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# Metabolic pathways fuelling protumourigenic cancerassociated fibroblast functions

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#### **Abstract**

Cancer-associated fibroblasts (CAFs) play many roles in supporting tumour growth and progression, and metabolic rewiring is known to be a hallmark of CAF activation. How to effectively target CAF metabolism is still an open question, however. Recent research shows that CAFs and cancer cells engage in complex metabolic crosstalk, which may offer strategies to metabolically target both tumour and stroma. CAF metabolic rewiring also regulates intrinsic CAF protumourigenic functions, by inducing epigenetic changes to maintain CAF activation and by promoting hallmarks of CAFs such as extracellular matrix (ECM) production and immunosuppression. Finally, the emerging field of CAF subpopulations has opened up possibilities for metabolically targeting specific protumourigenic subgroups and raises new questions about how we define and target CAFs.

#### Addresses

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## Keywords

CAF, Metabolism, Cancer, Epigenetics, Crosstalk signalling, CAF sub-populations, Extracellular matrix, Tumour microenvironment.

#### Introduction

Cancer-associated fibroblasts (CAFs) are one of the most abundant cell types of the tumour microenvironment (TME) and are known to play a key role in all stages of tumour progression, displaying both tumour-promoting and tumour-restraining properties (reviewed in studies reported by Kalluri, Santi et al. and Sahai et al.

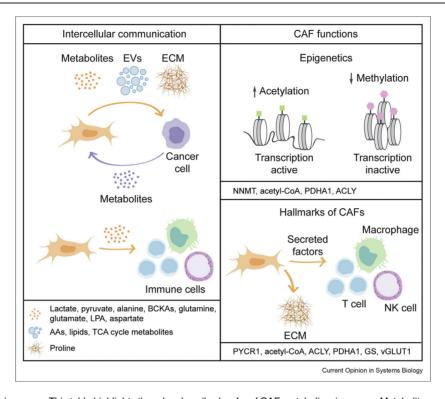
[1-3]). As the importance of metabolic rewiring in tumour cells has become increasingly clear in recent years, in parallel, metabolic rewiring of CAFs has been shown to be both intertwined with that of tumour cells and to be a vital aspect of the protumourigenic CAF phenotype. Activated CAFs vastly increase production of many proteins that influence both tumour cells and other cells of the TME, including growth factors, cytokines, extracellular matrix components and proangiogenic factors. This review will discuss recent evidence that CAFs further influence the TME through increased secretion of metabolites and that CAFs also rewire their metabolism to support their protumourigenic functions (see Figures 1 and 2). We also give perspectives on the future of the field and how new technologies can enhance our understanding of CAF metabolism in the context of the tumour.

# Cancer-associated fibroblast/cancer cell metabolic crosstalk

In the past decade, studies have shown that CAFs secrete metabolites which are taken up by tumour cells and used to support tumour progression. Initially, research focussed on the role of increased glycolysis and autophagy in CAFs, providing lactate, amino acids and ketone bodies to support tumour growth [4–7]. These studies provided initial evidence of metabolic crosstalk between CAFs and cancer cells and opened up the field of CAF metabolism for further investigation.

Increased lactate production owing to upregulation of glycolysis in CAFs is well-established; however, glycolysis-derived pyruvate is also emerging as a key protumourigenic metabolite. CAFs may be a major source of pyruvate in the TME. Pyruvate was secreted at high levels by CAFs derived from patients with breast cancer [8] and was also highly abundant in pancreatic ductal adenocarcinoma (PDAC) CAF-conditioned media [9]. Extracellular pyruvate maintained redox homoeostasis and enabled resistance to mitochondrial inhibitors in PDAC cells [9]. Pyruvate secreted by CAFs also promoted lymphoma cell survival [10], and extracellular pyruvate supported extracellular matrix (ECM) remodelling by metastatic breast cancer cells [11]. Therefore, CAF-secreted pyruvate has emerged as a key metabolite influencing several aspects of tumour progression.

Figure 1



Roles of CAF metabolism in cancer. This table highlights the roles described so far of CAF metabolism in cancer. Metabolites can be transferred to cancer cells and potentially (not yet shown) immune cells through their secretome, extracellular vesicles (EVs) and extracellular matrix proteins. CAF metabolism also controls intrinsic CAF functions via epigenetic regulation of histone modifications, regulation of signalling pathways and providing amino acids for extracellular matrix (ECM) production. After each section, there is a list of metabolites and enzymes that have been shown to contribute to the mechanisms represented in the drawing above. CAF, cancer-associated fibroblast.

Lipids have also emerged as protumourigenic CAFsecreted metabolites. Patient-derived CAFs from breast and colorectal cancers had increased fatty acid synthase (FASN) expression and produced more lipids, which were taken up by tumour cells and enhanced proliferation and metastasis [12,13]. CAF-derived lipids may be particularly relevant in pancreatic cancer in which CAFs are activated from resident pancreatic stellate cells (PSCs). Quiescent PSCs are rich in lipid droplets, but on activation, these are released. Auciello et al. [14] demonstrated that these lipids act as signalling molecules and fuel biomass production in pancreatic cancer cells and further discovered that PSCs are a major source of lysophosphatidic acid, activating phosphoinositide 3-kinase/RAC serine/threonine-protein kinase (PI3K/Akt) signalling in cancer cells.

Recent research has also highlighted the complexity of tumour cell-CAF crosstalk in rewiring CAF metabolism. The role of transforming growth factor beta (TGF-β) signalling and oxidative stress in stimulating glycolysis and autophagy in CAFs is well-documented [5,15]; however, it is becoming clear that cancer cells regulate CAF metabolism via a wide variety of mechanisms. TGF-β signalling was further shown to promote

production and secretion of branched-chain keto acids in PDAC patient-derived CAFs via increased branchedchain-amino-acid aminotransferase (BCAT1) expression. Branched-chain keto acids were then used by tumour cells as a source of carbon and nitrogen [16]. Extracellular vesicles secreted by tumour cells are also known to mediate CAF-cancer cell crosstalk. Breast cancer-derived exosomes were shown to activate protooncogene protein MYC signalling in fibroblasts and increase both glucose and glutamine metabolism [17]. Equally, CAF-derived exosomes can be a source of metabolites to support cancer cell growth [18]. CAFs also depend on tumour cell-derived metabolites to support their metabolic needs, and increased glycolysis in CAFs can be stimulated by tumour cell-derived glycogen [19], or lysophosphatidic acid [20]. Furthermore, supporting the complexity of CAF/cancer cell metabolism is a study in ovarian cancer, which found that CAFs upregulate glutamine production and secretion [21]. Conversely, cancer cells secreted glutamate that was used by CAFs, creating a cycle that supports both CAFs and cancer cells. Inhibiting both glutamine and glutamate production reduced tumour growth in vivo, providing a good example of how cotargeting CAF and cancer cell metabolism can treat tumours more effectively.

CAF metabolism is also regulated by other factors in the TME. The ECM is produced mostly by CAFs, but both CAFs and cancer cells influence ECM remodelling, crosslinking and stiffness. CAFs upregulated both glycolysis and oxidative phosphorylation on stiffer matrices. In addition, stiffer matrices induced a feedback loop between CAFs and cancer cells in which CAFs secreted aspartate that was taken up by cancer cells, and cancer cells secreted glutamate that was used by CAFs. This metabolic loop promoted tumour growth and invasion, and, crucially, could be disrupted by inhibiting glutaminase (GLS1) in both CAFs and cancer cells, giving the possibility to simultaneously target tumour and stroma [22]. Nutrient deprivation is also a common feature of the TME, and prostate cancer-derived CAFs were shown to support tumours under glutamine deprivation by upregulation of the pyruvate carboxylaseasparagine synthase cascade via p62 downregulation and cyclic AMP-dependent transcription factor ATF4. Stromal asparagine was used as a replacement nitrogen source by both CAFs and cancer cells [23]. Therefore, CAF metabolic rewiring can be stimulated through a combination of tumour cell-derived growth factors, metabolites and vesicles, as well as stressed such as nutrient deprivation, reactive oxygen species (ROS) and ECM stiffness. Feedback loops in which cancer cells and CAFs metabolically support each other may provide ways to simultaneously target CAFs and cancer cells.

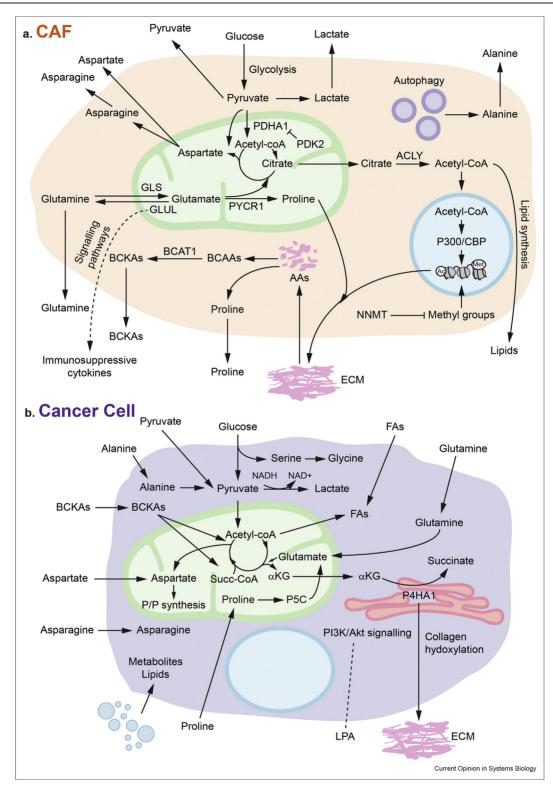
# Metabolism supports epigenetic changes and cancer-associated fibroblast hallmarks

Metabolic rewiring in CAFs can support other aspects of tumour development and the TME aside from providing nutrients to tumour cells. First, CAFs also rewire their metabolism to support their own phenotypic changes on activation. CAFs need to alter their epigenetic profile to maintain expression of genes involved in their protumourigenic phenotype. Nicotinamide N-methyltransferase (NNMT), which catalyses transfer of a methyl group from S-adenosyl methionine to nicotinamide, is upregulated in the stroma of ovarian, colorectal and gastric cancers [24–26] and associated with poor prognosis. NNMT reduced histone methylation in ovarian CAFs, and this led to widespread alterations in gene expression, including expression of CAF markers, tumour-promoting cytokines and ECM components [24]. Hypomethylation of promoters of glycolytic genes has also been observed in breast CAFs subjected to hypoxia [8]. Hypoxic signalling via hypoxia-inducible factor 1-alpha (HIF1-α) has previously been shown to induce a more glycolytic and autophagic CAF phenotype, supporting tumour cell metabolism via secretion of lactate and other metabolites [15,27]. Interestingly, the methylation pattern remained even when oxygen levels were restored, suggesting that stimuli in the TME can support an epigenetic shift in CAFs enables them that to maintain

protumourigenic phenotype even when those factors are removed. Decreased histone methylation often occurs with a corresponding increase in acetylation, and a study showed that breast CAFs have overall increased histone acetylation compared with normal fibroblasts (Kay et al., BioRxiv, doi: 10.1101/2020.05.30.125237). Histone acetvlation is supported by the metabolite acetyl-CoA, and the study further uncovered that CAFs upregulate acetyl-CoA production through pyruvate dehydrogenase (PDH) activation and that this supports histone acetylation and expression of collagens. Overall, research points to CAFs metabolically inducing an epigenetic shift towards transcription activation, consistent with their increased output of growth factors, ECM components and proinflammatory cytokines.

In addition to epigenetic rewiring, CAF metabolism can support further hallmarks of their activated phenotype. Collagen makes up a large proportion of the stromal ECM (role of the ECM in cancer reviewed in studies reported by Cox, Kai et al and Winkler et al. [28–30]). Collagen itself is also a means of metabolic crosstalk between CAFs and cancer cells because PDAC cancer cells can take up and degrade collagen as a source of amino acids, and especially a source of proline [31]. Collagen proteins contain unusually high levels of both glycine and proline, and therefore, their translation places unique metabolic pressures on CAFs to produce these amino acids. CAFs from patients with breast cancer upregulated proline production via pyrroline-5carboxylate reductase 1 (PYCR1), which was necessary to support collagen production. Stromal PYCR1 knockdown additionally reduced tumour growth and metastasis in vivo (Kay et al., BioRxiv, doi: 10.1101/ 2020.05.30.125237). Upregulated production of both proline and glycine to support collagen production was also observed in TGF-β-activated lung fibroblasts [32,33]. Immunosuppression is another hallmark of CAF activation. Netrin G1 (NetG1)+ CAFs from PDAC were shown to upregulate glutamine and glutamate synthesis, which were taken up and used as fuel by cancer cells. Interestingly, NetG1 also promoted immunosuppressive cytokine production by CAFs. Clustered regularly interspaced short palindromic repeats (CRISPR)-mediated knockout of either NetG1, glutamine synthetase (GS) or vesicular glutamate transporter 1 (VGlut1) reduced cytokine production and enabled natural killet (NK) cell-induced death of PDAC cells [34]. Although the role of CAF-secreted lactate is well-established as a fuel for tumour cells, lactate is also an immunosuppressive metabolite. Lactate promotes protumourigenic M2 macrophage polarisation, inhibits NK cell activity and reduces T cell infiltration in tumours [35–37]. Therefore, targeting CAF metabolism can not only affect cancer cells but also regulate other aspects of the TME that impacts tumour progression.

Figure 2



Metabolic crosstalk between CAF sand other tumour cells. (a). Summary of the pathways and metabolites regulating the communication between CAFs and other cell types and support hallmarks of CAFs. (b). Summary of the pathways and metabolites regulated by CAFs in the cancer cells. CAF, cancer-associated fibroblast.

# Cancer-associated fibroblast plasticity and subpopulations

A further layer of complexity to the CAF metabolic phenotype is the discovery of different CAF subpopulations, which have varied roles in the TME. The most commonly characterised subpopulations are the myofibroblastic CAFs (myofibroblastic, contractile, ECM producing) and the inflammatory CAFs, (inflammatory, cytokine-producing). These were first identified in PDAC, but similar populations have subsequently been found in other solid tumours including breast, ovarian and lung [38-40]. Further research has uncovered multiple subpopulations, including the antigenpresenting CAFs in PDAC [41] and up to eight populations in breast cancer [40]. As yet, little research has been performed into the metabolic phenotypes of these CAFs. Interestingly, expression of genes in the proline synthesis pathway is upregulated in myofibroblastic CAFs more than inflammatory CAFs, which supports proline availability being important for CAF ECM production (Kav et al., BioRxiv. doi: 2020.05.30.125237). This suggests that the metabolic status of CAF subpopulations can support their function. In PDAC, a novel CAF subpopulation with a highly active metabolic state (MeCAF) has recently been described [42]. MeCAF abundance correlated with poorer prognosis but better response to immunotherapy, suggesting that the metabolism of CAF subpopulations could be used to inform on therapeutic strategy. In addition, different subpopulations may be more or less prevalent in different types of tumours, as has already been shown in subtypes of breast cancer [43]. CAF metabolism, as determined by levels of glycolysis and oxidative phosphorylation (OXPHOS), has also been shown to differ between different breast cancer subtypes, and it will be interesting to determine whether this mirrors the presence of different CAF subpopulations [44]. The discovery of CAF subpopulations raises the question of whether it is possible to metabolically target specific subpopulations, and if so, which subpopulation(s) would have the most impact. In addition, CAF subpopulations appear to be plastic and able to differentiate between different subtypes depending on their position in the tumour and other context-dependent stimuli such as cytokine levels [38,40,45]. It seems likely that CAFs do not exist as clearly defined subgroups but instead exist across a spectrum of phenotypes. Given that the CAF phenotype can be regulated metabolically at the epigenetic level, it will be interesting to uncover whether targeting CAF metabolism can induce CAFs to differentiate between different subpopulations.

#### **Future directions**

Our understanding of the metabolic changes in CAFs and how this impacts tumour progression has expanded rapidly in recent years. However, there are still many questions to be addressed. It is becoming clear that the metabolic phenotypes of CAFs, cancer cells and other cells in the TME are closely intertwined and just as cancer cells depend on CAFs for nutritional support, so do CAFs rely on metabolites and factors produced by cancer cells to support their metabolism. Therefore, the most effective metabolic targets to target the tumour as a whole organ rather than focussing on only the tumour cells or cells of the TME are yet to be determined. Pathways such as proline or glutamine metabolism, which are upregulated in both CAFs and cancer cells and have protumourigenic functions in both, may be an efficient method of targeting several aspects of the TME. Alternatively, it may be necessary to target more than one pathway to disrupt metabolic crosstalk loops between CAFs and cancer cells. There are several emerging methods to further investigate metabolic crosstalk between CAFs and cancer cells in in vivo and in vitro systems. For example, tracing labelled metabolites into stable molecules such as proteins can eliminate the problems of rapid metabolite transfer between cell types and metabolite loss during cell sorting from tumours or three-dimensional coculture systems [46]. The recently developed flow cytometry-based method SCENITH (single-cell energetic metabolism by profiling translation inhibition) enables a seahorse-like analysis of mixed cell populations by inferring respiration, glycolysis and fatty acid oxidation (FAO) rates from changes in protein translation [47]. The growing field of mass spectrometry-based imaging, which enables spatial visualisation of metabolites and proteins within tissue sections [48], will also enable further investigation of the metabolic states of CAFs and cancer cells in the TME context.

The tools described previously can also be applied to uncover metabolic variations between CAF subpopulations. Recent and ongoing work into fibroblast heterogeneity and plasticity has opened up the possibility of targeting different subpopulations of CAFs within the TME, and it will be important to also distinguish the different metabolic phenotypes of these CAFs to determine the best therapeutic strategies for targeting cancer metabolism. Alpha smooth muscle actin (αSMA)-positive CAFs have previously been the main focus for targeting the stroma, but the emerging field of CAF subpopulations may uncover new definitions and markers for CAFs, and it remains to be determined whether CAF metabolic heterogeneity will play a role in this. Furthermore, it is becoming clear that CAFs can have both protumourigenic and antitumourigenic properties, particularly in PDAC in which stromal depletion enables tumour expansion [49,50]. Therefore, a good strategy to target CAFs may be to promote differentiation to a less tumour-promoting 'subpopulation', and targeting CAF metabolism could be a means to do this, potentially through metabolically altering the epigenetic profile of CAFs.

#### Conflict of interest statement

Nothing declared.

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