More indirectly, EVPs can be loaded with nanoparticle-carrying drugs or other therapeutic agents, which makes them functional carriers of membrane-soluble agents. Zhao and colleagues have reported the generation of breast cancer cellderived EVPs encapsulating cationic bovine serum albumin (CBSA) conjugated with anti-S100A4 siRNA, with EVPs dictating organ distribution while CBSA served as a non-antigenic and biodegradable deliverable. These EVPs successfully localized to the lungs of mice and prevented metastasis formation in a breast cancer mouse model (Zhao et al, 2020b).

EVPs can also be employed for the sensitization of tumor cells to other types of chemotherapy, such as sonodynamic and hypothermic therapy. Cancer cell-derived EVPs loaded with sinoporphyrin sodium, an organic sonosensitizer, spontaneously distributed to homotypic primary and metastatic tumors and simultaneously triggered DVDMS intracellular distribution to mitochondria and induction of cytotoxic ROS in response to ultrasound. The application of therapeutic ultrasound further potentiated the cytotoxic effect of EVP-associated DVDMS, reducing growth of primary and metastatic tumors (Liu *et al*, 2019d). Lv and colleagues showed the efficacy of EVP-thermosensitive liposomal hybrids to localize to metastatic peritoneal carcinoma and release their cargo of GM-CSF and docetaxel in response to localized hypothermia. In turn, the EVP content inhibited tumor cell proliferation directly (via doxorubicin), while activating the phagocytic activity of macrophages against tumor cells and promoting an anti-tumor adaptive immune response (via GM-CSF) (Lv *et al*, 2020a).

EVP-encapsulated nucleic acids are more protected from degradation by blood nucleases, ensuring better tissue delivery and achieving selective organotropism and thus have the potential to serve as tools for gene therapy delivery. For example, injection of siRNA encapsulated in Lamp2-ligand-expressing exosomes achieves a much more restricted tissue distribution than naked siRNA in mice and effectively depletes targets in recipient cells (Alvarez-Erviti et al, 2011). Survivin siRNA-loaded EVPs with tumor tropism dictated by surface PSMA aptamer-pRNA-3WJ, EGFR aptamer-pRNA-3WJ, and folate- pRNA-3WJ abrogated the growth of prostate, breast, and colorectal cancer, respectively (Pi et al, 2018). Importantly, EVP siRNA did not induce immune stimulation in vivo and achieved a level of target silencing comparable to fivefold higher amounts of naked siRNA. Kamarkar, Mendt and colleagues successfully hindered pancreatic cancer development and metastasis by silencing oncogenic Kras^{G12D} via siRNA and shRNAs loaded into fibroblast and MSC-derived EVPs and with much higher efficiency than engineered liposomes (Kamerkar et al, 2017; Mendt et al, 2018). Anti-miRNAs work as traps for endogenous miRNAs with known pro-cancerous effects. Liang and colleagues used 5fluorouracil and anti-miR-21 loaded HEK293T EVPs to induce expression of tumor-suppressor PTEN, growth arrest, and apoptosis of colorectal cancer cells, and reduction of tumor growth in vivo, while anti-miR-21 alone failed to reach a sufficient therapeutic effect (Liang et al, 2020a). Loading of miRNA-26 on Apo-A1-engineered EVPs allowed selective silencing of their targets Cyclin E2 and CDK6 and reduced migration and proliferation in liver cancer HepG2 cells (Liang et al, 2018). Several other miRNAs with anti-tumor functions were overexpressed in donor cells or directly transfected in EVPs, leading to their enrichment in EVPs that further induced cancer cell apoptosis and chemo- and radio-sensitivity, and reduced tumor growth in vivo (Gong et al, 2019; Pomatto et al, 2019; Liu et al, 2019b; Kobayashi et al, 2020; Konishi et al, 2020; Kulkarni et al, 2020; Yao et al, 2020; Sharif et al, 2021). Nucleic acids were also loaded into EVPs from dietary sources. Some studies have shown successful transfection of exogenous miRNA or pro-apoptotic and oncogene-directed siRNAs into raw bovine milk EVPs and delivery to cancer cells in vitro and in vivo (Aqil et al, 2019; Tao et al, 2020a; Del Pozo-Acebo et al, 2021; Munagala et al, 2021). In a similar manner, ginger-derived EVPs were conjugated with cholesterolpRNA-3WJ constructs and folic acid to deliver survivin siRNA to CRC cells expressing folate receptors (Li et al, 2018f). Together, these reports provide proof-of-principle evidence that engineered dietary EVPs are a nontoxic and cost-effective delivery tool for therapeutic nucleic acids.

Preclinical studies suggest that EVPs could also be engineered to induce phagocytosis of tumor cells. HEK293T EVPs overexpressing signal regulatory protein α (SIRP α) interact with the "don't eat me" CD47 signal on tumor cells, thus enhancing tumor cell phagocytosis *in vitro* and inhibiting tumor growth in immunocompetent mice. Both direct macrophage phagocytosis and infiltration of anti-tumor T cells were observed in tumors from mice treated with SIRP α -EVPs (Koh *et al*, 2017). Similarly, RAW264.7-derived EVPs decorated

Finally, some studies have demonstrated successful use of EVPs as immune adjuvants, with potential applications for cancer immunotherapy. Exosomes from DCs exposed to or expressing tumor antigens induce T cell activation and anti-tumor immunization (Zitvogel et al, 1998; Thery et al, 2002; Segura et al, 2005a; Lu et al, 2017; Li et al, 2018a). Additionally, by loading murine melanoma-derived EVPs with immunomodulatory cytosine-guanine dinucleotide (CpG) DNA, Morishita and colleagues achieved immunization of mice to tumor-specific antigens, protecting them from tumor initiation, growth, and metastasis. Specifically, CpG-loaded EVPs activated DCs and induced antigen presentation to T cells, eliciting an anti-tumor Th1 response (Morishita et al, 2016). Although similar results were obtained in response to CpG-conjugated liposomes and nanoparticles co-injected with tumor-associated antigens (de Jong et al, 2007; Yan et al, 2014a), CpG-loaded cancer EVPs contain a complete cargo capable of inducing activation and tumor antigen presentation within the same antigen-presenting cell for anti-tumor immunization.

EVPs as imaging tools

Engineered EVPs can be used as imaging agents. As discussed previously, optical imaging of fluorescence- or bioluminescence-labeled EVPs is an invaluable tool to study EVP functions in preclinical models, but it has the limitations of rapid photobleaching and low tissue penetration that render it impractical for clinical imaging. Instead, positron emission tomography (PET) imaging of EVPencapsulated radioactive isotopes, such as $^{64}\mathrm{Cu}$ and $^{68}\mathrm{Ga},$ allows for higher sensitivity localization of EVPs in animals (Shi et al, 2019; Jung et al, 2020). Despite these advantages, nuclear imaging may have safety limitations due to radionuclide handling and radiation exposure. Among all the available imaging techniques, intravital visualization of EVPs encapsulating or coated with superparamagnetic nanoparticles via magnetic resonance imaging (MRI) and CT scanning may be the safest (Qi et al, 2016; Li et al, 2018d; Zhuang et al, 2020; Cohen et al, 2021). Engineering of MSC exosomes to express a fusion product of membrane lactadherin and ferritin, naturally occurring MRI reporters, allows for exosome tracing in vivo via MRI imaging (Liu et al, 2020b). Alternatively, near-infrared (NIR) laser irradiation for cancer imaging has been tested. EVPs labeled with photoluminescent quantum dots engineered to target cell nuclei enabled concomitant intratumoral visualization and hyperthermia-mediated necrosis of tumor cells, due to their photothermal conversion when irradiated with an NIR laser (Cao et al, 2019). Autologous urinary EVPs were successfully loaded with nanocomposites of gold nanoparticles and the photosensitizer chlorine e6 to produce passion fruit-like EVPs with low immunogenicity and high tumor homing and retention. The release of nanoparticlechlorine e6 complexes in response to laser irradiation induced ROS generation and apoptosis of cancer cells (Pan et al, 2020). Through a different approach, re-assembled EVPs from pancreatic cancer cells were deprived of internal cargo and loaded with chlorine e6, enabling the photoacoustic imaging of subcutaneous murine melanoma tumors, due to their innate and potent tumor tropism. Simultaneously, these EVPs achieved active control of tumor growth by inducing both production of ROS in tumor cells upon laser

irradiation and systemic release of macrophage-derived chemoattractants, potentially owing to the transfer of tumor antigens to antigen-presenting cells (Jang *et al*, 2021b). Although these experiments were performed using human EVPs injected into mice, which may achieve a stronger immune response, they provide proof-ofprinciple evidence for the application of EVPs to *in vivo* imaging and immunostimulation. It is anticipated that, in the future, labeling EVPs with distinct tropism via these methods will allow visualization of different tumor types, pre-metastatic niches, and tumor prognostic features, such as vascular leakiness and dormancy.

Another potential frontier of cancer imaging is the labeling of endogenous EVPs. Chen and colleagues described the generation of a hydrogel-gold nanoparticle-based biosensor coupled with tumorspecific DNA aptamers, such as PSMA found in prostate cancer cells and EVPs, which could be visualized via surface plasmon resonance imaging. When incubated with prostate cancer patient serum or cell conditioned medium, the biosensor allowed the measurement of cancer cell-derived EVP levels in serum. This biosensor could potentially be applied to the magnetic separation of EVPs from bodily fluids, with possible analytical and therapeutic applications (Chen et al, 2020e). Further research in EVP-specific prognostic biomarkers and probes compatible with intravital EVP imaging will open the way to a new era of cancer imaging and management, where labeled EVPs might allow visualization of sites of vascular leakiness and PMN formation, currently not detectable via conventional clinical imaging.

Prevention of EVP uptake and production for cancer management

Overall, the available data on EVP-mediated cancer progression highlight the potentially immense utility of targeting EVP secretion and uptake for cancer treatment. Indeed, multiple studies have provided in vivo proof-of-principle evidence that interfering with EVP secretion and uptake reduces tumor growth, impedes metastatic progression, and inhibits systemic effects of cancer (Figure 2C). Notably, tumor cell depletion of Rab27 or Ral GTPases attenuated spontaneous lung metastasis of melanoma and mammary carcinoma in mice (Bobrie et al, 2012; Peinado et al, 2012; Ghoroghi et al, 2021). Similarly, treatment with GW4869 decreased tumor growth (Matsumoto et al, 2017; Richards et al, 2017) and impaired systemic effects of cancer, namely cachexia, in tumor-bearing mice (Hu et al, 2018; Qiu et al, 2020a). Conversely, enhancement of EVP uptake by decreasing 25-hydroxycholesterol, which blocks EVP internalization, on target cells via genetic deletion of cholesterol 25hydroxylase was shown to potentiate spontaneous melanoma metastasis to the lungs (Ortiz et al, 2019), suggesting that inhibiting uptake is anti-metastatic.

However, several challenges in effectively targeting EVP biogenesis and uptake exist. First, EVPs influence key developmental, physiological, and homeostatic functions. For example, exosomal secretion of the transferrin receptor is necessary for maturation of reticulocytes into erythrocytes (Harding *et al*, 1983; Pan & Johnstone, 1983). Transfer of exosomes plays an important role in optimizing communication between immune cells (Raposo *et al*, 1996; Zitvogel *et al*, 1998; Théry *et al*, 2002). EVPs also can contribute to cellular fitness by removing cytotoxic DNA (Takahashi *et al*, 2017; Yokoi *et al*, 2019). In addition, many of the molecular mediators of EVP biogenesis serve additional functions, which could lead to inappropriate inhibition of other pathways upon their blockade (Jahn & Scheller, 2006; Hurley, 2015; Zhen & Stenmark, 2015). Hence, the biological functions of EVPs and of molecular regulators of biogenesis raise important questions about systemic side effects associated with their inhibition. Furthermore, as detailed above, there are redundant pathways for seemingly all steps of biogenesis, as well as uptake, which could complicate effective target selection and pathway inhibition. Development of EVP-targeted therapies may therefore require a comprehensive understanding of how such pathways are regulated specifically in cancer and further interrogation into cancer-associated inducers of EVP production and uptake may reveal novel targets that can be safely inhibited.

Interestingly, there have been some investigations into repurposing already developed drugs for targeting EVP biogenesis or uptake. Screening of compound libraries has identified multiple candidates, including the microbial metabolite manumycin A, tipifarnib, neticonazole, climbazole, ketoconazole, and triademenol, which all reduce biogenesis (Datta et al, 2017, 2018). The mechanisms of action of some of these drugs appear to involve inhibition of Rasmediated signaling, which results in reduced levels of biogenesis mediators, such as Alix, nSMase2, and Rab27. They may therefore be primarily active in cancer cells compared with normal cells, making them attractive candidates for further investigation of preclinical efficacy in mouse models of metastasis. The statin simvastatin also was shown to impair EVP biogenesis, and this reduction was associated with decreased levels of Alix (Kulshreshtha et al, 2019). Finally, multiple drugs, including the anti-hypertensive drug reserpine and the anti-coagulant heparin, can block EVP uptake. Reserpine was shown to reduce uptake of cancer-cell-derived EVPs by non-cancer cells, preventing melanoma metastasis in vivo (Ortiz et al, 2019). Heparin can impair uptake of EVPs from glioblastoma and oral squamous cell carcinoma cell lines by other cancer and non-cancer cells, leading to diminished in vitro tumor cell proliferation, migration, and invasion and reduced oral squamous cell carcinoma xenograft tumor growth in vivo (Christianson et al, 2013; Sento et al, 2016).

In addition to establishing how best to target EVP biogenesis and uptake, it will also be critical to define when to provide treatments blocking these pathways. Other common treatments such as chemotherapy can increase secretion of pro-metastatic EVPs that enhance pre-metastatic niche formation in the lungs and consequent breast cancer lung metastasis (Keklikoglou et al, 2019). Thus, targeting EVP biogenesis or uptake in combination with standard therapies against the primary tumor may potentially mitigate prometastatic side effects that could result from therapy-induced EVP biogenesis. Also, inhibiting EVP uptake using reserpine as an adjuvant/neoadjuvant therapy in combination with tumor resection was found to markedly reduce lung metastasis and improve survival of mice with melanoma tumors, whereas reserpine treatment alone only had marginal effects on survival (Ortiz et al, 2019). These results further indicate that targeting EVP-dependent pathways for metastasis prevention may be most effective in the context of other standard treatments.

Conclusions and future perspectives

This review has summarized evidence that highlights the multifaceted effect of EVPs in cancer initiation, progression, and metastasis. One of the major revolutions in the field is the considerable technological advancement in the separation, analysis, and in vivo tracking of EVPs. This has led to the discovery of a previously unappreciated EVP heterogeneity and facilitated the molecular and functional characterization of distinct EVP subsets. As a result, EVP nomenclature is constantly evolving to fairly encompass and distinguish among the various EVP subclasses (Thery et al, 2018). The improvement of isolation strategies with higher resolution to remove contaminants and further separate specific EVP subsets is warranted to enhance the reproducibility and quality of studies involving EVPs and will further address the relevance of EVP subsets in cancer development. New visualization methods including super-resolution microscopy and real-time imaging will further advance our understanding of cargo packaging and biogenesis mechanisms, opening new avenues for therapeutic intervention, such as the discovery of more cell-specific and safer druggable targets of EVP biogenesis. Our knowledge on EVPs from different sources has also rapidly expanded. EVPs from most tumor cells, stroma cells, immune cells, microorganisms, and dietary sources play pivotal roles in cell-cell communication, even between life domains, during cancer development. In addition to promoting tumor growth, a major property of EVPs is to travel long distances via the hematogenous and lymphatic routes in order to shape the physiology of distant organs with the formation of PMNs and the induction of systemic effects of cancer. As shown by multiple preclinical studies, tumor-derived EVPs are determinants of organotropic metastasis, making them potential predictive/prognosis biomarkers and targets for metastasis-preventive therapies. Research into the organotropic distribution of EVPs has also opened the way to engineering "designer EVPs," which can be loaded with therapeutic or imaging molecules and endowed with the ability to image pre-metastatic sites, to tailor treatment to a selective organ site, and to reduce systemic toxicity associated with free drugs in preclinical models. The introduction of EVPs as therapeutic deliverable tools has not reached the clinic, with a few exceptions (Lamparski et al, 2002; Escudier et al, 2005; Viaud et al, 2011; Damo et al, 2015). Further strategy development on the cellular source and standardization of manufacturing pipelines for EVPs with high clinical quality are prerequisites for their further therapeutic application. Finally, by representing the phenotypic heterogeneity and invasive potential of cells of origin and the effect of therapeutic intervention in cancer patients, EVPs are among the most promising sources of liquid biomarkers for cancer detection and therapeutic response assessment. Standardization of EVP isolation and analysis pipelines, developing assays with acceptable specificity and sensitivity, and addressing the reproducibility and rigor of assays in large patient cohort studies will be necessary to introduce EVP biomarkers as diagnostic and prognostic tools in clinical settings.

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The authors declare that they have no conflict of interest.

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