



REVIEW

Metabolite transporters as regulators of macrophage polarization

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Abstract

Macrophages are myeloid immune cells, present in virtually all tissues which exhibit considerable functional plasticity and diversity. Macrophages are often subdivided into two distinct subsets described as classically activated (M1) and alternatively activated (M2) macrophages. It has recently emerged that metabolites regulate the polarization and function of macrophages by altering metabolic pathways. These metabolites often cannot freely pass the cell membrane and are therefore transported by the corresponding metabolite transporters. Here, we reviewed how glucose, glutamate, lactate, fatty acid, and amino acid transporters are involved in the regulation of macrophage polarization. Understanding the interactions among metabolites, metabolite transporters, and macrophage function under physiological and pathological conditions may provide further insights for novel drug targets for the treatment of macrophage-associated diseases.

Keywords Macrophage polarization · Metabolites · Metabolite transporters · Solute carriers

Abbreviations

PPP	Pentose phosphate metabolism pathways
OXPHOS	Oxidative phosphorylation
FAO	Fatty acid oxidation
SLCs	Solute carriers
GLUT1	Glucose transporter 1
MCTs	Monocarboxylate transporters
ETC	Electron transport chain
PGs	Prostaglandins
ABC	ATP-binding cassette superfamily

FA	Fatty acids
FATP1	Fatty acid transporter 1
iNOS	Inducible nitric oxide synthase
HIF-1 α	Hypoxia-inducible factor-1 α
TNF- α	Tumor necrosis factor α
IL-1 β	Interleukin-1 β
NO	Nitric oxide
Arg1	Arginase-1
ODC	Ornithine decarboxylase
AAs	Amino acids
LAT1	L-Amino acid transporters 1
EAs	Essential amino acids
SGLTs	Sodium-dependent glucose transporters
α -KG	α -Ketoglutarate
IKK- β	I κ B kinase- β
EAATs	Excitatory amino acid transporters
GSH	Glutathione
TME	Tumor microenvironment
LDHA	Lactate dehydrogenase
PGE2	Prostaglandin E2
GPR91	G-protein-coupled receptor 91
CVD	Cardiovascular disease

Highlights

- Metabolic reprogramming and changes in cell metabolism are required for macrophage polarization and activation.
- Metabolites participate in modification of macrophage polarization by altering metabolic pathways.
- Metabolite transporters regulate macrophage polarization by mediating the input/output of metabolites which cannot freely pass through the cell membrane.
- Metabolite transporters may represent novel drug targets for the treatment of macrophage-associated diseases.

The author confirm that no paper mill was used.

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Introduction

Macrophages are a key component of the innate immune system and represent critical players in host defense and tissue homeostasis (Lavin et al. 2015). To carry out these diverse

functions appropriately, macrophages exhibit a high functional plasticity and adopt different metabolic states. The two “extremes” of these states are defined as classically activated (M1) and alternatively activated macrophages (M2) (Mulder et al. 2021; Van Dyken and Locksley 2013). M1 and M2 macrophages exert different functions, with M1 (pro-inflammatory) macrophages being generally involving in fighting infections, pathogens, and tumors, while M2 (anti-inflammatory) macrophages exhibit potent capacity for phagocytosis and are thought to repair inflammation-related damage (Udalova et al. 2016). More recent data have suggested that an imbalance of macrophage polarization is present in atherosclerosis, asthma, metabolic disorders and obesity, rheumatoid arthritis (RA), and fibrotic diseases (Murray and Wynn 2011).

It has previously been shown that macrophage polarization is dependent on metabolic reprogramming and alterations in cellular metabolism (O'Neill and Pearce 2016). During the transition from resting state to activation, macrophages require a considerable amount of nutrients to provide energy (Newton et al. 2016). In the last decade, several studies have assessed how the immune metabolism affects macrophage polarization. It is now generally accepted that energy is generated via aerobic glycolysis and the pentose phosphate pathway (PPP) in M1 macrophages, while M2 macrophages mainly rely on oxidative phosphorylation (OXPHOS) and fatty acid oxidation (FAO) (Stunault et al. 2018).

There is now mounting evidence that suggests that cellular metabolites can also alter metabolic pathways. In particular active metabolites are known to mediate essential physiological functions of cells and are the key to cell survival. In addition, they can also influence the cellular microenvironment directly by modifying production and/or consumption of other metabolites (Hotamisligil 2017; Pålsson-McDermott and Diskin 2018). Tabas et al. reported that metabolic pathways of macrophages can be altered following ingestion of metabolites derived from other cells via efferocytosis (Tabas and Bornfeldt 2020). Most metabolites cannot pass freely through the cell membrane and therefore dedicated transporters are required (Hsu and Dzhagalov 2019). Membrane-bound metabolite transporters can mediate the absorption of nutrients and xenobiotics into the cells, thus providing energy for cells (Lin et al. 2015). In this review, we provide an overview of how metabolite transporters impact on macrophage polarization and how metabolite transporters may represent novel drug targets for the treatment of macrophage-associated diseases in the future.

Role of metabolite transporters in macrophage polarization

Macrophage activation is accompanied by rapid changes in nutrient flux to meet the energy requirements for immune activation. Previous studies have demonstrated that M1

macrophages do not rely on the citric acid (TCA) cycle to produce ATP but instead generate energy via glycolysis and PPP, while M2 macrophages rely on OXPHOS as well as FAO and undergo the TCA cycle (El Kasmi and Stenmark 2015). Accordingly, metabolic reprogramming in macrophages is not only important to supply the anabolic metabolism with substrates and ATP, but also regulates gene transcription and cell signaling events, and ultimately shapes cell polarization phenotypes. Interestingly, the regulation of cell metabolism and macrophage polarization is jointly realized through metabolite transporters (Hediger et al. 2013). In macrophages, metabolites are transported across the membrane by solute carriers (SLCs), including absorption and outflow of intracellular sugars, amino acids, and nucleotides (Perland and Fredriksson 2017). In addition, SLCs can also transport neurotransmitters and inorganic/metal ions, among other metabolites and nutrients (Zhu et al. 2015). Cells with incorrect transporter expressions may lack anabolic substrates or accumulate metabolites, leading to altered polarization (Fig. 1).

Glucose transporters and macrophage polarization

Glucose is a large polar molecule which cannot traverse the cellular lipid membrane via diffusion. It is the most important energy source of cells and is transported into cells via glucose transporters, after which it can be converted to ATP by glycolysis or OXPHOS to maintain the energy requirements for survival and growth (Hui et al. 2017). Glucose transporters can be subdivided into two types, including sodium-dependent glucose transporters (SGLTs) and diffusible glucose transporters (GLUTs) (Jurcovicova 2014). At present, the physiological significance of SGLTs is unknown.

The best characterized glucose transporters in macrophages are GLUT1 and GLUT3. GLUT1, also known as solute carrier family 2, facilitated glucose transporter member 1, or SLC2A1, is a critical regulator of glucose metabolism in macrophages (Freemerman et al. 2014), and overexpression of GLUT1 has been shown to promote glucose uptake, resulting in a proinflammatory macrophage phenotype (Freemerman et al. 2014). Furthermore, GLUT1-deficient bone marrow-derived macrophages (BMDMs) exhibited reduced release of pro-inflammatory metabolites such as succinate and showed an increased M2-related biomarkers and anti-inflammatory metabolites such as ornithine and polyamines (Freemerman et al. 2019). Of note, recent studies have shown that glucose uptake and utilization during GLUT1-mediated aerobic glycolysis contribute to efferocytosis (Morioka et al. 2018), i.e., the energy-intensive process of apoptotic cell removal (Doran et al. 2020; Verdone et al. 2015). Generally speaking, macrophages have been shown to promote the resolution of inflammation and tissue

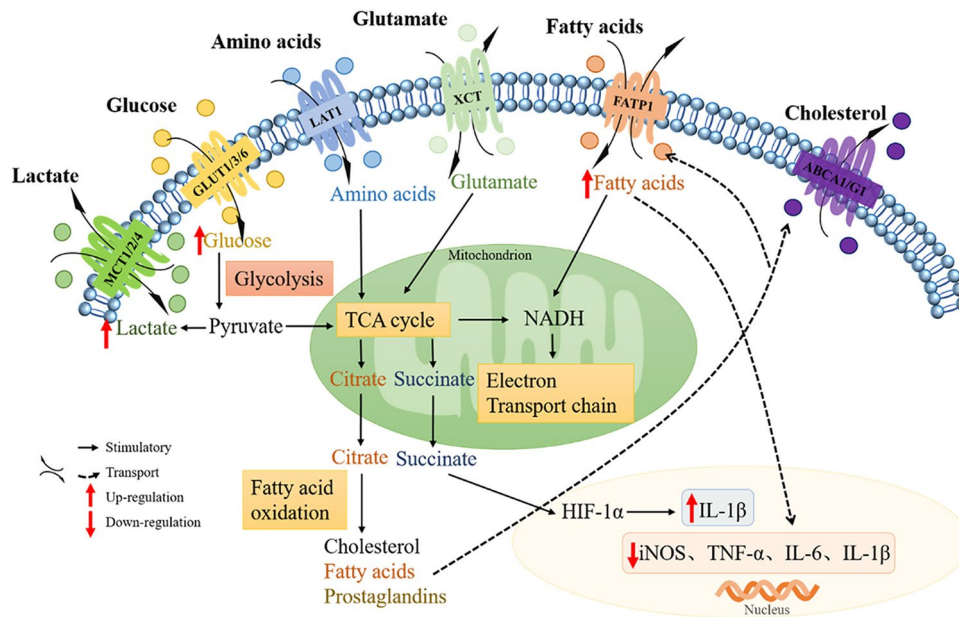


Fig. 1 The impact of metabolite transporters on macrophage polarization. Glucose transporter 1 (GLUT1) overexpression, promoting glucose uptake and glycolysis, leads to an M1 phenotype in macrophages which results in the production of large amounts of lactate and transport by monocarboxylate transporters (MCTS). In addition, pyruvate converted from glucose can enter the TCA cycle, where NADH is produced for use in the electron transport chain (ETC). Citrate in the TCA cycle is used for the synthesis of fatty acids (FA), cholesterol, and prostaglandins (PGs). Cholesterol is released into the extracellular space by ATP-binding cassette superfamily (ABC

A1 and ABCG1 transport, which promotes M2 macrophage polarization and reduces the risk of atherosclerosis, while FA taken up by fatty acid transporter 1 (FATP1) transport can also be oxidized to produce NADH. However, overexpression of FATP1 downregulates M1 markers including inducible nitric oxide synthase (iNOS), tumor necrosis factor α (TNF- α), and interleukin-1 β (IL-1 β) and IL-6. Notably, amino acids (AAs) (transported by L-amino acid transporters 1, LAT1) and glutamate (transported by XCT, SLC7A11) are important to the TCA cycle, and upregulation of LAT1 and XCT promotes M1 macrophage polarization

repair through efferocytosis (Poon et al. 2014). Interestingly, GLUT1-deficient BMDMs displayed decreased efferocytosis in vitro (Morioka et al. 2018). Further studies revealed that efferocytosis promotes metabolic gene programming of glucose uptake and subsequent glycolysis in phagocytes, downregulating genes associated with OXPHOS and FAO in macrophages (Kelly and O'Neill 2015; Morioka et al. 2018). Collectively, the GLUT1-mediated glycolytic metabolism may be involved in M2 polarization of macrophages, although efferocytic macrophages are more M2-like (Kelly and O'Neill 2015).

GLUT3 is the most abundant glucose transporter in the brain and has a higher affinity for glucose than other glucose transporters (Jurcovicova 2014). GLUT3 is considered to be an independent prognostic marker associated with the expression of inflammatory gene and is thought to induce macrophage activation in part through lactate regulation of C-X-C motif-chemokine ligand 8 (CXCL8) (Tsai et al. 2021). GLUT6, a low-affinity glucose transporter, can also be expressed in macrophages (Navale and Paranjape 2016). GLUT6 protein was significantly upregulated in LPS-induced inflammatory macrophages, while naive macrophages and IL-4-induced anti-inflammatory macrophages

do not express (Caruana et al. 2019). Interestingly, although GLUT6 has been shown to be significantly upregulated in M1 macrophages, glucose uptake or the glycolytic metabolism of M1 macrophage is not altered in GLUT6-knockout mice (Maedera et al. 2019).

Glutamine transporters and macrophage polarization

In addition to the glucose metabolism, macrophages employ glutaminolysis to meet their energetic and biosynthetic demands (Pearce and Pearce 2013). Glutamine is converted to glutamate by deamination and glutamate is then transformed to α -ketoglutarate (α -KG). α -KG is an anti-inflammatory metabolite that not only prevents M1 polarization by inhibiting the activation of I κ B kinase- β (IKK- β), but also enhances M2 polarization of macrophages via the α -KG-Jumonji domain-containing 3 (Jmjd3) pathway (Liu et al. 2017). However, not all of the cellular glutamine is used for metabolism. Recent studies have shown following knock-down of glutaminase, the key enzyme converting glutamine to glutamate, glutamine enters the TCA cycle and hexosamine pathways, thereby promoting the anti-inflammatory

polarization of macrophages in response to IL-4 stimulation. Conversely, LPS-stimulated inflammatory macrophages do not require glutamate (Jha et al. 2015), and instead, glutamine is transported out of the cell in exchange for essential amino acids (EAAs) that directly activate mTORC1 to promote protein translation and cell growth (Wise and Thompson 2010).

As glutamate is water-soluble, in order to enter the cell, it must be transported across the plasma membrane which is enabled by a variety of transporters. Glutamine transporters are subdivided into in four main families: SLC1, SLC6, SLC7, and SLC38 (Bhutia and Ganapathy 2016). Several glutamate transporter systems have been identified, including Na⁺-dependent excitatory amino acid transporters (EAATs), the Xc⁻ transport system, and the X_{AG} system (Greuer and Rauen 2005; Noda et al. 1999). Both EAATs and X_{AG} transport systems are Na⁺-dependent, while the anionic amino acid exchange Xc⁻ transport system is Na⁺-independent. The main component of the Xc⁻ transport system, XCT (SLC7A11), is induced by LPS in macrophages (Kobayashi et al. 2018), and the Xc⁻ transport system is highly specific for L-glutamate and L-cystine (La Bella et al. 2007). It has been reported that LPS induces the activity of cystine transport mediated by system Xc⁻ and upregulates the expression of cystine/glutamine transporter XCT/SLC7A11, promoting the conversion of cystine to cysteine and finally enabling the synthesis of glutathione (GSH) in mouse peritoneal macrophages (Sato et al. 1995; Bannai et al. 1991). In line with this, recent studies have demonstrated that increased activity of the XCT upregulates GSH levels, protecting cells from oxidative stress damage and maintaining the mercaptan redox state in macrophages (Song et al. 2020). Also, GSH promotes M1 polarization and enhances the immune activity through the potential ROS scavenging (Kwon et al. 2019). A high extracellular glutamate concentration inhibits cystine uptake via XCT, which in turn blocks GSH synthesis and induces oxidative stress-mediated cell death (Guo et al. 2021).

Lactate transporters and macrophage polarization

During glycolysis, one glucose molecule is converted to pyruvate two molecules, which are in turn converted to lactate by the cytoplasmic lactate dehydrogenase (LDH) (Rogatzki et al. 2015). Lactate is a pro-inflammatory signaling molecule, lactate promoting inflammation by increasing the expression of inflammatory genes and enhancing LPS-induced TLR4 and NF- κ B signaling (Samuvel et al. 2009). In line with this, lactate has been shown to increase the activity of LPS-stimulated monocyte matrix metalloproteinases and release of IL-1 β in obesity and type 1 diabetes (Nareika et al. 2005). Shime et al. found that lactate enhanced the expression of antigen-dependent

IL-17A during co-culture of CD4(+) T cells and BMDM (Shime et al. 2008). However, although lactate is primarily thought of as a pathological metabolite marker, recent studies have demonstrated that lactate can also act as a modulator of immune cell metabolism capable of reducing inflammation and representing a negative feedback signal high level of glycolysis, thereby alleviating the excessive inflammatory responses of pro-inflammatory immune cells (Hoque et al. 2014; Ratter et al. 2018). Zhang et al. found that in the late phases of inflammatory macrophage polarization, lactate could induce expression of genes involved in wound healing, such as arginase-1 (Arg1), via histone lactylation (Zhang et al. 2019a). Moreover, there is a fast-growing body evidence demonstrating that lactate produced by tumor cells can influence M2 polarization of macrophages in the tumor microenvironment (TME) (Spencer and Stanton 2019). For example, in human head and neck squamous cell carcinoma, lactate promotes the induction of an M2-like macrophage polarization by inhibiting LDH and GLUT1 expression, as well as the resulting increased secretion of vascular endothelial growth factor, via induction of hypoxia inducible factor-1 α (HIF-1 α) (Colegio et al. 2014; Ohashi et al. 2017). Importantly, efferocytic phagocytes have been shown to promote an anti-inflammatory phenotype in surrounding non-engulfing naive macrophages toward via lactate transporter-mediated lactate release, as well as anti-inflammatory factors, such as IL-10, released in the tissue microenvironment during efferocytosis (Han et al. 2016).

The effects of lactate on macrophages are predominantly mediated by proton-bound monocarboxylate transporters (MCTs) (Moreira et al. 2009). The MCT family, or solute carrier family 16 (SLC16), comprises 14 members, of which only the first four have been proven to be involved in the transport of lactate, including SLC16A1 (MCT1), SLC16A3 (MCT4), SLC16A7 (MCT2), and SLC16A8 (MCT3) (Halestrap 2013; Halestrap and Meredith 2004). In mammalian cells, these 4 subtypes exhibit functions related to the uptake and flux of lactate across the membrane (Halestrap and Meredith 2004). Previous work showed that macrophages have a higher expression of MCT1 and MCT4 than MCT2 (Imai et al. 2019). In high lactate microenvironments, MCT1 and MCT2 enable cellular lactate uptake, while MCT4 mediates lactate output (Contreras-Baeza et al. 2019; Diehl et al. 2018). MCT2 has been shown to have a higher affinity to lactate than MCT1 (Halestrap and Meredith 2004).

Crucially, MCTs are important regulators of glycolysis. Liang et al. found that MCT1 promoted classical microglial activation and MCT1 knockout reduced the rate of glycolysis as well as the expression of LPS-induced inflammatory markers, including inducible nitric oxide synthase (iNOS), interleukin-1 β (IL-1 β), and IL-6 (Kong et al. 2019). MCT4 contributes to the maintenance of the expression of

glycolytic and pro-inflammatory mediators in TLR4 agonist activated macrophages (Tan et al. 2015).

Fatty acid transporters and macrophage polarization

In mammals, there are two key sources of fatty acids (FAs): food and endogenous synthesis (i.e., *de novo* synthesis). The OXPHOS of FAs produces large amounts of ATP and represents an important energy source of M2 macrophages (Malandrino et al. 2015). Recent work showed that LPS increases fatty acid synthesis (FAS) in macrophages and promotes inflammation (Posokhova et al. 2008). However, enhanced FAO in macrophages not only reduces the accumulation of lipids, but also reduces the production of inflammatory cytokines regulating macrophage inflammation (Malandrino et al. 2015). As described above, in addition to recognition and clearance of apoptotic cells (ACs), efferocytosis induces the production of anti-inflammatory and tissue-restorative cytokines. A recent study has moreover shown that following an injury, IL-10 is upregulated during macrophage efferocytosis. This upregulation was not associated with glycolysis; instead, it was related to an increased FAO and the ETC of apoptotic cells, leading to M2 macrophage polarization and promoting tissue repair (Zhang et al. 2019b).

FAs are insoluble in water and therefore have to be imported into the mitochondria by members of the fatty acid transporter (FATP) family. The FATP family is composed of six isoforms, with FATP1 (SLC27A1) representing the most important subtype capable of mediating macrophage polarization (Nishiyama et al. 2018). FATP1 is an acyl-CoA synthase that inhibits macrophage inflammation by regulating lipid mediators and oxidative stress (Zhao et al. 2017), and it has been shown that the glucose metabolism is increased in FATP1 knockout mice, resulting in a pro-inflammatory macrophage proinflammatory (Johnson et al. 2016). Conversely, FATP1 overexpression has been shown to reduce glycolysis and decrease the production of iNOS, tumor necrosis factor- α (TNF- α), IL-6, and IL-1 β , thereby alleviating M1 macrophage-mediated inflammation (Johnson et al. 2016). Taken together, FATP1 acts as an important regulator of inflammatory signaling in macrophages.

Amino acid transporters and macrophage polarization

Amino acids (AAs) are the main components for protein synthesis and thereby constitute essential nutrients for all living cells. The cellular catabolism of AAs can be used for the production of ATP or act as a source of citric acid for the synthesis of fatty acids; it can also be used to maintain the immune activity of macrophages (Pålsson-McDermott and

Diskin 2018). Early evidence suggested that macrophages may inhibit tumor growth by Arg consumption and subsequent production of nitric oxide (NO), which prevents the repolarization of M1 to M2 macrophages (Currie 1978; Mills 1991). Moreover, as mentioned earlier, the clearance of ACs, during which macrophages take up arginine and ornithine, promotes injury regression (Arandjelovic and Ravichandran 2015). Macrophages metabolize arginine and ornithine to putrescine via Arg1 and ornithine decarboxylase (ODC), which introduces sustained efferocytosis and thereby inhibits inflammation and promotes tissue repair (Yurdagul et al. 2020). In addition, it has been recently reported that ODC inhibits M1 activation and macrophage antimicrobial activity via histone and chromatin modifications (Hardbower et al. 2017). Das et al. (2010) found that a variety of pathogens compete with iNOS for arginine and prevent NO production by an increased in Arg expression. In general, the AA metabolism during macrophage efferocytosis may provide novel therapeutic strategies for intervention in over-responsive or persistent inflammation. Importantly, current studies suggest that the AA metabolism is closely related to amino acid transporters (AATs).

AATs are membrane-bound transport proteins, most of which belong to the group of SLCs and are involved in nutrient uptake, cell signaling pathways, and the cell redox balance (Broer and Palacin 2011). Eleven members of the SLC family have been shown to represent AATs, including SLC1, SLC3, SLC6, SLC7, SLC15, SLC17, SLC18, SLC25, SLC32, SLC36, and SLC38 (Schweikhard and Ziegler 2012). The SLC7 family is further divided into two subfamilies, L-amino acid transporters (LATs) and cationic amino acid transporters (CATs) (Fotiadis et al. 2013). It has been shown that SLC7A5 (LAT1, L-amino acid transporter 1) is a key solute transporter in macrophages, and has been shown to be expressed higher in M1 than in M2 macrophages (Martinez et al. 2006). Increased LAT1 expression mediates leucine influx and enhances mTORC1-induced glycolysis, thereby elevating the production of pro-inflammatory IL-1 β in macrophages (Yoon et al. 2018). Conversely, macrophage downregulation of LAT1 significantly decreased levels of IL-1 β (Yoon et al. 2018). Interestingly, the expression of LAT1 in peripheral blood monocytes of RA patients has been shown to be significantly higher than that in healthy controls (Yoon et al. 2018). Thus, LAT1 can serve as an important indicator of inflammatory macrophages.

The other subfamily of SLC7 transporters, the cationic amino acid transporters 1–4 (CAT1–4), is responsible for the transport of extracellular L-Arg into cells (Bronte and Zanollo 2005). CAT2 is a key protein regulating the uptake of L-Arg by macrophages, and its expression is elevated in activated macrophages *in vitro* (Barry et al. 2011). Moreover, the synthesis of NO mediated by iNOS in M1 macrophages is dependent on CAT2 (Nicholson et al. 2001).

Cholesterol transporters and macrophage polarization

Cholesterol is the most abundant steroid compound in the body. It is not only an essential structural component of cell membranes, but is also the raw material for the synthesis of bile acids and steroids (Narwal et al. 2019). However, a cellular accumulation of cholesterol may cause hypercholesterolemia and lead to atherosclerosis (Groh et al. 2018). Cholesterol exits macrophages predominantly via ATP-binding cassette superfamily (ABCs) transporters which regulate intracellular cholesterol homeostasis, including ABCA1 and ABCG1 (Klaassen and Aleksunes 2010; Phillips 2014). Approximately two-third of the cellular cholesterol efflux are regulated by ABCA1 (Phillips 2014). Significantly, recent studies have shown that activation of central regulators of lipid homeostasis, liver X receptors (LXRs) LXR α and LXR β , upregulates the expression of ABCA1 and ABCG1, thereby stimulating cholesterol efflux from macrophages and promoting M2 macrophage polarization and reducing the atherosclerosis risk (Venkateswaran et al. 2000; Janowski et al. 1999; Schwartz et al. 2000). On the other hand, Sag et al. found that ABCG1-deficient macrophages transition from M2 polarization to anti-tumoral M1 macrophages and exhibited an increased NF- κ B activation in vitro (Sag et al. 2015).

The significance of metabolite transport for macrophage polarization and cellular communication

Metabolites can not only interact with the environment to coordinate cellular metabolism but also act as signaling molecules modifying gene expression and can thereby play an important role in cell survival, differentiation, and function (Curi et al. 2017). As a consequence, the transport of metabolites is critical for both the regulation of macrophage polarization and the communication between macrophages and other cells (Fig. 2).

Prostaglandin E2 (PGE2) is an effective immune regulator that can be secreted by macrophages and is transported into the extracellular space via OATP2A1/SLCO2A1 (Shimada et al. 2015), and it has been reported that the amount of PGE2 secreted from macrophages is significantly reduced in LPS-activated macrophages deficient for OATP2A1 compared to controls (Shimada et al. 2015). Interestingly, although PGE2 is generally considered a pro-inflammatory factor, it has also been shown to exhibit certain anti-inflammatory properties (Scher and Pillinger 2009). For instance, under inflammatory conditions, PGE2 released into the extracellular space by OATP2A1 binds to neutrophil EP4 receptors and removes neutrophils from

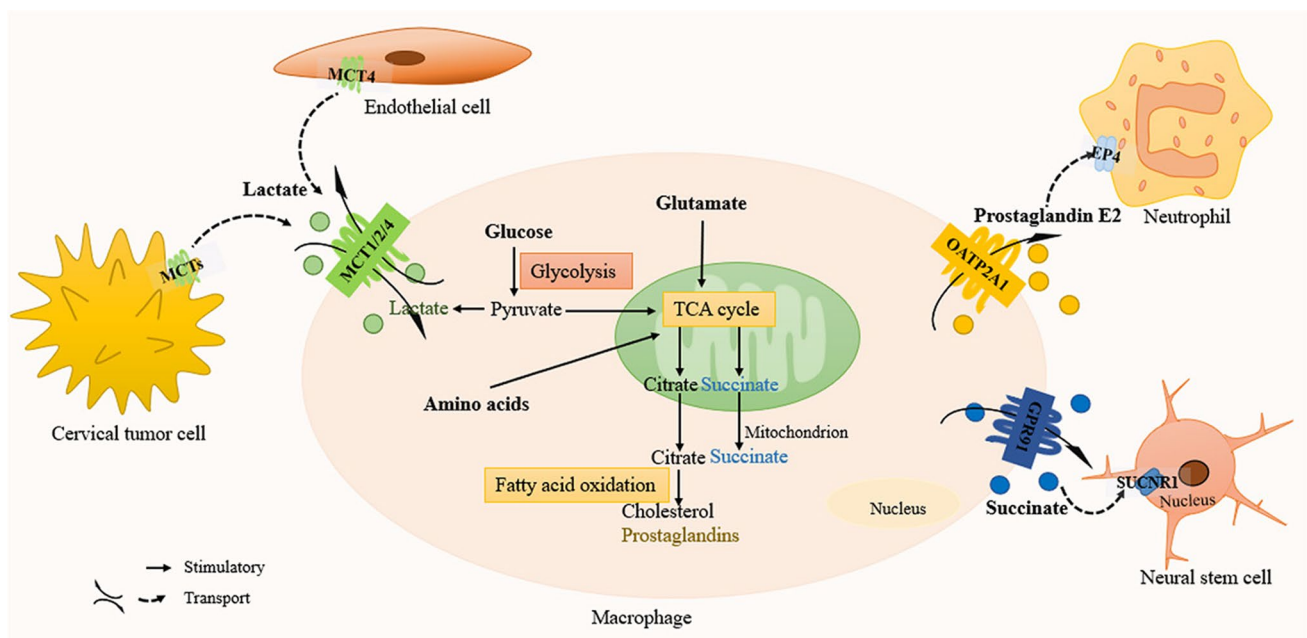


Fig. 2 Significance of metabolite transport in macrophage polarization and communication with other cells. Prostaglandin E2 (PGE2) secreted by macrophages is transported to the extracellular space by OATP2A1/SLCO2A1 and binds to EP4 receptor expressed on neutrophils, inhibiting inflammation. In addition, the pro-inflammatory mediator succinate is produced and released by M1 macrophages.

Succinate binds to the specific succinate receptor 1 (SUCNR1)/GPR91 on NSCs and induces expression of succinate transporters SLC13A3 and SLC13A5, thereby increasing extracellular succinate uptake and reducing inflammation. Notably, lactate derived from tumor cells and endothelial cells is taken up by macrophages via MCTs, promoting M2 polarization

inflammatory tissues, inhibiting inflammation (Loynes et al. 2018; Yamane et al. 2000).

Succinate, produced and released by M1 macrophages, is a highly pro-inflammatory mediator that results in upregulation of IL-1 β and induces a glycolytic metabolism in macrophages via stabilization and activation of HIF-1 α (Murphy and O'Neill 2018; Tannahill et al. 2013). Succinate is released into the extracellular space and binds to the G-protein-coupled receptor (GPR) 91, which is highly expressed on dendritic cells (DCs), acting synergistically with TLRs (Rubic et al. 2008). Recently, it was found that the release of succinate by classically activated macrophages activate specific succinate receptor 1 (SUCNR1)/GPR91 on NSCs, inducing the expression of succinate transporters SLC13A3 and SLC13A5 on NSCs (Gonzalez et al. 2016; Peruzzotti-Jametti et al. 2018). These transporters increase the uptake of extracellular succinate and thereby reduce succinate-mediated inflammation. In line with this, LPS-induced macrophages were shown to be reprogrammed toward an OXPHOS M2 phenotype when co-cultured with NSCs (Peruzzotti-Jametti et al. 2018).

As mentioned above, lactate is an active metabolite capable of inducing metabolic reprogramming and modifying the phenotype and function of macrophages. An increasing body of literature demonstrates increased levels of lactate secreted by tumor cells into the tumor microenvironment influence macrophage polarization as part of the Warburg effect (Domingo-Vidal et al. 2019; Stone et al. 2019). Zhang et al. (2020) recently found that endothelial cells release lactate via MCT4 and macrophages take it up via MCT1, after which it induces an anti-inflammatory phenotype and promotes muscle regeneration. Conversely, Stone et al. demonstrated that the conversion of cervical TAM to the M1 phenotype can be promoted by blocking either lactate synthesis or transport in cervical tumor cells (Stone et al. 2019).

Metabolite transporters as drug targets

Recent data indicate that 50% of SLC family members are related to human diseases (Cesar-Razquin et al. 2015). Significantly, there is accumulating evidence suggesting that metabolite transporters are involved in the etiology of a variety of metabolic and autoimmune diseases linked to macrophages due to their involvement in the transport of various metabolites, such as glucose, AAs, vitamins, neurotransmitters, and inorganic/metal ions (Borst and Elferink 2002; Zhang et al. 2019c). Based on the importance of metabolic requirements for macrophage polarization, metabolite transporters have become attractive targets for the regulation of macrophage polarization and the immune response (Table 1).

A prime example is the FA transporter GPR84, which is highly expressed in LPS-stimulated macrophages and is currently being investigated as a potential target for the treatment of fibrosis and metabolic diseases (Yin et al. 2020). PBI-4547, a GPR84 antagonist, has been shown to significantly increase the glucose and lipid metabolism and thereby reduce non-alcoholic fatty liver disease (NAFLD) scores (Simard et al. 2020). Another GPR84 antagonist, PBI-4050, has also been shown to reduce the expression of fibrotic and inflammatory markers and prevents the activation of fibroblast into pro-fibrotic myofibroblasts as well as inflammatory macrophage activation (Grouix et al. 2018). PBI-4050 has now entered phase II clinical trials as a lead drug candidate (Khalil et al. 2019).

ATP-binding cassette transporter A1 (ABCA1) is involved in the cellular cholesterol export and is highly expressed in liver- and other tissue-resident macrophages (Lawn et al. 2001). It has become an important new target for the removal of cholesterol from arterial macrophages and the treatment of atherosclerotic cardiovascular disease (CVD) (Oram and Vaughan 2006). ABCA1 is regulated by the expression and activity of liver X receptor α (LXR α) and peroxisome proliferator activated receptor γ (PPAR γ) (Soumian et al. 2005). Previously, PPAR γ agonists like the glitazones used in type 2 diabetes and LXR agonists (TO901317 and GW3965) have been shown to ameliorate atherosclerosis via upregulation transcription of ABCA1 and induction of cholesterol extravasation from macrophages in mouse models (Cabrero et al. 2003; Miao et al. 2004; Oram and Heinecke 2005; Joseph et al. 2002). Due to limitations of first-generation LXR agonists, the development and production of LXR agonists that effectively and selectively induce ABCA1 and other cholesterol transporters remains a major challenge (Repa et al. 2000).

In addition to the abovementioned therapeutic functions, metabolite transporters also represent potential cancer targets. The TME has been suggested to play a crucial role in carcinogenesis (Korniluk et al. 2017). Of note, a growing number of studies have shown that TAMs in the TME are involved in tumor progression and metastasis, and may therefore represent attractive therapeutic targets (Singh et al. 2017; Xu et al. 2018). Colegio et al. reported that the uptake of tumor-derived lactate by TAMs in the TME is mediated by MCT1, which promotes an M2 polarization (Colegio et al. 2014). AR-C155858 is a novel class of MCT1 inhibitor developed by AstraZeneca which inhibits the uptake of lactate, thereby inhibiting glycolysis (Guan et al. 2018). Taken together, the abovementioned findings emphasize the potential of metabolite transporters as immunoregulatory and cancer therapeutic targets.

Table 1 Targeting macrophage metabolic transporters for immunoregulation

Drug	Drug status	Transporters (gene name)	Substrate class	Effect	References
PBI-4547	Clinical Trial	GPR84	FA	Inhibition of GPR84 for the treatment of NAFLD and its complications via upregulation of the glucose and lipid metabolism and reduction of the NAFLD score	(Chen et al. 2020; Simard et al. 2020)
PBI-4050	Clinical Trial	GPR84	FA	Inhibition of GPR84 expression for the treatment of fibrotic diseases including idiopathic pulmonary fibrosis (IPF) and type 2 diabetes mellitus with metabolic syndrome by reduction of the expression of fibrosis/inflammation markers, inhibition of fibroblast transition to profibromyofibroblasts, and reduction of M1 macrophages activation	(Grouix et al. 2018; Khalil et al. 2019)
TO901317 GW3965	Clinical Trial	ABCA1	Cholesterol	Activation of LXR induces ABCA1 expression and enhances the lipid metabolism of M2 macrophages, thereby protecting from atherosclerosis	(Miao et al. 2004; Joseph et al. 2002)
Probenecid	Approved	ABCC	PGE2	Inhibition of ABCC transcription, thereby alleviating peritoneal inflammation via inhibition of PGE2 secretion by peritoneal M1 macrophages	(Leite et al. 2007)
Glitazones	Approved	ABCA1	Cholesterol	Activation and upregulation of ABCA1, upregulating ABCA1 transcription to reduce extravasation of M1 macrophages and alleviate atherosclerosis	(Oram and Heinecke 2005)
AR-C155858	Approved	MCT1/2 (SLC16A1)	Lactate	Inhibition of MCT1 expression of MCT1 to inhibit lactate uptake and glycolysis in M1 macrophages with therapeutic effects on cancer, including breast cancer	(Guan et al. 2018)
STF31	Approved	GLUT1 (SLC7A5)	Glucose	Inhibition of GLUT1 transcription for the treatment of neuroinflammation via inhibition of glucose uptake by M1 macrophages and downregulation of TNF- α and IL-1 β expression	(Wang et al. 2019)
Empagliflozin	Approved	SGLT2 (SLC5A2)	Glucose	Inhibition of SGLT2 to enhance adipocyte fat utilization by activated M2 macrophages, reducing obesity-induced inflammation and insulin resistance	(Xu and Ota 2018)

Table 1 (continued)

Drug	Drug status	Transporters (gene name)	Substrate class	Effect	References
Dapagliflozin	Approved	SGLT2 (SLC5A2)	Glucose	Inhibition of SGLT2 expression for inhibition of M1 macrophage infiltration, downregulation of IL-1 β expression, and alleviation of myocardial fibrosis	(Lee et al. 2017)
Riluzole	Approved	EAAT1 (SLC1A3)	Glutamate	Inhibition of EAAT1 to prevent glutamate release from M1 macrophages, exerting neuroprotective and anti-inflammatory effects	(Wu et al. 2020)

ABCC ATP-binding cassette C transporters, *PGE2* prostaglandin E2, *FA* fatty acids, *NAFLD* non-alcoholic fatty liver disease, *ABCA1* ATP-binding cassette transporter A1, *MCT1* monocarboxylate transporter 1, *LAT1* L-amino acid transporter 1, *GLUT1* glucose transporter 1, AAs amino acids, *SGLT2* sodium-glucose cotransporter 2, *EAAT1* excitatory amino acid transporter 1

Conclusions

Metabolite transporters are involved in modifying macrophage polarization. This review summarized the roles of metabolic transporters in macrophage polarization and macrophage-associated diseases. As evident from the presented literature, the immunometabolism is key for determining immunophenotypes and responses. The regulation of metabolite transporters has emerged as an attractive target for the manipulation of macrophage phenotypes and functions. Unfortunately, many SLC transporters currently lack crystallographic data and are known as orphan transporters, whose endogenous functions and substrates are unknown. It is likely that future studies will investigate these orphan SLCs. With a further understanding of metabolite transporters, more detailed knowledge of the pathogenesis and prevention of diseases associated with an imbalance of macrophage polarization will emerge and provide insights for new therapeutic targets.

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