



Stress responses in stromal cells and tumor homeostasis

Ilio Vitale^{a,b,c,**}, Gwenola Manic^d, Claudia Galassi^e, Lorenzo Galluzzi^{f,g,h,i,*}

^a Department of Biology, University of Rome 'Tor Vergata', Rome, Italy

^b Italian Institute for Genomic Medicine (IIGM), Turin, Italy

^c Candiolo Cancer Institute, FPO, IRCCS, Candiolo, Italy

^d IRCCS, Regina Elena National Cancer Institute, Rome, Italy

^e Istituto di Patologia Generale, Università Cattolica del Sacro Cuore, Rome, Italy

^f Department of Radiation Oncology, Weill Cornell Medical College, New York, NY, USA

^g Sandra and Edward Meyer Cancer Center, New York, NY, USA

^h Department of Dermatology, Yale School of Medicine, New Haven, CT, USA

ⁱ Université Paris Descartes/Paris V, Paris, France



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ABSTRACT

In most (if not all) solid tumors, malignant cells are outnumbered by their non-malignant counterparts, including immune, endothelial and stromal cells. However, while the mechanisms whereby cancer cells adapt to microenvironmental perturbations have been studied in great detail, relatively little is known on stress responses in non-malignant compartments of the tumor microenvironment. Here, we discuss the mechanisms whereby cancer-associated fibroblasts and other cellular components of the tumor stroma react to stress in the context of an intimate crosstalk with malignant, endothelial and immune cells, and how such crosstalk influences disease progression and response to treatment.

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1. Introduction

Non-malignant components of the tumor microenvironment (TME), which include endothelial, immune and stromal cells, numerically

exceed their transformed counterparts and play critical roles in all steps of the neoplastic process (Hanahan & Coussens, 2012; Quail & Joyce, 2013).

Cancer-associated fibroblasts (CAFs) constitute the most abundant stromal cell type of the TME (Kalluri, 2016; Shi, Du, Lin, & Wang, 2017) (Box 1). CAFs are particularly enriched in fibrotic neoplasms, such as breast, colorectal, pancreatic and prostate carcinomas (Yamauchi, Barker, Gibbons, & Kurie, 2018), where they can derive from either activation of tissue-resident fibroblasts (e.g., pancreatic stellate cells, PSCs) or differentiation of circulating bone marrow-derived MSCs (BM-MSCs). CAFs can also originate from the trans-differentiation of endothelial cells (via the so-called 'endothelial-to-mesenchymal transition'), epithelial cells (via the so-called 'epithelial-

Abbreviations: CAFs, cancer-associated fibroblasts; CSCs, cancer stem cells; CTLs, cytotoxic T lymphocytes; DDR, DNA damage response; ECM, extracellular matrix; EMT, epithelial-to-mesenchymal transition; RCD, regulated cell death; ROS, reactive oxygen species; SASP, senescence-associated secretory phenotype; TA-MSCs, tumor-associated mesenchymal stem cells; TAMs, tumor-associated macrophages; TME, tumor microenvironment.

* Correspondence to: Lorenzo Galluzzi, PhD, Weill Cornell Medical College, Stinch Radiation Oncology, 525 East 68th Street, Box # 169, New York NY 10065.

** Correspondence to: Ilio Vitale, Ph.D., University of Rome "Tor Vergata", Department of Biology, via della Ricerca Scientifica 1, 00133 Rome, Italy.

E-mail addresses: iliovit@gmail.com (I. Vitale), deadc80@gmail.com (L. Galluzzi).

Box 1
Stromal cell markers

Several morphological, phenotypic and functional markers have been harnessed to identify (and isolate) stromal cells from the TME. At the microanatomical level, CAFs generally display a spindle-like or stellate morphology, while TA-MSCs are rather heterogeneous (although they can present fibroblastoid features) (Kalluri, 2016; Shi et al., 2017). At the phenotypic level, CAFs express specific cell surface markers including (but not limited to): fibroblast activation protein alpha (FAP), platelet derived growth factor receptor alpha (PDGFRA) and PDGFRB, podoplanin (PDPN), transforming growth factor beta receptor 1 (TGFB1) and TGFB2, membrane metalloendopeptidase (MME, best known as CD10), and complement component 5a receptor 2 (C5AR2, best known as GPR77) (Kalluri, 2016). Conversely, CAFs are generally characterized by limited expression of caveolin 1 (CAV1) and CD36, and abundant levels of intracellular proteins involved in cell structure and motility, including actin alpha 2, smooth muscle (ACTA2), desmin (DES), S100 calcium binding protein A4 (S100A4, also known as FSP1), and vimentin (VIM). TA-MSCs express typical MSC markers, including 5'-nucleotidase ecto (5NTE, best known as CD73), Thy-1 cell surface antigen (THY1), endoglin (ENG, best known as CD104), but generally lack CAF biomarkers including FAP, ACTA2, S100A4, PDGFA and VIM, as well as proteins normally expressed by immune and hematopoietic cells, such as CD34 and protein tyrosine phosphatase receptor type C (PTPRC, best known as CD45) (Le Blanc & Mougiakakos, 2012; Shi et al., 2017). At the functional level, activated CAFs can be defined by their secretome, which encompasses: (1) growth factors like VEGFA, PDGFs, FGFs and epidermal growth factor (EGF); (2) cytokines like IL6, SDF1 and TGFB1; (3) metabolites like lactate, alanine and PGE₂; (4) ECM components such as type I and II collagen, fibronectin 1 (FN1), periostin (POSTN) and various members of the tenascin family; (5) ECM remodeling enzymes like lysyl oxidases and various metalloproteinases; and (6) other bioactive factors including WNT ligands (X. Chen & Song, 2019; Kalluri, 2016; Shi et al., 2017). That said, most of these markers taken individually are not CAF- or TA-MSC-specific, they are not always co-expressed, and their levels not only vary with tumor type, but also change over space (in different areas of the TME) and time (with disease progression), lending further support to the notion that stromal cells of the TME are highly heterogeneous.

to-mesenchymal transition', EMT), tumor-associated macrophages (TAMs), pericytes, adipocytes, or even malignant cells (Ohlund, Elyada, & Tuveson, 2014; Santi, Kugeratski, & Zanivan, 2018; Shi et al., 2017). The tumor stroma can also contain populations of (poorly characterized) tumor-associated mesenchymal stem cells (TA-MSCs), which derive from BM-MSCs and can potentially generate CAFs (Kalluri, 2016; Shi et al., 2017). Both CAFs and TA-MSCs are embedded in the extracellular matrix (ECM), which they help to synthesize and remodel, and display high degree of phenotypic and functional heterogeneity (Alexander & Cukierman, 2016; Costa, Kieffer, et al., 2018). Such an elevated heterogeneity coupled with a plastic nature and some degree of potency explains the apparently antithetic effects of stromal cells in tumor development and progression that have been reported thus far (Gascard & Tlsty, 2016; Kalluri, 2016; Shi et al., 2017; Valkenburg, de Groot, & Pienta, 2018).

The current view is that stromal cells become activated acutely to support the immunological elimination of pre-malignant lesions, but

can switch toward a tumor-supportive state on prolonged activation, hence acquiring the capacity to stimulate the proliferation and dissemination of cancer cells, as well as their ability to evade immune responses (Hanahan & Coussens, 2012; Kalluri, 2016; Klemm & Joyce, 2015; Quail & Joyce, 2013). That said, pro-tumor CAFs have been reported to co-exist with their anti-tumor counterparts, at least in some instances (Brechtbuhl et al., 2017; Costa, Kieffer, et al., 2018; Ohlund et al., 2017; Raz et al., 2018). Moreover, at least in specific pre-clinical and clinical settings, CAF depletion appears to accelerate rather than to halt tumor progression, potentially linked to an increased dissemination of cancer cells as a consequence of the partial resolution of local fibrosis (Carstens et al., 2017; Ozdemir et al., 2014; Rhim et al., 2014).

Thus, the stromal cell landscape of solid tumors is highly heterogeneous and dynamic, and hence can vary to considerable degrees depending on disease type and stage, as well as on a plethora of microenvironmental cues (Chen & Song, 2019). These cues include (but potentially are not limited to): (1) metabolic conditions such as nutrient and oxygen limitation (fostered by the harsh metabolic competition between malignant and non-malignant cells in a fibrotic and poorly vascularized TME) or the accumulation of metabolites produced in excess by malignant cells (e.g., lactate) (Bantug, Galluzzi, Kroemer, & Hess, 2018; Chang et al., 2015; Galluzzi, Kepp, Vander Heiden, & Kroemer, 2013); (2) immunomodulatory molecules released by cancer cells and/or tumor-infiltrating immune cells (D. S. Chen & Mellman, 2017; Galluzzi, Chan, Kroemer, Wolchok, & Lopez-Soto, 2018); (3) mechanical forces imposed by the ECM and the elevated hydrostatic pressure (Mohammadi & Sahai, 2018; Scherz-Shouval et al., 2014), and (4) exogenous toxic agents, encompassing pathogen-derived molecules as well as therapeutic interventions (Casey et al., 2015). Similar to their malignant counterparts, stromal cells respond to microenvironmental perturbations with mechanisms aimed at preserving cellular homeostasis or, if this cannot be achieved, promoting the demise (via regulated cell death, RCD) or permanent proliferative arrest (via cellular senescence) of cells irremediably damaged, in both cases along with the emission of signals for the maintenance of microenvironmental homeostasis (Galluzzi, Yamazaki, & Kroemer, 2018). Such cellular and microenvironmental responses to stress often involve changes in ECM as well as intricate paracrine circuitries interconnecting all the cellular compartments of the TME. Ultimately, the mechanisms whereby stromal cells adapt to stress have a major impact on the tumor-immune system co-evolution as they dictate the fate of malignant cells in the course of natural disease progression and response to treatment (Jiang, Hegde, & DeNardo, 2017; Shi et al., 2017; Valkenburg et al., 2018; Vitale et al., 2019).

Here, we outline how stromal cells adapt to stressful conditions, with a particular emphasis on the mechanisms whereby the signals released by stromal cells responding to stress affect cancer cells and tumor-infiltrating immune cells, and how these signals can be hijacked for therapeutic purposes.

1.1. Adaptive response of stromal cells to energetic cues

Stromal cells share with the other cellular compartments of the TME the same metabolic microenvironment and core bioenergetic circuitries, but their metabolic behavior and adaptive response to energetic perturbations are unique.

CAF and TA-MSCs are recruited to the tumor bed and activated by a variety of stressful conditions, including limited nutrient availability, low oxygen tension (hypoxia), pH deregulation and oxidative stress, often following the release of cytokines such as transforming growth factor beta 1 (TGFB1), platelet derived growth factor (PDGF), and C-X-C motif chemokine ligand 2 (CXCL2), and reactive oxygen species (ROS) from cancer cells (Cadamuro et al., 2013; Chaturvedi, Gilkes, Takano, & Semenza, 2014; Costa, Scholer-Dahirel, & Mechta-Grigoriou, 2014; Gilkes, Semenza, & Wirtz, 2014; LaGory & Giaccia, 2016). Similar to their transformed counterparts, CAFs display elevated degree of

metabolic flexibility, implying that they can rapidly adapt to conditions of poor glucose and oxygen availability, and hence they are less prone to undergo RCD in response to nutrient deprivation as compared to other cells of the TME (Yang, Achreja, et al., 2016). In particular, CAFs isolated from breast cancer patients can efficiently recycle metabolic byproducts such as lactate and ammonia as energy sources and nitrogen donors, respectively (Yan et al., 2018). Activated CAFs also resemble cancer cells in that they exhibit high biosynthetic activity and elevated proliferation rates, which they satisfy by robust glucose-driven anabolism coupled to fatty acid-driven mitochondrial respiration (Alexander & Cukierman, 2016; Santolla et al., 2012; Wu, Zhuo, & Wang, 2017). In this setting, increased glucose consumption coupled to extensive lactate secretion (Miller et al., 2017) is enabled by the upregulation of multiple glucose transporters and/or glycolytic enzymes encompassing hexokinase 2 (HK2), phosphoglycerate kinase 1 (PGK1) or lactate dehydrogenase A (LDHA) (Hu, Sun, Zhang, Xiong, & Mi, 2014; Shan et al., 2017; Shangguan et al., 2018; Wang et al., 2010; Wang, Xue, et al., 2016; Wu et al., 2018). The lactate-driven acidification of the TME supports the activation of TA-MSCs, which has been linked to increased stemness and chemoresistance in osteosarcoma cell lines *in vitro* (Avnet et al., 2017). Of note, enhanced glucose metabolism, and in particular increased metabolic flux via glycolysis, gluconeogenesis and the pentose phosphate pathway, has also been associated with the induction of cell senescence (James et al., 2015), which often characterizes the adaptive response of CAFs to genotoxic stress (see below). In cancer cell-fibroblast co-cultures as well as in the pancreatic TME, CAFs respond to microenvironmental perturbations by acquiring a secretive phenotype involving ECM components as well as ECM-remodeling enzymes, ultimately leading to extensive fibrosis (Spivak-Kroizman et al., 2013). Fibrosis limits the availability of nutrients and oxygen, hence setting off a feed-forward circuitry whereby accrued lactate accumulation, glucose deprivation and hypoxia foster the recruitment and activation of additional stromal cells.

Hypoxia has been linked to the rearrangement of core metabolic circuitries in stromal cells (Mitchell & Engelbrecht, 2017). In particular, hypoxia rewires stromal metabolism toward glycolysis via a process dependent on hypoxia inducible factor 1 subunit alpha (HIF1A), a transcription factor that transactivate multiple genes involved in glycolysis when oxygen concentrations fall below a specific threshold (Gonzalez, Xie, & Jiang, 2018). In PDGF-induced CAFs or primary CAFs from melanoma or colon cancer biopsies, decreased isocitrate dehydrogenase 3 (NAD(+) alpha (IDH3A) promotes glycolysis by stabilizing HIF1A as a consequence of fumarate and succinate accumulation (which inactivate the prolyl hydroxylases normally targeting HIF1A to degradation) (Selak et al., 2005; D. Zhang et al., 2015). In line with an impact for HIF1A activation in CAFs on tumor progression, both chronic hypoxia and the CAF-specific downregulation of egl-9 family hypoxia inducible factor 1 (EGLN1, an enzyme involved in HIF1A degradation best known as PDH2) have been shown to limit metastatic dissemination in an orthotopic breast cancer model (Kuchnio et al., 2015; Madsen et al., 2015). At least in some preclinical and clinical settings, such a tumor-supportive effect depends on the ability of glycolytic CAFs to secrete abundant levels of lactate, which can be taken up by cancer cells to fuel oxidative metabolism (Fiaschi et al., 2012; Romero, Mukherjee, Kenny, Litchfield, & Lengyel, 2015; Sanita et al., 2014; Wu, Fu, et al., 2017). This process, which is commonly known as 'reverse Warburg effect' (Galluzzi, Kepp, & Kroemer, 2012; Pavlides et al., 2009), has been linked, *in vitro*, to HIF1A stabilization in CAFs supported by cancer cell-imposed oxidative stress (Martinez-Outschoorn et al., 2013; Wilde et al., 2017). A similar metabolic cooperation involves CAF-derived pyruvate, in lymphoma models (Sakamoto et al., 2019), and CAF-derived glutamine, in prostate and ovarian cancer models (Mishra et al., 2018; Yang, Achreja, et al., 2016), which can directly feed into the Krebs cycle, as well as ketone bodies (Martinez-Outschoorn, Lisanti, & Sotgia, 2014), which can be harnessed for bioenergetic purposes by cancer cells overexpressing 3-oxoacid CoA-transferase 1 (OXCT1) (Huang, Li,

et al., 2016). Moreover, TGF β 1-activated CAFs can favor the mobilization of glycogen in cancer cells, although the molecular mechanisms underlying this process remain to be elucidated (Curtis et al., 2019). Along similar lines, *in vitro* experiments and studies from tumor biopsies suggest that CAFs favor glycolysis and the pentose phosphate pathway (hence supporting the anabolic metabolism and antioxidant defenses) by promoting the upregulation of key enzymes in these circuitries (Cruz-Bermudez et al., 2019; Sherman et al., 2017). Although the molecules at play in this setting remain to be characterized, CAF-derived exosomes (perhaps metabolism-relevant microRNAs or RNA species triggering pattern recognition receptor signaling) (Boelens et al., 2014; Nabet et al., 2017; Zhao et al., 2016) and cytokines stand out as potential messengers linking CAFs to cancer cells (La Shu et al., 2018; Zhao et al., 2016; Zhao, Ji, et al., 2017). Interestingly, in some settings CAFs have been reported to drive cancer cells into oxidative phosphorylation rather than glycolysis (Druzhkova et al., 2016). Potentially, this simply reflects the high degree of metabolic heterogeneity of both CAFs and malignant cells (Choi, Kim, Jung, & Koo, 2013).

CAF also respond to low oxygen tension by overexpressing G protein-coupled estrogen receptor 1 (GPER1), which not only supports the switch of breast CAFs towards glycolysis and fatty acid oxidation (Santolla et al., 2012; Yu et al., 2017), but also endows them with robust tumor-supportive functions including the secretion of pro-angiogenic molecules like vascular endothelial growth factor A (VEGFA) (De Francesco et al., 2013; De Francesco et al., 2017; Ren et al., 2015). Finally, hypoxia contributes to tumor progression by stimulating CAFs to release: (1) immunomodulatory molecules such as CXCL13, as shown, *in vitro* and *in vivo*, in prostate cancer models (Ammirante, Shalpour, Kang, Jamieson, & Karin, 2014), (2) growth factors such as insulin like growth factor 1 (IGF1), as observed in pancreatic tumor samples (Hirakawa et al., 2016), and hepatocyte growth factor (HGF) (Brauer et al., 2013; Kumar et al., 2018), as observed *in vitro* upon co-culturing fibroblasts with breast cancer cells, (3) antioxidants including ornithine and multiple polyamines (Ino et al., 2013), as described in pancreatic tissues, and (4) ECM remodeling enzymes like procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 (PLOD2) (Gilkes, Bajpai, Chaturvedi, Wirtz, & Semenza, 2013), as demonstrated in breast cancer models, *in vitro*. Taken together, these observations delineate metabolic, trophic and immunological circuitries activated by nutritional stress that link CAFs to endothelial cells in support of tumor progression. That said, HIF1A activity in CAFs can also underlie tumor-suppressive effects, at least in specific circumstances. Indeed, the deletion of *HIF1A* from CAFs reportedly accelerates tumor growth in a mouse model of breast cancer (Kim et al., 2012). This latter example lends further support to the notion that CAFs display elevated degrees of phenotypic and functional heterogeneity.

In response to dwindling amino acid levels, CAFs isolated from various tumors acquire the ability to secrete aspartate in direct support of cancer cell proliferation (Bertero et al., 2019), while pancreatic CAFs deposit increased amounts of collagen into the ECM, *de facto* constituting a reservoir of proline for malignant cells (Olivares et al., 2017). Along similar lines, CAFs experiencing nutrient deprivation secrete cytokines including CXCL12 (best known as SDF1) and interleukin 6 (IL6) that mediate antioxidant effects in malignant cells upon the activation of nuclear factor, erythroid 2 like 2 (NFE2L2, best known as NRF2) (Wu, Looi, Subramaniam, Masamune, & Chung, 2016). Likewise, CAFs have been shown to provide cysteine for glutathione synthesis to leukemia cells expressing low levels of the cystine transporter known as 'x_c system' (and hence being unable to synthesize glutathione from cystine) (Zhang et al., 2012).

Importantly, the metabolic circuitries relaying stressed CAFs to cancer cells are often bidirectional. In head and neck squamous cell carcinoma models, while CAF-derived HGF promotes glycolysis in cancer cells, fibroblast growth factor 2 (FGF2) secreted by malignant cells favors lactate uptake and oxidative metabolism in CAFs (D. Kumar et al., 2018). Similarly, CAFs appear to provide cancer cells with alanine

(supporting disease progression) in exchange of glutamate (driving oxidative phosphorylation in CAFs) (Bertero et al., 2019). Moreover, breast cancer cells can actively reprogram the metabolism of other cellular components of the TME including CAFs via the exosomal delivery of microRNAs that promote glutamine metabolism (e.g., miR-105) (Yan et al., 2018) and/or limit glucose utilization (e.g., miR-122) (Fong et al., 2015). Along similar lines, melanoma-derived exosomes have been shown to boost glycolysis in cultured CAFs, culminating with extracellular acidification downstream of lactate secretion (La Shu et al., 2018). The precise exosomal mediator of this latter effect, however, remains unknown. Similarly, a hitherto unidentified factor secreted by prostate cancer cells appears to favor extracellular acidification by promoting carbonic anhydrase 9 (CA9) expression on the surface of CAFs, culminating with accelerated disease progression (Fiaschi et al., 2013). Importantly, the net outcome of the abovementioned metabolic interactions is likely to depend on multiple parameters, including type of cancer, stage of the disease and the overall cellular composition of the TME.

Accumulating evidence indicates that macroautophagy – an evolutionary conserved mechanism for lysosomal degradation of dispensable or potentially toxic cytosolic material via double-membraned organelles known as autophagosomes (from here onward referred to as autophagy) (Galluzzi et al., 2017) – is key for CAF activation and survival (Goruppi, Clocchiatti, & Dotto, 2019). Accordingly, CAFs isolated from various tumors display elevated autophagic flux at baseline (Chaudhri et al., 2013; New et al., 2017) and increased levels of autophagy regulators including unc-51 like kinase 3 (ULK3) (Goruppi et al., 2017), most likely in response to the nutrient- and oxygen-poor conditions that characterize the TME. Importantly, autophagic responses in stressed stromal cells also support the survival and proliferation of cancer cells, at least *in vitro* (Sanchez et al., 2011; Zhou et al., 2017). In particular, autophagic PSCs have been shown to provide pancreatic cancer cells with alanine for oxidative metabolism upon intracellular conversion into pyruvate (Sousa et al., 2016). Similar observations have been made in co-culture experiments wherein autophagic CAFs provided breast cancer cells with glutamine in support of oxidative phosphorylation and anti-apoptotic signaling (Galluzzi et al., 2018; Ko et al., 2011). Apparently at odds with these observations, downregulation of the autophagic adaptor sequestosome 1 (SQSTM1, best known as p62) has been associated with both CAF activation (Valencia et al., 2014) and accelerated tumor progression as a consequence of increased asparagine supply to cancer cells experiencing glutamine deprivation (Linares et al., 2017). However, this metabolic effect seems independent of the autophagic

activity of p62. Altogether, these findings are in line with the increasingly better understood ability of cancer cells to use a variety of exogenous substrates for bioenergetic or biosynthetic purposes, substrates that are often provided by non-malignant cells (including CAFs) via autophagy (Katheder et al., 2017; Poillet-Perez et al., 2018).

In summary, the elevated heterogeneity and metabolic plasticity of stromal cells allow them to survive (and even become activated on) the harsh microenvironmental conditions that characterize most solid tumors, encompassing nutrient limitation, hypoxia, deregulated pH and increased oxidative stress. The adaptation of CAFs to metabolic stress also preserves tumor homeostasis by creating a protective niche that not only shields cancer cells from metabolic stress but also remodels their metabolic profile in support of their biosynthetic and bioenergetic needs (Fig. 1).

1.2. Adaptive response of stromal cells to therapeutic insults

Anticancer therapies, including those aimed at the (re)activation of tumor-targeting immunity, also threaten (most often unintentionally) the survival of stromal cells, *de facto* inducing multiple mechanisms of adaptation that influence therapeutic responses.

Despite increased proliferation rates (which are normally associated with an augmented sensitivity to stress) and evidence of apoptotic priming (*i.e.*, a proteomic profile compatible with an increased propensity for apoptotic cell death) (Lagares et al., 2017; Rizvi et al., 2014), stromal cells display an unusually elevated threshold for RCD activation by treatment. Thus, stromal cells are intrinsically resistant to most conventional therapeutic agents, which is at least in part linked to their autophagic proficiency and their ability to secrete pro-survival factors in response to stress (Chaudhri et al., 2013). Presumably, such a resistance to RCD also evolves over time in response to chronic stress signals from the TME of established tumors, *de facto* sparing CAFs from activation-driven apoptosis (and consequent phagocytic clearance), which seals the fate of normal fibroblasts (*e.g.*, upon wound healing) (Desmouliere, Redard, Darby, & Gabbiani, 1995). Accordingly, CAFs exhibit increased resistance to therapeutic insults as compared to other non-malignant cells of the TME. Thus, CAFs resist treatment with bortezomib (a proteasomal inhibitor commonly employed for multiple myeloma patients) (Garg et al., 2017) along with a TGF β 1-driven increase in autophagic flux that ultimately favors chemoresistance in leukemic cells as well (Frassanito et al., 2016). Similar autophagy-dependent cytoprotective responses in CAFs impacting the sensitivity

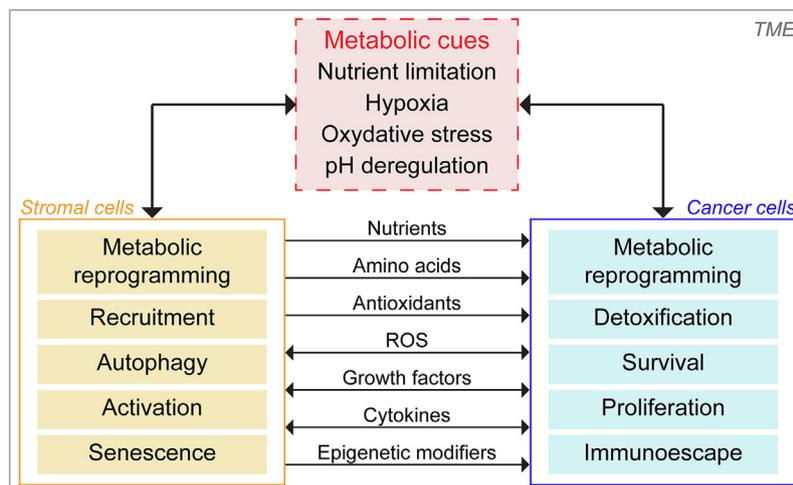


Fig. 1. Metabolic crosstalk between stromal cells and cancer cells in the TME. The tumor microenvironment (TME) of solid neoplasms is generally characterized by relatively harsh metabolic conditions, encompassing nutrient shortage, hypoxia, oxidative stress and pH alterations. All these factors have a direct effect on the metabolic and functional profile of all cellular compartments of the TME, including stromal and malignant cells (both of which exhibit elevated resistance to metabolic challenges). Alongside, metabolic perturbations of the TME enable an intimate, bidirectional crosstalk between stromal and malignant cells whereby the former ultimately support the survival, proliferation and resistance to treatment of the latter. ROS, reactive oxygen species.

of cancer cells to treatment *in vitro* and/or *in vivo* have also been observed in ovarian cancer (Wang, Xue, et al., 2016), multiple myeloma (Yang, Zheng, Zhang, Cao, & Jiang, 2017), colorectal carcinoma (Yang, Xu, Zhu, Zhang, Wu, Wu, et al., 2016), and pancreatic cancer (Zhang et al., 2018). Apparently at odds with these findings, administration of the autophagy inhibitor chloroquine to CAFs reportedly favors the resistance of co-cultured pancreatic cancer cells to gemcitabine *in vitro* (Molejon et al., 2018). That said, chloroquine is not specific for autophagy but inhibits all processes converging on lysosomal degradation (Galluzzi, Bravo-San Pedro, Levine, Green, & Kroemer, 2017), implying that these latter findings may reflect an autophagy-independent function of lysosomes.

The elevated resistance of CAFs to a variety of DNA-damaging agents including radiation therapy (Gorhcs et al., 2015; Lotti et al., 2013; Richards et al., 2017; Tommelein et al., 2018) suggests that these cells can mount a proficient cell cycle arrest and DNA damage response (DDR), in thus far resembling cancer stem cells (CSCs, the malignant cell subpopulation responsible for tumor initiation, progression and therapeutic resistance) (Manic et al., 2018; Vitale, Manic, De Maria, Kroemer, & Galluzzi, 2017). Most likely, however, this does not reflect genetic alterations (as in the case of CSCs), but rather epigenetic changes, because CAFs from distinct tumor types are usually described as genetically stable (Hosein et al., 2010; Qiu et al., 2008; Sonnenberg et al., 2008; Wang et al., 2015). Interestingly, CAFs infiltrating breast carcinomas appear to rely (at least in part) on ATR serine/threonine kinase (ATR, a transducer of the cellular response to replication stress) for their survival (Al-Ansari & Aboussekhra, 2014), in spite of reduced ATR expression levels (Al-Ansari & Aboussekhra, 2018) and other alterations in the DDR machinery including low checkpoint kinase 2 (CHEK2) expression (Al-Rakan, Hendrayani, & Aboussekhra, 2016) and, in lung CAFs, defective tumor protein p53 (TP53) signaling (Arandkar et al., 2018). Of note, the activation of TP53 following DNA damage in CAFs isolated from lung cancer biopsies can be relayed to activation of the DDR in adjacent cells that did not experience genotoxic insults (Schmid et al., 2012). The molecular mechanisms underlying this phenomenon, however, remain to be elucidated. Of interest in this setting, lung and pancreatic CAFs responding to genotoxic insults including irradiation and the DNA replication poison gemcitabine (which is commonly used in the clinical management of pancreatic tumors) (Gravett, Trautwein, Stevanovic, Dalglish, & Copier, 2018) tend to undergo cellular senescence rather than RCD (Hellevik et al., 2012; Toste et al., 2016). Such an induction of cell senescence has been observed in CAFs from distinct tumors, including (but possibly not limited to) ovarian, lung and pancreatic cancer (Capparelli et al., 2012; Hellevik et al., 2012; Pitiyage et al., 2011; Wang, Notta, et al., 2017; Yang et al., 2006). Taken together, these observations indicate that CAFs experiencing DNA-damaging conditions are prone to successfully repair damage or undergo cellular senescence, rather than succumbing to apoptosis driven by the DDR. Further investigations are required to shed light on the molecular bases of such a resistance.

The response of CAF to therapeutic agents involves profound transcriptomic modifications (also occurring in CAF-interacting cancer cells) that (1) rely on the transcriptional activity of multiple nuclear receptors, as observed in CAFs from squamous cell carcinoma biopsies (Chan et al., 2018), and (2) support the establishment of a high apoptotic threshold and resistance to therapy, as observed *in vitro*, in breast CAFs (Marusyk et al., 2016). In particular, activation of specific nuclear receptors in stressed CAFs drives the synthesis and release of biologically active factors that act on cancer cells via paracrine circuitries to support resistance to treatment. Paracrine circuitries of this sort have been described for (1) CAF-derived HGF, underlying the resistance of melanoma cells with B-Raf proto-oncogene, serine/threonine kinase (BRAF) mutations to BRAF inhibitors (Straussman et al., 2012; Wilson et al., 2012), lung cancer cells with ALK receptor tyrosine kinase (ALK) translocations to ALK inhibitors (Yamada et al., 2012), and breast cancer cells to epidermal growth factor receptor (EGFR) inhibitors (Mueller

et al., 2012); (2) CAF-derived FGF2, which supports the resistance of breast cancer cells to hormone therapy and targeted therapies with phosphoinositide-3-kinase (PI3K) inhibitors (Shee et al., 2018); (3) glial cell derived neurotrophic factor (GDNF), which limits the sensitivity of prostate cancer cells to mitoxantrone, an anthracycline inducing immunogenic cell death, and docetaxel, a microtubular poison (Galluzzi, Buque, Kepp, Zitvogel, & Kroemer, 2017; Huber et al., 2015); and (4) various insulin-like growth factors (IGFs), which drive the resistance of pancreatic cancer cell to gemcitabine (Ireland et al., 2016). Of note, IGF2 is also released by cancer cells responding to monoclonal antibodies specific for insulin like growth factor 1 receptor (IGF1R) (J. S. Lee et al., 2015), a process that indirectly promotes resistance to treatment upon the recruitment of additional CAFs to the tumor bed, at least in colorectal cancer models (Unger et al., 2017).

CAF also contribute to the resistance of cancer cells to chemotherapy and immunotherapy owing to their ability to secrete ECM components and remodelers. Indeed, a stiff ECM provides malignant cells with a physical barrier against chemotherapeutics and tumor-infiltrating immune cells (see below) (Jacobetz et al., 2013; Miao et al., 2017; Olive et al., 2009; Provenzano et al., 2012; Whatcott et al., 2017). This situation is particularly pronounced in pancreatic tumors, which often display a dense stromal reaction commonly referred to a desmoplastic stroma (Neesse, Algul, Tuveson, & Gress, 2015). In line with the ability of the desmoplastic stroma to support chemoresistance, agents that favor ECM loosening, such as protein tyrosine kinase 2 (PTK2, best known as FAK) inhibitors or pegylated recombinant human hyaluronidase (PEGPH20, a hyaluronic acid-degrading enzyme), have been reported to improve gemcitabine uptake by pancreatic tumors and consequently favor therapeutic responses (Hingorani et al., 2016; Jacobetz et al., 2013; Liang et al., 2017; Provenzano et al., 2012; Whatcott et al., 2017). In this context high levels of intratumoral hyaluronic acid have been suggested to predict the ability of by PEGPH20 to sensitize patients with untreated metastatic pancreatic ductal adenocarcinoma to gemcitabine-based chemotherapy (Hingorani et al., 2018). That said, the desmoplastic stroma also constitutes a barrier against metastatic dissemination (Yamauchi et al., 2018), implying that therapeutic strategies targeting the ECM may ultimately favor distant recurrence. Interestingly, resistance to gemcitabine in pancreatic cancer also involves drug scavenging by stromal cells (Hessmann et al., 2018), as well as the release of transglutaminases by cancer cells, culminating with CAF-dependent ECM remodeling (J. Lee et al., 2016). Moreover, chemotherapy resistance in ovarian and colorectal cancers also arises from inefficient drug delivery due to tumor vasculature deregulation by CAFs (Leung et al., 2018), and to ECM remodeling supported by therapy-driven hypoxia (Rahbari et al., 2016), respectively. Furthermore, changes in the ECM have been linked to increased chemoresistance in cancer cells secondary to the activation of autophagy (Li et al., 2016; Liao et al., 2018) and inhibition of apoptosis via diverse mechanisms (Castells et al., 2013; Hirata et al., 2015; Muerkoster et al., 2008; Seip et al., 2016).

CAF undergoing senescence in response to DNA damage (as in the context of gemcitabine treatment) or cell cycle blockage acquire the so-called 'senescence-associated secretory phenotype' (SASP), which supports the growth of malignant cells and protects them from therapy (Galluzzi & Vitale, 2018; Guan et al., 2017; Toste et al., 2016). Along similar lines, senescent fibroblasts boost tumor inflammation to support disease recurrence and exacerbate the adverse effects of chemotherapy, as least in the breast cancer setting (Demaria et al., 2017). Mitogen-activated protein kinase 14 (MAPK14, best known as p38^{MAPK}) appears to mediate a key role in the acquisition of the SASP by CAFs (Alspach et al., 2014). SASP components that have been linked to chemoresistance in this setting include tumor necrosis factor (TNF) (Acharyya et al., 2012), IL6 (Karakasheva et al., 2018; Qiao et al., 2018; Xu et al., 2018), CXCL8 (J. S. Lee et al., 2015), CXCL13 (Ammirante et al., 2014), serine protease inhibitor Kazal type I (SPINK1) (F. Chen et al., 2018), and serpin family E member 1 (SERPINE1, best known as

PAI-1) (Che et al., 2018). In this setting, TNF favors the activation of the anti-apoptotic transcription factor NF- κ B coupled to the recruitment of immunosuppressive cells that favor chemoresistance in breast cancer (Acharyya et al., 2012), IL6 supports esophageal and ovarian cancer cell proliferation by promoting signal transducer and activator of transcription 3 (STAT3) activation (Karakasheva et al., 2018; Qiao et al., 2018; Xu et al., 2018), CXCL8 supports neo-angiogenesis and metastatic dissemination (J. S. Lee et al., 2015), while SERPINE1 inhibits the activation of apoptosis by treatment in esophageal squamous cell carcinoma as a consequence of AKT serine/threonine kinase 1 (AKT1) signaling (Che et al., 2018). Conversely, the pathways activated by CAF-derived CXCL13 and SPINK1 in cancer cells remain obscure. Similar to autophagy, senescence appears to be important also for CAF activation in the course of tumorigenesis, at least in part linked to the downregulation of recombination signal binding protein for immunoglobulin kappa J region (RBPJ, an effector of NOTCH signaling) and either TP53 (Menietti et al., 2016; Procopio et al., 2015) or the stress-responsive transcriptional modulator activating transcription factor 3 (ATF3) (D. E. Kim et al., 2017). Intriguingly, autophagy has been proposed not only to support cellular senescence in multiple settings (Dou et al., 2015; Galluzzi, Bravo-San Pedro, & Kroemer, 2016), but also to modulate RBPJ levels (Goruppi et al., 2018), which suggests the existence of an intimate connection between these two processes in stressed CAFs. Together with promising results from the use of senolytic agents for the treatment of age-associated disorders (Justice et al., 2019), these observations support senescence as potential therapeutic target for cancer therapy.

Additional factors produced by CAFs experiencing therapeutic stress in support of resistance to treatment include (1) Wnt family member 16 (WNT16) and secreted frizzled related protein 2 (SFRP2), two components of the WNT signaling machinery (Galluzzi, Spranger, Fuchs, & Lopez-Soto, 2019) that limit the sensitivity of cancer cells to genotoxic therapies *in vitro* and *in vivo* (Sun et al., 2012; Sun et al., 2016); (2) exosomes, which (by a hitherto unidentified mechanism) activate snail family transcriptional repressor 1 (SNAIL) in pancreatic cancer cells to increase their resistance to gemcitabine (Richards et al., 2017); (3) glutathione and cysteine, which not only can be taken up by prostate cancer cells to strengthen their defense against treatments causing oxidative stress (e.g., radiation therapy) (Cheteh et al., 2017), but also counteract the intracellular accumulation of specific chemotherapeutics (e.g., cisplatin) in lung and ovarian cancer cells (Galluzzi et al., 2013; Wang, Kryczek, et al., 2016).

Recent data suggest that a specific subset of CAFs (CD10⁺GPR77⁺) drives chemoresistance by specifically promoting the survival of CSCs, at least in the setting of breast cancer (S. Su et al., 2018). Potentially, this process relies on autophagy activation in CAFs, culminating with the release of the non-histone nuclear protein high mobility group box 1 (HMGB1) and consequent Toll-like receptor 4 (TLR4) activation in malignant cells (Zhao, Lin, et al., 2017). CAFs surviving conventional DNA-damaging chemotherapeutics, such as 5-fluorouracil (5-FU) and oxaliplatin, also promote the expansion of colorectal CSCs by releasing IL17A (Lotti et al., 2013) or exosomes (Y. Hu et al., 2015), a process that is exacerbated by hypoxia (as shown in preclinical and clinical settings) (Tang et al., 2018). Of note, differentiated malignant cells have been reported to indirectly stimulate stemness upon the induction of Hedgehog signaling in breast CAFs (Cazet et al., 2018). Whether this circuitry promotes resistance to treatment, however, is unclear. Beyond protecting stromal and malignant cells, CAF-secreted IGFs and SDF1 also drive tumor relapse upon radiotherapy by favoring bioenergetic and behavioral changes in cancer cells surviving treatment (Hirakawa et al., 2016; Tommelein et al., 2018; Wang, Gan, et al., 2017). Of note, in head and neck squamous cancers, tumor repopulation upon radiotherapy also depends on the activation of Hedgehog signaling in both stromal and cancer cells (Gan et al., 2014), pointing to a key role for CSCs in this setting. However, despite encouraging preliminary results (Olive et al., 2009), the abrogation of Hedgehog signaling by

Box 2

Strategies to reverse CAF activation

Over the past decade, along with the recognition that CAFs play a key role in tumor initiation, progression and resistance to treatment, great interest has been attracted by the possibility to deplete or inactivate CAFs as a means to sensitize malignant lesions to therapy (X. Chen & Song, 2019; Valkenburg et al., 2018). In this context, several strategies have been conceived to drive CAFs into quiescence and/or to limit their capacity to deposit ECM constituents. For instance, both these goals can be achieved by autophagy inhibitors, reflecting the key role of autophagy in CAF activation (Goruppi et al., 2017) as well as in the ability of CAFs to secrete ECM constituents (Endo et al., 2017). However, inhibition of autophagy has also been reported to exacerbate the tumor-supportive functions of CAFs, at least in some settings, by preventing the autophagic degradation of IL33 (Ding et al., 2018). CAF quiescence has also been achieved by perturbing the transcriptional reprogramming of CAFs with calcipotriol (a vitamin D analogue) or all-trans retinoic acid (ATRA), which was accompanied by restored tumor sensitivity to gemcitabine (Carapuca et al., 2016; Sherman et al., 2014), and diminished metastatic dissemination (Chronopoulos et al., 2016; Froeling et al., 2011). Similar results have been obtained with minnelide (a water soluble pro-drug of an active compound from a Chinese herb) in a model of pancreatic cancer, in which CAF quiescence is accompanied by decreased TGF β 1 signaling (Dauer et al., 2018). Likewise, preventing therapy-induced CAF activation with low-dose metronomic chemotherapy improved therapeutic efficacy in a preclinical model of breast cancer (T. S. Chan et al., 2016). CAFs are also particularly sensitive to BET inhibitors (which operate as epigenetic modifiers) (Clocchiatti et al., 2018), inhibitors of protein synthesis (limiting ECM deposition) (Duluc et al., 2015), and FAK inhibitors (also influencing ECM deposition) (Jiang et al., 2016; Santos, Jung, Aziz, Kissil, & Pure, 2009). All these interventions drive CAFs into quiescence as they mediate anticancer effects in a variety of preclinical tumor models (Duluc et al., 2015; Huang, Nahar, et al., 2016; Yamamoto et al., 2016). That said, CAFs have been shown to participate in tumor infiltration by CTLs (Kilvaer et al., 2018; Koeck et al., 2017). Moreover, CAF depletion strategies may mediate toxic effects, at least in some settings (Roberts et al., 2013; Tran et al., 2013). Thus, caution should be taken with the development of CAF-targeting strategies for translation to the clinics.

smoothed, frizzled class receptor (SMO) inhibitors accelerated tumor development and progression in mouse model of pancreatic cancer (J. J. Lee et al., 2014). Moreover, SMO inhibitors provided limited therapeutic benefits when combined with chemotherapy (in metastatic colorectal or pancreatic cancer patients) or used as maintenance agents (in patients with ovarian cancer) (Berlin et al., 2013; Catenacci et al., 2015; Kaye et al., 2012). This is in line with the role of stromal Hedgehog signaling in restraining rather than supporting oncogenesis (Rhim et al., 2014), limiting enthusiasm on the modulation of the Hedgehog network for anticancer purposes.

Taken together, these observations indicate that stromal cells not only are poorly sensitive to conventional and targeted anticancer therapies, but also respond to these agents by endowing cancer cells with treatment resistance, increased stemness, and superior potential for progression. Accordingly, several strategies to reverse CAF activation have been shown to mediate antineoplastic effects (Box 2).

1.3. Impact of stromal cells on anticancer immunity

It is now clear that oncogenesis, tumor progression and responses to (immuno)therapy are governed by an intimate crosstalk between malignant cells and non-malignant components of the TME (Jiang et al., 2017; Junttila & de Sauvage, 2013; Turley, Cremasco, & Astarita, 2015).

Stromal and immune cells engage themselves in a bidirectional interaction involving the release of soluble mediators as well as cell-to-cell physical interactions. Thus, pro-inflammatory cytokines released by tumor-infiltrating immune cells (e.g., TNF, IL1B) favor the recruitment of stromal cells to the developing tumors and their activation, as shown in a mouse model of squamous skin carcinogenesis (Erez, Truitt, Olson, Arron, & Hanahan, 2010). In turn, activated CAFs can further aggravate inflammation not only by contributing to TNF and IL1B release, but also by secreting a variety of chemokines that initially sustain the recruitment of immune cells to the tumor bed (e.g., CXCL2, IL6) (Erez et al., 2010; Erez, Glanz, Raz, Avivi, & Barshack, 2013). However, recruited immune cells are generally polarized towards an immunosuppressive phenotype that supports (rather than limits) tumor progression (Kato et al., 2018). Moreover, as CAFs deposit increasing amounts of ECM (Jiang et al., 2017; Klemm & Joyce, 2015), the resulting fibrotic stroma constitutes a physical and functional barrier to tumor infiltration by immune effectors cells (Carstens et al., 2017; Kaur et al., 2019), *de facto* limiting the efficacy of a variety of immunotherapeutic regimens (Elahi-Gedwillo, Carlson, Zettervall, & Provenzano, 2019; Hartmann et al., 2014; Jiang et al., 2016; Zhao et al., 2018).

The functional cooperation between CAFs and TAMs is a crucial determinant of tumor progression (Erez et al., 2010; Hashimoto et al., 2016). Stromal cells promote the recruitment of TAMs to the TME and their polarization toward an anti-inflammatory, tumor-supportive phenotype (so-called 'M2') not only by secreting chemoattractants for circulating monocytes such as IL6, SDF1, colony stimulating factor 1 (CSF1), and chitinase 3 like 1 (CHI3L1) (Cho et al., 2018; Cohen et al., 2017; Comito et al., 2014; Jia et al., 2016; Zhang et al., 2017) but also by promoting ECM remodeling (Mazur, Holthoff, Vadali, Kelly, & Post, 2016). Activated CAFs also limit the ability of colony stimulating factor 1 receptor (CSF1R) inhibitors to deplete M2 TAMs or repolarize them toward an immunostimulatory, anticancer phenotype (so-called 'M1') by driving granulocytic infiltration of the tumor bed, as shown in murine models of lung cancer and biopsies from non-small cell lung carcinoma patients (Kumar et al., 2017). Stromal cells and their progenitors also recruit myeloid-derived suppressor cells (MDSCs, an immature population of bone marrow-derived myeloid cells that exerts potent immunosuppressive effects) (Allaoui et al., 2016; Mace et al., 2013; Ren et al., 2012; Yang, Lin, et al., 2016; Yen et al., 2013), CD4⁺CD25⁺FOXP3⁺ regulatory T cells (a lymphoid cell population that also exerts potent immunosuppression) (Givel et al., 2018; Kato et al., 2018; Rashedi, Gomez-Aristizabal, Wang, Viswanathan, & Keating, 2017), and can polarize helper T cell responses toward a T_H2 profile, which supports (rather than limits) tumor progression (De Monte et al., 2011).

Immunosuppression by stromal cells also involves the inhibition of multiple effectors of the anticancer immune response (Galluzzi, Chan et al., 2018). For instance, CAFs limit the ability of natural killer (NK) cells to mediate anticancer effects by inhibiting the expression of the NK cell-activatory receptor killer cell lectin like receptor K1 (KLRK1, best known as NKG2D) (Lopez-Soto, Gonzalez, Smyth, & Galluzzi, 2017) on their surface and/or expression of its cognate ligands on the surface of malignant cells (Costa, Vene, et al., 2018; Ziani et al., 2017). Along similar lines, stromal cells can inhibit the activity of CD8⁺ cytotoxic T lymphocytes (CTLs) by secreting immunosuppressive cytokines (e.g., IL10, TGFB1, SDF1) and metabolites (*i.e.*, adenosine) (de Lourdes Mora-Garcia et al., 2016; Feig et al., 2013; Garcia-Rocha et al., 2015; B. Garg et al., 2018; Kerkela et al., 2016; Saldanha-Araujo et al., 2011). The metabolic rewiring of activated CAFs is indeed especially relevant for their ability to quench tumor-targeting CTL-driven immune responses. In particular, stromal cells overconsume glucose, arginine and

Fibroblasts		CAFs
Mesoderm	Origin	Diverse
High	Genetic stability	High
High	Epigenetic stability	Low
Silent	Metabolic profile	Plastic
Low	Autophagic flux	High
Low	Motility	High
Low	Proliferation	High
Inactive	Status	Active

Fig. 2. Side-by-side comparison of CAFs and normal fibroblasts. As compared to their normal counterparts (which derive from the mesoderm), cancer-associated fibroblasts (CAFs, which originate from diverse tissues), exhibit increased epigenetic instability, a plastic metabolic profile generally coupled with increased autophagic proficiency, elevated motility and superior proliferative rates. Such an activated status render CAFs highly resistant to both metabolic and therapeutic challenges.

tryptophan, all of which are required for the optimal expansion of CTLs to mediate robust effectors functions (Bantug et al., 2018; Chang et al., 2015), as a consequence of intense glycolytic metabolism as well as of the elevated expression of indoleamine 2,3-dioxygenase 1 (IDO1) and arginase 1 (ARG1) (J. Y. Chen et al., 2014; Ino et al., 2013; J. Su et al., 2014; Takahashi et al., 2017). Besides depleting CTLs of essential nutrients, this metabolic profile results in the synthesis of actively immunosuppressive molecules including lactate (Comito et al., 2019) and kynurenine (a product of tryptophan metabolism) (Chen et al., 2014; Hsu et al., 2016; Kadle et al., 2018). Moreover, CAFs can inhibit CTL proliferation by secreting nitric oxide (Cremasco et al., 2018) and prostaglandin E₂ (Kobayashi, Omori, & Murata, 2018), and directly delete potentially tumor-reacting CTLs by presenting tumor antigens in the context of death signals (Lakins, Ghorani, Munir, Martins, & Shields, 2018). Finally, CAFs not only express high levels of the co-inhibitory ligands CD274 (best known as PD-L1) and programmed cell death 1 ligand 2 (PDCD1LG2, best known as PD-L2) (Chinnadurai, Copland, Patel, & Galipeau, 2014; Davies, Heldring, Kadri, & Le Blanc, 2017; Ebine et al., 2018; Miyoshi et al., 2016; Yang, Liu, et al., 2017), especially in response to therapeutic challenges (Yang, Liu, et al., 2017), but also favor the recruitment of PD-L1-expressing granulocytes to the tumor bed by secreting IL6 (Cheng et al., 2018).

Taken together, these observations exemplify the multipronged immunosuppressive functions of stromal cells. Accordingly, most (if not all) therapeutic strategies based on stromal cell suppression or inactivation (Box 2) reinstate the ability of the host immune system to mediate antineoplastic effects and sensitize tumors to immunotherapy with immune checkpoint blockers (Feig et al., 2013; Mace et al., 2018; Steele et al., 2016; Wang et al., 2014).

2. Concluding remarks

Accumulating preclinical evidence indicates that stromal cells populating the TME are considerably different from their normal counterparts (Fig. 2) and particularly resistant to a variety of environmental perturbations, reflecting not only their ability to mount robust responses to stress, but also their elevated phenotypic, metabolic and behavioral plasticity. Importantly, such an intrinsic resistance also favors the survival and adaptation of malignant cells, via metabolic, trophic and immunological circuitries. Thus, stromal cells most often support oncogenesis, tumor progression and resistance to treatment, *de facto* standing out as promising targets for the development of novel anticancer regimens. That said, none of the strategies employed so far to delete or inactivate CAFs has progressed into clinical drug development (Chen & Song, 2019). Although many reasons can be invoked to explain such a deceit, we surmise that the elevated

heterogeneity and plasticity of the stromal compartment of most solid tumors constitute major obstacles against the development of clinically useful stroma-targeting agents. In this context, elucidating the precise molecular mechanisms that underlie the ability of CAFs and TA-MSCs to cope with stress and elude RCD may identify potentially actionable therapeutic targets. Alongside, it will be important to deconvolute the paracrine circuitries that regulate the interaction between stromal cells and other cellular compartments of the TME, and to explore the relevance of precise CAF subpopulations (e.g., PDPN⁺ CAFs, CD10⁺GPR77⁺ CAFs or so-called 'CAFs-S1') (Cesta, Kieffer, et al., 2018; Su et al., 2018; Yoshida et al., 2015). Clarifying these aspects of the CAF immunobiology may not only open novel avenues of investigation but also identify previously unexplored CAF-targeting therapeutic strategies.

Disclosures

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Author contributions

IV and LG conceived the article, prepared the first version of the manuscript and addressed comments from reviewers. GM and CG performed bibliographical searches in support of manuscript preparation. GM prepared display items with inputs and revisions from IV and LG. All authors approved the final version of the article.

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