

Reprogramming of tumor-associated macrophages by metabolites generated from tumor microenvironment

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ABSTRACT

The tumor microenvironment comprises both tumor and non-tumor stromal cells, including tumor-associated macrophages (TAMs), endothelial cells, and carcinoma-associated fibroblasts. TAMs, major components of non-tumor stromal cells, play a crucial role in creating an immunosuppressive environment by releasing cytokines, chemokines, growth factors, and immune checkpoint proteins that inhibit T cell activity. During tumors develop, cancer cells release various mediators, including chemokines and metabolites, that recruit monocytes to infiltrate tumor tissues and subsequently induce an M2-like phenotype and tumor-promoting properties. Metabolites are often overlooked as metabolic waste or detoxification products but may contribute to TAM polarization. Furthermore, macrophages display a high degree of plasticity among immune cells in the tumor microenvironment, enabling them to either inhibit or facilitate cancer progression. Therefore, TAM-targeting has emerged as a promising strategy in tumor immunotherapy. This review provides an overview of multiple representative metabolites involved in TAM phenotypes, focusing on their role in pro-tumoral polarization of M2.

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Introduction

Cancer, a leading cause of death worldwide, is not simply a genetic disease. The tumor microenvironment (TME), encompassing both cellular and acellular components, plays an important role in tumor initiation, growth, invasion, metastasis, and resistance to treatment. According to the classical theory, oncogenic mutations in malignant cells initiate cancer. This is accompanied by the release of various intercellular communicators, including cytokines, chemokines, and vesicles, which recruit and adapt to surrounding non-transformed cells, resulting in TME formation and close interaction with cancer cells (Balkwill et al. 2012). Chronic inflammation or wound-healing processes in an abnormal microenvironment can also trigger oncogenic signals and drive tumor development (Mantovani et al. 2008; Capp 2017; Deng et al. 2019; Todorovic and Karin 2019).

Recently, immunotherapy encompassing checkpoint inhibitors (Pardoll 2012; Abril-Rodriguez and Ribas 2017) and adoptive cell therapy (D'Aloia et al. 2018; June and Sadelain 2018) has shown promise in cancer treatment, demonstrating durable clinical responses

(Sharma P et al. 2011). Nevertheless, in most cancer types, some patients are either unresponsive or resistant to therapy (Bagley and O'Rourke 2020; Meric-Bernstam et al. 2021). Investigations into tumor-induced immunosuppressive mechanisms to overcome immunotherapeutic resistance have identified multiple suppressor cell populations within the TME. Notably, tumor-associated macrophages (TAMs) account for a major component of immune cell types in the TME. Plasticity is a hallmark of macrophages, allowing them to respond to environmental cues by exhibiting different forms of polarization, including the pro-inflammatory M1 and the anti-inflammatory M2 phenotypes (Zhou et al. 2014; Locati et al. 2020). M1 macrophages have tumor-killing properties, whereas M2 macrophages have anti-inflammatory properties that may indirectly promote tumor growth (Aras and Zaidi 2017). Therefore, TAMs have been proposed as novel emerging targets for immunomodulatory therapies in cancers (Cassetta and Kitamura 2018; Zhang M et al. 2018).

Despite the generation of diverse types of metabolites in the TME through metabolic pathways and

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their profound influence on the tumor developmental process, the metabolites have been considered as mere metabolic waste or detoxification products and thus overlooked. However, recent evidence has revealed new and important oncogenic roles of metabolites within malignant tumors (Huang S et al. 2021; Martinez-Reyes and Chandel 2021).

TME composition

The TME is a crucial factor in augmenting the efficiency of cancer therapy. The vigorous interaction of cancer cells with the cellular and non-cellular components of TME promotes progression and metastasis, increasing resistance to anticancer therapy. Cancer cells are surrounded by fibroblasts, endothelial cells, pericytes, and immune cells, such as T and B cells, macrophages, neutrophils, and dendritic cells, critically involved in the promotion or suppression of tumor growth. Paracrine signaling mediates intercellular communication by secreting chemokines, cytokines, and growth factors within the TME.

The highly complex and heterogeneous TME, formed by the recruitment of non-cancerous host cells and remodeling of the vasculature and extracellular matrix (ECM), including collagen, hyaluronan, laminin, and fibronectin, is regulated by cancer cells (Jahanban-Esfahlan et al. 2017; Jahanban-Esfahlan et al. 2018; Lee TW and Lee 2022). Critical networks for intercellular communication in the TME encompass various cell-to-cell interactions, including paracrine signaling, through the production of cytokines, growth factors, and chemokines (Shi et al. 2019; Song et al. 2020; Jin Y et al. 2023). Adhesion molecules, such as integrins, selectins, and cadherins, regulate tumor growth and suppression through signal transduction by promoting cell-to-cell interactions and cell-ECM adhesion (Kechagia et al. 2019; Yeini et al. 2021; Hwang et al. 2023). The ECM plays a pivotal role in the storage of secreted molecules, promoting adhesion and migration and activating intercellular communication. The interaction between cancer cells and the ECM establishes a dynamic reciprocity between neoplastic cells and the tumor stroma within the TME (Gonzalez-Avila et al. 2020; Li et al. 2020).

Exosomes originating from different cancer cells communicate with non-cancerous host cells, including immune cells, endothelial cells, and cancer-associated fibroblasts, thereby promoting tumor invasion (Huang XY et al. 2020), migration (Chen C et al. 2023), and immune escape (Liu J et al. 2020). Exosomal secretion of long non-coding RNAs from cancer cells influences various biological processes, such as metastasis (Yao et al. 2022) and tumor growth (Ni et al. 2023). Extracellular vesicles contain different molecules, including RNA,

DNA, metabolites, and proteins, which act as bioactive cargoes that affect target cells and mediate intercellular communication (Dong et al. 2023; Serrati et al. 2023; Uemura et al. 2023; Zhang Y et al. 2023).

Metabolic reprogramming of cancer cells is a hallmark of malignancy. It allows cancer cells to adapt to hypoxic and nutrient-poor environments and alters their metabolism to maintain growth and proliferation (Ward and Thompson 2012; Bhagat et al. 2019; Watson et al. 2021; Jin HR et al. 2023). Tumor cells influence the metabolic environment within the TME by consuming nutrients and producing metabolites (Elia and Haigis 2021). These metabolites regulate transcriptional responses and modulate the expression of target genes via transactivation or transrepression domains (Angelin et al. 2017; Feng et al. 2017; Kuang et al. 2017; Walton et al. 2018). Furthermore, the metabolic reprogramming of tumor-infiltrating cells leads to differentiation and acquisition of effector functions (Stone et al. 2019; Wang H et al. 2020; Han et al. 2023; Wang Z et al. 2023).

TAM

Macrophages, the main components of immune infiltrates, can efficiently infiltrate tumors and are abundant within the TME (Lee H et al. 2022; Cassetta and Pollard 2023). Concurrent with the growing understanding of TAM function, its clinical significance in solid tumors is widely being studied. Elevated TAM infiltration correlates with advanced tumor stages, as observed in esophageal (Li et al. 2019), ovarian (Yuan et al. 2017), breast (Qiu et al. 2018), and pancreatic cancers (Di Caro et al. 2016). In addition, higher TAM densities are related to poor patient outcomes (Qian and Pollard 2010; Medrek et al. 2012; Wang XL et al. 2016; Wu P et al. 2016; Kitano et al. 2018; Li et al. 2019; Wang C et al. 2022) owing to their facilitation of tumor growth, invasion, metastasis, angiogenesis, and drug resistance (Mantovani 1978; De Palma and Lewis 2013; Cassetta and Pollard 2018). Initially, the tissue-resident macrophages were thought to be derived from blood monocytes (Volkman and Gowans 1965); however, it is now known that they arise either from circulating monocytes or from primitive macrophages originating in the embryonic yolk sac and fetal liver (Ginhoux and Guilliams 2016). Therefore, TAMs can be derived from both the infiltration of tumors by circulating monocytes and tissue-resident macrophages from the surrounding tissues (Loyher et al. 2018; Laviron et al. 2022).

As mentioned earlier, activated macrophages are frequently classified into two phenotypes depending on their polarization: pro-inflammatory M1 and anti-inflammatory M2 (Mills et al. 2000; Mantovani et al. 2002). M2

macrophages can be further subdivided into four subtypes based on changes in their microenvironment and stimuli: M2a, M2b, M2c, and M2d (Roszer 2015). Among these subtypes, M2d macrophages (sometimes called TAMs) are involved in angiogenesis and tumor progression, induced by adenosine A2 receptors and leukemia inhibitory factor (an IL-6 cytokine). They also contribute to the secretion of vascular endothelial growth factor (VEGF), IL-10, and TGF- β (Roszer 2015). In general, M1 macrophages promote inflammatory responses against invading pathogens and inhibit tumor progression, while M2 macrophages exert an immunosuppressive phenotype that favors tissue repair and tumor progression (Bingle et al. 2002; Lewis and Pollard 2006; Zaynagetdinov et al. 2011; Seth et al. 2017). Thus, it is reasonable to assume that most pro-tumoral TAMs are M2-like macrophages, and their reprogramming into M1-like macrophages is a promising therapeutic approach for cancer treatment (Zhang J, Zhou, et al. 2022). However, cancer-associated inflammation induced by M1-like macrophages triggers heightened inflammation, continuous cell proliferation, angiogenesis, and the survival of damaged or transformed cells, resulting in neovascularization and rapid tumor expansion (Coussens and Werb 2002). Moreover, M1-like TAMs have been found to increase tumor cell mobility and facilitate cancer metastasis (Wang H et al. 2014; Xiao et al. 2018).

TAM polarization

Although M1-like and M2-like classifications in TAM studies are predominant (Mantovani et al. 2002; Mantovani et al. 2013), it is important to consider that macrophage polarization only refers to the state of macrophage activation at a particular time-point. Moreover, because of plasticity, the polarization state of macrophages is not fixed and can change based on the integration of multiple signals from the TME (Bardi et al. 2018; Boutilier and Elsawa 2021; Laroni et al. 2022).

TAM polarization is regulated by cytokines, chemokines, growth factors, and other signals derived from the TME (Qian and Pollard 2010). M1-like TAMs are activated by IFN- γ , TNF- α , and GM-CSF. They express CD68, CD80, and CD86 and secrete cytokines including IL-1 β , IL-6, IL-12, IL-23, CXCL9, and CXCL10. In contrast, M2-like TAMs are stimulated by CSF-1, C-C motif ligand 2 (CCL2), IL-10, or TGF- β . They express CD163, CD204, CD206, and stabilin-1, and secrete IL-10, IL-12, TGF- β , CCL17, CCL18, CCL22, and CCL24 (Lewis and Pollard 2006; Algars et al. 2012; Biswas et al. 2013; Ruffell and Coussens 2015; Koelzer et al. 2016; Jeannin et al. 2018).

Recently, TAM markers that are not defined by conventional M1 and M2 polarization but are associated

with prognostic factors have been reported. For instance, the CXCL9:SPP1 ratio in TAMs of patients with head and neck squamous cell carcinoma is strongly associated with prognosis (Bill et al. 2023). Additionally, CCL8 and SIGLEC1 expressing TAMs in breast cancer indicate shorter disease-specific survival (Cassetta et al. 2019).

The two most well-documented factors among these are CSF-1 and CCL2, which act as macrophage recruiters and M2 stimulators (Mantovani and Sica 2010; Xu R et al. 2019), (Poh and Ernst 2018). The main factor influencing M2 macrophage polarization is the interaction of chemokine/cytokine receptors with their ligands present within the TME, leading to the activation of several signaling pathways, including the PI3 K/AKT, JAK/STAT6, STAT3, and TGF- β /SMAD-dependent pathways (Gao et al. 2022; Kerneur et al. 2022).

Epigenetic alterations are universal features of all human cancers and are now known to interact with genetic alterations to influence cancer phenotypes (Sharma S et al. 2010; Baylin and Jones 2016). Epigenetic regulators reshape chromatin structures, pack the genome, and alter gene expression patterns without altering the DNA code. These alterations involve DNA methylation, post-translational modifications of histone proteins, chromatin remodeling, non-coding RNAs, and other chromatin components (Baylin and Jones 2016; Cheng et al. 2019). Because epigenetic modifications play a significant role in macrophage polarization (Hoeksema and de Winther 2016; Kapellos and Iqbal 2016), pharmacological modulators or inhibitors can protect TAMs from M2 polarization and tumor progression (de Groot and Pienta 2018; Niu et al. 2022).

Macrophages are highly sensitive to changes in metabolite concentrations (O'Neill 2011; Tannahill et al. 2013; Kim S et al. 2014), substrates (Pesce et al. 2009; Rodriguez-Prados et al. 2010), certain lipids (El Kasmi et al. 2013), oxygen tension (Pfau et al. 2004; Fumagalli et al. 2015), environmental pH (Wu H et al. 2019), tissue osmolality (Ip and Medzhitov 2015), and other molecular components of the microenvironment (El Kasmi et al. 2014). Therefore, additional non-cytokine pathways are required for macrophage polarization (Colegio et al. 2014; El Kasmi et al. 2014) along with the primary cytokine-mediated pathway.

TME metabolites regulate TAM

Lactate

Cancer cells produce lactate through glycolysis. The released lactate engages in metabolic symbiosis with other cells in the TEM, where it enters the TCA cycle and generates ATP through oxidative phosphorylation.

In addition, lactate can influence macrophages towards pro-angiogenic and anti-inflammatory phenotypes through several mechanisms. Pyruvate and lactate compete with α -ketoglutarate for the prolyl hydroxylases of HIF-1 α (Lu et al. 2002; Kim MJ et al. 2023). Hydroxylated HIF-1 α is ubiquitinated and subsequently undergoes proteasomal degradation (Lu et al. 2005). Therefore, heightened pyruvate and lactate levels inhibit the proline hydroxylation of HIF-1 α , leading to its stabilization in a hypoxia-independent manner, thereby increasing the expression of anti-inflammatory Arg1 and VEGF in TAMs (Bohn et al. 2018).

In addition to HIF-1 α , lactate can stabilize HIF-2 α and endow it with the pro-angiogenic phenotype of TAMs (Liu N et al. 2019). Furthermore, lactate downregulates the expression of ATP6V0d2, a vacuolar ATPase involved in the lysosomal-mediated degradation of HIF-2 α , in TAMs through the mTORC1-mediated inhibition of the transcription factor EB. Decreased lysosomal degradation of HIF-2 α , coupled with increased tumor incidence, was observed in *Atp6v0d2*^{-/-} mice. A correlation between ATP6V0d2 expression and the survival rate has also been reported in patients with lung adenocarcinoma (Liu N et al. 2019).

The lactate within TAMs can participate in the post-translational modification of proteins, and lactate-derived lactylation of histone lysine residues has emerged as a novel epigenetic modification that induces the expression of genes related to the pro-tumorigenic polarization of macrophages, such as those of arginase 1, HIF-1 α and VEGF-A (Zhang D et al. 2019). However, the process mechanism as well as enzymes involved in the addition or removal of lactate remain unknown.

Instead of entering cells via the monocarboxylate transporter (MCT), lactate can act on G-protein-coupled receptor 132 (Gpr132) on the plasma membrane and initiate signaling for the M2 polarization of TAMs (Chen P et al. 2017). Gpr132 is a lactate-signaling sensor that forms an interplay between cancer cells and macrophages within the acidic environment of the TME. Induction and stimulation of Gpr132 in macrophages by tumor-derived lactate promotes adhesion, migration, and invasion of breast cancer cells in vitro and in vivo (Chen P et al. 2017). Patients with breast cancer exhibit a positive correlation between Gpr132 expression, M2 macrophages, metastasis, and poor prognosis, making lactate-Gpr132 signaling a potential therapeutic target (Chen P et al. 2017). The macrophage odorant receptor Olfr78 is a heterodimeric partner of Gpr132 that senses lactate in the TME and generates pro-tumoral M2 TAMs (Vadevoo et al. 2021). In Gpr132-mediated signaling, the cAMP-mediated expression of

inducible cAMP early repressor may be involved in the pro-angiogenic, pro-tumorigenic phenotype of TAMs. This is because of the increased anti-inflammatory expression of Arg1, VEGF-A, and HIF-1 α in macrophages (Bohn et al. 2018).

Lactate activates the ERK/STAT3 axis, mediates M2 polarization, and is responsible for angiogenesis, along with cancer cell migration and invasion. The inhibition of ERK/STAT3 in MCF7 breast cancer cells reduced macrophage M2 polarization and decreased breast cancer proliferation and angiogenesis in vitro. Growth of the implanted tumor cells and progression and angiogenesis were inhibited in vivo as well (Mu et al. 2018).

TCA cycle intermediates

Succinate. Succinate, present in large quantities in tumors, is a byproduct of either hypoxia-induced glycolysis in tumor cells or reduced succinate dehydrogenase activity because of genetic mutations and/or epigenetic regulation (King et al. 2006; Killian et al. 2014; Richter et al. 2016; Wu J-Y et al. 2020). Within cells, succinate stabilizes and activates HIF-1 α by competing with α -ketoglutarate to inhibit HIF-prolyl hydroxylase activity (Selak et al. 2005). Various types of cancer cells, including those of lung, breast, and colon cancers, secrete succinate, which directs TAM polarization towards the M2 phenotype and contributes to cancer progression as a metabolic signal (Wu J-Y et al. 2020; Trauelson et al. 2021). Succinate in the TEM can bind to succinate receptor 1 (SUCNR1), also known as Gpr91, in macrophages. SUCNR1 is highly expressed on the surface of immature dendritic cells and macrophages and is involved in the succinate-driven recruitment of macrophages. Inhibition by anti-SUCNR1 antibodies reduces the migration of succinate-treated macrophages. Succinate-induced SUCNR1 activation leads to intracellular signaling events in TAMs. The PI3K-HIF-1 α axis is a potential downstream mediator of SUCNR1, which induces a pro-angiogenic phenotype in TAMs. Succinate-induced TAMs enhance cancer cell migration in vitro and promote cancer metastasis in vivo (Wu J-Y et al. 2020). Succinate increases the expression of M2 type macrophages, such as Arg1, Fizz1, and Mgl1/2, within TAMs in a dose-dependent manner. Conversely, SUCNR1 inhibition using small interfering RNA or inhibition of PI3K by LY294002 suppresses their expression (Wu J-Y et al. 2020).

α -Ketoglutarate. α -Ketoglutarate is an essential co-substrate of HIF-prolyl hydroxylases (Epstein et al. 2001; Fong and Takeda 2008) that can affect HIF-1 α degradation. This induces the M1 polarization of macrophages. α -Ketoglutarate is also involved in the M2

polarization of macrophages by facilitating fatty acid oxidation and jumonji domain-containing protein 3-dependent epigenetic changes in genes involved in M2 polarization (Liu P-S et al. 2017). The ratio of α -ketoglutarate to succinate may be a factor driving M1 and M2 polarization, as low and high ratios of α -ketoglutarate to succinate are related to the M1 and M2 polarization of macrophages, respectively (Liu P-S et al. 2017).

Itaconate. Itaconate, a cis-aconitate metabolite, has recently emerged as an important regulator of immunity and inflammation (Feng et al. 2023). It inhibits succinate dehydrogenase, thereby blocking the production of reactive oxygen species (ROS) from complex 1 and leading to the inhibition of HIF-1 α activity and interferon-1 β production. Inhibition of M2 polarization by itaconate was demonstrated through the inhibition of the JAK1/STAT6 pathway and succinate dehydrogenase, which increased succinate levels (Runtsch et al. 2022).

Adenosine

Adenosine is produced in many different types of tumors, and high levels in the TME suppress local antitumor immune responses (Antonioli et al. 2013). Tumor cells express the ecto-5'-nucleotidase, CD73, which hydrolyzes extracellular ATP, ADP, and AMP to adenosine that acts on adenosine receptors (Montalbán Del Barrio et al. 2016). Hypoxia and HIF-1 α induce transcription of CD73 (Kobayashi et al. 2000; Synnestvedt et al. 2002), and upregulation of CD73 in hypoxic TME causes accumulation of extracellular adenosine (Hatfield et al. 2014). Four distinct adenosine receptors, A1, A2A, A2B, and A3, are G-protein-coupled transmembrane receptors that are differentially expressed in various cell types, including cancer, endothelial, immune, and inflammatory cells (Eltzschig et al. 2012; Haskó and Pacher 2012). Tumor-protective effects are associated with A2A and A2B receptors that stimulate adenylyl cyclase, elevate intracellular cAMP levels, and lead to the activation of cAMP response element-binding (CREB) protein (Ohta et al. 2006). The adenosine pathway within cells creates a TME with tumor-protective effects. Deletion of CD73 or the A2A receptor has been shown to reduce tumor growth, inhibit metastasis, and evoke a potent antitumor immune response in mice (Stagg et al. 2011; Beavis et al. 2013; Cekic et al. 2014). Expression of A2A and A2B receptors is heightened in activated macrophages, and they are predominantly involved in M1 and M2 macrophage activation, respectively (Csoka et al. 2012). Adenosine inhibits the pro-inflammatory consequences of M1 activation, such as the secretion of TNF- α and IL-12 (Hasko et al. 2000), and polarizes macrophages into M2-like macrophages

that produce anti-inflammatory IL-10 to suppress immune cells and produce VEGF to support angiogenesis (Csoka et al. 2012). Thus, metabolic alterations within the TME that facilitate adenosine accumulation in interstitial spaces may cause immunosuppression by facilitating M2 polarization.

The A2A receptor and adenosine have been implicated in the proliferation of macrophages, high levels of which are correlated with poor prognosis in patients with hepatocellular carcinoma (Wang J, Wang, et al. 2021). These proliferating macrophages, which constitute a major macrophage pool in the TME of hepatocellular carcinoma, are poorly differentiated and immunosuppressive. Tumor-stimulated TAMs secrete GM-CSF, which acts on TAMs to induce the A2A receptor in an autocrine manner, thereby allowing tumor-derived adenosine to promote the proliferation and activation of TAMs through A2A and the PI3 K/Akt and MEK/ERK pathways (Wang J, Wang, et al. 2021). Because adenosine exhibits pro-tumorigenic effects and protection from antitumor immune responses, modulation of macrophage function via adenosine or adenosine receptor-targeted therapies may be beneficial in cancer treatment.

Lipid metabolites

Prostaglandin E₂. Prostaglandin E₂ (PGE₂) is derived from arachidonic acid through cyclooxygenase (COX) and PGE₂ synthase (PGES) and is synthesized in most types of cells. COX-1, expressed constitutively, is linked to cytosolic PGES, whereas COX-2 is functionally associated with microsomal PGES-2, which is rapidly induced by pro-inflammatory stimuli (Weigert et al. 2018). PGE₂ is a pro-inflammatory and pro-tumorigenic factor and is a major prostaglandin responsible for both inflammatory responses and tumor progression. Various cancer cells, including both established cell lines and human samples, produce high amounts of PGE₂, which is involved in tumor formation, progression, metastasis, and immune evasion (Stolina et al. 2000; Eruslanov et al. 2009; Wang D et al. 2015; Nagaraja et al. 2016; Hsu et al. 2017; Zang et al. 2017). The significance of PGE₂ in tumors treated with aspirin and COX-2 inhibitors has been studied in human cancers, including mesothelioma and colorectal cancer, as well as in mouse models with implanted cancer cells (DeLong et al. 2003; Haas et al. 2006; Nan et al. 2015). PGE₂ acts on cancer cells and other cell types in the TME in a paracrine manner. It binds to the G protein-coupled receptors EP1, EP2, EP3, and EP4 to transfer signals that induce angiogenesis, lymphangiogenesis, epithelial-mesenchymal transition, and immune evasion (Dehne et al. 2017). Recent studies have reported that PGE₂ influences the transformation of M1 macrophages into immunosuppressive

M2 macrophages (Bi et al. 2020; Wang J, Liu, et al. 2021; Xu M et al. 2021; Wang W et al. 2023). COX-2 in TAMs is upregulated by molecules from cancer cells and produces PGE₂, which induces the pro-tumorigenic M2 phenotype in TAMs (Inaba et al. 2003; Weigert et al. 2018). Multiple factors from apoptotic cancer cells, including sphingosine-1-phosphate and lysophatidylcholine, recruit macrophages to the tumor and stimulate them to upregulate COX-2 and mPGES-2, besides producing PGE₂ in a feed forward manner (Dehne et al. 2017).

The crosstalk between macrophages and tumor cells contributes to hepatocellular carcinoma progression. TAM-derived PGE₂ upregulates tumor ubiquitin-like proteins with PHD and ring finger domain 1 (*UHRF1*), an oncogene that is highly expressed in hepatocellular carcinoma. UHRF1 recruits histone 3 lysine 9 methyltransferase, leading to epigenetic changes in the cancer genome. Methylation of the Krüppel-like factor promoter decreases KLF6 expression, which correlates with hepatocellular carcinoma progression. UHRF1 also increases CSF-1 expression, which in turn recruits and activates TAMs, thus forming a reciprocal loop within the TME to promote hepatocellular carcinoma growth and tumor metastasis (Zhang J, Zhang, et al. 2022).

Sphingosine-1-phosphate. Sphingosine-1-phosphate (S1P) is a bioactive metabolite that regulates various cellular processes. S1P produced by cancer cells is a pro-survival and pro-tumorigenic factor that induces tumor cell transformation, viability, migration, and angiogenesis (Pyne Nigel et al. 2012). S1P released by apoptotic breast cancer cells polarizes macrophages toward an M2-like phenotype (Weigert et al. 2007). The effects of S1P on tumor cells, macrophages, and subsequent tumor growth have been reported in various studies. Although the effects of these components remain unexplored, enzymes involved in the production of S1P and S1P receptors are important regulators of macrophage polarization (Weigert et al. 2019).

Polyunsaturated fatty acids. Polyunsaturated fatty acids, such as linoleic acid, can act as fatty acid ligands in serous ovarian carcinoma ascites, activating PPAR β/δ and thus promoting the polarization of TAMs into an M2 phenotype (Schumann et al. 2015). Moreover, tumor cells promote lipid accumulation in TAMs, which also polarizes them towards the M2 phenotype (Qiao et al. 2023).

Amino acids

Depletion of glucose and non-essential amino acid (NEAA) affects immunity and is often observed in the TME. Due to continual glucose uptake and lactate

secretion, glucose is rapidly depleted in the TME (Ho et al. 2015; Kamphorst et al. 2015), thus suppressing inflammatory macrophage differentiation and simultaneous promotion of M2 macrophage polarization (Schworer et al. 2019). Amino acids are the primary source of carbon for proliferating cells (Hosios et al. 2016). NEAAs, including glutamine, serine, and cysteine, may be depleted within tumors (Kamphorst et al. 2015). Depletion of cysteine and serine in the TME promotes ROS accumulation to toxic levels in inflammatory macrophages and suppresses M1 activity during chronic anti-tumor responses (Schworer et al. 2019).

Conclusion

The focus of cancer research and treatment has shifted from a primary emphasis on the cancer itself to a more comprehensive approach centered on the TME, recognizing its growing importance in understanding cancer biology. Despite the recognition, the effectiveness of therapeutic approaches specifically targeting TME cells or pathways remains unsatisfactory. Therefore, identification and targeting of immunosuppressive factors within the TME may provide valuable insights into the mechanisms underlying tumor formation and progression.

TAMs represent a distinct population of immune cells abundant in the TME (Cassetta and Pollard 2023). Inhibiting TAM recruitment (Mantovani and Allavena 2015) and reprogramming of the phenotype from M2 to M1 (Ugel et al. 2015) have emerged as potential therapeutic strategies for effectively arresting tumor growth and preventing metastasis.

While extracellular nutrients are crucial in providing necessary components for cell growth, the metabolites generated during this process can directly affect neighboring stromal cells, including TAMs. This is achieved by activating signal transduction cascades, thereby exerting paracrine effects (Oh et al. 2010; Lorendeau et al. 2015; Schworer et al. 2019) (Figure 1).

Although no known metabolite modulators act specifically on TAMs, various cancer metabolites mentioned earlier can affect the polarization of macrophages. Therefore, inhibitors of enzymes that produce metabolites or antagonists of transporters or receptors can be used as immunomodulating agents to target TAMs. For instance, lactate dehydrogenase inhibitors such as oxamate (Zhao et al. 2015; Yu et al. 2020), gossypol (Van Poznak et al. 2001; Rani and Kumar 2016), and galloflavin (Manerba et al. 2012), or MCT inhibitors such as 7ACC2 (Corbet et al. 2018), CHC (Sonveaux et al. 2008), and DIDS (Amorim et al. 2015), can prevent lactate-induced polarization of TAMs. NF-56-EJ40 is a SUCNR1 inhibitor that can prevent immune cell migration and

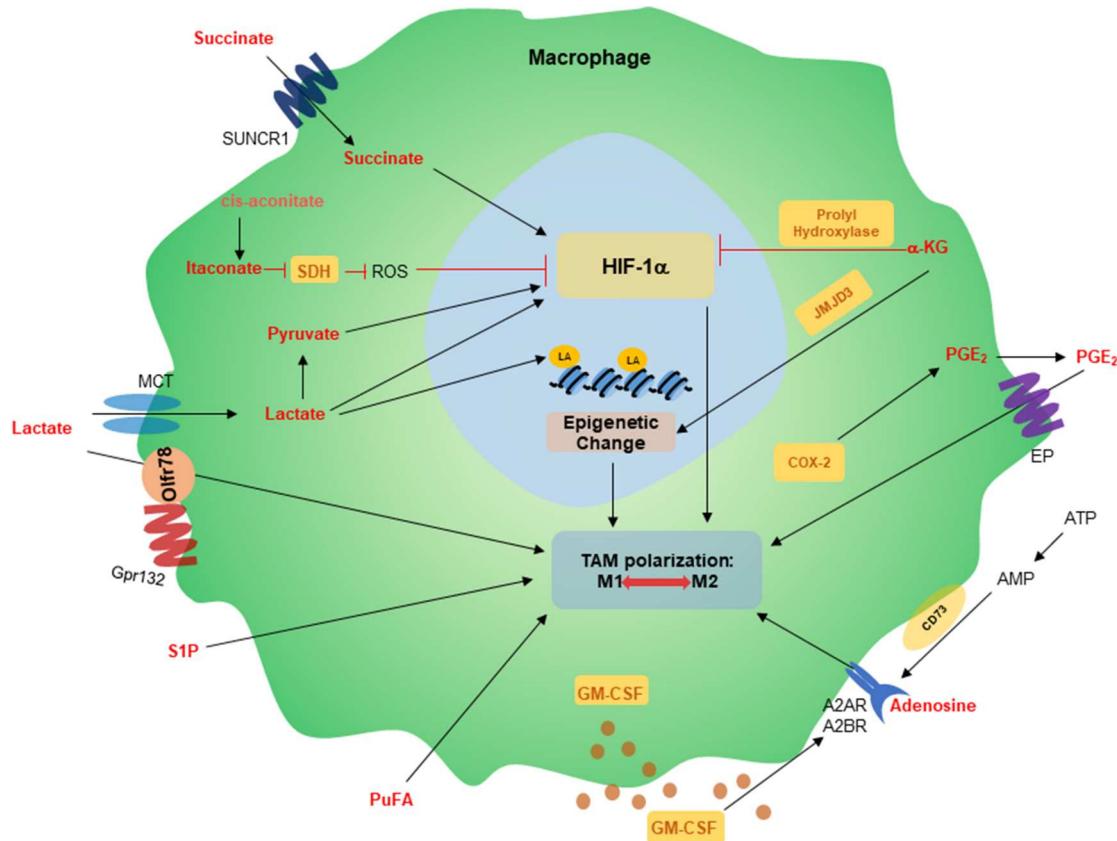


Figure 1. Metabolites generated in the tumor microenvironment affect TAM polarization. Schematic shows the roles of metabolites in macrophages. Metabolites can either stabilize or degrade HIF-1 α , which induces TAM polarization. Lactate-derived lactylation of histone lysine residues promotes tumorigenic polarization of macrophages. A2AR, A2A adenosine receptor; A2BR, A2B adenosine receptor; COX, cyclooxygenase; EP, E prostanoïd receptor; Gpr132, G Protein-Coupled Receptor 132; JMJD3, jumonji domain-containing protein-3; PGE₂, prostaglandin E2; PuFA, polyunsaturated fatty acids; S1P, sphingosine-1-phosphate; SDH, succinate dehydrogenase; SUNCR1, succinate receptor; TAM, tumor-associated macrophage.

inhibit succinate-induced M2 polarization of TAMs (Trauelsen et al. 2021). In addition, oleclumab (Bendell et al. 2023) and durvalumab (Lim et al. 2022), inhibitors of CD73 that produces adenosine from AMP, and AZD4635 (Atif et al. 2022; Lim et al. 2022), a selective A2AR antagonist, can inhibit adenosine-induced M2 polarization. Celecoxib, a selective COX-2 inhibitor, can also modulate the polarization of TAMs by inhibiting the production of PGE₂ (Song et al. 2016; Xun et al. 2021). Thus, the development of metabolite modulators and antagonists of transporters or receptors that can specifically act on TAMs is expected to promote anti-tumor immune responses by modulating the TME.

Disclosure statement

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