

Myeloid cells: key players in tumor microenvironments

Qiaomin Hua^{1,2,*}, Zhixiong Li^{1,2,*}, Yulan Weng^{1,*}, Yan Wu (✉)¹, Limin Zheng (✉)^{1,2}

¹Guangdong Provincial Key Laboratory of Pharmaceutical Functional Genes, MOE Key Laboratory of Gene Function and Regulation, School of Life Sciences, Sun Yat-sen University, Guangzhou 510275, China; ²State Key Laboratory of Oncology in South China, Guangdong Provincial Clinical Research Center for Cancer, Sun Yat-sen University Cancer Center, Guangzhou 510060, China

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Abstract Cancer is the result of evolving crosstalk between neoplastic cell and its immune microenvironment. In recent years, immune therapeutics targeting T lymphocytes, such as immune checkpoint blockade (ICB) and CAR-T, have made significant progress in cancer treatment and validated targeting immune cells as a promising approach to fight human cancers. However, responsiveness to the current immune therapeutic agents is limited to only a small proportion of solid cancer patients. As major components of most solid tumors, myeloid cells played critical roles in regulating the initiation and sustenance of adaptive immunity, thus determining tumor progression as well as therapeutic responses. In this review, we discuss emerging data on the diverse functions of myeloid cells in tumor progression through their direct effects or interactions with other immune cells. We explain how different metabolic reprogramming impacts the characteristics and functions of tumor myeloid cells, and discuss recent progress in revealing different mechanisms—chemotaxis, proliferation, survival, and alternative sources—involved in the infiltration and accumulation of myeloid cells within tumors. Further understanding of the function and regulation of myeloid cells is important for the development of novel strategies for therapeutic exploitation in cancer.

Keywords myeloid cells; ICB treatment; immune therapy; tumor microenvironments

Introduction

Cancer results from the evolving crosstalk between neoplastic cell and its immune microenvironment, of which T lymphocytes have been regarded as key players [1,2]. Accordingly, immune therapeutics targeting T lymphocytes, such as immune checkpoint blockade (ICB) and CAR-T, have made significant progress in cancer treatment. However, responsiveness to the current immune therapeutic agents is limited to only a small proportion of solid cancer patients. One of the major reasons for that lies in the lack of consideration of immune system as a complex interactive network which comprises both T lymphocytes and large amounts of myeloid cells [3–5]. As major components of most solid tumors, myeloid cells played critical roles in regulating the initiation and sustenance of adaptive immunity, tumor angiogenesis, matrix remodeling, as well as cancer

cell biology, thus determining tumor progression as well as therapeutic responses [6–10]. A renewed focus on myeloid cells in cancer research has yielded significant new insight into the critical roles of these cells in cancer therapies.

Myeloid cells belong to the innate arm of immune system. They harbor a broad specificity toward pathogens and constitute the “first-line” defense against infections [11]. As a heterogeneous group of populations, myeloid cells consist of monocytes, macrophages, granulocytes (which include neutrophils, basophils, eosinophils and mast cells), dendritic cells (DCs), and myeloid-derived suppressor cells (MDSCs, which are further categorized into monocytic MDSCs or granulocytic/polymorphonuclear (PMN) MDSCs in both mouse and human) [12–16]. Many markers have been applied to distinguish different myeloid cell subsets. For example, combinations of CD11c, CD14, CD68, Fcγ RIII/CD16, Fc gamma RI/CD64, and CCR5 are regarded as DC markers, and cell surface markers used to identify human and mouse macrophages include CD11b/Integrin alpha M, CD14, CD68, Fcγ RIII/CD16, Fc gamma RI/CD64, and CCR5, along with F4/80 in mouse [17,18]. While

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Correspondence: Yan Wu, wuyan32@mail.sysu.edu.cn;

Limin Zheng, zhenglm@mail.sysu.edu.cn

*These authors contributed equally.

CD11b⁺Gr1⁺Ly-6C⁻Ly-6G⁺ and CD11b⁺Gr1⁺Ly-6C⁺Ly-6G^{-/low} could be generally used to distinguish mouse PMN MDSCs and monocytic MDSCs, markers for human MDSCs vary across different tumor types. CD11b⁺CD14⁻CD15⁺/CD66b⁺ and CD14⁺CD15⁻HLA-DR^{-/low} could be used to identify human PMN MDSCs and monocytic MDSCs, and lectin-type oxidized low-density lipoprotein receptor 1 has emerged as a specific human PMN MDSCs marker [9,19]. Of note, some researches proposed that the most viable standard to define MDSCs is their ability to inhibit immune responses [9,20,21].

Recent years have seen large amounts of publications revealing roles of myeloid cells in tumor microenvironments (TME). This review will briefly discuss the diverse functions of myeloid cells in tumor progression through their direct effects or interactions with other immune cells, and then explore how different metabolic pathways shift and impact the characteristics of tumor myeloid cells. We also discuss how different mechanisms—chemotaxis, proliferation, survival, and alternative origins—contribute to the infiltration and accumulation of myeloid cells within tumors. For simplicity and clarity, we mainly focus on monocytes/macrophages and MDSCs. Other myeloid cells such as granulocytes and DCs have been reviewed elsewhere and have not been discussed in this review.

Functions of TAM and MDSC in tumor microenvironments

A majority of tumor-associated macrophages (TAMs) originate from bone marrow (BM)-derived monocytic precursors, but tissue-resident macrophages originate from embryonic precursors that seed organs in embryonic life also contribute to sustaining macrophage levels within tumors [12]. In contrast, it has been proposed that pathological activation arising from persistent stimulation of the myeloid cell compartment owing to the prolonged presence of myeloid growth factors and inflammatory signals in the settings of cancer, chronic infections or inflammation, gives rise to MDSCs [9]. While monocytes/macrophages are double-edged swords with dual potential in cancer, MDSCs were generally regarded as pro-tumor populations [9,12,22,23].

Direct effects on tumor cells

Macrophages can directly impact different characteristics of cancer cells. For instance, high densities of CD68⁺ cells had been associated with improved survival in colon, gastric and endometrial cancer [7,24]. Macrophages could directly kill cancer cells through the release of nitric oxide, reactive oxygen species (ROS), and tumor necrosis factor (TNF). When appropriately

activated, macrophages could mediate phagocytosis of cancer cells and cytotoxic tumor killing [12,25]. Recent studies found that Kupffer cell lineage-determining factor ID3 endowed Kupffer cells, but not monocyte-derived TAMs, with the ability to phagocytose live cancer cells and orchestrate the recruitment, proliferation and activation of immune effector cells in the liver to restrict the tumor growth [26,27]. Interestingly, whole beta-glucan particle could lead to a trained immunity phenotype in lung interstitial macrophages, resulting in inhibition of tumor metastasis and survival prolongation in multiple mouse models of metastasis [28].

However, within many tumors, macrophages often exhibited pro-tumor functions and their infiltration had been a negative prognostic factor [7,29]. Cytokines and growth factors, such as IL-6, TNF, EGF, creatine released by TAMs supported the survival and proliferation of cancer cells [7,30,31]. TAMs also produced large amounts of proteases such as matrix metalloproteinases (MMPs) or cathepsins that degraded collagen fibers, and cross-linking enzymes that modulated the stiffness of the extracellular matrix [7,30,32]. TAMs-derived TGF- β , CCL18, and Cathepsin B facilitate the epithelial-to-mesenchymal transition (EMT) of cancer cells to promote metastasis [7,30,33]. In hepatocellular carcinoma (HCC), we previously found that tumor necrosis factor alpha (TNF- α) and IL-1 β derived from tumor-activated monocytes synergistically induced cancer cell autophagy in the invading edges, which facilitated the EMT of cancer cells and promoted tumor metastasis [34]. Moreover, TAMs played important roles in promoting tumor angiogenesis through vascular endothelial growth factor (VEGF), IL-8, and SEMA4D. It has been reported that TAMs expressing the angiopoietin receptor Tie2 accumulated at the perivascular areas, where they supported angiogenesis and tumor growth [7,23,30,35]. Monocytes/macrophages were also involved in the process of pre-metastatic niche formation. Once activated by tumor-derived cues, tissue resident macrophages helped establish a pro-tumoral environment by enhancing cancer cell extravasation, transmitting survival signals to support cancer cell survival, promoting inflammation, suppressing anti-tumor immune responses, or inducing endothelial cell-mediated production of niche components, thus creating a favorable environment for disseminating cancer cells. Premetastatic niches continually recruited monocytes to replenish local macrophages, facilitating a positive pro-metastatic feedback loop [30,36–39]. Similar effects on cancer cell transformation and the establishment of premetastatic niche could also be observed in MDSCs. MDSCs could stimulate cancer cell stemness and EMT via production of IL-6 and TGF β as well as cancer cell invasion and dissemination via secretion of MMPs [40]. Furthermore, MDSCs could promote metastasis by enhancing the

engraftment by circulating tumor cells, escorting tumor cells into the circulation, promoting their metastatic potential, inhibiting their killing by immune cells, and promoting their extravasation into the tissues [9,20,40].

It should be noted that the different functions exhibited by TAMs can be attributed to distinct macrophage subsets with different origins, or the same population changing its phenotypes according to different environmental cues or from different developmental stages. Progress in single cell analysis technique in recent years has provided more sensitive characterization of TAM phenotypes and functions across various cancer types, but protein level analysis is warranted for the validation and proper interpretation of scRNA-seq data [41,42].

Modulation of tumor microenvironments

In addition to direct interactions with tumor cells, myeloid cells can also orchestrate multiple immune cells, especially effector T cells, within the TME to influence tumor progression [38,43]. The immune modulation by tumor-associated myeloid cells is supported by a diverse array of molecular mechanisms. These mechanisms span from the depletion of critical nutrients within the tumor microenvironment, providing cytokine signals, to cell-to-cell interaction. Here, we described the multifaceted roles of myeloid cells in promoting or inhibiting tumor progression through their interactions with TME components.

It is well-established that TAMs and MDSCs can produce high levels of immunoregulatory enzymes that deplete essential nutrients for T cells [44]. Arginase 1 (Arg1) served as a marker of alternatively activated macrophages [45] and exhibited high expression levels in MDSCs [46]. It catalyzed the conversion of L-arginine into urea and L-ornithine. By depleting L-arginine, myeloid cells suppressed CD3 ϵ re-expression and inhibited antigen-specific T cell proliferation, fostering an immunosuppressive TME [47]. Similarly, TAMs and MDSCs utilized indoleamine 2,3-dioxygenase (IDO) to deplete L-tryptophan [48]. Moreover, the resultant L-kynurenine inhibited the proliferation and function of T and NK cells [49–51], and supported the expansion of Treg cells [52]. In addition to depriving lymphocytes of essential nutrients, myeloid cells also suppressed anti-tumor immune responses by inducing an oxidative stress milieu through the expression of inducible nitric oxide synthase (iNOS) and the production of ROS [53–55]. iNOS-mediated nitric oxide production led to peroxynitrite formation, which disrupted the interaction between the T cell receptor (TCR) and the major histocompatibility complex (MHC) by nitrating tyrosine residues in the TCR-CD8 complex [56]. Consequently, this nitration impeded antigen recognition and hindered effective immune activation. Synergizing with iNOS,

ROS contributed to the suppression of T cell responses [56]. ROS could downregulate CD3 ζ expression in T cells [57], impairing T cell activation and cytokine production [58], thereby promoting tumor immune evasion [59,60]. Moreover, both TAMs and MDSCs could convert extracellular adenosine triphosphate (ATP) to adenosine via the ectonucleotidases CD39 and CD73, leading to an immunosuppressive milieu [61,62].

Myeloid cells shaped adaptive immune responses not only by altering the metabolic microenvironment but also by delivering immunosuppressive cytokine signals. IL-10, an important immunomodulatory cytokine, was notably produced by TAMs and MDSCs [63–65]. In addition to its inhibitory effects on antigen-presenting cells and CD4 $^{+}$ T cells [63,66,67], IL-10 directly modulated CD8 $^{+}$ T cells by increasing N-glycan branching on their surface glycoproteins, resulting in reduced antigen sensitivity [68]. Moreover, TAMs and MDSCs released TGF- β , which suppressed the cytotoxic activity of T cells and NK cells, and induced Treg generation [69–73]. TREM2 $^{+}$ monocyte-derived macrophages impaired NK cell function and recruitment by secreting IL-18BP to intercept IL-18 and the infiltration of TAMs was associated with a decreased number and dysfunction of NK cells in various human cancers [70,74,75].

Additionally, tumor-associated myeloid cells could suppress anti-tumor function of lymphocytes through direct cell-to-cell contact. By expressing immune checkpoint ligands including B7-H4, programmed cell death ligand 1 (PD-L1), and PD-L2, TAMs interacted with the related receptors on T cells and suppressed adaptive immune responses [40,76]. Within the tumor tissue, TAMs regulated CD8 $^{+}$ T cell exhaustion by forming antigen-specific and long-lasting synapses, especially within the tumor hypoxia region [77]. In addition to promoting T cell exhaustion, recently identified Tim-4 $^{+}$ macrophages could selectively sequester viable and cytotoxic T cells by interacting with phosphatidylserine, thereby preventing their infiltration into the tumor to exert anti-tumoral effects [78].

In addition to T cells and NK cells, research on human ovarian cancer has highlighted that within TME, large stromal leukocyte aggregates featured a dynamic intermingling of T cells, tumor-infiltrating B cells, and macrophages [79]. There was a reciprocal regulatory relationship between tumor-infiltrating myeloid cells and B cells during tumor progression and immunotherapy [80–83]. In HCC and colorectal cancer liver metastasis, TAMs selectively recruited IgG $^{+}$ plasma cells, which in turn, fostered the polarization of protumorigenic macrophages within the HCC [81]. Moreover, distinct myeloid cell subsets could be colocalized within specific tumor regions to amplify immunosuppression and accelerate tumor progression [84,85]. Depending on cell contact, tumor-induced MDSCs could reduce the IL-12

production by macrophages, while simultaneously increasing their own secretion of anti-inflammatory cytokine IL-10 [86,87]. The interactions between MDSCs and macrophages could also lead to decreased MHC II expression in macrophages, potentially regulated by IL-10 through the induced expression of MARCH1 [88]. Interestingly, under the condition of tumor hypoxia, M-MDSCs could differentiate into TAMs with a more immunosuppressive phenotype [89,90]. These mutual interactions could be further enhanced by the chemotaxis among myeloid subsets [84].

Although current research on TAMs predominantly highlights their protumorigenic roles, emerging studies have identified that in certain tumor types and tissue regions, TAMs may also fulfill protective roles for the host. In human HCC tissues, CD169⁺ macrophage was a potential anti-tumor subset with high expression levels of HLA-DR and CD86 [91]. Moreover, in primary breast tumors, a distinct population of human tissue-resident FOLR2⁺ macrophages has recently been identified to exhibit anti-tumor properties [92]. PD-L1⁺ macrophages were predominantly recognized for their role in dampening immune responses within TME. Nonetheless, in human HCC and breast cancer tumors, PD-L1 expression on macrophages was correlated with an active immune microenvironment and better prognosis [93,94]. These PD-L1⁺ macrophages in breast cancer tumor tissue exhibit closer spatial contact with CD8⁺ T cells compared to PD-L1⁻ macrophages and were able to enhance T cell proliferation and cytotoxic activity [94]. That could reflect the nature of macrophages that activated cells also highly express inhibitory molecules, e.g. PD-L1 [59,60]. Therefore, even among myeloid cells with the same phenotype, their functions could vary dramatically in different tissue types and TME, influenced by local environmental signals and neighboring cells, including the expression pattern of receptors on target cells that transduce either pro- or anti-tumor functions of macrophages. Integrating high-throughput *in situ* detection and analysis techniques is warranted to enhance our understanding of the true roles of myeloid cells within the tumor milieu.

The metabolic rewiring of TAM and MDSC

Immunometabolism describes the changes in intracellular metabolic pathways in immune cells during their growth, differentiation, and function [95]. Solid tumors are fast-growing and metabolically demanding tissues, and this largely influences the features in the TME, including altered nutrient availability, hypoxia and immunosuppressive metabolite production. These changes could induce immune cell metabolic rewiring, then affect their survival and function, and eventually regulate tumor progression. In light of recent progress in the field, we

discuss the metabolic landscape of TAMs and MDSCs, including the immunoregulatory roles of glucose, fatty acids, and amino acids. A binary metabolic schema is currently used to characterize macrophages immunological phenotypes: glycolysis promotes the activation of classic M1 macrophage, which generates ROS and other inflammatory factors, whereas oxidative phosphorylation (OXPHOS) stimulates alternative M2 macrophage to support tissue repair and immunosuppression. However, this classification likely underestimates the variety of states *in vivo*. Understanding these nuances will be significant when developing interventional metabolic strategies.

Glucose metabolism

Glucose was usually metabolized through glycolysis, the Krebs or tricarboxylic acid (TCA) cycle and the pentose phosphate pathway (PPP). Glucose metabolism led to the accumulation of metabolites such as lactate and succinate that could regulate epigenetic remodeling and signaling transduction [96]. Therefore, glucose metabolism in tumor associated myeloid cells coordinated an intrinsic immune-metabolism crosstalk via integrating gene-, protein-, and metabolite-based regulatory mechanisms, consequently determining the function of TAMs and MDSCs [96] (Fig. 1).

Glucose uptake (GLUT1)

In TME, myeloid cells had the greatest capacity to uptake glucose and maintained a higher glycolysis rate than tumor-infiltrating T cells and cancer cells [97]. M2-like TAMs were recently shown to be the subset of immune cells with the strongest glucose uptake capacity [33], suggesting that nutrient acquisition and metabolism preferences between macrophages and tumor cells were complex. Macrophages sensed the glucose concentration and took glucose into the cytoplasm through glucose transporter protein 1 (GLUT1) and specific deletion of GLUT1 in macrophages dramatically decreased glycolysis and tumor burden [98]. However, in the murine mammary tumor model, a subset of MDSCs suppressed antitumor immunity by overexpressing GLUT3 [99]. GLUT3 knockdown significantly triggered apoptosis and reduced glucose uptake in these cells [99].

Glycolysis

With the glucose uptake capacity increased, the levels of glycolysis in TAMs were further enhanced [100]. Inhibiting glycolysis in TAMs with a competitive inhibitor to hexokinase-2, 2-deoxyglucose, was sufficient to disrupt their pro-metastatic phenotype. Tumor-derived soluble factors, including hyaluronan fragments, could

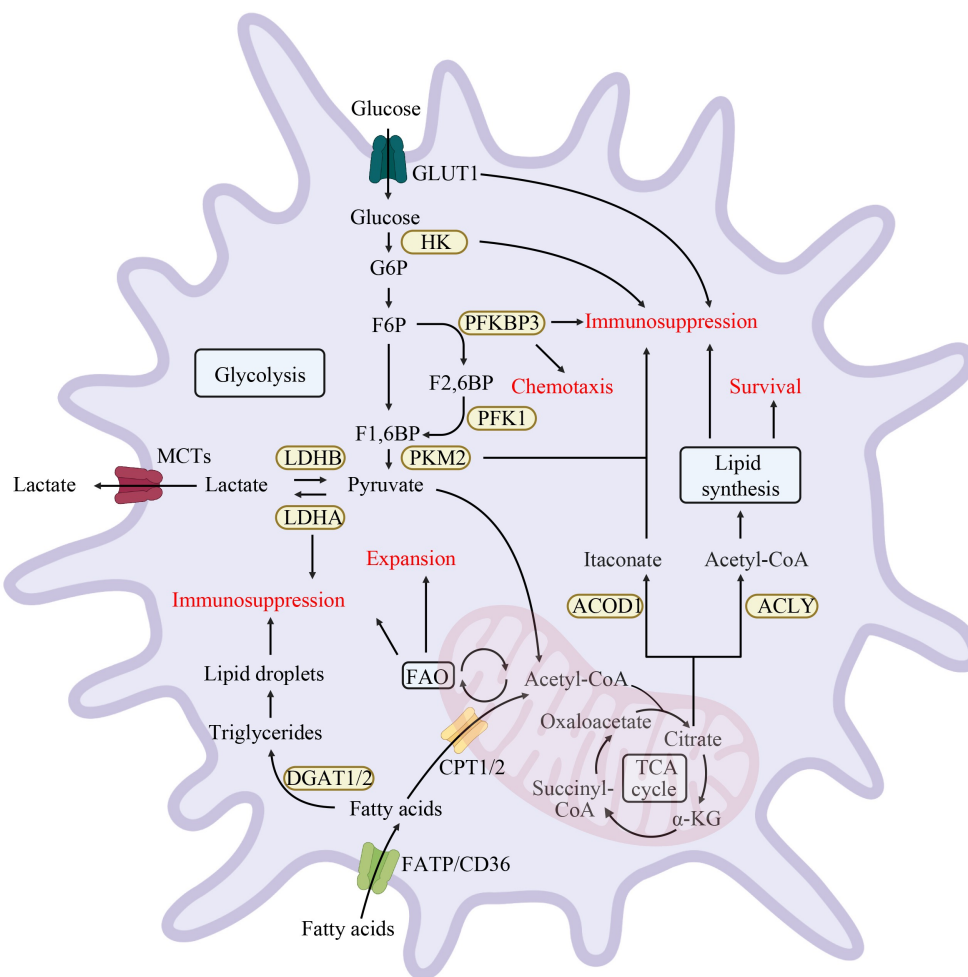


Fig. 1 The glucose and lipid metabolic landscape of tumor-associated myeloid cells. The diagram depicts the different metabolic pathways in myeloid cells, especially, glycolysis, lipid accumulation and oxidation are frequently upregulated in tumor associated myeloid cells, coordinated with their infiltration and protumor function (highlighted in red). G6P, glucose-6-phosphate; F6P, fructose-6-phosphate; F1,6BP, fructose-1,6-bisphosphate; F2,6BP, fructose-2,6-bisphosphate. This figure was created using BioRender.com.

significantly enhance glycolysis by upregulating a key glycolytic enzyme, PFKFB3, in TAMs. This enzyme modulated the cellular metabolic switch and mediated the increased expression of PD-L1 on macrophages, subsequently attenuating anti-tumoral responses. Consistently, the levels of PFKFB3⁺ TAMs infiltration were negatively correlated with overall survival in patients with HCC [101]. The activation of glycolysis also led to the production of large amounts of CXCL2 and CXCL8, which effectively recruited peripheral neutrophils and sustained their survival, subsequently facilitating disease progression in human HCC [84]. PFKFB3 overexpression in TAMs was indicative of a higher risk of tumor relapse in patients with colon cancer [102]. As the enzyme that regulates the final rate-limiting step of glycolysis, pyruvate kinase M2 exerted control over TAM expression of PD-L1 in pancreatic cancer, while also supporting tumor cell growth, exemplifying the dual benefit of glycolytic perturbation [103]. Thus,

M2-like TAMs could be highly glycolytic and utilize glucose to support their maintenance and suppressive activity. However, the macrophage anti-tumor response also depended on glycolysis, at least in some circumstances. Wenes *et al.* reported that enhanced glycolysis in hypoxic TAMs could reduce endothelial glucose availability and promote the formation of an organized tumor vasculature, which helped to restore oxygenation and prevented metastasis in subcutaneous lung cancer and orthotopic mammary tumor mouse models [104]. There was no coincidence that chloroquine reprogrammed macrophage metabolism toward glycolysis and induced TAMs proinflammatory polarization to ameliorate TME in mice bearing subcutaneous melanoma or hepatocarcinoma ascites [105].

MDSCs also had high glucose and glutamine uptake rates, a reduced oxygen consumption rate and most of the ATP generated was obtained through a glycolysis-dependent mechanism. A high glycolytic flux was needed

for the maturation and survival of MDSCs and suggested an indirect mechanism by which the consumption of carbon sources by MDSCs results in the suppression of effector T cells [9]. Although MDSCs were also shown to use OXPHOS, under hypoxic conditions, the activation of hypoxia-inducible factor 1 α (HIF-1 α) induced the switch from OXPHOS to glycolysis in MDSCs [9]. As a critical regulator of MDSCs in the TME, HIF-1 α could not only facilitate the differentiation of MDSCs [90]; but also enhance immunosuppressive function of MDSCs via glycolysis [106]. Deleting HIF-1 α in MDSCs reactivated antitumor T cell responses and effectively impaired tumor radioresistance [107]. However, MDSCs isolated from tumor tissue of patients with HCC had a dormant metabolic phenotype and failed to utilize glucose [108]. This peculiar metabolic phenotype was mediated by the accumulation of methylglyoxal in MDSCs and MDSCs suppressed T cell activation by transferring methylglyoxal to T cells [108]. Whether these findings could be recapitulated in other conditions remains to be determined.

Lactate

Lactic acid production from the end product of glycolysis, pyruvate, by the enzyme lactate dehydrogenase A was associated with immune suppressive TME in certain tumors. Lactate could promote HIF-1 α stabilization and M2 polarization in the absence of IL-4. In addition, exposure of mouse BM-derived macrophages to an acidic pH (6.8) *in vitro* increased the expression of anti-inflammatory genes [109]. Consistently, depletion of lactate dehydrogenase A in myeloid cells skewed M1-like polarization of macrophages with reduced pro-angiogenic VEGF expression and triggered antitumor properties. Conversely, LDHB could transform lactate to pyruvate and its expression was downregulated in TAMs. LDHB downregulation increased aerobic glycolysis and lactogenesis in TAMs and subsequent tumor growth [110].

Lactate was transported across the plasma membrane by proton-linked monocarboxylate transporters (MCTs) such as MCT1 (mainly lactate import) and MCT4 (mainly lactate export) [111]. High levels of circulating lactate caused expansion of MDSCs and such effect was significantly reduced by inhibition of MCT1 [112]. Lactate transporter MCT2 transcription downregulation led to reduced intracellular lactate levels, blunted MDSCs differentiation, and enhanced TAMs maturation [113]. Besides, lactate-enhanced tumor-promoting activity of MDSCs contributed to the radioresistance of pancreatic cancer [107]. Therefore, lactic acid could foster an immunosuppressive environment by modulating the differentiation and function of myeloid cells.

Lactate also served as a key bridge linking glucose metabolism and epigenetics in TAMs. Lactate derived

lactylation of histone lysine residues in macrophages could directly stimulate gene transcription [114]. For example, histone lactylation in M1 macrophages induced expressions of homeostatic genes, including VEGF and Arg1, and promoted M1 to M2 macrophage transition [114]. Tumor-derived factors induced high glycolysis and lactate production in TAMs, and intracellular lactate-driven histone lactylation promoted IL-10 expression [100]. Another study showed that tumor derived lactate mediated H3K18 lactylation was also important for IL-6 expression in TAMs, which endowed macrophages with tumor-promoting functions via activation of signal transducer and activator of transcription 3 (STAT3) signaling in tumor cells [115]. These studies pointed out different ways by which lactate production was linked to epigenetic remodeling for the direction of TAMs polarization and tumor progression. The discrepancy might be related to a dynamic change in glucose supply and metabolism in TME during different stages of tumor development, which resulted in differential patterns of epigenetic regulation of gene expression in TAMs.

TCA cycle/Krebs cycle

During proinflammatory macrophage activation, there was an accumulation of the TCA cycle intermediates succinate and citrate, and the TCA cycle-derived metabolite itaconate. In TAMs, high OXCT1 expression induced the accumulation of succinate, which promoted Arg1 transcription and CD8⁺ T cell exhaustion [116]. Myeloid-specific Bmal1 knockout rendered TAMs aberrant HIF-1 α activation and metabolic shift for glycolytic metabolism and succinate accumulation, contributing to an immunosuppressive TME [117]. Besides, itaconate produced by aconitate decarboxylase 1 (ACOD1) inhibited the expression of inflammatory genes in TAMs and the infiltration of CD8⁺ T cells into tumor sites [118]. Deletion of aconitate decarboxylase 1 in mice suppressed the growth of multiple tumors and enhanced the efficacy of anti-PD-(L)1 immunotherapy [118]. Similarly, metabolic reprogramming via aconitate decarboxylase 1 depletion enhanced function of human induced pluripotent stem cell-derived CAR-macrophages in solid tumors [119]. These studies suggested succinate and itaconate maybe immunosuppressive regulators of TAMs.

However, the role of the TCA cycle in tumor associated MDSCs was still unclear. Dihydrolipoamide succinyl transferase, a subunit of α -ketoglutarate decarboxylase complex in the TCA cycle, was found to be the most significantly elevated gene in tumor-primed myeloid cells [120]. The inhibition of dihydrolipoamide succinyl transferase reduced OXPHOS, immunosuppressive marker expression and function in myeloid cells [120]. Triggering STAT3 signaling via β 2-adrenergic receptor

activation enhanced glutamine consumption via the TCA cycle in MDSCs [121]. Then the metabolized glutamine generated itaconate could downregulate mitochondrial ROS and the oxidative stress response to promote MDSC survival [122].

Hexosamine biosynthetic pathway

The hexosamine biosynthetic pathway was a glucose metabolic pathway essential for the synthesis of UDP-GlcNAc, which regulated protein N-glycosylation and O-GlcNAcylation. Recently, Cao *et al.* revealed that TAMs increased glycolysis through the hexosamine biosynthetic pathway and O-GlcNAcylation to promote tumor metastasis and chemoresistance [33]. Consistently, glucose flux promoted O-GlcNAcylation in TAMs and induced an M2-like phenotype in patients with hyperglycemia [123]. Hedgehog signaling enhanced UDP-GlcNAc biosynthesis and STAT6 O-GlcNAcylation to promote the immune suppressive polarization of TAMs [124]. Given that TAMs had the strongest glucose uptake capacity in the TME, it was important to further identify how O-GlcNAcylation linked glucose uptake and utilization in TAMs to their tumor-promoting functions.

The product of hexokinase enzymes, glucose-6-phosphate, could be metabolized through glycolysis or directed to alternative metabolic routes, such as the PPP to generate anabolic intermediates. Although glycolysis and the PPP were indispensable in the activation of inflammatory macrophages, the role of PPP in tumor associated myeloid cells still needs to be illustrated.

Lipid metabolism

In response to different stimulus, cellular lipid metabolism could be dynamically altered and influence the heterogeneity of TAMs and MDSCs from several aspects [125]. Not only as an important energy source, lipids could also serve as essential components of cell membranes and as signaling molecules to modulate various myeloid cell functions. Besides, lipids modified proteins to regulate cell functions and acted as ligands for some key transcription factors (Fig. 1).

Lipid synthesis

Tumor-exposed macrophages had a strong upregulation of lipid biosynthesis pathways, an increased total lipid content and enriched levels of intracellular lipids. Inhibition of lipid biosynthesis by the FASN inhibitor C75 in TAMs significantly reversed the increased inflammatory cytokines and the capacity to produce ROS [126]. The disruption of SREBP1-dependent *de novo* fatty acids synthesis could impede TAMs survival and their tumor-promoting activity. Targeting SREBP1

pathway could improve anti-PD1 treatment efficacy in tumor-bearing mice [127]. However, *de novo* lipogenesis, not exogenous fatty acids, was also critical for CpG-activated macrophages anti-tumoral activity [128].

Lipid synthesis also influenced MDSCs. Ginger polysaccharide could decrease MDSCs proliferation and promote their apoptosis by inhibiting expression of FASN and diacylglycerol acyltransferase 2 [129]. The downregulation of RIPK3 in tumor-infiltrating MDSCs potentiated NF- κ B activation, cyclooxygenase-2 expression and the release of the immunosuppressive mediator, prostaglandin E2 (PGE2). PGE2, in turn, further reduced RIPK3 and promoted the immunosuppressive activity of MDSCs and tumorigenesis [130]. Thus, enhanced lipid synthesis in TAMs and MDSCs could promote their survival and protumor characteristics.

Fatty acid oxidation

Fatty acid oxidation (FAO) mainly occurred in mitochondrial matrix and was a source of ATP, especially when glucose availability was limited. In addition to bioenergetics, FAO may produce multiple metabolites that influence signal transduction and/or gene regulation [125]. Oxidative stress-induced oncogenic KRAS protein released from pancreatic cancer cells was essential for TAMs polarization via STAT3-dependent FAO [131]. Peroxisome proliferator-activated receptor γ (PPAR γ)-dependent fatty acid absorption and FAO induction could enhance protumor macrophage polarization, regulated by S100A4 or Hedgehog signaling [124,132]. Nevertheless, FAO was also critical for stimulating anti-tumorigenic functions in macrophages [128,133].

MDSCs relied on FAO as the major metabolic fuel for their immunosuppressive function. The increased fatty acid uptake and activated FAO were found in both peripheral blood MDSCs from patients with cancer and tumor-infiltrating MDSCs in murine tumor models. FAO inhibition blocked tumor-infiltrating MDSCs immunosuppressive effects and induced a significant antitumor effect [134]. scRNA sequencing analysis also showed that immunosuppressive myeloid cells with characteristics of fatty acid oxidative metabolism dominated the immune-cell landscape in ICB-resistant subjects. Furthermore, PIM1, a serine/threonine kinase, was confirmed in regulating MDSCs lipid oxidative metabolism and their immunosuppressive function via PPAR γ -mediated activities. PIM kinase inhibition not only improved the efficacy of PD-L1 blockade but also overcame ICB resistance in nonresponders [135]. Besides, β 2-adrenergic receptor signaling triggered by stress was an important physiologic regulator of OXPHOS and FAO in tumor-infiltrating MDSCs, which increased expression of fatty acid transporter CPT1A and PGE2 production [136]. Although targeting FAO maybe

a useful approach to limit the immune-suppressive function of TAMs and MDSCs, the specific factors responsible for this shift among the TCA, glycolysis, and FAO pathways in the TME and the molecular networks involved in the energy metabolic reprogramming of TAMs and MDSCs are still unknown.

Lipid droplet

Several studies revealed that lipid-associated macrophages were present in the TME, normally showed high cellular granularity and enriched lipid droplets and lipid metabolism related genes. These cells could exert immune-suppressive activities and support tumor growth and progression. Our recent study found LDs-laden macrophages were enriched in HCC tissues and associated with disease progression. These TAMs displayed immunosuppressive phenotypes and attenuated the antitumor activities of CD8⁺ T cells. LDs prolonged their survival and promoted CCL20 secretion, which further recruited CCR6⁺ Tregs to HCC tissue. Inhibiting these TAMs formation by targeting diacylglycerol acyltransferase 1 and diacylglycerol acyltransferase 2, which catalyze the synthesis of triglycerides, significantly reduced Treg recruitment and delayed tumor growth [137]. TAMs and MDSCs highly expressed scavenger receptor CD36 that was implicated in lipid scavenging and accumulation, and consequently augmented FAO and OXPHOS to fuel their protumorigenic functionality [138]. Although CD36 acted as a central regulator of both immune and metabolic pathways mainly through transporting of long-chain fatty acids, there were other lipid receptors to be revealed. Lipid receptor TREM2 drove a gene expression program involved in phagocytosis and lipid metabolism, the accumulation of TREM2⁺ TAMs was confirmed using scRNA-seq analysis and immunohistochemistry [139]. Furthermore, a subpopulation of monocyte-derived STAB1⁺TREM2^{high} TAMs with immune suppressive capacities was expanded and correlated to ICB resistance in patients with triple-negative breast cancer. These TAMs were induced by cancer-associated fibroblast-driven CXCL12-CXCR4 axis. TREM2⁺ TAMs were also significantly increased in pulmonary breast cancer metastasis lesions, and showed enrichment of genes implicated in lipid metabolism, extracellular matrix remodeling and immunosuppression, but reduced capacity for phagocytosis [140]. As a sensor for β -glucosylceramide, Mincle was essential for lipid accumulation, pro-tumorigenic properties and suppressive activity of TAMs in mouse melanoma model [141]. In prostatic adenocarcinoma, the formation of lipid-loaded TAMs was dependent on Marco-mediated oxidized low-density lipoprotein (LDL) uptake [142]. Fatty acid transport protein 2 promoted lipid accumulation and suppressive activity of MDSCs [143]. The accumulated

lipids could generate oxidized lipids via myeloperoxidase (MPO) in MDSCs. The transfer of oxidized lipids from MDSCs to DCs was implicated in the negative regulation of tumor-associated antigen cross-presentation *in vivo* by DCs, which was substantially improved in MDSC-depleted or MPO-deficient tumor-bearing mice [144]. The release of oxygenated lipids from MDSCs induced by ferroptosis could limit T cells activity [145]. If lipid accumulation became an established feature of TAMs and MDSCs, the mechanisms of lipid intake and the source of lipids still need to be fully illustrated.

Cholesterol metabolism

Cholesterol homeostasis was a dynamic process, involving synthesis, influx, efflux and esterification, which was implicated in the regulation of cell growth and differentiation. Moreover, it has been reported that the TCA cycle might be the possible intracellular source of acetyl-CoA for cholesterol synthesis [125]. Many cancers rewired cholesterol metabolism to support tumor progression and therapeutic resistance [146]. Notably, cholesterol metabolism could also impact TME and anti-tumor immune responses. The cholesterol metabolism feature and its potential role in tumor associated myeloid cells has recently been explored (Fig. 2).

Hypoxia induced nuclear translocation and activation of sterol regulatory element binding protein 2 (SREBP2) in monocytes, an essential regulator of cholesterol biosynthesis. In tumor-bearing mouse models, inhibiting cholesterol biosynthesis with atorvastatin significantly reduced tumor growth, angiogenesis, infiltration of monocytes/macrophages, and expression of Ccl2 [147]. A novel potent colony-stimulating factor 1 receptor (CSF1R) inhibitor, PXB17, significantly reprogrammed TAMs to M1 phenotype. Compared with M2 macrophages, PXB17-treated cells showed reduction of cholesterol content and downregulation of cholesterol biosynthesis related genes, including 3-hydroxy-3-methylglutaryl coenzyme A reductase (HMGCR), squalene epoxidase (SQLE) and SREBP2 [148]. DHCR7, another key enzyme in cholesterol biosynthesis, was significantly elevated in tumor-supportive macrophages. DHCR7 ablation in macrophages effectively suppressed cholesterol supply and activated T cell immunity [149]. SQLE catalyzed the stereospecific oxidation of squalene to (S)-2,3-epoxysqualene and was a rate-limiting enzyme in cholesterol biosynthesis. Dysregulation of SQLE resulted in altered cholesterol metabolism in TAMs and an immune suppressive TME, favorable for tumor growth and progression [150]. However, Liu *et al.* showed that β -glucan-induced antitumor activity of macrophages in a melanoma mouse model required SQLE-catalyzed squalene epoxidation, which not only produced 24(S),25-epoxycholesterol for liver X receptor (LXR) activation

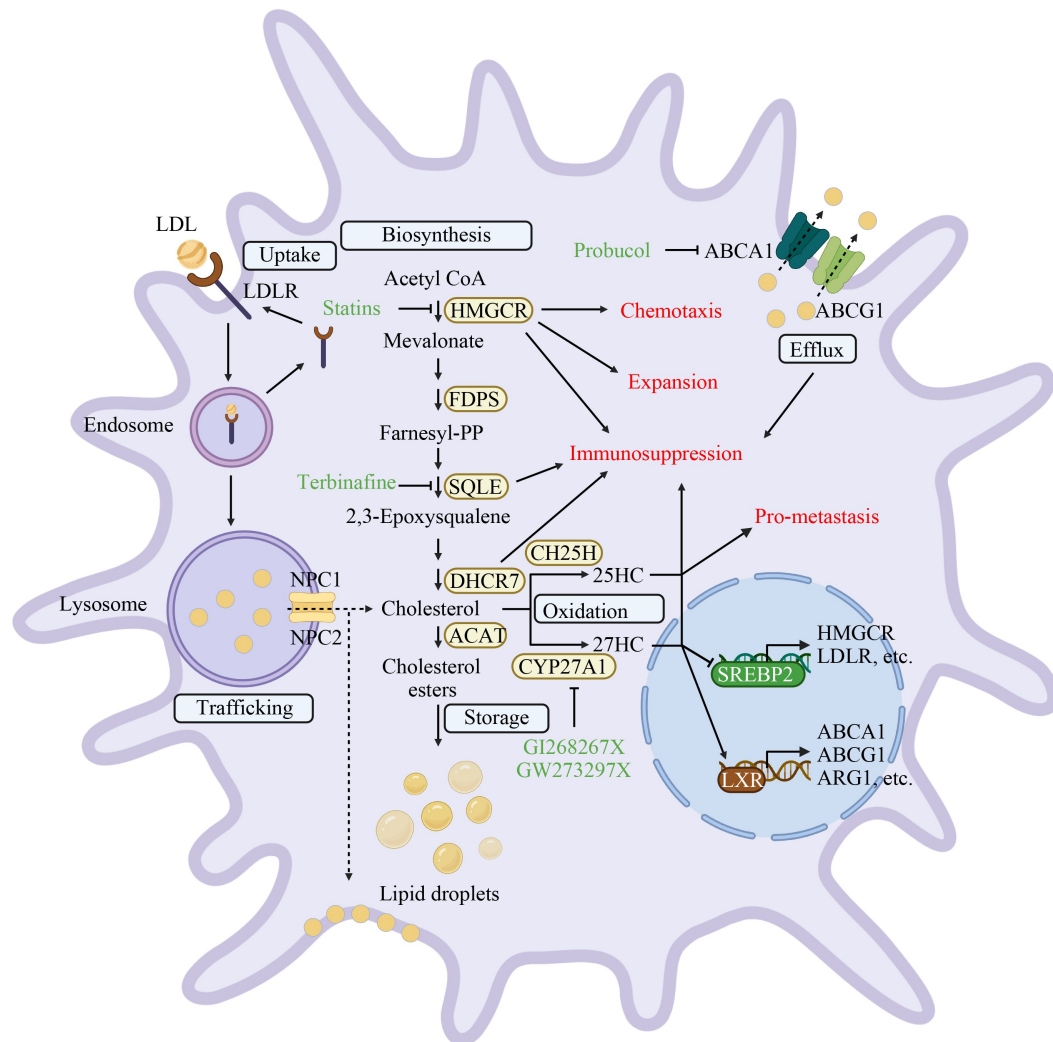


Fig. 2 Cholesterol metabolism in tumor-associated myeloid cells. Cholesterol is synthesized with acetyl-CoA from the TCA cycle, using HMGCR, farnesyl diphosphate synthase (FDPS), SQLE and DHCR7 as the rate-limiting enzymes (highlighted in blue). In addition to *de novo* biosynthesis, cholesterol carried by LDL particles can be taken up by LDL receptor. Excess cholesterol is exported to the blood by ABCA1 and ABCG1. Cholesterol can also be fluxed into cholesterol ester by ACAT (or SOAT) for storage in lipid droplets. Besides, cholesterol can further be converted into 25-hydroxycholesterol by CH25H or 27-hydroxycholesterol (27HC) by CYP27A1. These oxysterols can decrease cholesterol synthesizing genes by inhibiting SREBP2 and activating LXR-mediated cholesterol efflux. Moreover, cholesterol synthesis, oxidation and efflux are frequently upregulated in tumor associated myeloid cells, coordinated with their infiltration and protumor function (highlighted in red). This figure was created using BioRender.

and ensuing reprogramming of histone modification and chromatin accessibility but also generated ROS for glycolytic induction [151].

Cholesterol production might promote the expansion and immunosuppressive activity of MDSCs. In tumor-bearing mouse models, cholesterol promoted BM cell immature differentiation into MDSCs, and increased the levels of MDSC signature molecules, PD-L1 and ROS. The inhibition of cholesterol biosynthesis by HMGCR knockdown resulted in a reduction in cholesterol levels as well as the expression of PD-L1 and ROS in MDSCs [152]. However, RIPK3 deficiency led to cholesterol abrogation in MDSCs, which induced the translocation of LXR β into nuclear to transcript Arg1, consequently,

cholesterol deficiency profoundly elevated the immunosuppressive activity of tumor-infiltrating MDSCs [153]. PD-1 ablation in myeloid cells skewed the fate of myeloid cells away from immunosuppressive MDSCs, but toward a functional effector monocyte/macrophage and DC differentiation, which was associated with cholesterol accumulation [154]. Therefore, the exact role of cholesterol in MDSCs should be further illustrated.

Oxysterols, the oxidized forms of cholesterol or its precursors, could also modulate tumor immunity. Xiao *et al.* show that TAMs exhibited elevated expression of cholesterol-25-hydroxylase (Ch25h), resulting in lysosome-accumulated 25-hydroxycholesterol that activates AMPK α to promote STAT6-dependent Arg1

production. CH25H-deficient macrophages switched “cold tumors” into “hot tumors” and improved anti-PD1 treatment efficacy [155]. In human breast cancer specimens, TAMs highly elevated the CYP27A1 expression and the conversion of cholesterol to 27-hydroxycholesterol (27HC), which promoted tumor growth and metastasis. Besides, 27HC-treated macrophages exhibited a strong immunosuppressive effect on T cell activation and function in an LXR-dependent manner [156]. It was worth noting that MDSCs were also required for the pro-metastatic effects of 27HC [157].

Although myeloid cells could produce cholesterol, they could not catabolize the molecule and therefore needed to dispose of the excess out of the cell or store it as cholesteryl esters in LDs. ATP binding cassette subfamily A member 1 (ABCA1) and ATP binding cassette subfamily G member 1 (ABCG1) were responsible for cholesterol efflux, which regulated plasma membrane cholesterol levels and profoundly influenced macrophage responses to extracellular stimuli. For example, ABCG1 deficiency in macrophages increased their pro-inflammatory phenotype and reduced tumor growth [158]. In a mouse model of metastatic ovarian cancer, tumor cells promoted membrane cholesterol efflux and depletion of lipid rafts from macrophages. Genetic deletion of ABCA1 and ABCG1 could revert the tumor-promoting functions of TAMs and reduce tumor progression [159]. Granulocyte-macrophage colony-stimulating factor (GM-CSF)/PPAR γ signaling increased fatty acid synthesis and cholesterol efflux, yet decreased cholesterol esterification in TAMs from lung adenocarcinoma. TAMs transferred cholesterol to lung adenocarcinoma cells, which increased EGFR phosphorylation and promoted tumor progression. Macrophages could also transfer cholesterol to prostate tumor cells, enhancing androgen receptor activation *in vitro* [160]. Cholesterol depletion was a key feature of TAMs in human lung adenocarcinoma and HCC. Li *et al.* observed that the coordination of exogenous cholesterol and tumor-derived factors promoted ABCA1-mediated cholesterol efflux and decreased cellular cholesterol levels in human primary monocytes/macrophages, resulting in immature and immunosuppressive macrophages. High numbers of ABCA1⁺ TAMs in HCC were correlated with reduced CD8⁺ T cell infiltration and poor clinical outcome [161]. These studies suggested selective modulation of cholesterol metabolism in TAMs may represent a novel strategy for cancer treatment.

Amino acid metabolism

Amino acids played a major role in regulating important cellular events including hormones and peptides synthesis, signal transduction and regulation of gene expression. In myeloid cells, the consumption of amino acids and their

availability were key drivers of cellular identity impacting development, functional polarization, and interaction with other cells [162]. Here, we discussed recent progress and emerging concepts in our understanding of the impact amino acid availability and consumption had on myeloid cell phenotype, with a major focus on three amino acids: arginine, glutamine and tryptophan.

Arginine metabolism

Arginine could be degraded by Arg1. It was highly expressed in TAMs, which was in part dependent on HIF-1 α signaling, lactate, GM-CSF and creatine [163]. Arg1-expressing myeloid cells could inhibit T cell proliferation in an *in vitro* culture system. SLC7A2-mediated arginine uptake in tumor myeloid cells also suppressed T cell proliferation *ex vivo* [164]. Those observations suggested that the Arg1-mediated arginine consumption in TAMs and MDSCs might have an immunosuppressive function. Arginase inhibition enhanced arginine concentration and cytotoxic immune cell infiltration and delayed tumor development [165]. Moreover, studies in pancreatic cancer identified arginine as the most depleted metabolite [166], and Arg1 deletion in myeloid cells suppressed murine tumor progression, which was associated with increased cytotoxic CD8⁺ T cell infiltration and activation [167]. The arginine-polyamine pathway was induced in myeloid cells to promote their survival, and depletion of polyamine prolonged tumor-bearing mouse survival [168]. Myeloid cells also produced creatine from arginine to feed tumor cells to allow their survival in the hypoxic niche [31]. Arginine was also a substrate for proline, which promoted the production of collagen fibrils and subsequent fibrosis, leading to the immune exclusion from tumors [169].

Arginine catabolism through nitric oxide synthase 2 (NOS2) was another key suppressive mechanism of TAMs or MDSCs. Their release of nitric oxide or peroxynitrite could induce T cells apoptosis as well as T cell function and migration inhibition [9,31]. Traditional Chinese medicine saposchnikovia root extract Prim-O-glucosylcimifugin could inhibit the proliferation, metabolism and immunosuppressive ability of MDSCs by inhibiting arginine metabolism and the TCA cycle. Prim-O-glucosylcimifugin could also increase CD8⁺ T cell infiltration in the tumors and enhance the antitumor effect of PD-1 inhibitor [170]. These observations suggested that different arginine catabolism pathways coordinated its pro-tumor phenotype, but the exact mechanisms and functions of such metabolic rewiring in TAMs and MDSCs remained to be investigated.

Glutamine metabolism

As a major source of carbon and nitrogen, glutamine was

essential for production of amino acids, purine, pyrimidines, and lipids. Additionally, glutamine-derived glutamate could be utilized in synthesis of glutathione, which was used to neutralize ROS and maintain redox balance. Glutamine-derived α -KG was required for the differentiation of macrophages to an anti-inflammatory, immunosuppressive phenotype [171]. Glutamine deprivation and glutaminolysis inhibition decreased expression of immunosuppressive genes while upregulating inflammatory genes in macrophages [172]. Therefore, glutamine metabolism contributed to the polarization of macrophages toward an immunosuppressive phenotype like those of TAMs in the TME. Our previous work found that human suppressive immature myeloid cells from colon and breast tumor tissues exhibited high glycolytic metabolism [173]. However, the generation of immature myeloid cells relied on glutaminolysis, regardless of glucose availability. Glutamine metabolism not only supported the expansion of immature myeloid cells with glutamine-derived α -KG but also regulated the suppressive capacity through the glutamate–NMDA receptor axis. Moreover, inhibition of glutaminase GLS1 enhanced the therapeutic efficacy of anti–PD-L1 treatment, with reduced Arg1^+ myeloid cells, increased CD8^+ , $\text{IFN}\gamma^+$ and granzyme B^+ T cells, and delayed tumor growth in an ICB-resistant mouse model [173]. Tumor-primed myeloid cells showed increased immunosuppressive marker expression and OXPHOS fueled by glutamine, inhibiting the glutamine metabolic pathway decreased OXPHOS and immunosuppressive activity [120]. These findings suggest a tumor-promoting role of myeloid glutamine/glutamate catabolism, but its specific function in TAMs and MDSCs remains to be determined.

Glutamine metabolism was a promising target for sensitizing tumors and their immunosuppressive microenvironments toward immunotherapy. JHU083, a prodrug version of the glutamine antagonist 6-diazo-5-oxo-L-norleucine, was a glutamine metabolism inhibitor that was selectively activated in the TME to mitigate toxicity; it was shown to inhibit tumor growth and promote survival in tumor-bearing mice, particularly in combination with immunotherapy [174]. Administration of this prodrug augmented endogenous antitumor immunity, as it promoted activation, proliferation, and memory in tumor-infiltrating lymphocytes [174]. Additionally, JHU083 inhibited the recruitment of immunosuppressive MDSCs to the TME and induced their apoptosis, simultaneously reprogramming MDSCs and TAMs to a proinflammatory antitumor phenotype [175]. Notably, glutamine inhibition via JHU083 increased the effectiveness of anti-PD1 and anti-CTLA4 checkpoint blockade in tumors that did not benefit from monotherapy [175].

Tryptophan metabolism

IDO was an intracellular, tryptophan-metabolizing enzyme that functions through its catalysis of the rate-limiting step of the kynurenine pathway. IDO was highly expressed in TAMs and MDSCs in the TME and played a role in tumor immune escape. Our previous study found that activated CD69^+ T cells fostered immune privilege by upregulating IDO expression in TAMs [176]. Tryptophan metabolism and subsequent depletion via IDO expression in macrophages had been shown to inhibit antigen-specific T cell proliferation and activation [48]. Additionally, kynurenine had been shown to activate the aryl hydrocarbon receptor (AhR), and this activation led to the generation of immunosuppressive Tregs and the resistance of solid tumors to oncolytic adenoviruses treatments [52]. IL-4-induced-1 (IL4I1), an L-amino-acid oxidase, had recently been identified as a potent activator of the AhR pathway by promoting tryptophan catabolism to indole metabolites and kynurenic acid [177]. IL4I1^+ TAMs could prevent T cell proliferation and cytokine production, decrease the CD8^+ T cell response, and promote the differentiation of naive CD4^+ T cells into Tregs. In addition to suppressing the antitumoral T cell response, IL4I1 expression was also shown to recruit immunosuppressive MDSCs to the TME [178]. scRNA-seq analyses revealed that an enriched $\text{IL4I1}^+\text{IDO}^+\text{PD-L1}^+$ TAMs subset was associated with T cell dysfunction in multiple human tumors [179]. In addition to AhR, kynurenine was also bound to the cell surface receptor G-protein coupled receptor 35 (GPR35), GPR35 depletion in myeloid cells suppressed tumor development in genetic and carcinogen-induced tumor models [180].

MDSCs also decreased levels of tryptophan via the expression of IDO in the external environment to impair cytotoxic T cell responses and survival. In patients with breast cancer, increased IDO-expressing MDSC populations were correlated with increased amounts of Tregs and a poor prognosis [181]. In fact, IDO^+ MDSCs tended to be more suppressive than their IDO^- counterparts. Moreover, a recent study showed that IDO vaccine ablated immune-suppressive myeloid populations and enhanced antitumor effects [182].

Current clinical therapeutics targeting myeloid cell metabolism

At present, several clinical trials are underway to evaluate the efficacy of targeting the aforementioned metabolic pathways in various cancers (Table 1). IM156 and IACS-010759, small molecules targeting the OXPHOS pathway, were primarily in Phase I clinical trials (NCT03291938, NCT03272256 and NCT05497778). Cyclooxygenase-2, a rate-limiting enzyme involved in the synthesis of PGE2, is currently being explored as a

Table 1 Therapeutic approaches targeting metabolism pathway in myeloid cells

Targets	Drug type	Drug name	Phase	Trial identifier	Combination regimen	Targeted disease	Clinical outcomes
Oxidative phosphorylation pathway inhibitor	Small molecule	IACS-010759	I	NCT03291938	Monotherapy	With advanced solid tumors and lymphoma	No results posted
	Small molecule	IM156	I	NCT03272256	Monotherapy	Advanced solid tumors and lymphoma	No results posted
	Small molecule	IM156	I	NCT05497778	Gemcitabine and nab-paclitaxel	Advanced pancreatic cancer	No results posted
Cyclooxygenase-2 inhibitor	Small molecule	Celecoxib	II	NCT03026140	Ipilimumab and nivolumab	With stage 1–3 adenocarcinoma of the colon with no signs of distant metastases	No results posted
	Small molecule	Celecoxib	II	NCT03926338	Toripalimab	Mismatch-repair deficient or microsatellite instability-high locally advanced colorectal cancer	No results posted
E-type prostanoid receptor 4 antagonist	Small molecule	TPST-1495	I	NCT04344795	Monotherapy and with pembrolizumab	Advanced solid tumors	No results posted
Glutaminase inhibitor	Small molecule	CB-839	I/II	NCT02861300	Capecitabine chemotherapy	Colon cancer, rectal cancer, and other solid tumors	Results submitted
	Small molecule	CB-839	I	NCT03944902	Niraparib	Platinum-resistant BRCA wild-type ovarian cancer patients	No results posted
Arginase 1 inhibitor	Small molecule	INCB001158	I	NCT02903914	Monotherapy and with pembrolizumab	Advanced/metastatic solid tumors	Well tolerated with early responses observed in pretreated MSS CRC patients
NOS2 inhibitor	Small molecule	L-NMMA	I	NCT03236935	Pembrolizumab	Unresectable or metastatic tumor mutational burden-high solid tumors	No results posted
Aryl Hydrocarbon Receptor (AHR) Inhibitor	Small molecule	IK-175	I	NCT04200963	Monotherapy and with nivolumab	Locally advanced or metastatic solid tumors and urothelial carcinoma	No results posted
	Small molecule	BAY2416964	I	NCT04069026	Monotherapy	Advanced solid tumors	No results posted
	Small molecule	BAY2416964	I	NCT04999202	Pembrolizumab	Advanced solid cancers including head and neck cancer, lung cancer and bladder cancer	No results posted
IDO1 inhibitor	Small molecule	NLG802	I	NCT03164603	Monotherapy	Recurrent advanced solid tumors	No results posted
	Small molecule	D-1MT	I	NCT00739609	Monotherapy	Relapsed or refractory solid tumors	No results posted

Abbreviations: IACS, inhibitor of ATP synthase complex; CRC, colorectal cancer; MSS, microsatellite stable; BRCA, breast cancer susceptibility gene; NOS2, nitric oxide synthase 2; AHR, aryl hydrocarbon receptor; IDO1, indoleamine 2,3-dioxygenase 1; NCT, national clinical trial identifier; MSS CRC, microsatellite stable colorectal cancer; SC, subcutaneous; IV, intravenous.

therapeutic target in several clinical trials (NCT03026140 and NCT03926338). PGE2, in turn, reprogramed myeloid cells toward an immunosuppressive function via interaction with the E-type prostanoid receptor 4. The E-type prostanoid receptor 4 antagonist TPST-1495 was still undergoing clinical trials as both a monotherapy and in combination with pembrolizumab (NCT04344795). Other clinical trials concerning amino acid metabolism pathways included those targeting glutaminase (NCT02861300 and NCT03944902), arginase 1 (NCT02903914) and NOS2 (NCT03236935). The AHR

inhibitor IK-175 associated with tryptophan metabolism was undergoing Phase I clinical trials as a monotherapy and in combination with nivolumab in solid tumors and urothelial carcinoma (NCT04200963). Another AhR inhibitor BAY2416964 has been evaluated as a monotherapy (NCT04069026) or in combination with pembrolizumab (NCT04999202) in advanced solid cancers including head and neck cancer, lung cancer and bladder cancer. While Phase II clinical trials showed that the combination of IDO inhibitors and immune checkpoint blockade was well tolerated and achieved an

objective response rate of 55% [183], this combination therapy failed in Phase III trials [184,185]. Additionally, metabolic pathways concerning iron metabolism were also being investigated as novel therapeutic targets.

To be noted, in the TME, myeloid cells exhibit plasticity and heterogeneity, rather than binary polarization. Therefore, there is a pressing need to comprehensively explore the metabolic networks among these diverse myeloid subsets. Additionally, most metabolic pathways currently under clinical investigation are not exclusive to myeloid cells, and the same metabolic products may lead to opposite effects depending on their interactions with different cell types such as T cells or tumor cells. This complexity presents challenges but also opportunities for developing therapeutic strategies that selectively target myeloid cell metabolism.

The accumulation of TAM and MDSC

Given that cells of the myeloid compartment were generally short-lived, this growing and fast-turnover pool of tumor-associated myeloid cells needed prompt and continuous regeneration, which could be achieved by enhancing peripheral recruitment, promoting survival and proliferation within the tumor, and biasing host hematopoietic activity toward myeloid cells differentiation.

Chemotaxis

Different immune cells traffic into the TME and modulate immune responses in primary tumors and metastatic sites. Chemokines, small secreted proteins, are pivotal in immune cell trafficking and lymphoid tissue development. In the TME, chemokines can be expressed by tumor cells as well as immune and stromal cells. In response to specific chemokines, different immune cell

subsets migrate into the TME and regulate tumor immune responses in a spatiotemporal manner [186] (Fig. 3).

Monocytes continuously egressed from the BM in a strictly CCR2-dependent manner, initially circulating in the bloodstream as classical or “inflammatory” CCR2^{hi} monocytes with a half-life of approximately one day [187]. Under steady-state conditions, these monocytes could be recruited at a low rate to tissues, differentiating into macrophages that supplement the tissue-resident macrophages established during embryogenesis to maintain tissue homeostasis. However, in the context of the tumor milieu, tumor cells employed various mechanisms to upregulate chemokine expression, thereby enhancing the recruitment of monocytes, which subsequently differentiated into TAMs. The chemokine C-C motif ligand 2 (CCL2), also known as monocyte chemoattractant protein 1 (MCP-1), facilitated the migration of monocytes into the tumor sites by binding to its receptor CCR2. Elevated levels of CCL2 have been observed in several malignancies, including HCC [188,189], breast cancer [190], and colorectal cancer [191]. Blockade of the CCL2/CCR2 signaling pathway inhibited the recruitment of monocytes and their subsequent M2 polarization, generally enhancing T cell immunity and reducing the growth of various tumors, which indicated that their pro-tumoral activities most often outweigh their anti-tumoral ones [189,192–195]. CCL2 also facilitated the recruitment of MDSCs to tumors. Studies across numerous animal models and cancer patient samples have demonstrated that increased CCL2 levels correlate with heightened MDSCs accumulation in the TME, thereby promoting tumor progression [196–199]. This indicated that, in addition to CCR2, other receptors expressed on TAMs and MDSCs, such as CCR1, CCR5, CXCR1, and CXCR2, may serve as alternative mechanisms for tumor infiltration. This provided opportunities to reduce the accumulation of these cells in the TME by interfering with these receptors

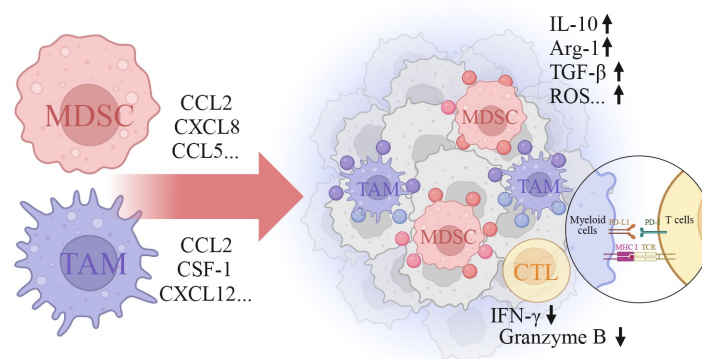


Fig. 3 Tumor-driven recruitment of tumor-associated myeloid cells. Tumor-derived chemokines such as CCL2, CXCL8, CXCL12, and CSF-1 recruit MDSCs and TAMs into the TME. These myeloid cells contribute to immune evasion by producing immunosuppressive mediators and upregulating PD-L1, suppressing CTL effector functions and facilitating tumor progression. This figure was created using BioRender.com.

or their ligands' signaling. For instance, the MDSCs attractant CXCL8, whose receptors were CXCR1 or CXCR2, was found to be elevated in various cancer types, such as breast, colon, ovarian, pancreatic, prostate, and several hematological malignancies [200]. The inhibition of CXCR1 or CXCR2 has shown a potential to enhance sensitivity to ICB therapy and restrict tumor metastasis [201,202]. In a recent study, CAR T cells engineered with CXCR1 or CXCR2 demonstrated increased accumulation within tumors, leading to a significant reduction in tumor burden [203]. CCR5 is also expressed in both monocytes and MDSCs. Therefore, CCR5, along with its associated ligands, is a key element in the recruitment program of monocytes and MDSCs. Meanwhile, CCR5 was also expressed in cytotoxic T lymphocytes (CTLs), which were a major source of its ligand CCL5 [204] and were often considered as part of the type 1 immune response. This suggested that these chemokine-receptor signaling pathways facilitate T cell interactions with monocytes or macrophages in inflamed tissue environments. Additionally, CCR5 expressed on CD8⁺ T cells in immunogen-draining lymph nodes permitted these cells to be guided to sites of DCs-CD4⁺ T cell interaction where the cognate chemokines CCL3 and CCL4 were produced [205]. Finally, activated CTLs could produce CCR5 ligands CCL3 and CCL4. This accelerated the recruitment of distant CCR5⁺ T cells and further speeded up swarming behavior [206]. Further investigation is required to elucidate the role of CCR5 in distinct immune cell types within the TME, including its function on TAMs and T cells.

In addition to chemokine-receptor signaling pathways, the signaling factor CSF-1 (also known as colony-stimulating factor-1 or M-CSF) served as a critical attractant for macrophages. The interaction of CSF-1 with its receptor CSF-1R orchestrated a cascade of downstream signaling pathways involving the phosphoinositide 3-kinase (PI3K)-AKT pathway, mitogen-activated protein kinase (MAPK) pathway, and JAK-STAT pathway. These pathways collectively regulated macrophage activation, polarization, and proliferation, illustrating that CSF1 function governs macrophage biology and diseases involving macrophage dysfunction. CSF-1 was highly expressed in multiple tumors and subsequently enhanced the accumulation and migration of TAMs. Recent research has shown that IL-1 β enhances the expression of HIF-1 α , PD-L1, and CSF1, facilitating the infiltration of TAMs and MDSCs through the CSF-1/CSF1R axis. Knockdown of CSF1 attenuated intra-tumoral TAMs and MDSCs infiltration and HCC metastasis [207]. In some studies, CSF-1 has been found to elevate the expression of CCL2 in macrophages [208]. Given that CSF-1/CSF1R signaling was instrumental in shifting macrophage polarization toward a tumor-promoting phenotype, targeting the CSF-1/CSF-1R axis

emerged as a promising therapeutic strategy.

Survival

Tumors possess a unique physicochemical environment that differs significantly from that of normal tissues, resulting in complex metabolic patterns such as hypoxia, elevated lactate levels, and reduced glucose availability. These features collectively create an adverse environment that impairs the survival and function of recruited immune cells. Despite their typically short lifespan, their substantial presence in tumor tissues indicates that these cells have developed intricate mechanisms to adapt to the tumor-specific environment. Understanding how tumor-associated myeloid cells survived in the inhospitable TME is of significant importance [15] (Fig. 4).

Circulating monocytes play a crucial role in innate immune surveillance. In a steady-state, these monocytes have a short lifespan, with most either leaving the circulation or undergoing apoptosis. However, in an inflammatory environment, chemokines and pathogen signals guide monocytes across blood vessels into damaged or infected tissue areas, where they rapidly differentiate into macrophages or dendritic cells to perform their respective immune functions. Unlike monocytes, macrophages have a significantly extended lifespan, ranging from months to years. Cytokines such as M-CSF, GM-CSF, and IL-34 were crucial for the survival and proliferation of macrophages, stimulating at least three signaling pathways: the PI3K pathway, the MAPK pathway, and the JAK-STAT pathway. Mice lacking M-CSF showed deficiencies in most tissue-resident macrophages [209], while IL-34-deficient mice displayed selective reductions in Langerhans cells and microglia [210]. Thus, targeting M-CSF or its corresponding receptor was an effective strategy for depleting macrophages within the TME in cancer therapy. This approach could reduce the recruitment of macrophages and increase the apoptosis of existing TAMs. Previous studies have shown that RG7155 was a selective inhibitor of CSF-1R dimerization, effectively blocking both ligand-dependent and ligand-independent receptor activation. Administration of RG7155 to patients led to significant reductions in CSF-1R⁺CD163⁺ macrophages in various solid malignancies, which also altered the T cell composition and contributed to a more favorable immune response against the tumors [211]. Additionally, inhibiting the CSF-1/CSF-1R signaling pathway could enhance the effectiveness of various immunotherapies, including CD40 agonists [212], PD-1 inhibitors [213], CTLA-4 antagonists [214], and adoptive T cell therapies [215]. Therapeutic blockade of GM-CSF effectively depleted TAMs by reducing their viability and altering their polarization, which was correlated with decreased STAT5 phosphorylation. This strategy functionally

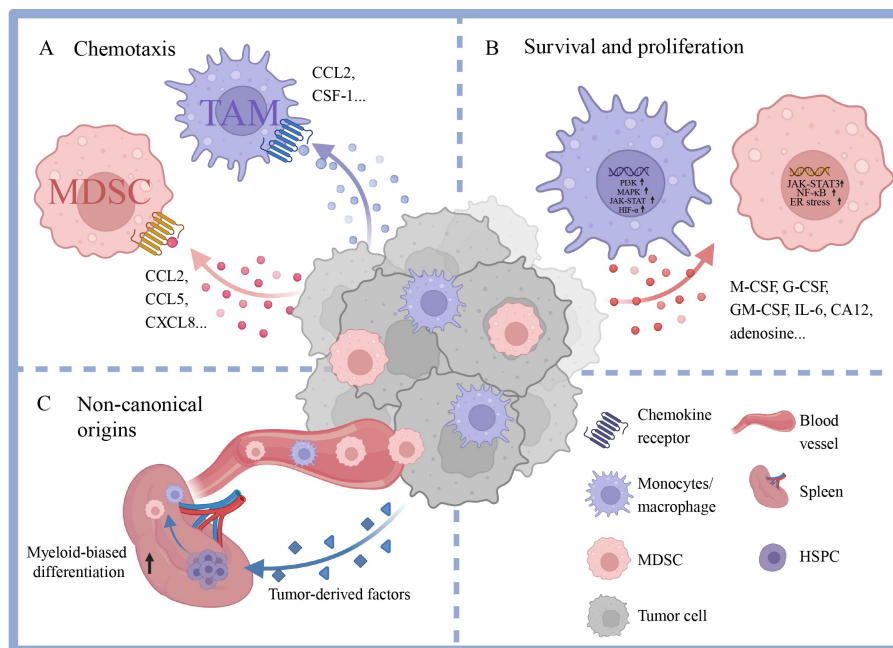


Fig. 4 Different mechanisms mediate the accumulation of TAMs and MDSCs in TME. The accumulation of tumor-associated myeloid cells can be facilitated through several mechanisms: (A) enhancing the recruitment of myeloid cells from peripheral sources, (B) promoting their survival and proliferation within TME, and (C) skewing host hematopoietic activity toward the differentiation of myeloid cells. This figure was created using BioRender.com.

reprogrammed myeloid cells, resulting in enhanced cytotoxic T cell engagement [216].

The metabolic state of macrophages significantly influences their survival and function under various physiologic and pathological conditions. Research has shown that transient glycolytic activation of peritumoral monocytes can induce carbonic anhydrase 12 upregulation in both monocytes and macrophages through HIF-1 α and an autocrine cytokine-dependent pathway. This mechanism supports the survival of monocytes and macrophages in acidic microenvironments and may help explain the relatively high levels of infiltration of these cells observed in HCC tumor tissues [217]. Another study demonstrated that β -glucosylceramide derived from tumor cells drove the reshuffling of lipid composition and saturation in the endoplasmic reticulum membrane of macrophages. This process promoted pro-tumorigenic polarization in macrophages, enhancing their survival capacity within the TME [141]. Similarly, recent research has shown that tumor-induced lipid reshuffling and TNF- α -mediated uptake of tumoral fatty acids contribute to the formation of lipid droplets in TAMs, thereby extending their survival [218]. A detailed understanding of the signaling pathways and metabolic states regulating TAMs survival could lead to novel therapeutic strategies to control their accumulation.

MDSCs generally have a short lifespan; however, their survival dynamics vary considerably across different pathological contexts and tissue environments. A critical

regulator of MDSC survival is the STAT3 signaling pathway, which is activated by tumor-derived factors like G-CSF, GM-CSF, and IL-6. Activated STAT3 orchestrated essential functions in MDSCs, including cell survival, proliferation, differentiation, and apoptosis regulation. It upregulates key proteins like MYC, cyclin D1, and B cell lymphoma-extra large, which resisted cell death and contributed to the expansion and maintenance of MDSCs. In addition to STAT-related signaling pathways, the NF- κ B pathway plays a significant role in the survival and activation of MDSCs. This pathway is activated by inflammatory cytokines, such as TNF- α , which binds to TNF receptor-2. This interaction upregulates c-FLIP expression and inhibits caspase-8 activity, thereby promoting the survival of MDSCs in murine models [219]. A distinguishing characteristic of MDSCs, compared to monocytes and neutrophils, is the activation of the ER stress pathway [220,221]. This activation leads to the upregulation of DR5, a key receptor in the TRAIL pathway [221], providing a potential therapeutic target for selectively inducing apoptosis in MDSCs. For instance, the agonistic DR5 antibody DS-8273a has been tested in phase I clinical trials, showing potential for selectively inducing MDSCs apoptosis and enhancing antitumor immunity [222]. Recent research indicated that autophagy might also play a role in the survival of MDSCs. Inhibition of autophagy increased the apoptosis of MDSCs, indicating that autophagy enhanced their survival. This process was

mediated by HMGB1 and highlighted the role of autophagy in sustaining MDSCs viability [223]. Collectively, these insights underscored the complex regulation of TAMs and MDSCs survival. Therapeutic strategies targeting molecules like M-CSF/CSF-1R and STAT3 to modulate TAMs and MDSCs functions hold promise for disrupting their pro-tumor functions and enhancing immune therapy efficacy.

Proliferation

In addition to the recruitment of myeloid cells, the proliferation of pre-existing myeloid cells within tissues also contributes significantly to the abundance of myeloid cells in the TME. This local expansion of myeloid cells is driven by various factors, including cytokines, growth factors, and other signaling molecules secreted by tumor and stromal cells. These factors not only attract myeloid cells to the tumor site but also stimulate their proliferation and survival once they arrive. This dual mechanism ensures a continuous supply of myeloid cells, which play crucial roles in supporting tumor growth, suppressing anti-tumor immune responses, and promoting metastasis (Fig. 4).

It was long believed that TAMs primarily originated from circulating monocytes. However, recent evidence suggested that some macrophages in tissues such as the liver and brain were established from progenitors derived from the yolk sac and fetal liver. The pool of macrophage could be maintained through monocytes input and proliferation. Adenosine, a metabolic product of ATP conversion to AMP, typically accumulates in tumors due to increased CD73 expression during tumor growth. While adenosine is essential for maintaining tissue homeostasis and preventing excessive immune responses during inflammation and infection, it can also hinder immune responses against tumor cells by disrupting cytotoxic anti-tumor immune responses. Recent studies indicated that HCC-derived adenosine could induce TAMs proliferation via the adenosine/A2A pathway [224]. Both *in vitro* and *in vivo* models showed that PD-L1 antibody treatment enhanced spontaneous proliferation, survival, and activation of mouse and human macrophages, which was linked to the upregulation of mTOR pathway. These findings suggested that targeting PD-L1 signaling in macrophages could reverse their immune-suppressive state and boost antitumor activity [225]. Previous research has shown that phosphoglycerate dehydrogenase (PHGDH), the first rate-limiting enzyme in the serine synthesis pathway, was activated in IL-4 induced M2 macrophages and was critical for their anti-inflammatory function. High levels of PHGDH expression have been observed in TAMs isolated from murine orthotopic lung tumors. Inhibiting PHGDH has been found to reduce IL-4-induced M2

polarization and macrophage proliferation. These findings suggest that PHGDH could be a potential target for modulating TAM infiltration to enhance the body's immune response against tumors [226].

The same growth factors that facilitated regular myelopoiesis in the BM, namely GM-CSF, G-CSF, and CSF1, also promoted the accumulation of MDSCs [227]. Therefore, the dysregulated production of such growth factors and the constant presence of inflammatory mediators in the context of chronic inflammation and tumor resulted in the expansion and accumulation of MDSCs. The activation of mTOR signaling in tumor cells has also been described as a major driver of this process through increased secretion of G-CSF [228]. In addition to the growth factors mentioned above, VEGF was a potent stimulator of MDSCs expansion owing to its ability to inhibit the differentiation of immature myeloid cells [229–231]. The JAK/STAT3 pathway was crucial for promoting the expansion of MDSCs. Consequently, cytokines that activated this pathway, including GM-CSF, G-CSF, and IL-6, were key contributors to MDSC proliferation [227]. On the one hand, STAT3 activation upregulated MYC, B cell lymphoma-extra large, and cyclin D1, which were essential for the proliferation and survival of MDSCs. On the other hand, STAT3 also promoted MDSCs proliferation by upregulating the expression of S100A8 and S100A9, whose receptors were also present on the surface of MDSCs. The STAT3-inducible upregulation of S100A9 in myeloid progenitor cells inhibited the differentiation of DCs and macrophages, leading to the accumulation and expansion of MDSCs. Conversely, MDSCs expansion was not observed in S100A9-deficient mice following tumor challenge [232]. IL-6 was also reported as an important cytokine mediating MDSCs expansion via STAT3. In mice, the overexpression of PPAR γ , which was defined as an anti-inflammatory molecule, upregulated IL-6 levels to activate STAT3 and expand MDSCs [233]. Further study demonstrated that in a mouse model of breast cancer, MDSCs secreted IL-6 at the tumor site, thus inducing pSTAT3 expression by tumor cells and promoting tumor progression and metastasis [234].

Non-canonical origins

The BM was the primary hematopoietic organ, playing a crucial role in maintaining homeostasis and responding to pathological conditions. Under homeostasis, BM tightly regulated the process of hematopoiesis, generating various blood cells, including erythrocytes, leukocytes, and platelets. Hematopoietic stem and progenitor cells (HSPCs) were central to this process, possessing the abilities of self-renewal and multipotent differentiation. At a steady-state, HSPCs resided primarily in the BM and remained largely quiescent, only entering the cell cycle

when needed to produce specific lineages of blood cells. This regulation ensured a balanced production of blood cells, meeting the physiologic demands of the organism without exhausting the HSPCs pool. In recent years, studies have found that HSPCs could directly sense environmental signals and pro-inflammatory cytokines, allowing them to actively participate in initiating the immune response. These mechanisms provided a basis for tumor-regulated emergency myelopoiesis, which altered BM niche and HSPCs activity by a range of factors, such as cytokines and chemokines. Emergency myelopoiesis became crucial in tumors where the short lifespan of myeloid cells necessitated rapid and sustained regeneration from HSPCs, biased toward generating myeloid cells with tumor-promoting properties. Studies across various solid tumors, including hepatocellular, breast, cervical, esophageal, gastrointestinal, lung, and ovarian cancers, consistently showed circulating HSPCs skewed toward granulocytic differentiation [235]. Both human and murine studies provided evidence supporting the generality and importance of hematopoietic skewing observed in cancers [235–239].

Hematopoietic alteration was not restricted to BM, it has also been observed in multiple extramedullary organs. Recent research underscored the spleen as a pivotal site of extramedullary hematopoiesis. The spleen was primarily known for its roles in blood filtration, differentiation, and activation of T cells and B cells, as well as for antibody production. In addition to studies on the expansion of myeloid precursors in the spleen [240–242], the spleen had been found to be the reservoir of a large number of HSPCs, including HSCs and granulocyte/macrophage progenitors (GMPs). Their descendants, including monocytes and neutrophils, were relocated to tumor sites and exerted tumor-promoting functions [236,243]. It suggested that splenic monocytes and granulocytes might have received distinct signals compared to those in the BM. Although phenotypically and functionally, there were no notable differences between the two counterparts, this mechanism could not be formally excluded. Consistently, our investigation revealed that the spleen accumulated a population of HSPCs that was functionally distinct from those in the BM, profoundly expanding and supporting myeloid-biased myelopoiesis in various types of solid tumors [238]. These findings suggested the generality of splenic myelopoiesis. The mechanisms underlying the activity of splenic HSPCs and the adaptation of the extramedullary hematopoiesis niche to the organism's environment remained not fully elucidated. However, these processes are likely attributed to two key factors. On one hand, there may be selective recruitment of HSPCs to the spleen, potentially mediated by pathways like the CCL2/CCR2 axis. On the other hand, HSPCs might engage in a dynamic interplay with their niche through the secretion of various cytokines that

regulate their own function. This HSPCs-niche interaction could be crucial in adapting to the demands of the microenvironment [244]. Understanding the regulatory mechanisms of splenic myelopoiesis was vital for controlling myeloid cell responses and fostering tumor suppression. Thus, targeting splenic myelopoiesis presented substantial potential for inhibiting tumor-promoting myeloid cell responses and shifting the balance toward tumor suppression. A comprehensive understanding of the functional specialization and regulatory mechanisms of splenic myelopoiesis will be essential for managing myeloid cell responses at their origin.

It was also noteworthy that the conventional understanding was that myeloid cells primarily developed from HSPCs originating in the BM or migrating to the spleen via myelopoiesis. In normal physiology, HSPCs differentiated into common myeloid progenitors, which then further differentiated into GMPs or megakaryocyte/erythrocyte progenitors (MEPs), ultimately giving rise to myeloid cells or erythrocytes/platelets. Such studies have convincingly demonstrated that lineage fate may be predetermined earlier than the common myeloid progenitors stage with advancements in single-cell sequencing, lineage tracing, and other technologies. Zhu *et al.* found that tumor-derived GM-CSF mediated the transdifferentiation of CD45⁺ erythroid progenitor cells (CD45⁺Ter119⁺CD71⁺, EPCs) into the myeloid lineage, known as erythroid-derived myeloid cells (EDMCs), thereby supporting and supplementing tumor-promoting myeloid cell generation at its source [245,246]. Interestingly, Cao *et al.* reported one population of tumor-inducible, erythroblast-like cells (Ter-cells, CD45⁻Ter119⁺CD71⁺) deriving from megakaryocyte-erythroid progenitor cells. Ter-cells that were enriched in the enlarged spleen of hosts bearing advanced tumors produced artemin, a neurotrophic factor, and facilitated tumor progression [247]. Given the powerful immunosuppressive capabilities of EPCs in the TME, further understanding of the tumor-induced erythrocyte immune regulation mechanisms and investigating their developmental origins are crucial from a therapeutic standpoint.

Current clinical therapeutics targeting myeloid cell accumulation

In clinical research, one strategy for targeting myeloid cells is to inhibit their infiltration into tumors. Targeting these chemotaxis-related pathways reduced myeloid cell infiltration and increased anti-tumoral immunity in preclinical studies [248–250]. Accordingly, a broad range of clinical trials was initiated to explore the inhibition of myeloid cell chemotactic pathways (Table 2), including those mediated by CCL2–CCR2, CCL5–CCR5, CSF1–CSF1R, CXCR1, CXCR2, CXCR4, and IL-8 in

Table 2 Therapeutic approaches targeting myeloid cells accumulation

Therapeutic target	Drug type	Drug name	Phase	Trial identifier	Combination regimen	Targeted disease	Clinical outcomes	
CSF1R antagonists	Small molecule	AMG 820	Ib/II	NCT02713529	Pembrolizumab	Select advanced solid tumors	Limited clinical activity but was well tolerated at the recommended dose of 1100 mg AMG 820 with 200 mg pembrolizumab	
	Small molecule	ARRY-382 (PF-07265804)	Ib/II	NCT02880371	Pembrolizumab	PD1/PDL1-refractory tumors, platinum-refractory ovarian cancer, and PDAC	Despite limited clinical benefits, the combination was well tolerated	
	Small molecule	ARRY-382 (PF-07265804)	I	NCT01316822	Monotherapy	Solid tumors	No results posted	
	Small molecule	Pexidartinib (PLX3397)	I	NCT01790503	Radiotherapy and temozolomide	Recurrent glioblastoma	Safety and efficacy data reported. Minimal impact observed on PFS and OS	
	Small molecule	Pexidartinib (PLX3397)	I	NCT02777710	Durvalumab	CRC, PDAC, metastatic cancer, advanced cancer	No results posted	
	Small molecule	Pexidartinib (PLX3397)	I	NCT02452424	Pembrolizumab	Melanoma and other solid tumors	Terminated for lack of clinical efficacy	
	Small molecule	Pexidartinib (PLX3397)	I/II	NCT01596751	Eribulin	Metastatic breast cancer	Well tolerated at 1000 mg/day, but with limited efficacy	
	Antibody	LY3022855 (Lilly)	I	NCT02718911	Durvalumab or tremelimumab	Advanced solid tumors	No efficacy, but well tolerated	
	Antibody	LY3022855 (Lilly)	I	NCT02265536	Monotherapy	Breast and prostate cancer	Well tolerated with evidence of immune modulation; limited clinical efficacy observed	
	Antibody	LY3022855 (Lilly)	I	NCT03153410	Cyclophosphamide, GVAX and pembrolizumab	PDAC	No results posted	
	Antibody	LY3022855 (Lilly)	I/II	NCT03101254	Cobimetinib and vemurafenib	Melanoma	Poorly tolerated; limited efficacy. Phase II halted	
	Antibody	Cabiralizumab (BMS-986227, FPA008)	II	NCT04050462	Nivolumab	HCC	No results posted	
	Antibody	Cabiralizumab (BMS-986227, FPA008)	I/II	NCT03335540	Nivolumab	Solid tumors	No results posted	
	Antibody	Cabiralizumab (BMS-986227, FPA008)	II	NCT03336216	Nivolumab with and without chemotherapy	PDAC	Limited efficacy	
	Antibody	Cabiralizumab (BMS-986227, FPA008)	II	NCT03697564	Nivolumab and gemcitabine	PDAC	No results posted	
	Antibody	Cabiralizumab (BMS-986227, FPA008)	II	NCT03768531	Nivolumab	Biliary tract cancer	Withdrawn	
	Antibody	Cabiralizumab (BMS-986227, FPA008)	II	NCT03927105	Nivolumab	Relapsed/refractory T cell lymphoma	Safety data reported	
	Antibody	Cabiralizumab (BMS-986227, FPA008)	I	NCT03431948	Nivolumab and radiotherapy	Advanced metastatic cancers	No results posted	
	CSF1 antagonists	Antibody	Lacnotuzumab (MCS110)	I/II	NCT02807844	PDR001	Solid tumors	Safety reported
		Antibody	Lacnotuzumab (MCS110) (Novartis)	II	NCT02435680	Carboplatin and gemcitabine	TNBC	Safety reported, no efficacy

(Continued)

Therapeutic target	Drug type	Drug name	Phase	Trial identifier	Combination regimen	Targeted disease	Clinical outcomes
	Antibody	Lacnotuzumab (MCS110) (Novartis)	I/II	NCT03742349	Spartalizumab and LAG525	TNBC	No results posted
	Antibody	Lacnotuzumab (MCS110)	I/II	NCT02807844	PDROO1	Solid tumors	Preliminary safety and limited efficacy
	Antibody	Lacnotuzumab (MCS110)	II	NCT02435680	Carboplatin and gemcitabine	TNBC	Safe, limited efficacy
	Antibody	Lacnotuzumab (MCS110)	I/II	NCT03742349	Spartalizumab and LAG525	TNBC	No results posted
CCR2 antagonists	Small molecule	PF-04136309 (PF-6309)	Ib/II	NCT01413022	FOLFIRINOX	PDAC	Potential efficacy signal
	Small molecule	PF-04136309 (PF-6309)	Ib/II	NCT02732938	Nab-paclitaxel	PDAC	No efficacy signal and increased toxicity
	Small molecule	BMS-813160 (BMS CCR2/5 inhibitor)	II	NCT04123379	Nivolumab	HCC/NSCLC	No results posted
	Small molecule	BMS-813160 (BMS CCR2/5 inhibitor)	I/II	NCT03767582	GVAX, radiotherapy and nivolumab	PDAC	No results posted
	Small molecule	BMS-813160 (BMS CCR2/5 inhibitor)	I/II	NCT03496662	Gemcitabine, paclitaxel and nivolumab	PDAC	Results reported in <i>ClinicalTrials.gov</i>
CXCR2/IL-8 antagonists	Small molecule	AZDS5069 (AstraZeneca)	I/II	NCT02499328	Durvalumab	HNSCC	Safety data reported, no efficacy
	Small molecule	AZDS5069 (AstraZeneca)	I/II	NCT02583477	Durvalumab	PDAC	Minimal efficacy observed
	Small molecule	AZDS5069 (AstraZeneca)	I/II	NCT03177187	Enzalutamide	Metastatic castrate-resistant prostate cancer	Terminated
	Antibody	BMS-986253 (HuMax-IL8)	I/II	NCT03689699	Nivolumab and degarelix	Hormone-sensitive prostate cancer	No results posted
	Antibody	BMS-986253 (HuMax-IL8)	I/II	NCT04050462	Nivolumab	HCC	No results posted
	Antibody	BMS-986253 (HuMax-IL8)	I	NCT04123379	Nivolumab	HCC, NSCLC	No results posted
	Antibody	BMS-986253 (HuMax-IL8)	I/II	NCT03400332	Nivolumab or nivolumab and ipilimumab	Metastatic or unresectable solid tumors	No results posted
	Antibody	BMS-986253 (HuMax-IL8)	I	NCT04572451	Radiotherapy and nivolumab	Metastatic solid tumors	No results posted
CXCR4 antagonists	Small molecule	USL311	I/III	NCT02765165	Monotherapy or with lomustine	Advanced solid tumors; relapsed/recurrent glioblastoma multiforme	Due to early termination of study in phase 1, efficacy outcomes were not analyzed for subjects in part 1a or part 1b
	Peptide	LY2510924	I	NCT02737072	Durvalumab	Advanced refractory solid tumors	No dose-limiting toxicities observed. Recommended phase 2 dose: 40 mg LY2510924 SC daily with 1500 mg durvalumab IV, showing acceptable safety and tolerability
	Peptide-drug conjugate	MB1707 conjugated CXCR4 peptide antagonist	I	NCT05465590	Conjugated with paclitaxel	Advanced cancer	Withdrawn

Abbreviations: CSF1R, colony-stimulating factor 1 receptor; PD1, programmed cell death protein 1; PDL1, programmed death-ligand 1; PDAC, pancreatic ductal adenocarcinoma; CRC, colorectal cancer; TNBC, triple-negative breast cancer; HCC, hepatocellular carcinoma; NSCLC, non-small cell lung cancer; PK, pharmacokinetics; GVAX, granulocyte-macrophage colony stimulating factor vaccine; CTLA4, cytotoxic T-lymphocyte antigen 4; HNSCC, head and neck squamous cell carcinoma; IL-8, interleukin 8; GBM, glioblastoma multiforme; SC, subcutaneous; IV, intravenous; FOLFIRINOX, combination chemotherapy regimen (5-FU, leucovorin, irinotecan, and oxaliplatin).

various types of solid cancer [14].

Preclinical studies have shown enhanced efficacy of CCR2 inhibition in various cancer treatments including chemotherapy and immunotherapy [251–255]. A phase 1b study of CCR2 inhibition with the small molecule inhibitor PF-04136309 combined with FOLFIRINOX (leucovorin, fluorouracil, irinotecan, and oxaliplatin) chemotherapy showed an increase in efficacy over the group with FOLFIRINOX alone (NCT01413022). Although CCL2–CCR2 blockade could impair the recruitment of circulating monocytes, the tissue resident macrophages in PDAC were demonstrated as key regulators in cancer progression [256] and should be considered as therapeutic targets. Interestingly, despite the improved efficacy, patients receiving CCR2 inhibition showed increased tumor-infiltrating CXCR2⁺ TAN following treatment. This compensatory recruitment of alternative myeloid subsets may lead to a persistent immunosuppressive TME, highlighting the potential consideration of combined inhibition of myeloid cell chemotactic pathways [257]. In various cancers, inhibitors AMG 820 targeting the CSF1R as monotherapy or combination with pembrolizumab (NCT02713529) had not shown significant anti-tumor effects [258]. The limitations in the efficacy of CSF1R inhibitors might be due to insufficient depletion of heterogeneous protumoral macrophage populations and diverse protumorigenic compensatory mechanisms. In colorectal cancer, anti-CSF1R therapy selectively targeted and reduced the number of pro-inflammatory macrophages within the tumor, while a population of pro-angiogenic macrophages persisted [259]. Moreover, inhibition of CSF1R conversely caused the recruitment of PMN-MDSCs and was accompanied by the accumulation of Foxp3⁺ regulatory T cells, which limited the efficacy of the treatment [260,261]. Similar compensatory mechanism was observed in the treatment of small-molecule inhibitor of CXCR1 and CXCR2, possibly due to co-expression of CXCR1 and CSF1R on macrophages [262]. These observations underscored the need for further investigation into the potential benefits of the combination of targeting multiple chemotaxis-related pathways.

Despite the association of TAM and MDSC infiltration in tumors with poor prognosis and treatment resistance, the clinical translation of therapies that solely inhibit overall myeloid cell infiltration remains challenging. This may be primarily due to the heterogeneity of tumor-associated myeloid cells. The pro- and anti-tumor myeloid subtypes often simultaneously coexist within the tumor milieu, potentially competing for the balance of the local myeloid response. Our recent studies revealed that the balance of microenvironmental myeloid cell response significantly impacts the TIME status, tumor progression,

and efficacy of immunotherapy in both mice and patients [263,264]. Therefore, further understanding the environmental factors and key subsets involved in pro-tumor myeloid responses may provide an alternative approach to tipping the balance of myeloid response toward tumor suppression, thereby enhancing the benefits of myeloid-targeted therapy.

Conclusions and perspective

In addition to their tumor-promoting activities, myeloid cells are also critical players in mediating the immune surveillance and therapeutic efficacy against tumors. That could explain that direct targeting myeloid cells or lineages failed to achieve therapeutic benefit. Recent studies, especially those concerning the metabolic rewiring (involving multiple metabolic pathways) and accumulation (including the non-canonical mechanisms) of myeloid cells within tumors, have greatly advanced our understanding about the diverse routes leading to the specific characteristics and functions of these cells, thus providing novel targets for stand-alone or combinational anti-tumor treatments.

Myeloid cells might simultaneously exhibit activatory and inhibitory properties. For example, activated monocytes/macrophages often express high levels of PD-L1 in many tissues. The ultimate functions of these cells depend on the composition of and receptors expressed by their surrounding cells. Therefore, deciphering the interaction network between regional myeloid and non-myeloid cells is of utmost importance to determine the key molecules/pathways in regulating their functions. In addition, as proposed by Song *et al.* in their new concept of onco-spheres in cancer ecosystem, cancer cells should be conceived as “living organisms” and it is important to explore their interacting with cellular or noncellular components in the host internal environment, not only within local TME, but also with distant organ niche, host’s nervous, endocrine and immune systems [106]. Technologies including scRNA-seq, multiplex IHC, and mass cytometry, have greatly improved our ability to explore the diversity of tumor-associated myeloid cells, and future advances in the field will provide more insights to build up myeloid-based models for precision medicine. Future studies will also enable the next wave of cancer immunotherapy agents that will selectively target pro-tumoral myeloid cell subsets, while leaving those anti-tumoral ones unimpacted, to further enhance the clinical outcomes for patients.

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Compliance with ethics guidelines

Conflicts of interest Qiaomin Hua, Zhixiong Li, Yulan Weng, Yan Wu, and Limin Zheng have declared that no conflict of interest exists.

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