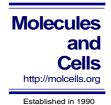
Minireview



The Role of Macrophage Polarization in Infectious and Inflammatory Diseases

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Macrophages, found in circulating blood as well as integrated into several tissues and organs throughout the body, represent an important first line of defense against disease and a necessary component of healthy tissue homeostasis. Additionally, macrophages that arise from the differentiation of monocytes recruited from the blood to inflamed tissues play a central role in regulating local inflammation. Studies of macrophage activation in the last decade or so have revealed that these cells adopt a staggering range of phenotypes that are finely tuned responses to a variety of different stimuli, and that the resulting subsets of activated macrophages play critical roles in both progression and resolution of disease. This review summarizes the current understanding of the contributions of differentially polarized macrophages to various infectious and inflammatory diseases and the ongoing effort to develop novel therapies that target this key aspect of macrophage biology.

INTRODUCTION

Macrophages (M ϕ) represent a ubiquitous yet complex and nuanced population of immune cells that play essential roles in both disease and homeostasis throughout the body (Hume, 2008). In addition to monocytes and M ϕ circulating throughout the bloodstream, specialized tissue-resident M ϕ can be found in most major organs, including Kupffer cells in the liver, Langerhans cells in the skin, microglia in the brain, splenic red pulp M ϕ , lung alveolar M ϕ , adipose tissue M ϕ , and bone osteoclasts, to name a few (Davies et al., 2013; Gautier et al., 2012; Ji et al., 2013; You et al., 2013). While some identify these populations as the endpoint of bone marrow monocyte maturation, several lines of evidence indicate that tissue resident M ϕ originate during embryogenesis in association with their specific tissue independently from blood monocytes and monocytes/M ϕ recruited to sites of inflammation (Davies et al., 2013; Gomez and Geissmann,

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2013; Schulz et al., 2012). Regardless of their location, Mφ are responsible for the maintenance of healthy tissues through phagocytic clearance of apoptotic cells and foreign materials and through tissue repair and remodeling during wound healing (Duffield, 2005; Ghavami et al., 2014; Majai et al., 2014; Mantovani et al., 2013). Μφ are also major regulators of the inflammatory response to disease and infection, acting as a bridge between innate and adaptive immunity by monitoring the microenvironment through an array of surface receptors and secreting appropriate cytokines and chemokines (Heydtmann, 2009; Schwabe et al., 2006).

Depending on the stimuli they encounter, tissue resident and circulatory $M\phi$ populations can be directed to distinct phenotypic programs in a process known as $M\phi$ polarization (Fig. 1, Table 1). The diverse properties of different $M\phi$ subsets can have drastic effects on health and disease within the tissues where they reside; while the induction of a particular subset can be protective during homeostasis or disease, this process can be altered or subverted to enhance pathogenesis and disease progression (by, for example, inappropriately dampening the immune response or exacerbating harmful inflammation) (Murray and Wynn, 2011). Therefore, this review aims to summarize recent findings regarding the identity, properties, and roles of polarized $M\phi$ in various disease models and the development of therapeutic strategies that target both the process of $M\phi$ polarization and individual $M\phi$ subsets.

PHENOTYPIC POLARIZATION OF MO

The most well-described and commonly reported paradigm of M ϕ polarization is the M1/M2 polarization axis (Mantovani et al., 2004; Martinez et al., 2009; Sica et al., 2013). Originally named to reflect relationships to Th1/Th2 polarization of immune responses, M1 and M2 M ϕ are also referred to as classically or alternatively activated M ϕ , respectively (Gordon, 2003; Mills et al., 2000).

Classical activation is stimulated by microbial products and proinflammatory cytokines (IFN γ and/or LPS or TNF), and the resulting M1 M ϕ are characterized by high antigen presentation, high production of IL-12 and IL-23, and high production of nitric oxide (NO) and reactive oxygen intermediates (ROI) (Verreck et al., 2004). M1 M ϕ have been shown to produce several other inflammatory cytokines like TNF α ; IL-1, -6, and -12; Type I IFN; CXCL1-3, 5 and 8-10; CCL2-5 and 11; CXCL16; and CX3CL1 (Mantovani et al., 2004; Sica and Mantovani, 2012).

By contrast, alternative/M2 activation is mediated by IL-4, IL-

Table 1. SR, scavenger receptor; MR, mannose receptor; HO-1, heme oxygenase-1; VEGF, vascular endothelial growth factor; SD-1, sulfire-docin-1; TR-reductase, thioredoxin-reductase (Kadl et al., 2010; Leitinger and Schulman, 2013; Murray and Wynn, 2011)

Polarization state	Gene expression	Cytokines	Chemokines
M1	CD80, CD86, MHC I/II, IL-1R I, TLR2, TLR4, iNOS	TNFα, IL-1, IL-6, IL-12, IL-15, IL-23, ROS, iNOS, type I IFN	CXCL1-3, CXCL5, CXCL8-10, CXCL16, CCL2-5, CCL8, CCL11, CCL15, CCL20, CX3CL1
M2a	CD163, MHC II, SR, CD206, MR, IL-1R II, YM-1, Fizz1, Arg-1	IL-10, TGFβ, IL-12, IL-1Ra	CCL1, CCL2, CCL24, CCL22, CCL17, CCL18
M2b	CD86, MHC II	IL-10, IL-1, TNF α , IL-6	CCL1, CCL20, CXCL1, CXCL2, CXCL3
M2c	CD163, TLR1, MR, Arg-1, YM-1, TLR8	IL-10, TGFβ	CCL16, CCL18
M2d	VEGF	IL-10, VEGF	CCL5, CXCL10, CXCL16
M4	?	TNFlpha	CCL18, CCL20
Mhem	HO-1	IL-10	?
MOx	HO-1, SD-1, TR-reductase	?	?

10, and IL-13, which were initially thought to produce "deactivated M\(\phi\)" (Martinez et al., 2009). M2 M\(\phi\) are marked by the upregulation of several surface molecules including Dectin-1, DC-SIGN, mannose receptor (MRC1/CD206), scavenger receptor A (CD204), scavenger receptor B-1, CD163, CCR2, CXCR1, and CXCR2 (Gordon, 2003; Mantovani et al., 2004; Martinez et al., 2009). M2 M\$\phi\$ exhibit altered cytokine and chemokine production, and typically produce high levels of IL-10 and low levels of IL-12 (Mosser, 2003). CCL1, CCL2, CCL17, CCL18, CCL22, CCL24, and IL-1Ra are also made by alternatively activated Mo (Mantovani et al., 2004). Genetic studies of M2 M\$\phi\$ in mouse models have identified additional signatures of alternative activation, including arginase 1 (Arg1), YM1 (a member of the chitinase family) and FIZZ1 (found in inflammatory zone 1, RETNLA) (Raes et al., 2002; 2005). Generally, the M2 polarization state is characterized by little to no secretion of proinflammatory cytokines, increased secretion of anti-inflammatory cytokines, enhanced scavenging of cellular debris, promotion of tissue remodeling and repair, and, in some cases, increased capacity to fight parasitic infections (Alfano et al., 2013). Additionally, the concept of resolution of inflammation has evolved and is no longer perceived as a passive process that simply occurs when the insult disappears, but rather as a highly orchestrated response coordinated by a complex regulatory network of cells and anti-M1 mediators called pro-resolving mediators (Rius et al., 2012).

M2 Mφ can be further divided into subtypes according to their inductive stimuli and secreted chemokines (Martinez et al., 2008). M2a Mφ are stimulated by IL-4 and IL-13 and produce CCL24, CCL22, CCL17, and CCL18, which are recognized by CCR3, CCR4, and CCR8 and promote recruitment of eosinophils, basophils, and Th2 cells. M2b Mφ result from activation with immune complexes and TLR agonists (like LPS) and produce CCL1, which recruits Tregs. IL-10 drives Mφ polarization to M2c cells, which produce CCL16 and 18, recruiting eosinophils and naïve T cells, respectively. M2d Mφ accumulate in the tumor microenvironment and present an IL-10^{hi}VEGF^{hi} M2 profile, but also exhibit some M1 characteristics such as expression of INFγ-inducible chemokines CCL5, CXCL10, and CXCL16 (Duluc et al., 2009).

A full understanding of the M1/M2 paradigm of M ϕ polarization, however, contains some caveats. First, M1 and M2 M ϕ as defined in the foundational literature most likely do not exist as

distinct categories, but rather should be considered as extremes at either end of a continuum of overlapping functional states (Mosser and Edwards, 2008). Indeed, Mo with combinations of M1 and M2 markers can be found in atherosclerotic plaques and some murine tumors (Kadl et al., 2010; Umemura et al., 2008). Second, unlike the irreversible phenotypic changes seen in lymphocytes after exposure to polarizing cytokines, Mo polarization is both transient and plastic (Biswas and Mantovani, 2010; Biswas et al., 2008; Sica et al., 2013; Stout and Suttles, 2004). For example, M2 M∮ can be reprogrammed to express M1 genes following exposure to TLR ligands or IFN γ (Mylonas et al., 2009; Stout et al., 2005). Finally, while there is partial overlap of M1-and M2-identifying markers in murine and human studies, there are still markers in each system that fail to translate to the other. The chitinase-like proteins YM1 and YM2, along with FIZZ1, are markers of murine M2 polarization which lack human orthologs, while CCL14, CCL18, and CCL23 are human-restricted M2 markers with no murine orthologs (Chang et al., 2001; Martinez et al., 2009; Raes et al., 2002). Finally, there are other specially activated M\(\phi\) (M4, Mhem, and Mox) that have been described in atherosclerosis and may lie on a separate activation axis from M1/M2 M\$\phi\$ (Fig. 1). These atherosclerotic Mo subsets have been discussed in recent reviews (Fenyo and Gafencu, 2013; Leitinger and Schulman, 2013), but will not be examined in detail here.

SIGNALING PATHWAYS INVOLVED IN M Φ POLARIZATION

The network of molecular mediators that regulate M1/M2 polarization in response to various stimuli is incompletely understood, but several signaling pathways have been implicated in this process (Fig. 2). One of the major pathways identified is the JAK/STAT pathway, which mediates responses to a collection of different cyotkines and growth factors and regulates processes from hematopoiesis and immune development to lactation and adipogenesis (Rawlings et al., 2004). Binding of IFN γ to its cell surface receptor leads to activation of receptor-associated JAKs, which in turn cause STAT1 to dimerize and translocate to the nucleus where it initiates transcription of genes that promote M1-associated functions like enhanced microbicidal activity and proinflammatory cytokine production (Hu et al., 2007; Rauch et al., 2013). M ϕ -specific deletion of SOCS3, an inhibitor

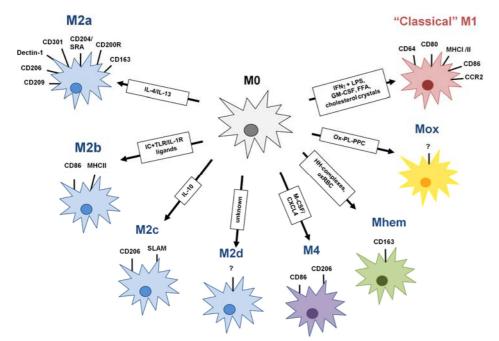


Fig. 1. Schematic representation of Mφ polarization. While M1/ classically activated macrophages are typically induced by IFNγ and microbial products like LPS, different stimuli lead to the development of an array of finely tuned alternately activated states. IC, Immune complex; HH, Haptohemoglobin; OxRBC, oxidized red blood cells; Ox-PL-PPC, ox-PL 1-palmitoyl-2arachidonoyl-sn-glycero-3-phosphorycholine; FFA, free fatty acid.

of cytokine and JAK/STAT signaling, was found to increase levels of the M1 genes IL-1 β , IL-6, IL-12, IL-23, and iNOS (Qin et al., 2012a) and increase phosphorylation of STAT1 and STAT3 (Qin et al., 2012b).

In contrast, STAT6 is activated by IL-4 and IL-13 to induce M2 polarization (Daley et al., 2009; Moreno et al., 2003; Stolfi et al., 2011). C-Jun N-terminal kinase (JNK), a mitogen-activated protein kinase (MAPK) involved in cell proliferation, transformation, differentiation, and apoptosis is likely involved in this pathway (Zhou et al., 2013). Upon activation, JNK can phosphorylate serine 707 on STAT6, thereby deactivating it (Shirakawa et al., 2011). A study of Mo polarization in obesity showed that mice lacking the JNK activator MLK3 were also deficient in M1 Mφ polarization (Gadang et al., 2013). The transcription factors PPARγ and PPARδ are activated by STAT6 and necessary for M2 polarization, and PPARδ Mφ exhibit enhanced activation of JNK following treatment with adipocyte-conditioned medium, which contains the M2 cytokines IL-4 and IL-13 (Kang et al., 2008; Odegaard et al., 2007). The zinc-finger transcriptional regulator Krüppel-like factor 4 (KLF4) is involved in this pathway as well and cooperates with STAT6 to skew polarization towards M2 by sequestering coactivators of NF-κB (Liao et al., 2011).

Furthermore, the phosphoinositol-3-kinase (Pl3K) signaling pathway, which activates multiple kinase cascades through the production of the second messenger PlP3, regulates $M\varphi$ survival and gene expression \emph{via} activation of the Akt family of serine/threonine protein kinases (Liu et al., 2001; Luyendyk et al., 2008). Knockout studies have demonstrated that M1 polarization depends on the activation of Akt2 while M2 polarization requires Akt1 (Arranz et al., 2012). In addition, the Pl3K/Akt signaling pathway controls the activation of mTOR, which promotes M2 polarization (Byles et al., 2013; Mercalli et al., 2013; Weichhart and Säemann, 2008).

Interferon-regulatory factor (IRF) proteins are also regulators of $M\phi$ polarization. IRF5 is associated with M1 polarization and promotes the transcription of genes encoding IL-12 while re-

pressing the gene that encodes IL-10 (Krausgruber et al., 2011). Notch signaling through the nuclear transducer RBP-J controls expression of IRF8, which induces M1 gene expression (Xu et al., 2012). IRF4 is highly expressed in adipose tissue M $_{\varphi}$ (ATM) and its deletion leads to increased production of IL-1 $_{\beta}$ and TNF $_{\alpha}$ and expression of M1 markers, indicating that IRF4 activation contributes to M2 polarization (Eguchi et al., 2013). The IRFs also underlie the ability of GM-CSF and M-CSF to induce polarization: GM-CSF leads to downstream activation of IRF5 (M1) while M-CSF leads to IRF4 (M2) activation (Lawrence and Natoli, 2011).

BACTERIAL INFECTIONS

Given the ability of Mo to acquire enhanced microbicidal abilities following stimulation with microbial products and the preeminent roles of Mo in both innate and adaptive immune responses, one might predict that pathogens would evolve strategies to redirect and alter Mo activation in their favor. Several transcriptome analysis studies have established that innate immune cells, particularly $M\phi$, engage in a common response to pathogen challenge that involves a shared pattern of gene expression (Jenner and Young, 2005; Nau et al., 2002). A multi-study review of transcriptional responses of mononuclear phagocytes to bacteria and bacterial components focusing specifically on genes involved in Mo polarization identified a common response program that mainly involved the upregulation of M1associated genes, including the cytokines TNF, IL-6, IL-12, IL-1β, the cytokine receptors IL-7R and IL-15RA, the chemokines CCL2, CCL5, and CXCL8, and the chemokine receptor CCR7 (Benoit et al., 2008). This M1 activation program is typically associated with protection against disease, and M1 polarization has been shown to aid host control of several bacteria, including Listeria monocytogenes, Salmonella typhimurium, Mycobacterium tuberculosis, Mycobacterium ulcerans, and Chlamydia infections (Benoit et al., 2008; Chacón-Salinas et al., 2005; Jouanguy et al., 1999; Kiszewski et al., 2006; Rottenberg et al.,

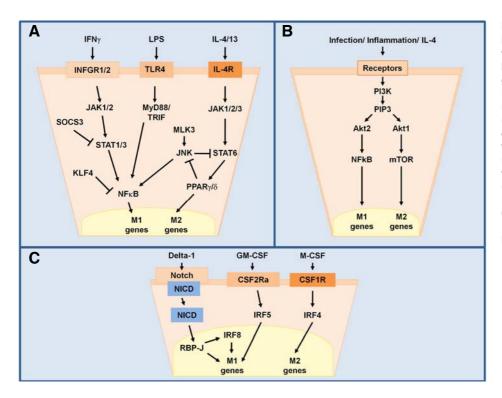


Fig. 2. Major signaling pathways involved in M1/M2 Mb polarization. STAT1/3 and STAT6 regulate transcription of M1 and M2 genes following recognition of IFN_γ or IL-4/13 by their surface receptors and activation of JAKs (A). Differential activation of Akt1 or Akt2 via PI3K and PIP3 leads to either M2 or M1 polarization, respecively (B). Upon activation, the intracellular domain of Notch (NICD) is cleaved and activates IRF8 to promote M1 polarization. GM-CSF triggers M1 polarization via IRF5 while M-CSF induces M2 polarization via IRF4 (C).

2002; Shaughnessy and Swanson, 2007).

Consequently, several pathogenic bacteria, especially intracellular species, have developed mechanisms to interfere with Mø polarization in order to enhance their own survival. Some species accomplish this by blunting M1 polarization to reduce inflammation and microbicidal functions of Mo. The intracellular form of the enteropathogen Shigella flexneri produces an altered, hypoacetylated form of LPS that evades recognition by TLR4 and elicits decreased production of proinflammatory cytokines from murine bone marrow derived Mo (BMDM) (Paciello et al., 2013). During pulmonary infection in mice, Staphylococcus aureus induces Akt1 signaling to enhance SOCS1 activity and inhibit NF-κB activity, shifting Mφ from an antimicrobial M1 phenotype to a functionally inert one (Xu et al., 2013). M. tuberculosis secretes the virulence factors lipoarabinomannan and early secretory antigenic target-6 (ESAT-6), which inhibit M1 activation by inhibiting phagosome maturation and NF-κB activation, respectively (Lugo-Villarino et al., 2011). M. tuberculosis also subverts the inflammatory response by stimulating Wnt6 signaling in infected Mo in granulomatous lesions in the lung, driving M2-like polarization (Schaale et al., 2013). S. aureus biofilms are resistant to Mφ invasion, but those Mo that do successfully penetrate catheter-associated biofilms in vitro display decreased expression of IL-1 β , TNF α , and iNOS expression but robust Arg1 expression, signifying an M2 profile (Thurlow et al., 2011). S. typhimurium has been shown to preferentially associate with M2 M ϕ , and PPAR δ expression is upregulated in Salmonella-infected Mφ while PPARδ deficiency severely inhibits bacterial replication and persistence (Eisele et al., 2013). Interestingly, the dependency of *S. typhimurium* on PPARS expression was shown to be due to its metabolic effects rather than its ability to reduce production of antimicrobial mediators by promoting M2 polarization, and it remains to be determined whether S. typhimurium directly augments PPARS

activity to promote persistence.

VIRAL INFECTIONS

Similar to evasion strategies employed by bacterial pathogens, many viruses take advantage of the Mo polarization system to enhance their own growth and virulence. However, unlike bacterial pathogens, which generally tend to thrive within and encourage production of M2-polarized Mφ, viral pathogens more commonly activate M1 polarization. This inflammatory phenotype is often correlated with disease severity. Hepatitis C virus preferentially infects hepatocytes and establishes a chronic inflammatory infection, often leading to fibrotic cirrhosis and hepatocellular carcinoma (HCC) (Lavanchy, 2011). It has been demonstrated that the viral protein NS3 enhances IL-12 and TNFα production by THP-1 M_Φ, implicating M1 polarization in sustaining inflammation (Hajizadeh et al., 2013). Furthermore, activation of Mo with TLR agonists triggers the secretion of TNFα, which promotes HCV entry into polarized hepatoma cells by relocalizing the tight junction protein and HCV entry factor occludin (Fletcher et al., 2013). Of the three common clades of avian H5N1 influenza virus circulating in poultry in China (2.3.2, 2.3.4, and 7), clade 2.3.4 is the most successful at infecting, replicating within, and inducing cytopathic effects in clade 2.3.4 also stimulated the highest expression of IL-1\beta, IL-6, IL-8, TNF α , IFN γ , and MCP-1 in MDMs (Sun et al., 2013). M2 M
 polarization by S. aureus, which is commonly present among the airway mucosal microbiota, inhibits influenza-mediated lung injury, implying that M1 Mo exacerbate flu infection (Wang et al., 2013).

Nonetheless, some viruses do benefit by skewing M\phi polarization towards an M2 phenotype. During infection by severe acute respiratory syndrome coronavirus (SARS-CoV), lung

damage resulting from both intrinsic viral infection and dysregulation of the host immune response rapidly progresses to diffuse alveolar damage, resulting in acute respiratory distress syndrome and pulmonary fibrosis (Franks et al., 2003; Peiris et al., 2003). A recent study revealed that SARS-CoV-infected mice lacking hematopoeitic STAT1 expression have greater weight loss and lung pathology associated with upregulation of the M2 indicators YM1, FIZZ1, IL-4, and IL-13 (Page et al., 2012). Absence of lung disease and prefibrotic lesions in infected STAT1/STAT6^{-/-} double-knockout mice also supported the notion that M2 M\$\phi\$ contribute to SARS-CoV pathogenesis. Human cytomegalovirus (HCMV) has a more complex relationship with Mφ polarization. The HCMV gene UL111A encodes a homolog of human IL-10 that is capable of polarizing monocytes towards an anti-inflammatory M2c phenotype including high expression of the scavenger receptor CD163, suppression of MHC expression, and exppression of heme oxygenase 1 (which suppresses TNF α and IL-1 β) (Avdic et al., 2013). Additionally, HCMV optimally infects M2- but not M1-polarized M∮ and latephase HCMV infection is dependent on the M2-promoting activation of mTOR (Poglitsch et al., 2012). Despite this, HCMVactivated M₀ have been shown to adopt an M1 transcriptome profile (Chan et al., 2008). HIV-1 similarly seems to benefit from M2 polarization: HIV-1 displays impaired viral DNA synthesis, delayed proviral integration, and reduced proviral transcription in M1 Mø, while the M2a surface receptor DC-SIGN facilitates HIV-1 entry, DNA synthesis, and transmission from infected Mo to CD4+ T cells (Cassetta et al., 2013; Cassol et al., 2010; 2013). Notably, clathrin-mediated endocytosis of HIV-1 is increased in M1 and decreased in M2 Mø, but this method of endocytosis leads to increased viral degradation and is unlikely to result in productive infection (Gobeil et al., 2012). Yet, like HCMV, HIV-1 infection of MDMs drives them toward M1 polarization, and the viral protein Nef is preferentially taken up by M2 M
 and stimulates an M2-to-M1 transition (Cassol et al., 2010; Chihara et al., 2012; Lugo-Villarino et al., 2011). These contradictions may be explained by a viral survival strategy that takes M2 M ϕ as a reservoir of replication and M1 M ϕ to recruit fresh immune cells to spread the infection. This can also be inferred from the ability of proinflammatory cytokines and chemokines from HCMV-infected Mo to enhance virus replication and dissemination (Alfano et al., 2013; Smith and Bentz, 2004a; 2004b).

DIABETES, OBESITY, AND NON-ALCOHOLIC STEATOHEPATITIS

Type 1 diabetes is an autoimmune disease that results in high blood sugar following the destruction of insulin-producing pancreatic beta cells via activation of innate immunity and expansion of auto-reactive T cells and autoantibody-producing B cells. proinflammatory profile (high levels of TNFα, IL-6 and IL-1β) when compared to normal subjects (Bradshaw et al., 2009; Devaraj et al., 2006; Shanmugam et al., 2004). Moreover, elevated levels of glucose and islet amyloid polypeptide (IAPP) deposition lead to the activation of TLRs and inflammasomes, resulting in beta cell death and decreased insulin secretion (Henao-Mejia et al., 2013). Recently, it has been suggested that M1 M₀ may contribute to diabetes-related complications such as cardiovascular diseases by altering the immune system of type 1 diabetics (Burke and Kolodgie, 2004). Furthermore, the sustained increase of growth hormone in murine models of type 1 diabetes leads to a reduction of diabetes

symptoms by attenuating the apoptosis and increasing the expansion of beta cells (Villares et al., 2013). Growth hormone also triggers M2 polarization of $M\phi$ *via* modulation of the cytokine milieu, stimulating the activity of suppressor T cells and limiting Th17 cell activation (Villares et al., 2013).

Obesity is a major health problem in western countries and a risk factor for insulin resistance, type 2 diabetes, hepatic steatosis, and artherosclerosis. Obesity is closely associated with chronic inflammation in adipose tissues, suggesting that the chronic excess of nutrients triggers an immune response in adipose tissues (Goh et al., 2011; Hotamisligil, 2006; Kanneganti and Dixit, 2012). White adipose tissues store energy in the form of fat and regulate systemic metabolism through the release of adipokines by adipocytes that control insulin sensitivity in the liver and skeletal muscle (Sun et al., 2011; Tateya et al., 2013). In lean subjects and mice, adipose tissue M\(\phi\) (ATM) present an M2 phenotype and are critical to maintaining insulin sensitivity in adipocytes through IL-10 production (Liao et al., 2011; Lumeng et al., 2007a; 2007b). In metabolic homeostasis, M2 ATMs are maintained by IL-4 and IL-13 secreted by adipocytes in a PPARy/δ/β- and KLF4-dependent manner (Wynn et al., 2013; Zhou et al., 2013). In obese subjects and mice, adipocytes release proinflammatory mediators (i.e. CCL2/MCP-1, TNFα, CCL5, CCL8 and free fatty acid), promoting the infiltration of Ly6Chi inflammatory monocytes which differentiate into M1-polarized ATMs that express high levels of TNFα, iNOS, IL-6 and IL-1ß (Cinti et al., 2005; Lumeng et al., 2007a; Olefsky and Glass, 2010; Tateya et al., 2013; Weisberg et al., 2003, 2006). Therefore, the severity of obesity-related metabolic dysfunctions correlates with M1 ATM infiltration whereas chronic inflammation in adipose tissue inhibits the production of adiponectin, thus contributing to the development of insulin resistance in surrounding adipocytes (Lumeng et al., 2007a; Weisberg et al., 2003; 2006).

Recently NAFLD (Non-alcoholic fatty liver disease) has emerged as an obesity-related health problem characterized by steatosis (accumulation of lipids in hepatocytes). Hepatic steatosis can evolve to non-alcoholic steatohepatitis (NASH) when accompanied by liver injury (ballooning hepatocytes) and hepatic inflammation, which may be associated with fibrosis and eventually culminates in cirrhosis and HCC. The development of the complex pathology of NASH involves a variety of liver cells including hepatocytes, hepatic Mo, and stellate cells. Inflammatory mediators, especially those derived from adipose tissues, the gut, and the liver, have recently been reported to play a major role in initiating and controlling the progression of NASH by regulating lipid metabolism (Day and James, 1998; Racanelli and Rehermann, 2006; Tilg and Moschen, 2010). In particular, the activation of innate immune cells such as Kupffer cells and infiltrating blood-derived monocytes is a major event of NASH development. In homeostatic conditions, Kupffer cells perform immune surveillance by removing pathogens and toxins from the circulation and maintain liver tolerance through IL-10 secretion (Thomson and Knolle, 2010). Kupffer cells communicate with a variety of hepatic immune cells and interact directly with hepatocytes passing through the space of Disse (Racanelli and Rehermann, 2006). In early mouse models of diet-induced steatohepatitis, Kupffer cells are the first innate cells responding to injured hepatocytes and differentiate toward M1 Mφ, promoting the recruitment of blood-derived CD11b^{int} Ly6C^{hi} monocytes through secretion of TNF α and chemokines (MCP-1 and IP-10) (Tosello-Trampont et al., 2012). The recruitment of these inflammatory M1-polarized Ly6C+ blood-derived monocytes is dependent of CCR2 and MCP1 (Karlmark et al.,

2009; Klein et al., 2007; Miura et al., 2012; Obstfeld et al., 2010). The hallmarks of NASH (i.e. steatosis, low-grade inflammation, and hepatic recruitment of M1-polarized M ϕ) are reduced/delayed following specific depletion of Kupffer cells or by silencing of TNF α in myeloid cells (Tosello-Trampont et al., 2012). Moreover, M1-polarized Kupffer cells also produce inflammatory mediators such as IL-1 β and ROS, which induce hepatic steatosis and fibrosis (Miura et al., 2012; Schwabe and Brenner, 2006). NF-κB and JNK activation in Kupffer cells may contribute to the development of hepatic inflammation by promoting M1-like M ϕ polarization (Zhou et al., 2013).

Liver Mo are also implicated in the severity of NASH via the expression of Toll-like receptors (TLR2, TLR4, TLR9, MyD88) and scavenger receptors (scavenger receptor A and CD36) (Bieghs et al., 2010; Miura et al., 2010; 2012; 2013). TLRs and scavenger receptors trigger proinflammatory responses following recognition of hepatic free fatty acids, damage-associated molecular pattern (DAMPs) expressed by steatotic hepatocytes, and/or bacterial products derived from the gut (Farrell et al., 2012; Roh and Seki, 2013). NASH patients show increased intestinal permeability, resulting in greater hepatic abundance of bacterial products and other TLR ligands derived from the gut via portal vein circulation (Zhu et al., 2013). The imbalance of gut flora may influence liver disease by activating TLRs expressed on liver cells and leading to the activation of NLPR3 (Csak et al., 2011; Farrell et al., 2012; Henao-Mejia et al., 2013; Roh and Seki, 2013). In models of diet-induced NASH and obesity, inflammasome-deficient mice develop more severe NASH which is fully transferable to WT mice upon prolonged cohousing, suggesting that commensal bacteria in the GI tract play an important role in NASH disease progression (Csak et al., 2011; Henao-Mejia et al., 2012; 2013; Weisberg et al., 2003).

CANCER

Mo are a highly influential cell type in most varieties of cancer and are recruited to all solid tumors (Cassetta et al., 2011). The contributions of different subsets of polarized M\(\phi \) to the tumor microenvironment and cancer progression are therefore a subject of great interest. M1 Mo are generally considered to be beneficial to the host, and peritumoral Mo that express M1 cytokines like IFN γ , IL-1 β , and IL-6 have been shown to have antitumoral effects and are associated with improved prognoses (Dumont et al., 2008; Klimp et al., 2002; Niino et al., 2010; Öberg et al., 2002; Zhou et al., 2010). M1 Mo may have the opposite effect in virally induced cancers, however: administration of IFN γ or TNF α to patients infected with Kaposi sarcoma virus enhances disease progression (Monini et al., 1999). Proinflammatory Mo are also harmful in intraocular tumors, where TNFα- and iNOS-dependent antitumor responses lead to necrosis of bystander cells and destruction of the eye (Coursey et al., 2012).

M2-polarized tumor-associated M ϕ (TAM), on the other hand, have been repeatedly and consistently associated with unfavorable effects like tumor growth, angiogenesis, and metastasis in malignant cancers (Alfano et al., 2013). The M2 cytokines IL-4, IL-13, and IL-10 are present within the tumor microenvironment and TAMs from various cancer models have been shown to express an M2 activation profile that includes enhanced expression of CD163, MRC-1, c-type lectins, IL-10, and Arg-1 and decreased production of IL-12 (Beck et al., 2009; Biswas et al., 2006; Schmieder et al., 2012; Sica et al., 2002). The small secretory lectin Reg3 β is an important inhibitor of inflammation in pancreatic and intestinal tissues, and deficiency of Reg3 β

(an activator of the STAT3 pathway) drastically impairs pan-and towards M1 (Gironella et al., 2013). M2 TAMs have also been shown to increase fibroblastic morphology, vimentin and snail expression, metalloproteinase activity, and proliferation and migration of pancreatic cancer cells, implicating them in the development of eptihelial-mesenchymal transition and metastasis (Liu et al., 2013). In HCC, high expression of the heparinsulfate proteoglycan glypican-3 (GPC3) on the surface of cancer cells is associated with increased Mo infiltration in human patients, and human/mouse xenograft transplantation with a GPC3-overexpressing cell line leads to infiltration by Mo expressing M2-specific markers (Takai et al., 2009a; 2009b). M2 TAMs worsen HCC both by promoting tumor growth and angiogenesis and by encouraging liver fibrosis through IL-13 and TGFβ secretion (Sica et al., 2013).

Given that M ϕ play important roles in maintaining tissue homeostasis and fighting disease, polarized M ϕ subsets that specifically contribute to the pathogenesis or amelioration of various diseases present themselves as attractive targets for therapeutic intervention. Different therapeutic strategies include either targeting the polarized M ϕ themselves or manipulating the signaling pathways involved in the process of M ϕ polarization to a desirable outcome.

Bacterial biofilms that form on body surfaces or on surgical implants lead to chronic and recurrent infections, and are difficult to treat with antibiotics (Donlan and Costerton, 2002; Otto, 2008). Early, local administration of M1 Mo or the C5a receptor agonist EP67, which stimulates M1 polarization, significantly attenuated biofilm formation in a mouse model (Hanke et al., 2013). Furthermore, treatment of established biofilms significantly reduced bacterial burden compared to antibiotic treatment, suggesting the potential of a therapeutic alternative (Hanke et al., 2013). Microbes themselves may also prove to be useful sources of therapeutics that modulate M\phi polarization. In vitro application of extracellular polysaccharide secreted by an oligotrophic bacteria found in Lop Nur Desert, Bacillus sp. LBP32, was found to limit LPS-induced inflammation in the Mo cell line RAW 264.7 by inhibiting NF-κB and JNK activation, and may prove useful in diseases characterized by excessive M1 polarization (Diao et al., 2013). Similarly, the small-molecule compound bis-N-norgliovictin isolated from the marine-derived endophytic fungus S3-1-c inhibits LPS-induced M1 polarization of RAW 264.7 cells and murine peritoneal Mo, and improves survival in mouse models of sepsis (Song et al., 2013). As a proof of concept for treating inflammatory gastrointestinal diseases, a lab strain of E. coli was created that secretes a Herpes virus homolog of IL-10 via a Sec-dependent transporter construct. Viral IL-10 delivered in this manner was shown to activate STAT3 and suppress TNF α production in the J774.1 murine

IKKβ, a downstream mediator of insulin resistance and activator of the NF- κ B pathway (and therefore of M1 polarization), is inhibited by anti-inflammatory salicylates like aspirin, which attenuates hyperglycemia and hyperinsulinemia in obese rodents (Yin et al., 1998; Yuan et al., 2001). Several small trials in patients with type 2 diabetes have demonstrated that treatment with salicylates results in a marked reduction of diabetic metabolic parameters and improved glycemic control (Tateya et al., 2013).

Apolipoprotein A-I mimetics are a class of therapeutic mole-

cules that attempt to modulate HDL to treat atherosclerosis and are the subject of extensive clinical and mechanistic study, as reviewed in Leman et al. (2013). Interestingly, the mimetic D4F also has potential for cancer therapy: D4F inhibits the M2-associated scavenger receptor CD204/SRA on TAMs, preventing metastatic spread (Neyen et al., 2013).

Anticancer therapies also seek to convert protumoral M2 M ϕ into M1 M ϕ . M2 M ϕ generated by IL-6 and prostaglandin E2 secreted by cervical cancer cells can be repolarized to M1 by coculture with Th1 cells, and this interaction could possibly be reproduced by activation with CD40L and IFN γ (Heusinkveld et al., 2011). Moreover, IFN γ was shown to successfully switch M2 TAMs purified from human ovarian tumors to an M1 phenotype, and the addition of IFN γ skewed *de novo* tumor-induced M2 differentiation of monocytes to favor M1 polarization (Duluc et al., 2009). Other potentially therapeutic molecules found to repolarize TAMs from an M2 to an M1 phenotype include zoledronic acid, CpG oligonucleotide, and histidine-rich glycoprotein (Coscia et al., 2010; Huang et al., 2012; Rolny et al., 2011).

CONCLUSION

The integral importance of $M\phi$ in the maintenance of nearly every tissue throughout the body and their position as the first line of defense against many diseases guarantees that they play critical roles in both disease progression and in resolution, and that altering the behavior of these cells can mean the difference between healthy recovery and severe illness. $M\phi$ polarization itself is an extremely nuanced and fine-tuned process and can produce nearly infinite variations of endpoint phenotypes, each of which has the potential to affect various diseases in different ways. While polarized $M\phi$ subsets and the polarization process itself are attractive and novel therapeutic targets in both infectious and inflammatory disease, better understanding of how polarization is controlled and how polarized $M\phi$ modulate specific diseases is necessary to fully harness the potential of these strategies.

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