INVITED REVIEW



Macrophages in vascular inflammation and atherosclerosis

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Abstract Atherosclerosis is characterized by lipid accumulation and chronic inflammation of the arterial wall, and its main complications-myocardial infarction and ischemic stroketogether constitute the first cause of death worldwide. Accumulation of lipid-laden macrophage foam cells in the intima of inflamed arteries has long been recognized as a hallmark of atherosclerosis. However, in recent years, an unexpected complexity in the mechanisms of macrophage accumulation in lesions, in the protective and pathogenic functions performed by macrophages and how they are regulated has been uncovered. Here, we provide an overview of the latest developments regarding the various mechanisms of macrophage accumulation in lesion, the major functional features of lesion macrophages, and how the plaque microenvironment may affect macrophage phenotype. Finally, we discuss how best to apprehend the heterogeneous ontogeny and functionality of atherosclerotic plaque macrophages and argue that moving away from a rigid nomenclature of arbitrarily defined macrophage subsets would be beneficial for research in the field.

Keywords Atherosclerosis \cdot Inflammation \cdot Macrophages \cdot Immune cells

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Introduction

Atherosclerosis is a chronic inflammatory disease of the vascular wall, and its complications, in particular myocardial infarction and stroke, constitute the first cause of death in the world. Macrophages are the most abundant immune cell type in atherosclerotic lesions and have an essential role during all stages of the disease, from lesion initiation to plaque rupture. Hence, thoroughly understanding macrophage biology in vascular inflammation and atherosclerosis appears as a prerequisite to develop novel therapeutic strategies aiming at taming the disease burden associated with this pathology.

A long standing paradigm regarding the major steps of macrophage-dependent vascular inflammation in atherosclerosis could be briefly described as follows: in areas of non-laminar vascular blood flow, endothelial dysfunction permits circulating low density lipoprotein (LDL) infiltration into the vascular intima, which is increased under conditions of hyperlipidemia. In the vessel wall, LDL undergoes modifications such as oxidation, and modified LDL activates endothelial cells and resident immune cells leading to expression of chemokines and adhesion molecules that attract circulating monocytes to the vessel wall and allow their adhesion, rolling and transendothelial migration, resulting in monocyte infiltration in the intima. Once in the intima, monocytes differentiate into macrophages and ingest modified lipoprotein to become foam cells. Gradually accumulating foam cells die in the intima through apoptosis and, when not promptly disposed of, become necrotic, progressively leading to the formation of a thrombogenic and proinflammatory necrotic core. Macrophages further fuel lesion inflammation through secretion of cytokines, and their proteolytic activity promotes plaque destabilization and rupture that leads to atherothrombosis and the associated ischemic events such as myocardial infarction or stroke. Although this view is still considered generally valid and an important underlying mechanism of lesion formation,

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recent research has revealed an unexpected complexity in the mechanisms of macrophage accumulation in atherosclerotic plaques, in the functions performed by macrophages, and in the mechanisms determining macrophage phenotype in lesions. In this review, we provide a brief overview of the origins of macrophages in the vessel wall, their fundamental function, and how these are regulated. Finally, we will discuss how to best apprehend investigations of macrophage phenotypic heterogeneity and its implications in disease, and how moving beyond the macrophage polarization paradigm might be beneficial for research in the field.

Mechanisms of macrophage accumulation in the vessel wall

Recruitment of bone marrow and spleen-derived circulating monocytes

Recruitment of circulating monocytes to the inflamed vessel wall is instrumental in the initiation and progression of atherosclerotic lesions. In mice, hypercholesterolemia induces monocytosis and more particularly a rise in levels of circulating Ly6C^{hi} monocytes, the equivalent of human CD14⁺ CD16⁻ monocytes [120, 123]. Ly6C^{hi}CCR2⁺ monocytes are considered to be the major precursors of plaque macrophages, and their recruitment to plaques depends on expression of the chemokine receptors CCR2, CCR5, and CX3CR1 [120, 123] and receptors that bind various adhesion molecules expressed on endothelial cells [46]. Interestingly, the systemic control of circulating monocyte levels appears to have a crucial role in lesional macrophage accumulation as plaque macrophage content is directly correlated to circulating monocyte levels [30]. Medullary hematopoiesis has long been considered as the major-if not sole-source of monocytes in atherosclerosis, and hyperlipidemia as well as associated comorbidities, such as hyperglycemia, promote monocyte production in the bone marrow [81, 114]. Bone marrow monocytes are mobilized to the bloodstream mainly in response to chemokine/chemokine receptor signaling, in particular CCL2/CCR2 [30, 107]. However, it is now well established that also extramedullary hematopoiesis in the spleen significantly contributes to atherosclerosisassociated monocytosis and that monocytes originating from the spleen participate in macrophage accumulation within lesions [97]. Mechanistically, hematopoietic stem cells (HSCs) migrate from the bone marrow to the spleen, where the microenvironment supports their progressive differentiation towards mature monocytes [97]. Interestingly, mobilization of monocytes from the splenic reservoir appears to be independent of CCR2, but relies on angiotensin II signaling through its type 1 receptor AT1 [121], and may also depend on splenic B cells, although the underlying mechanisms are still unclear [78].

Local proliferation of macrophages

Proliferation of macrophages in atherosclerotic plaques has been observed in human and animal models more than 20 years ago [49, 95, 102], but its quantitative contribution to macrophage accumulation in lesions has long remained enigmatic. A study based on a model of parabiosis, where the blood circulation of two mice is joined, shed new light on this paradigm. By allowing a discriminating of the origin of cells in tissue from either recruited circulating or locally expanded cells, macrophage proliferation was proposed to account for ~87% of macrophage accumulation in established lesions, while recruitment of circulating monocytes was only instrumental in the early phases of the disease [98]. However, data from the same study using a long-term bone marrow chimera model showed that all macrophages in established lesions ultimately originate from circulating precursors, and a proportional increase in monocyte recruitment with lesion progression was also reported [119]. In contrast to the work by Robbins et al. [98], a recent report suggested that macrophage proliferative activity was higher in early rather than in advanced lesions [69]. To add another layer of complexity, it was recently found that a substantial proportion of macrophages in established lesions are senescent, thus by definition incapable of proliferating, and that their clearance through pharmacological intervention significantly reduces macrophage content in established lesions [23]. The fact that highly proliferative and plastic vascular smooth muscle cells can adopt a macrophagelike phenotype and express classical macrophage markers such as Mac3 or Mac2 (Lgals3) in lesions (as discussed below) further complicates interpretation of studies investigating macrophage proliferation in atherosclerosis [20, 40, 109].

VSMC transdifferentiation into macrophage-like cells

Cells co-expressing markers of macrophages and vascular smooth muscle cells (VSMCs) have been described in human atherosclerotic lesions 20 years ago [8], and a study recently showed that up to 50% of cells identified as macrophage foam cells co-expressed smooth muscle cell markers [7]. However, these studies based on immunohistological analyses cannot determine whether these cells originate from macrophages upregulating VSMC markers or VSMCs transdifferentiating into macrophage foam cells. Convincing evidence of VSMC transdifferentiation into macrophage-like cells in lesions has been obtained from lineage fate mapping of VSMCs in murine atherosclerosis. Using pulse-labeling of VSMCs in reporter Apoe^{-/-}-ROSA26 mice expressing the tamoxifen-inducible Cre recombinase under the control of a VSMC-specific promoter in the SM22 α gene locus, Feil et al. demonstrated loss of VSMC markers and conversion to a macrophage-like cell phenotype of clonally expanded VSMC-originating cells in advanced lesions [40]. Using a similar fate mapping strategy, albeit with expression of inducible Cre under the control of another VSMC-

specific promoter, Shankman et al. demonstrated that a vast proportion of pulse-labeled cells lost expression of VSMC markers and acquired expression of macrophage or mesenchymal stem cell markers. Furthermore, it was demonstrated that this phenotypic transition depended on expression of the transcription factor Klf4 [109]. A recent report using a model of stochastic multicolor fate mapping further suggested that a subset of highly proliferative plastic VSMCs can clonally expand in lesions and that progeny of a single VSMC can adopt different phenotypes, including conversion to a macrophage-like phenotype with expression of the macrophage marker Mac3 [20].

In in vivo studies, VSMC-derived macrophage-like cells could form foam cells, but these are likely functionally different from bona fide macrophages [40, 109]. This notion is corroborated by in vitro studies, where cholesterol-loading induces VSMC transdifferentiation to macrophage-like cells [101]. Indeed, these VSMC-derived macrophage-like cells have a transcriptional profile that largely differs from bone marrow-derived macrophages and perform poorly in classical macrophage function tests, such as phagocytosis and efferocytosis [131].

Resident aortic macrophages and differentiation of local precursors

In the absence of hypercholesterolemia and atherosclerotic disease, healthy arteries already contain resident macrophages and dendritic cells. This was recently demonstrated with the help of genetic fate mapping models, and it could be revealed that murine arteries contain a resident population of macrophages derived from two distinct sources, namely CX3CR1⁺ embryonic precursors and bone marrow-derived monocytes that colonize arterial tissue during embryonic development and in the first few days after birth, repsectively [35]. This arterial macrophage population appears to self-renew during homeostasis and after infection-induced depletion [35]. The role of this resident macrophage population in atherosclerosis remains to be determined, but it is conceivable that they may impact disease initiation in a similar fashion as vascular resident dendritic cells that take up lipids and form foam cells at very early stages of lesion formation [86]. Their proliferative ability also suggests that they may contribute to macrophage accumulation during lesion progression. In addition to resident arterial macrophages, some studies have furthermore suggested that a population of adventitial macrophage progenitor cells resides in the adult mouse aorta and may locally differentiate to contribute to macrophage accumulation in atherosclerosis [90, 91].

The notion that a large part of resident tissue macrophages arise from stem cells during embryonic development has challenged the general "monocyte-derived macrophage" paradigm [47, 87]. The exact developmental origin of these macrophages, however, is still debated [47, 87]. It appears that macrophages in any given tissue originate from various sources of precursors such as yolk sac-derived progenitors, fetal hematopoietic stem cells (HSCs), or adult HSC-derived monocytes, both during homeostasis and inflammation [47]. It remains to be determined whether ontogeny has functional implications in mature macrophages [47], and it will be interesting to investigate not only the contribution of resident arterial macrophages and macrophage progenitors to macrophage accumulation in atherosclerosis, but also the impact of macrophage origin on disease-relevant functions.

Macrophages and plaque regression

Atherosclerotic plaques-and their macrophage content-can regress, as shown in particular in murine models of hypercholesterolemia reversal [39, 42, 89]. However, the exact underlying mechanisms are still debated. Some reports based on models of atherosclerotic aortic transplantation proposed that egress of mature macrophages from lesions drove plaque regression in a process involving liver X receptor (LXR)-dependent induction of CCR7 in macrophages [38] and that this is hampered by expression of the adhesion molecule JAM-C on endothelial cells [17]. It was further proposed that lesional macrophages can express retention molecules such as netrin-1 and its receptor UNC5b, which inhibit their emigration from lesions and thereby promote plaque progression [129]. Another study proposed that regression of lesional macrophage burden was independent of CCR7-driven macrophage emigration, but rather relied on suppression of monocyte recruitment and steady local apoptosis of plaque macrophages [89].

Functions of macrophages in atherosclerosis

Production of inflammatory cytokines and proteases

Once in lesions, macrophages actively participate in vascular inflammation through secretion of proinflammatory cytokines and the production of chemokines to promote further recruitment of immune cells. Plaque macrophages express proinflammatory cytokines which have been assigned a proatherogenic role such as TNFa [84], IL-18 [75, 138], and IL-12 [67]. Although affecting all hematopoietic cells and not only macrophages, experimental studies of lethal irradiation and bone marrow reconstitution in atherosclerosis-prone mice have been essential in establishing the crucial role of macrophage-derived cytokines in plaque inflammation. IL- 1α and IL-1 β deficiency in bone marrow-derived cells was shown to reduce lesion formation and inflammation in $Apoe^{-7}$ mice [59], although a subsequent study proposed that only leukocyte-derived IL-1 α , but not IL-1 β , has a crucial role in atherogenesis [44]. CCL2 overexpression in bone marrow cells increased macrophage recruitment to lesions, showing that leukocyte-derived chemokines can fuel plaque inflammation [3]. Plaque macrophages also produce anti-inflammatory

cytokines, and leukocyte-specific deficiency in IL-10 or IL-13 increased plaque inflammation and lesion formation [19, 88].

Proteolytic activity in lesions is associated with the progression towards a vulnerable and rupture-prone phenotype [112]. Lesional macrophages are known to have a strong proteolytic activity and are thus considered to substantially participate in plaque destabilization and rupture [92]. A proof-ofconcept for the critical role of macrophage-mediated proteolysis in plaque destabilization was obtained in $Apoe^{-/-}$ mice overexpressing active matrix metalloproteinase (MMP)-9 specifically in advanced lesion macrophages, which induced features of plaque disruption [50]. Conversely, MMP-14 deficiency in bone marrow-derived cells led to formation of stable plaques with increased collagen content in $Ldlr^{-/-}$ mice, suggesting a role of macrophage-derived MMP-14 in plaque destabilization [105].

Foam cell formation

Formation of macrophage foam cells in the vascular intima is a hallmark of atherosclerosis. The extent to which macrophages accumulate intracellular lipids represents the balance between extracellular lipid uptake and reverse lipid transport from the intracellular compartment to extracellular lipid acceptors. Macrophages take up modified LDL through various scavenger receptors such as CD36, scavenger receptor A1 (SR-A1, also known as MSR1), scavenger receptor B1, LDL receptor-related protein 1 (LRP-1), and lectin-like oxLDL receptor-1 (LOX-1) [122]. Experimental studies in mice deficient for scavenger receptors have investigated their role in foam cell formation and atherogenesis. $Ldlr^{-/-}$ mice with macrophage-specific deficiency in LRP-1 have decreased cholesterol accumulation in macrophages upon highfat diet feeding but accumulate cholesterol and triglycerides in the bloodstream, hampering interpretation of the specific role of LRP-1 in lesion macrophages [72]. Several studies have demonstrated reduced foam cell formation in mice with total or macrophage-specific deficiency in CD36 [36, 37] and MSR1 [10, 118]. However, another report in $Apoe^{-/-}$ mice deficient for CD36 or MSR1 demonstrated normal lesional foam cell accumulation despite reduced cholesterol accumulation in peritoneal macrophages, suggesting that alternative pathways of lipid uptake can compensate for the loss of CD36 or MSR1 [79]. In addition to its role in lipid uptake, a critical role for MSR1 has been identified in macrophage proliferation in advanced lesions [98]. Recent research demonstrated that the adhesion receptor CD146 (also known as melanoma cell adhesion molecule, MCAM), which is expressed on human and murine plaque macrophages, promotes the accumulation of oxidized LDL in macrophages by aiding CD36 internalization. Interestingly, CD146 also appears to promote macrophage retention within lesions [73].

Intracellular cholesterol can be removed from macrophages through an active reverse cholesterol transport process from the intracellular compartment to extracellular lipid acceptors such as Apolipoprotein A-1 (ApoA-1), a major constituent of high-density lipoprotein (HDL) [141]. Macrophage cholesterol efflux depends on the ATP-binding cassette transporters (ABC) ABCA1 and ABCG1 [141]. Accordingly, hypercholesterolemic mice lacking ABCA1 and ABCG1 expression in leukocytes display enhanced atherosclerotic lesion formation, likely in part due to increased accumulation of macrophage foam cells [139]. However, the role of ABCA1 and ABCG1dependent cholesterol efflux pathways goes beyond the regulation of foam cell formation. Indeed, ABCA1 and ABCG1 are suppressors of hematopoietic stem and progenitor cell (HSPC) proliferation and mobilization [136, 140], and Acba1^{-/-}Abcg1^{-/-} mice show uncontrolled HSPC proliferation, leukocytosis [140], and increased extramedullary hematopoiesis [136], which altogether promote immune cell accumulation within lesions [140].

Proliferation and senescence, survival, and apoptosis

Given its recently appreciated importance in lesional macrophage accumulation (see above), proliferative ability can also be considered an important functional trait of lesion macrophages. As macrophage proliferation has been proposed to be preferentially activated in advanced lesions [10], deciphering the mechanism underlying the transition from a nonproliferative to a proliferative state would be of interest. In contrast to proliferating macrophages, lesions also contain cells with terminal loss of proliferative ability, namely senescent cells. Although a general pathogenic role of senescence in atherosclerosis was already suspected [22, 134], a recent report proposed that senescent macrophage foam cells within the vascular intima were pathogenic during the whole atherogenic process [23]. Intimal macrophage foam cells expressing senescent markers were abundantly found in the intima of the lesion-prone lesser curvature of the aortic arch in $Ldlr^{-/-}$ mice after 9 days of atherogenic diet feeding, and their pharmacological clearance reduced mRNA expression of *Tnfa*, *Vcam1*, and Mcp1, suggesting a role of these cells in lesion initiation. Senescent markers were also found in ~20% of macrophage foam cells in established lesions, and sorted senescent macrophages had increased mRNA expression of some proinflammatory cytokines ($II1\alpha$, Mcp1) and metalloproteases (Mmp12, *Mmp13*). Accordingly, clearance of senescent cells from established lesions halted lesion progression and was associated with features of plaque stability [23]. Thus, senescence can be considered as a novel deleterious dysfunctional state of macrophages in lesions.

Survival and apoptosis in plaques represent critical aspects of macrophage biology in atherosclerosis as they dictate not only formation of the necrotic core, but can also underlie plaque regression and resolution of inflammation upon normalization of blood lipid levels [89]. In line, it is still unclear how modulation of macrophage survival impacts atherosclerosis, as contrasting results have been reported in various genetic mouse models that showed that increased macrophage survival appeared either beneficial [16, 104] or deleterious [11, 12, 48, 143]. Whether increased macrophage survival or apoptosis ultimately determines plaque progression or regression most likely depends on the plaque stage and total efferocytotic ability of surrounding viable macrophages.

Efferocytosis and authophagy

Efferocytosis corresponds to the immunologically silent clearance of apoptotic cells by phagocytes and is essential in the maintenance of self-tolerance [51]. Several lines of evidence indicate that macrophage efferocytotic ability has a critical impact on atherosclerotic lesion formation and progression [130]. Evidence supporting this concept mostly stems from genetic mouse models in which major pathways of apoptotic cell recognition by phagocytes have been invalidated. MFG-E8 bridges apoptotic cells to macrophages through binding of exposed phosphatidilyserine (PS) on the membrane of apoptotic cells and $\alpha v\beta 3/\beta 5$ integrins on macrophages, and $Ldlr^{-/-}$ mice with immune cell-specific deficiency in MFG-E8 displayed increased atherosclerosis and necrotic core formation [4]. Apoptotic cells can also be recognized by the PSbinding protein GAS6, which binds the receptor MER-TK on macrophages. Increased atherosclerosis, accumulation of apoptotic cells, and plaque necrosis were observed in Apoe-*Mertk*^{-/-} mice [126] and in $Ldlr^{-/-}$ mice [5] with immune cell MER-TK deficiency. In line, it was recently proposed that proteolytic cleavage of MER-TK from the macrophage surface triggers defective efferocytosis in advanced lesions, as $Ldlr^{-/-}$ mice expressing a cleavage-resistant MER-TK showed improved efferocytosis and decreased necrosis in lesions [18]. Blockade of TIM-1 or TIM-4, which are expressed by macrophages and recognize PS on apoptotic cells [43], or genetic deficiency in the complement C1q, known to be involved in apoptotic cell clearance, also increased lesion formation in $Ldlr^{-/-}$ mice [14]. Apoptotic cells can also express "do not eat me" signals such as CD47, which inhibit efferocytosis upon binding to its receptor SIRP α on macrophages, and therapeutic neutralization of CD47 via monoclonal antibodies was recently shown to promote efferocytosis and reduce lesion formation in murine models of atherosclerosis [63]. This further shows that efferocytosis is a crucial and therapeutically targetable function of atherosclerotic lesion macrophages. Beyond its role in preventing accumulation of secondary necrotic cells, efferocytosis also has a profound impact on macrophage phenotype. Notably, phagocytosis of apoptotic cells reprograms macrophages towards an antiinflammatory profile, with increased expression of antiinflammatory IL-10 and TGF β , and decreased expression of proinflammatory IL-12 and TNF α [25]. Furthermore, apoptotic cell phagocytosis triggers LXR-dependent expression of MER-TK by phagocytes, further promoting efferocytosis [83]. Given the multifaceted anti-atherogenic functions of LXR-mediated gene expression in macrophages [38, 57, 115], LXR activation through efferocytosis may further participate in a beneficial macrophage phenotype.

Autophagy can be induced in response to oxidative and endoplasmic reticulum (ER) stress in plaque macrophages, and disruption of this process through genetic deficiency in the autophagy-related gene 5 (Atg5) increased plaque macrophage apoptosis and necrosis. Additionally, apoptotic Atg5deficient macrophages were less efficiently efferocytosed by viable macrophages [71]. These findings suggest that macrophage autophagy plays a protective role in advanced atherosclerosis.

Microenvironmental determinants of macrophage function in atherosclerosis

In lesions, macrophages are exposed to a vast variety of stimuli that can profoundly impact on their phenotype. In response to microenvironmental factors, several intracellular pathways involving signaling hubs such as, e.g., nuclear factor "kappalight-chain-enhancer" of activated B cells (NF- κ B), various signal transducer and activation of transcription (STAT) transcription factors or nuclear receptors, notably of the peroxisome-proliferator activating receptor (PPAR) family, are activated and control macrophage phenotype [29]. To illustrate the complexity of the plaque microenvironment and of the determinants of lesional macrophage phenotype, we here provide a brief and non-exhaustive overview of some of the major cues governing macrophage function in atherosclerosis (Fig. 1).

Lipids

Within lesions, macrophages are exposed to native and modified lipoproteins and accumulate intracellular lipids. Efferocytosis of apoptotic cells can also contribute to macrophage accumulation of intracellular lipids. How this affects macrophage phenotype is still unclear [122]. Lipid loading itself was unexpectedly shown to inhibit, rather than to activate inflammatory gene expression in peritoneal macrophage foam cells of $Ldlr^{-/-}$ mice fed a high-fat diet, a process that depended on accumulation of the lipid intermediate desmosterol and activation of LXR target gene expression [115]. This suggests that the plaque microenvironment, rather than lipid loading itself, controls proinflammatory functions of lesional macrophages. On the other hand, excess intracellular cholesterol accumulation has toxic effects in



Fig. 1 Nonexhaustive overview of microenvironmental and intrinsic modulators of atherosclerotic plaque macrophage phenotype. In lesions, macrophages are exposed to a variety of microenvironmental signals that either promote a pathogenic phenotype (in *red*), or in contrast attenuate pro-atherogenic features (in *green*). The exact influence of some microenvironmental signals (e.g., hypoxia) is still poorly defined. Abbreviations: *ABCA1/G1* ATP binding cassette transporter A1/G1, *ATP* adenosine triphosphate, *CHOP* C/EBP homologous protein, *CLEC4e* C type lectin domain family 4 member E, *dsDNA* double-stranded deoxyribonucleic acid, *FABP4* fatty acid binding protein 4,

Neutro neutrophils, *NETs* neutrophil extracellular traps, *eRNA* extracellular ribonucleic acid, *HDL* high-density lipoprotein, *HSPs* heat-shock proteins, *IFN* interferon, *IL* interleukin, *NF-xB* nuclear factor "kappa-light-chain-enhancer" of activated B cells, *NLRP3*, *NACHT*, *LRR* and *PYD* domain-containing protein 3, *OxLDL* oxidized low-density lipoprotein, *PKC* protein kinase C, *PS* phosphatidylserine, *ROS* reactive oxygen species, *TGF* β transforming growth factor- β , *TLR* Toll-like receptor, *ER* stress endoplasmic reticulum stress, *TNF* α tumor necrosis factor- α , *UPR* unfolded protein response

macrophages through activation of endoplasmic reticulum (ER) stress, which also has proinflammatory effects (see below) [41]. Fatty acid accumulation in macrophages can also promote a proinflammatory macrophage phenotype through activation of the fatty acid binding protein (FABP)-4 [74].

Oxidized phospholipids and lipoproteins (ox-LDL) promote macrophage inflammation [68], notably through the scavenger receptor CD36, which induces proinflammatory effects through promotion of the formation of a Toll-like receptor (TLR)-4/TLR-6 heterodimer upon ox-LDL binding [116].

Recently, it was proposed that HDL, which is essential in macrophage reverse cholesterol transport and generally considered atheroprotective, could induce a proinflammatory phenotype in macrophages, with increased secretion of IL-12, IL-1 β , and TNF α and reduced IL-10 production. This study proposed that HDL-dependent passive cholesterol efflux led to depletion of membrane cholesterol and disruption of lipid

rafts, leading to activation of several protein kinase C isoforms and proinflammatory effects mediated by NF- κ B and STAT-1 signaling [128]. In contrast, ABCA1- and ABCG1-dependent active cholesterol efflux to HDL is thought to have antiinflammatory effects in macrophages, as ABCA1/G1 double-deficient lesional macrophages display a clearly proinflammatory profile [137].

A family of anti-inflammatory, pro-resolving lipid mediators has a crucial role in the resolution of inflammation particularly through promotion of macrophage efferocytosis, suppression of proinflammatory, and activation of antiinflammatory gene expression [108]. The concentration of two of these pro-resolving mediators, Maresin 1 and Resolvin D2, was recently found to decrease in vascular tissue during plaque progression, and their therapeutic delivery favored an antiatherogenic macrophage phenotype and decreased lesion formation [132].

Cholesterol crystals

In lesions, cholesterol crystals can form both intra- and extracellularly, and cholesterol crystal deposits can be detected even in early atherosclerotic lesions [33]. Importantly, cholesterol crystals can activate the NLRP-3 inflammasome, which converts the proinflammatory cytokines IL-1ß and IL-18 to their mature and secretable form, and cholesterol crystal-mediated activation of the NLRP-3 inflammasome has been suggested to be essential in atherogenesis [33]. Formation of cholesterol crystals in macrophages and subsequent NLRP-3 inflammasome activation depends on CD36 [110]. Besides their direct proinflammatory effects in macrophages, cholesterol crystals also induce formation of extracellular traps (NETs) by neutrophils. NETs, in turn, prime macrophages for proinflammatory cytokine production, notably IL-1 α and IL-1 β , at the transcriptional level, disclosing cholesterol crystals not only as a direct inducer of macrophage inflammation but also as an indirect priming signal through NETosis [135].

Hypoxia

In advanced lesions, growing distance from the vessel lumen to the plaque core and increased metabolic demand creates areas of hypoxia. Hypoxia induces stabilization of the oxygen-sensing transcription factor hypoxia-inducible factor-1 α (HIF1 α), a process that can be further substantiated by inflammatory signaling pathways such as NF-κB [85, 96]. Although the critical role of HIF1 α in macrophage function is well established [31, 85], contradictory findings on its effects in atherosclerosis have been obtained. Reduced atherosclerosis in LysM^{cre}Hifla^{flox} mice with myeloid cell-specific HIF1 α deficiency was reported after 16 weeks of highcholesterol diet, and HIF1 α -deficient macrophages showed decreased apoptosis and inflammatory cytokine expression in vitro [1]. Another study showed no differences in early lesion formation in the same model at 6 weeks of high-fat diet feeding [21]. In contrast, increased early lesion formation and IL-12 expression by antigen-presenting cells were evidenced in CD11c^{cre}Hif1a^{flox} mice where Cre-mediated recombination occurs not only in dendritic cells but also in some macrophages and T cells [2, 21]. Given that Cre expression driven by the LysM promoter is not macrophage specific, and that not all macrophages may be affected in *CD11c^{cre}Hif1a^{flox}* mice, these results are altogether difficult to interpret. One could speculate that HIF1 α differentially affects distinct macrophage subsets and has disease stage-specific functions. Hifla activation can also induce expression of netrin-1 and Unc5b in lesional macrophages [94], a process that could promote their retention in lesions [129], although this has yet to be addressed experimentally.

Endoplasmic reticulum stress and the unfolded protein response

In lesions, several factors (e.g., lipid loading, metabolic stress, inflammatory signaling) can induce an impairment of the endoplasmic reticulum (ER) function in macrophages, leading to activation of the unfolded protein response (UPR) [56]. The UPR/ER stress response appears to have a crucial role in the control of macrophage apoptosis in lesions (for detailed review about the role of ER stress and UPR in atherosclerosis, we refer the reader to references [56, 58]). Indeed, macrophage cholesterol loading induces ER stress and triggers cell death through a mechanism depending on the transcription factor CHOP, a major effector of the UPR [41]. CHOP deficiency drastically reduced apoptotic cell accumulation and necrotic core formation in advanced lesions in $Ldlr^{-/-}$ and $Apoe^{-/-}$ mice [127]. Other effector proteins of the UPR such as XBP1 or IRE1 α may also have a substantial role in the control of lesional macrophage phenotype [26, 56].

Necrotic cells

During atherosclerotic plaque progression towards advanced and unstable phenotypes, accumulation of apoptotic cells is thought to eventually overcome macrophage efferocytic ability, leading to local secondary necrosis of plaque cells and formation of the necrotic core. In contrast to apoptotic cells, recognition and engulfment of necrotic cells elicit proinflammatory responses in macrophages [99]. Loss of cell membrane integrity allows leakage of intracellular molecules that are recognized by macrophages as damage-associated molecular patterns (DAMPs) such as double-stranded DNA (dsDNA), RNA, heat shock proteins (HSPs), or nucleotides (e.g., ATP) [100]. Notably, HSPs and dsDNA promote macrophage inflammation via Toll-like receptors (TLRs) [142], and extracellular RNA was recently shown to promote atherosclerosis, presumably in part through induction of proinflammatory cytokine secretion (e.g., TNF α , IL-1 β) by macrophages [113]. A recent study demonstrated a critical role of the necrotic cell sensor C type lectin receptor 4e (CLEC4e) in the control of lesional macrophage phenotype [26]. In vitro, activation of CLEC4e increased macrophage lipid accumulation by reducing Abca1 and Abcg1 expression and inhibiting reverse cholesterol transport, without affecting ox-LDL uptake. CLEC4e signaling also activated the UPR in macrophages in vitro, with increased expression of the UPR/ER stress-associated proteins inositol-requiring enzyme-1 α (Ire1 α) and Chop and splicing of Xbp1 mRNA. Although the role of the UPR/ER stress response and particularly of CHOP in lesional macrophage apoptosis is well established [41, 127], as previously mentioned, Clec4e signaling was not associated with increased macrophage cell death, but instead promoted a proinflammatory macrophage phenotype and macrophage proliferation

through upregulation of macrophage colony-stimulating factor (CSF1). Accordingly, $Ldlr^{-/-}$ mice with CLEC4edeficient bone marrow cells showed decreased atherosclerosis associated with reduced lesional macrophage content and proliferation, lower plaque lipid accumulation, and diminished inflammatory cytokine expression [26].

Growth factors, proinflammatory and anti-inflammatory cytokines, and interaction with other immune cells

In lesions, macrophages are exposed to growth factors such as granulocyte-macrophage colony-stimulating factor (CSF2) or CSF1 that control macrophage survival, proliferation, and various aspects of their function [26, 32]. CSF2 was also shown to indirectly induce plaque macrophage apoptosis through upregulation of IL-23 expression [117]. The plaque microenvironment also contains a plethora of pro- and antiinflammatory cytokines that impact macrophage phenotype [6, 124]. Cytokines such as IL-1 β , TNF α , or IFN γ promote acquisition of a pro-atherogenic macrophage phenotype with increased expression of proinflammatory cytokines and chemokines, proteases, and can in addition also affect macrophage lipid metabolism [93]. Type I interferons seem to particularly influence foam cell formation, as IFN- α promotes lipid uptake [70] while IFN- β both increases uptake and reduces efflux of cholesterol in macrophages [15]. In contrast, IL-10 confers anti-atherogenic properties to macrophage by reducing their expression of inflammatory cytokines and proteases and a modulation of the lipid metabolism [54]. The antiatherogenic cytokine IL-33 limits foam cell formation by reducing macrophage lipid uptake and increasing reverse cholesterol transport [77]. Likewise, IL-13 has been shown to promote an anti-atherogenic plaque phenotype [19].

In line, interaction with other cytokine-producing immune cell types shapes lesional macrophage phenotype. CD4⁺ T cells primed by antigen presenting cells in atherosclerotic vessels express IFN γ and TNF α and promote modified LDL uptake by lesional macrophages, as demonstrated in an ex vivo aortic explant model [64]. Co-culture with activated CD8⁺ T cells promotes secretion of CCL2 and CXCL1 by macrophages, and aortas from atherosclerotic mice display reduced *Ccl2* and *Cxcl1* mRNA levels after CD8⁺ T cell depletion [28]. CD8⁺ T cell-derived TNF α was also proposed to potentiate macrophage-mediated inflammation in lesions, and CD8⁺ T cell production of cytotoxic enzymes granzyme-B and perforin trigger macrophage cell death in lesions [66], indicating a potential role of CD8⁺ T cells in the control of plaque macrophage phenotype.

Other microenvironmental and intrinsic factors

In lesions, macrophages are exposed to reactive oxygen species (ROS) produced by other vascular cells such as endothelial cells and VSMCs that may impact their phenotype. ROS production can be activated in macrophages in response to modified LDL and is thought to have proinflammatory effects, as demonstrated in macrophages deficient for the NADPH-oxidase component Nox2 [13]. ROS also promote cellular senescence [134]. Exposure to hemostatic factors in lesions can also impact macrophage phenotype [62], and we could for example recently demonstrate that coagulation factor XII induced a proinflammatory macrophage phenotype and promoted lesion formation [133]. Epigenetic regulation of gene expression plays a role in defining macrophage phenotype in lesions, and changes in acetylation or methylation of specific histones associated with plaque progression have been observed in human lesion macrophages [52]. How these epigenetic marks are acquired and how they influence gene expression and macrophage function remain to be determined. Non-coding RNAs such as microRNAs [60] or long-noncoding RNAs [55] may also affect gene expression and macrophage function in atherosclerosis.

Some studies indicate that macrophage phenotype could be in part predetermined before their precursors reach atherosclerotic lesions. In particular, it has been demonstrated that hypercholesterolemia leads to hematopoietic stem cell priming in the bone marrow towards a proinflammatory phenotype [106]. In a model of gastrointestinal infection, resident bone marrow natural killer cells were shown to educate monocytes during medullar development and to prime them towards regulatory functions [9]. As developing and mature monocytes are in contact with a plethora of other immune cells in the bone marrow and spleen, one could speculate that this concept of monocyte pre-education at their production sites may be relevant in atherosclerosis.

Atherosclerotic lesion macrophage identity: moving beyond the polarization paradigm

Limits of the M1/M2 paradigm and its variations

It has long been recognized that macrophages can adopt a wide range of phenotypes in response to specific stimuli. A commonly used classification of macrophage phenotypes relies on the in vitro defined M1/M2 paradigm and its variants. Macrophages stimulated with IFN γ and LPS adopt a M1 phenotype, characterized by high expression of proinflammatory cytokines and chemokines, expression of inducible nitric oxide synthase (iNOS), and production of ROS, associated with pathogen destruction [76, 80, 111]. In contrast, macrophages exposed to the Th2 cytokines IL-4 and IL-13 adopt an anti-inflammatory M2 phenotype and secrete IL-10 and TGF β [76, 80, 111]. Using various stimulation cocktails, variants of the M2 phenotype (M2a, M2b, M2c) have further been described [76, 80, 111].

The M1/M2 polarization states were defined in specific conditions in vitro and represent extreme, artificial ends of a spectrum of macrophage phenotypes. However, the M1/M2 classification is commonly used to attempt defining macrophage phenotype in in vivo contexts. For example, expression of genes associated with M1/M2 polarization (e.g., Arginase-1, CD206, iNOS) is employed to infer macrophage function in disease models in vivo. This represents at best an approximation but could potentially be misleading: recently, in an obesity model, adipose tissue macrophages expressing the M2 marker CD301b were shown to induce weight gain and glucose intolerance, which is in contrast to the predicted beneficial role of M2-polarized macrophages in this setting [61, 65]. Although prototypical M1/M2 phenotypes associated with the expression of respective markers can be faithfully recapitulated in specific contexts in vivo (e.g., allergy or parasitic infection), the M1/M2 paradigm cannot be readily transposed to any disease setting where macrophages are exposed to a more complex microenvironment [76, 111]. In light of the complexity of the atherosclerotic plaque environment (Fig. 1), the M1/ M2 paradigm is unlikely to embrace the complexity of macrophage phenotypic heterogeneity in atherosclerosis.

Despite these widely recognized limitations, the M1/M2 paradigm is nevertheless ubiquitously used in the atherosclerosis research literature, and analysis of M1/M2-associated gene expression is a request that often arises during manuscript peer review. Researchers attempting to decipher macrophage functional heterogeneity in atherosclerosis and apprehend its role in disease have elaborated on the M1/M2 paradigm and proposed several macrophage polarization states induced by specific stimuli (e.g., M4, induced by CXCL4; Mheme, induced by Heme; Mox, induced by oxidized phospholipids) presumably associated with particular functions relevant to atherosclerosis [24, 27]. Although this approach has some merits as it attempts to integrate the role of plaquespecific stimuli in the control of lesional macrophage function, it still appears drastically reductive when considering the variety and complexity of plaque macrophage phenotypic determinants.

In line, recent articles have questioned the use of a rigid nomenclature to classify macrophage subsets in the context of cardiovascular diseases and atherosclerosis. Tabas and Bornfeldt proposed "that the phenotype of lesional macrophages cannot be classified into predetermined subsets but rather is a consequence of the lesional microenvironment and the activation of specific intracellular signaling pathways" [122]. Nahrendorf and Swirski argued that the M1/M2 paradigm constitutes a hurdle in deepening our understanding of macrophage function and should be abandoned in favor of a function-focused identification of macrophage phenotypes [82]. As true functional features of macrophages dictated by the plaque environment, rather than their affiliation to arbitrarily defined subsets, determines their contribution to atherosclerosis, we fully concur with these views. For a better understanding of their role in various stages of atherosclerosis, defining macrophages based on their origin and a set of disease-relevant functions would be much more informative than assigning them a putative polarized state based on very limited information (e.g., expression of a set of predefined markers). Efforts aiming at establishing a unifying nomenclature for macrophage activation and polarization have been made, and it was proposed to define macrophages based on their source, activators, and a consensus collection of markers [80]. Although this is convenient to implement in in vitro experiments, such an approach may not be readily applicable to lesional macrophages in vivo, as the definition of micro-environmental activators may be close to impossible and no consensus has yet been established for plaque macrophage subsets and their markers. Nevertheless, it now appears technically feasible to elaborate on a similar idea and to attempt defining lesional macrophages based on their origin, activation of intracellular signaling pathways, and functional features.

Methodological limitations and future avenues

To date, the most commonly used methodological tools unfortunately fail to embrace the full spectrum of macrophage functional heterogeneity in vivo. Use of arbitrarily defined sets of markers associated with in vitro macrophagepolarized states in flow cytometric or immunohistochemical analyses of lesion macrophages does not allow deducing functional features. Transcriptomics analyses of bulk lesion macrophage populations, even if presorted according to putative subset markers, produce averaging effects that likely mask discrete, intermediate phenotypes, and it is likely that proposed lesional macrophage subsets such as M4 or Mox actually encompass macrophages with diverse phenotypes. Recent technological advances may provide researchers with better tools to investigate macrophage functional heterogeneity in atherosclerosis and its impact on disease. For example, recent genetic fate-mapping or parabiosis models allow discriminating lesion macrophages and macrophage-like cells of different origin [35, 40, 98, 109]. High-dimensional flow cytometry analyses and mass cytometry could be used to simultaneously analyze an increasingly growing number of cell surface and intracellular markers in lesion macrophages [53, 103]. This would for example allow analyzing expression of functionally relevant cell surface proteins such as ABCA1, MER-TK, SIRP α , CD36, MSR1, and others in flow cytometric analyses of macrophages directly extracted from the lesion environment, and could help identify and sort more precisely defined macrophage subsets using a wide array of markers, some of which likely remain to be identified. Single-cell transcriptomics approaches such as single-cell RNA-sequencing are able

to identify cells endowed with distinct phenotypes within seemingly homogenous immune cell populations and have for example revealed phenotypes in Th17 T cells ranging from regulatory to highly pathogenic in experimental autoimmune encephalomyelitis [45]. This individual cell approach could represent a powerful tool to analyze macrophage phenotype in atherosclerosis while avoiding bias associated with arbitrary predefinition of cell subsets. Although these methods are still costly and require a significant level of technical expertise that may preclude their routine use in many laboratories, the higher resolution that they offer may be a way to dwell deeper into lesional macrophage biology in the future.

Understanding the complex biology and function of macrophages in vascular inflammation and atherosclerosis constitutes as prerequisite for the development of novel therapeutic approaches. Precisely identifying the mechanisms of macrophage accumulation and functional regulation in lesions could pave the way towards the development of original strategies targeting these processes and limiting lesion formation or progression towards a vulnerable phenotype. This could also facilitate the development of novel imaging strategies [34] or the emergence of new biomarkers [125] to help evaluate plaque phenotype and the associated atherothrombotic risk in patients.

Conclusion

Recent research has revealed an unexpected complexity in the mechanisms of macrophage accumulation in atherosclerosis, protective and pathogenic functions performed by macrophages in lesions, and how these functions are regulated. Major recent conceptual shifts and challenges to long-standing paradigms highlight the need to constantly reevaluate how we apprehend research on the role of macrophages in atherosclerotic disease. In the near future, higher resolution analysis of macrophage phenotype in atherosclerotic lesions through novel methods will allow researchers in the field to establish more precise macrophage "identity cards" taking into account their origin and disease-relevant functional features. This will hopefully pave the way for the development of therapeutic strategies targeting macrophages to reduce the disease burden caused by atherosclerosis and associated pathologies.

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