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Making a difference: Monocyte Heterogeneity in Cardiovascular Disease

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Abstract

Monocytes are frequently described as bone marrow-derived precursors of macrophages. Although many studies support this view, we now appreciate that monocytes neither develop exclusively in the bone marrow nor give rise to all macrophages and dendritic cells. In addition to differentiating to specific leukocyte populations, monocytes, as monocytes, are functionally and ontogenically heterogeneous. In this review we will focus on the development and activity of monocytes and their subsets in mice (Ly-6C^{high/low}) and humans (CD14^{+dim/-} CD16^{+/-}) in the context of atherosclerosis and its complications.

Keywords

monocyte subsets; monocyte heterogeneity; Ly-6C; CD14; CD16; macrophage; dendritic cells; atherosclerosis; myocardial infarction; cardiovascular disease; extramedullary hematopoiesis; inflammation

Introduction

Monocytes, macrophages and dendritic cells are essential to the development of atherosclerosis [1]. According to a current paradigm, monocytes infiltrate atherosclerotic lesions and develop into macrophages and dendritic cells. Macrophages are the most numerous cells in atheromata, accumulate lipids, secrete multiple inflammatory cytokines and growth factors, and participate at all stages of atherogenesis. Depletion of monocytes and their progeny in an experimental mouse model decreases the development of atherosclerosis [2], but wholesale ablation of monocytes and macrophages is not a viable therapeutic option because of these cells' essential role in immunity.

Leukocytosis and monocytosis have been associated with cardiovascular diseases in numerous epidemiological studies, prompting speculation on the functional role of these cells. Many studies have documented heterogeneity among human monocytes, but it was the discovery and characterization of monocyte subsets in the mouse that enabled investigation into the relevance of monocyte heterogeneity in cardiovascular disease models [3]. In this review we will focus on recent work that has enriched our understanding of monocyte and macrophage biology in atherosclerosis and its complications. We will consider monocyte development and function. We will discuss how insights from experimental studies can be used to test the clinical relevance of monocyte heterogeneity in cardiovascular disease.

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Finally, we will assess human monocyte heterogeneity in the context of clinical and epidemiological studies.

Development of monocyte subsets

Monocytes are a major population of circulating white blood cells. Morphologically, monocytes are larger than lymphocytes and, unlike granulocytes, contain a characteristic horseshoe or kidney-like nucleus. Functionally, they are phagocytic and can develop into macrophages and dendritic cells in vitro and in vivo. In humans and mice at least two monocyte subsets have been described. In humans they are usually classified according to CD14 and CD16 expression levels (see extended discussion below). In mice, monocytes are defined by their expression of Ly-6C, which is an epitope of Gr-1. Ly-6C^{high} (Gr-1⁺) monocytes are CCR2^{high} CX₃CR1^{low} CD62L⁺, whereas Ly-6C^{low} (Gr-1⁻) monocytes are CCR2^{low} CX3CR1^{high} CD62L⁻ [3]. Originally, Ly-6C^{high} monocytes were called “inflammatory” because they preferentially accumulate in the peritoneum in response to an inflammatory stimulus, and Ly-6C^{low} monocytes were called “resident” because of their apparent indiscriminate accumulation in tissue in the steady state. Subsequently, investigators have called Ly-6C^{low} monocytes “patrolling” because of their ability to crawl along the endothelium and “reparative” because of their role in mediating healing after injury. Others have proposed to call Ly-6C^{high} monocytes, in analogy to human monocytes, “classical” and Ly-6C^{low} monocytes “non-classical”, a nomenclature that, although convenient, offers no functional insight.

Nomenclature aside, an important early question was how subsets relate to each other. It has been known for a long time that monocytes arise from the common myeloid progenitor (CMP), a self-renewing bone marrow precursor that, in addition to monocytes, also gives rise to neutrophils, megakaryocytes, basophils and mast cells. A downstream progenitor of the CMP restricted toward the monocyte lineage, the macrophage and dendritic cell progenitor (MDP) was identified in 2006 [4], and, at the molecular level, transcription factors such as PU.1, KLF4, IRF-8 and MafB have proven to be particularly important for monocyte development [5]. The question remains, however, whether the MDP is a common progenitor for both subsets and whether Ly-6C^{high} monocytes convert to Ly-6C^{low} monocytes. The first study in favor of conversion utilized monocyte-depleting clodronate-loaded liposomes, showing that repopulation of the monocyte pool following depletion occurs in two phases: Ly-6C^{high} monocytes appear after 1 day while Ly-6C^{low} monocytes appear only after 4 days [6]. Direct fate-mapping experiments supported this view. Labeled Ly-6C^{high} monocytes adoptively transferred and tracked in the circulation gave rise to Ly-6C^{low} monocytes, presumably in the bone marrow [7, 8]. Both studies are the foundation of the idea that Ly-6C^{low} monocytes arise from Ly-6C^{high} monocytes.

Conversion alone, however, may not fully explain the relationship between the two subsets. The biphasic re-emergence of monocyte subsets after clodronate-mediated depletion, while intriguing, can also reflect differences in life-span and cell development; Ly-6C^{low} monocytes are the more long-lived cells. The in vivo adoptive transfer studies are a strong case in favor of conversion, but the number of cells retrieved in those experiments was low, and thus it is difficult to gauge the relative importance of conversion in generating Ly-6C^{low} monocytes. In vitro, the rapid differentiation of monocytes to macrophages makes it impossible to study conversion. Two insights in gene-knockout animals, however, may help to resolve the issue. First, it has been documented that Nur77^{-/-} mice lack mature Ly-6C^{low} monocytes but contain a Ly-6C^{high} monocyte population [9]. Does Nur77 convert Ly-6C^{high} monocytes or is it guiding Ly-6C^{low} monocyte production upstream in ontogeny, perhaps independently of Ly-6C^{high} monocytes? Second, Kruppel-Like Factor 4 (KLF4) deficient bone marrow chimeras lack Ly-6C^{high} monocytes in blood and spleen but still

contain low numbers of Ly-6C^{low} monocytes [10]. Is this evidence that Ly-6C^{low} monocytes can develop from a committed progenitor without a Ly-6C^{high} intermediate? These mice represent new tools to elucidate the mechanisms that link the development of Ly-6C^{high} and Ly-6C^{low} monocytes.

A comprehensive map of the developmental relationships between monocyte subsets requires a location. Since the 1960s it has been known that monocytes arise in the bone marrow, circulate in the blood, and develop to macrophages in peripheral tissue. The bone marrow contains specialized hematopoietic niches whose composition and function are the subject of multiple studies [11, 12]. Aside from the bone marrow and blood, monocyte subsets can also be found in the spleen as part of a reservoir that can be mobilized in response to distant inflammatory stimuli such as myocardial infarction [13]. The reservoir, which relies on angiotensin II signaling, appears to be important in post-injury healing [14].

In the context of continued or chronic inflammation the spleen becomes monocytopoietic, complementing the bone marrow's capacity to produce inflammatory cells. In apolipoprotein E deficient (ApoE^{-/-}) and LDL receptor deficient mice hematopoietic stem cells progressively seed the splenic red pulp to produce Ly-6C^{high} monocytes locally in response to GM-CSF and IL-3 [• 15]. In myocardial infarction and stroke the continuous demand for monocytes likewise transforms the spleen into a monocytopoietic organ [16]. The phenomenon occurs in a tumor model, thus broadening the scope of extramedullary monocytopoiesis in inflammatory diseases [17]. Although these insights add a new dimension to monocyte heterogeneity – the site of origin – the extent to which different hematopoietic environments influence monocyte function remains to be elucidated.

Function of monocyte subsets in cardiovascular disease

Our understanding of how monocyte subsets participate in cardiovascular disease is largely based on mouse models of atherosclerosis and myocardial infarction (Figure 1). In the steady state, the proportion of circulating Ly-6C^{high} and Ly-6C^{low} monocytes is nearly equivalent. In murine models of atherosclerosis, hypercholesterolemia induces monocytosis in the bone marrow, blood and spleen [18, 19]. Of the two subsets, Ly-6C^{high} monocytes increase in number preferentially. Recent work has shown that hypercholesterolemia induces proliferation of hematopoietic stem cell progenitors (HSPC) involving the cholesterol efflux pathway and its central molecular components ApoE and ATP-binding cassette transporters ABCA1 and ABCG1. HSPC secrete ApoE which binds to proteoglycans on the cell surface and mediates cellular cholesterol efflux via ABCA1 and ABCG1 to HDL. ApoE deficiency impairs cholesterol efflux, increases membrane cholesterol content as well as the surface expression of the IL-3/GM-CSF receptor [• 20, 21]. IL-3 and GM-CSF stimulate proliferation and survival of HSPC in the bone marrow and the spleen and thus contribute to monocytosis and neutrophilia [• 15]. Although cholesterol sensing pathways have been known to play important roles in atherosclerosis [22], these recent mechanistic studies have forged a previously unknown link with monocytes.

Mice deficient in apolipoprotein E develop large and complex lesions when fed a diet high in fat and cholesterol. Ly-6C^{high} monocytes accumulate in the growing atheromata preferentially via CCR2 and CX3CR1 [18, 19, 23]. Invading Ly-6C^{high} monocytes of medullary and extramedullary origins are sources of IL-1 β , reactive oxygen species, and proteases and may directly contribute to the lipid load in atherosclerotic lesions by ingesting lipids prior to accumulating in lesions [• 15]. Ly6C^{low} monocytes, which also ingest lipids [24], infiltrate atherosclerotic lesions less frequently via CCR5, but may still contribute to atherosclerosis in other important ways. Nur77^{-/-} ApoE^{-/-} mice and LDLR^{-/-} mice reconstituted with Nur77^{-/-} bone marrow have fewer Ly-6C^{low} monocytes. The mice

develop large lipid-laden lesions with more macrophages that express higher levels of TNF α , CD36 and SR-A [25]. The observations suggest that Ly-6C^{low} monocytes are atheroprotective. However, Nur77 deficiency also heightens inflammatory cytokine production by Ly-6C^{high} monocytes and macrophages [25, 26], rendering it difficult to judge the relative importance of Ly-6C^{low} monocytes in atherosclerosis.

In a mouse model of myocardial infarction two monocyte phases can be distinguished. Ly-6C^{high} monocytes infiltrate the healing myocardium on day 1 and dominate the first inflammatory phase. This subset secretes proteases and pro-inflammatory TNF α , and removes debris through phagocytosis. The second phase begins on day 4 and is dominated by the preferential accumulation of Ly-6C^{low} monocytes which secrete VEGF and promote myofibroblast accumulation, angiogenesis, and granulation tissue formation [• 27]. The biphasic monocyte recruitment pattern is orchestrated by increased MCP-1/CCL2 expression in infarcts in the first phase, which attracts Ly-6C^{high} CCR2^{high} monocytes, and increased Fractalkine/CX₃CL1 expression in the second phase, which favors Ly-6C^{low} CX₃CR1^{high} monocytes. A balanced and coordinated subset recruitment is likely important because atherosclerotic ApoE^{-/-} mice with Ly-6C^{high} monocytes have impaired healing of the infarcted myocardium [28].

The functional characterization of monocyte subsets in cardiovascular disease models has raised interesting therapeutic possibilities with regard to monocyte recruitment. Most of the interest has focused on targeting accumulation of Ly-6C^{high} monocytes, which are typically regarded as the central inflammatory culprits. Monocyte accumulation occurs through a series of distinct steps. First, chemokines attract monocytes via chemokine receptors. Silencing the chemokine receptor CCR2, which is highly expressed on Ly-6C^{high} monocytes, via nanoparticle-mediated transfer of short interfering RNA decreases Ly-6C^{high} monocytes and their progenies in peripheral tissues and attenuates inflammation associated with atherosclerosis and myocardial infarction [29]. Second, selectins and their ligands mediate leukocyte capture and rolling, a crucial step to be blocked by specific antibodies. The P-selectin glycoprotein ligand-1 (PSGL-1) on leukocytes interacts with P- and E-selectins on activated endothelium and platelets [30, 31]. Ly-6C^{high} monocytes express PSGL-1 at higher levels compared to Ly-6C^{low} monocytes and thus accumulate in the growing lesion preferentially [32]. L-selectin, which is also selectively overexpressed in Ly-6C^{high} monocytes, mediates secondary capture at sites of atherosclerosis [33]. The third stage involves activation of integrins which bind to their cognate receptors on the endothelium to mediate firm arrest. Therapeutically, interference with VLA-4/VCAM-1, LFA-1/ICAM-1 and Mac-1/CD40L interaction reduces monocyte adhesion and macrophage lesion content [34–• 38]. Beyond lipid lowering, statins and other anti-inflammatory drugs are thought to be atheroprotective in part because they interfere with endothelial activation and monocyte recruitment [39, 40]. Many of the therapeutic approaches mentioned above remain to be tested in humans.

Differentiation beyond the monocyte

Monocytes are precursors of macrophages and dendritic cells, the key phagocytic and antigen presenting cells in lymphoid and non-lymphoid tissues. Macrophages and dendritic cells are phenotypically and morphologically heterogeneous, a fact that has fueled considerable debate about how to define and categorize them [41]. Regardless of name, everyone agrees that these populations participate in many important biological processes. From the perspective of monocyte biology, one of the most exciting questions is whether subsets are restricted to give rise to macrophages/dendritic cells with defined functions, or whether the subset differences disappear once monocytes accumulate in tissue.

Functionally distinct macrophages can be derived from monocytes in vitro. Classical macrophage activation, which involves culture of bone marrow cells with M-CSF, LPS or IFN- γ yields M1 macrophages which are TNF α , IL-1 β , IL-6, IL-12 and iNOS-secreting, and thus “inflammatory”. Alternative activation involves culture with IL-4, IL-10 or IL-13 and generates M2 macrophages which are defined by their high expression of “anti-inflammatory” arginase 1, IL-10, CD206 and Fizz. These definitions have dominated thinking about macrophage heterogeneity and, although convenient for in vitro studies and elegant in their simplicity, should be used with caution in the in vivo setting. In the steady state, most organs contain their own particular macrophages, many of which do not derive from the bone marrow or from monocytes [42–45]. The spleen, for example, contains red pulp macrophages, metallophilic macrophages, classical dendritic cells, and undifferentiated monocytes, among others [13, 46]. Precisely how monocyte subsets contribute to macrophage and dendritic cell populations in the steady state is still unknown.

In disease, macrophage and dendritic cell heterogeneity magnifies. Uptake of oxidatively modified lipids via scavenger receptors and toll-like receptors drives inflammatory cytokine expression and M1 polarization of macrophages [47, 48], while engulfment of cholesterol crystals activates the NLRP3 inflammasome and leads to the over-expression of the M1 cytokine IL-1 β . Cholesterol metabolites and fatty acids serve as ligands for nuclear liver-X-receptor (LXR) and peroxisome-proliferator-activated receptors (PPARs). Activation of these receptors favors alternative macrophage polarization, inhibiting inflammatory gene expression and mediating cholesterol efflux [22, 49]. Platelet chemokine CXCL4 induces differentiation into M4 type macrophages that are weak in phagocytosis and oxLDL uptake [50], whereas Mox macrophages arise when macrophages are stimulated with oxidized phospholipids [51]. Whether these are separate populations or simply states that any lesional macrophage can adopt is perhaps secondary to the fact that the atheroma is a bustling microenvironment of functionally heterogeneous activity [52].

The relationship between circulating monocyte subsets and lesional macrophages is still poorly understood. Ly-6C^{high} monocytes give rise to lesional CD11b⁺ F4/80^{high} macrophages [• 15, 18], but whether they preferentially give rise to a subset of macrophages, and whether macrophages differentiate from one phenotype into another locally, is yet to be clarified. It has been proposed that Ly-6C^{low} monocytes, which express low levels of CD11c, preferentially give rise to CD11c⁺ dendritic cells in atherosclerotic lesions [19]. However, low yield of adoptively transferred cells in aortas has compromised sophisticated fate mapping studies. Not all macrophages in aortic lesions derive from a circulating progenitor, however. Recently, it was shown that adventitial Sca-1⁺ progenitors in C57Bl/6 and ApoE^{-/-} aortas give rise to macrophages locally [53]. Given the rare frequency of these progenitors in aortic tissue their functional in vivo relevance remains to be determined.

In addition to macrophages, the atherosclerotic lesion contains subsets of dendritic cells (DCs). DCs in the steady state aorta and in the growing lesion express high levels of MHCII and CD11c. They stimulate T cells but, unlike macrophages, are poor phagocytes [54, 55]. Aortic CD11c⁺ DCs may be divided into two major subsets: CD11b⁺ CD103⁻ F4/80⁺ DCs and CD11b⁻ F4/80⁻ CD103⁺ DCs. CD11b⁺ CD103⁻ DCs are believed to be monocyte derived while CD103⁺ DCs resemble classical DC and derive from common DC progenitors (CDP) without a monocyte intermediate. Flt3 depletion in LDLR^{-/-} mice selectively ablates CD103⁺ DC and worsens atherogenesis [55]. Likewise, depletion of plasmacytoid DC, although only sparsely detected in atherosclerotic lesions, increases lesion size [56]. These studies suggest that monocyte-derived macrophages and DC are atherogenic whereas classical DCs are atheroprotective. The complex interplay between these various subsets in shaping disease is yet to be described.

Relationship between mouse and human monocyte subsets

Monocytes are heterogeneous in humans [57]. Human monocytes have been classified according to different expression of surface receptors CD14 and CD16. So-called classical CD14^{high} CD16⁻ monocytes constitute ~70–80% of monocytes in the peripheral blood and can be distinguished from smaller monocytes coexpressing high levels of CD16 and lower levels of CD14 [58]. CD16⁺ monocytes produce high levels of TNF α in response to LPS stimulation and rise in number during infection. For this reason they were first named “inflammatory” [59, 60]. However, it is the classical CD14^{high} CD16⁻ monocyte subset, and not the “inflammatory” CD16⁺ subset, that resembles mouse “inflammatory” Ly-6C^{high} monocytes: The CD16⁻ subset expresses high levels of CCR2, CD62L, CD64 and low levels of CX₃CR1 [3, 57]. This had led to some confusion as to whether and how human and murine monocytes correspond.

Recent studies have taken advantage of gene array analysis and hierarchical clustering to compare monocyte subsets in the two species. In one study, the investigators gated, or grouped, human monocyte subsets according to their CD16 expression. The dominant “classical” subset was sorted as a CD14⁺ CD16⁻ cell population whereas the less numerous “non-classical” subset was sorted as a CD16⁺ cell population that contained a broad range of CD14 expression (CD14^{+/low/-}). The authors concluded that, in general, CD16⁻ monocytes resemble murine Ly-6C^{high} monocytes and CD16⁺ monocytes are similar to murine Ly-6C^{low} monocytes [61]. Several differences between the species were noted, however, including converse expression of several scavenger receptors.

Another study gated human monocytes into three populations: A numerically dominant CD16⁻ subset, an intermediate CD14⁺ CD16⁺ subset, and a CD14^{low/dim} CD16⁺ subset [62]. By performing principal component analysis and by comparing the three subsets to each other and to murine subsets, the authors concluded that CD14^{high} CD16⁻ and CD14⁺ CD16⁺ monocytes cluster with the murine Ly-6C^{high}/Gr-1⁺ monocytes whereas CD14^{dim} CD16⁺ monocytes cluster with Ly-6C^{low} monocytes. The study challenges the importance of using CD16 as a discrimination marker and argues for using CD14 as the essential marker for defining 2 monocyte subsets. Even so, the authors supplement their phenotypic characterization with functional assays of all 3 subsets. In response to LPS CD14⁺ CD16⁺ monocytes secrete TNF α , IL1 β and IL-6 while CD14^{high} CD16⁻ cells preferentially produce CCL2, IL-10, IL-8, reactive oxygen species and myeloperoxidase and high levels of IL-6. CD14^{dim} CD16⁺ monocytes, which express low levels of CCR2 but highest levels of CX₃CR1, and which also exhibit patrolling behavior, resemble murine Ly-6C^{low} counterparts. Stimulation of these CD14^{dim} cells with TLR7 and 8 agonists selectively upregulated inflammatory cytokine expression [62]. Other groups have reported that CD14^{dim} monocytes can produce TNF α in response to LPS [63, 64]. These observations argue against describing any particular subset as “inflammatory” since every cell is “inflammatory” in its own particular way and is specialized in how it responds to different stimuli. If one were to compare the three transcriptionally distinct human monocyte subsets [64, 65] to the two murine subsets based on phenotype and behavior, both CD16⁻ CD14^{high} and CD16⁺ CD14⁺ monocytes resemble Ly-6C^{high} monocytes while CD14^{dim} monocytes correspond to Ly-6C^{low} monocytes (Table).

Monocyte subsets and human cardiovascular disease

Many cohort and case-control studies have documented an association of leukocytosis with cardiovascular diseases. Elevated leukocyte counts were identified as an independent risk factor for developing disease and as a negative prognostic indicator in patients with coronary heart disease, myocardial infarction, peripheral artery disease and stroke [66–69].

Neutrophils show the strongest and most consistent correlation with disease occurrence and outcome [70, 71]. Monocytosis was found to predict cardiovascular events in some studies [70, 72–74] but not in others [75, 76], and lymphocyte counts seem to be inversely correlated with coronary heart disease and its complications [77]. While differences in study design may account for some of the discrepancies regarding the correlation of monocyte counts and adverse cardiac events in epidemiological studies, the use of flow cytometric analysis to distinguish monocyte subsets has allowed for more sophisticated and nuanced risk stratification.

Many studies investigated the relationship between cardiovascular risk factors and monocyte subsets. A weak but positive correlation of CD14^{dim} CD16⁺ monocytes with total plasma cholesterol and triglyceride levels was first described in 1999 in hypercholesterolemic patients with a positive stress ECG indicative of coronary heart disease [78]. Numbers of CD16⁺ monocytes but not overall monocyte counts positively correlate with Body-Mass-Index, insulin resistance/diabetes and intima-media-thickness. Weight loss after gastric bypass surgery in severely obese patients is associated with a significant reduction of CD16⁺ monocytes [79, 80]. Likewise, exercise training reduced numbers of CD16⁺ monocytes in a physically inactive study population [81]. CD14⁺ CD16⁺ monocytes but not total monocyte counts predict cardiovascular events in patients with chronic kidney disease and end stage renal disease on dialysis, a patient population at increased risk for atherosclerotic complications [79, 82].

In patients with symptomatic coronary artery disease compared to healthy controls the percentage of CD16⁺ monocytes was found to be increased according to a first small case-control study in 2004, even after adjustment for common risk factors [83]. This finding was confirmed in another small study where numbers and proportion of monocyte subsets were measured according to their differential capacity for magnetic nanoparticle uptake [84]. Assessment of plaque vulnerability by optical coherence tomography and computed tomography in patients with both stable and unstable angina pectoris revealed an increase in CD16⁺ monocytes with more vulnerable plaques. In fact, monocyte subset proportions did not differ significantly between healthy controls and patients with non-vulnerable plaques. Statin treatment decreased the percentage of CD16⁺ monocytes [85, 86]. CD16⁺ monocytosis after stent placement in patients with myocardial infarction also positively correlated with late in-stent restenosis [87]. Interestingly however, among a study population with stable coronary artery disease, those patients with more than 5 cardiovascular risk factors and especially with a positive family history for coronary artery disease presented relatively higher percentages of CD14^{high} CD16⁻ monocytes [88]. A prospective cohort study recently reported that an increased number and percentage of classical CD14^{high} CD16⁻ monocytes predicted future cardiovascular events independently of other risk factors in a general population [x• 89].

A number of studies have explored how monocyte subsets change during acute cardiovascular events. In stroke patients, CD14⁺ CD16⁺ monocytes increased preferentially within the first week, but the proportion of CD14^{high} CD16⁻ monocytes on admission positively correlated with infarct size and predicted worse clinical outcome and mortality [90]. After acute myocardial infarction (MI) and revascularization total blood monocyte counts tend to rise temporarily, peaking between day 2 and 3 after intervention. However, CD14^{high} CD16⁻ CCR2⁺ monocytes peak within the first 3–4 days whereas CD16⁺ CX₃CR1⁺ monocytes peak thereafter, a pattern reminiscent of the biphasic response observed in mice [• 27]. However, no data are yet available on subsets in heart tissue. Patients with unstable angina undergoing intervention do not show a shift in monocyte subsets suggesting that the observed effects are MI related. The peak value of CD16⁻ monocytes shortly after MI negatively correlates with myocardial salvage and gain of left

ventricular function at follow up [91]. With worsening congestive heart failure the percentage of intermediate CD14⁺ CD16⁺ monocytes has been reported to increase preferentially [92]. More recently, a small study in MI patients compared CD14⁺ CD16⁺ and CD14^{dim} CD16⁺ monocytes. The most pronounced increase was reported for intermediate CD14⁺ CD16⁺ monocytes within the first 3 days post MI and intervention. CD14^{high} CD16⁻ monocytes also increased during the first 3 days, as reported earlier, while CD14^{dim} CD16⁺ monocyte levels did not change over time. At 30 days after MI, monocyte subset distribution and numbers equaled those of patients with stable coronary artery disease [93]. Altogether, most studies report an association of CD14⁺ CD16⁺ monocytes with active cardiovascular disease, whereas some suggest that CD14^{high} CD16⁻ monocytosis is a negative prognostic indicator. Altogether, these important epidemiologic studies, which are necessarily descriptive, underscore the need of studying monocyte subset biology in mouse models. The observations that CD14⁺ CD16⁺ and CD14^{high} CD16⁻ monocytes are closely related to mouse Ly-6C^{high} monocytes, and given that mouse models position Ly-6C^{high} monocytes as central culprits of cardiovascular inflammation, lend further credibility to the potential translation of mouse studies to human disease.

Concluding remarks

Cardiovascular diseases are characterized by a highly diversified and heterogeneous response of the myeloid leukocyte population. How cell subsets shape pathogenesis is the current focus of many laboratories, and the therapeutic goal is to neutralize functionally distinct subsets that promote disease while augmenting or sparing those subsets that are protective. Achieving this will rely on mechanistically-oriented, high quality in vivo animal studies that can show how lesion growth, plaque rupture, and infarct healing can be controlled. Translating insights from the mouse to the human will no doubt continue to be a challenge, but it will be the combination of basic insights and increasingly sophisticated clinical studies that will likely harness the significance of monocyte and macrophage heterogeneity in cardiovascular disease.

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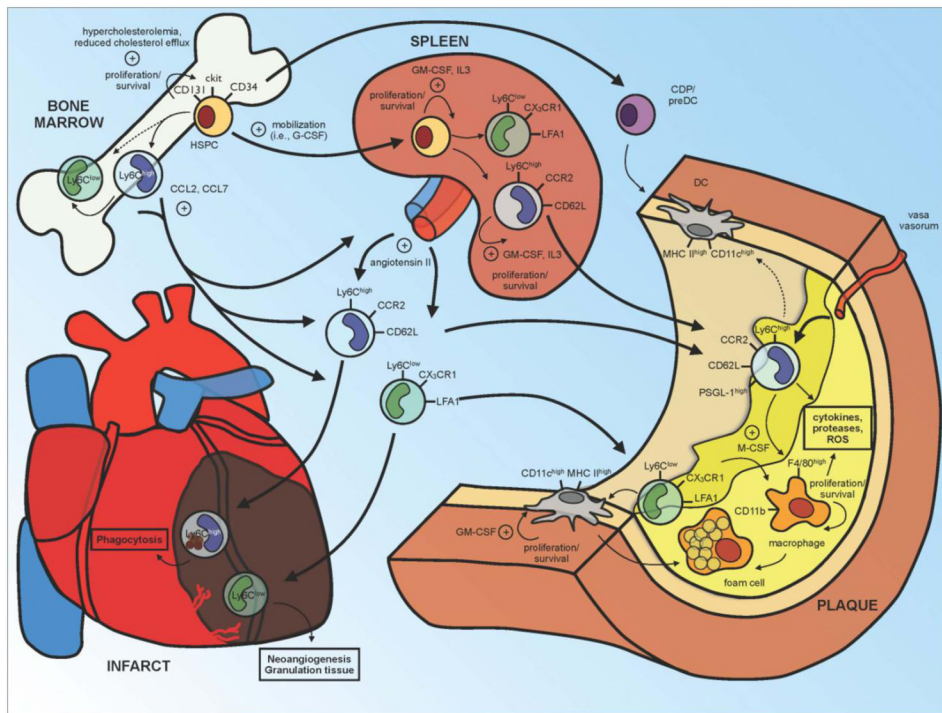
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Figure 1.

Monocyte subsets decisively engage in cardiovascular disease. Hypercholesterolemia and impaired cholesterol efflux promote hematopoietic stem progenitor cell (HSPC) proliferation and predominant Ly-6C^{high} monocytopoiesis. While monocyte bone marrow egress largely depends on CCR2 signaling, an interplay of multiple growth factors, chemokines and proteases mediates mobilization of progenitor cells. During murine atherosclerosis progenitor cells seed the spleen to locally supplement monocytopoiesis. Ly-6C^{high} monocytes from bone marrow and spleen preferentially enter atherosclerotic lesions and develop into macrophages and foam cells. Both monocytes and macrophages are sources of inflammatory cytokines, proteases and reactive oxygen species (ROS). Aortic dendritic cells (DC) derive either from monocytes or common dendritic cell progenitors (CDP) and develop into foam cells. In myocardial infarction Ly-6C^{high} and Ly-6C^{low} monocytes of medullary and extramedullary origins accumulate in the ischemic myocardium sequentially for phagocytosis, debris removal, granulation tissue formation, and neoangiogenesis. Thick arrows depict spatial relationships, thin arrows developmental relationships, and dashed arrows uncertain relationships.

Table

Monocyte subset profiles in mice and men

		Mouse		Human	
Subset	Profile	Subset	Profile	Subset	Profile
Ly-6C ^{high} /Gr-1 ⁺	CCR2 ^{high} , CCR5 ^{low} , CX ₃ CR1 ^{low} , CD62L ⁺ , PSGL-1 ^{high} , CD11a ^{low} , CD11b ⁺ , CD11c ⁻ , F480 ^{int} , CD36 ⁻ , CD64 ⁺ , MHCII ⁻	Classical CD14 ^{high} CD16 ⁻	CCR2 ^{high} , CCR5 ^{low} , CX ₃ CR1 ^{low} , CD62L ⁺ , PSGL-1 ^{high} , CD11a ^{high} , CD11b ⁺ , CD11c ⁻ , CD36 ^{high} , CD64 ^{high} , CD86 ^{low} , HLA-DR ^{low/-}	strong phagocytosis, preferential homing to inflamed tissue	strong phagocytosis; unclear migratory behavior in vivo
		intermediate CD14 ⁺ CD16 ⁺	CCR2 ⁺ , CCR5 ⁺ , CX ₃ CR1 ⁺ , CD62L ^{low/-} , CD11a ^{low} , CD11b ⁺ , CD11c ^{low} , CD36 ⁺ , CD64 ^{int} , CD86 ⁺ , HLA-DR ^{high} , Tie2 ⁺		strong phagocytosis; unclear migratory behavior in vivo
Ly-6C ^{low} /Gr-1 ⁻	CCR2 ^{low} , CCR5 ^{low} , CX ₃ CR1 ^{high} , CD62L ⁻ , PSGL-1 ^{low} , CD11a ^{high} , CD11b ⁺ , CD11c ^{low} , F480 ^{int} , CD36 ⁺ , CD64 ⁺ , MHCII ^{low}	non-classical CD14 ^{dim} CD16 ⁺	CCR2 ^{low} , CCR5 ⁻ , CX ₃ CR1 ^{high} , CD62L ⁻ , PSGL-1 ^{low} , CD11a ^{low} , CD11b ^{low} , CD11c ^{low} , CD36 ^{low} , CD64 ⁻ , CD86 ⁻ , HLA-DR ⁺	strong phagocytosis, patrolling behavior in vivo	poor phagocytosis; patrolling behavior in vivo