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Marie Benoit, Benoît Desnues, and Jean-Louis Mege

Converging studies have shown that M1 and M2 macrophages are functionally polarized in response to microorganisms and host mediators. Gene expression profiling of macrophages reveals that various Gram-negative and Gram-positive bacteria induce the transcriptional activity of a “common host response,” which includes genes belonging to the M1 program. However, excessive or prolonged M1 polarization can lead to tissue injury and contribute to pathogenesis. The so-called M2 macrophages play a critical role in the resolution of inflammation by producing anti-inflammatory mediators. These M2 cells cover a continuum of cells with different phenotypic and functional properties. In addition, some bacterial pathogens induce specific M2 programs in macrophages. In this review, we discuss the relevance of macrophage polarization in three domains of infectious diseases: resistance to infection, infectious pathogenesis, and chronic evolution of infectious diseases. The Journal of Immunology, 2008, 181: 3733–3739.

Antigen-presenting cells such as monocytes/macrophages play major roles as sentinels for first line alerts or as mediators that shape the adaptive immune response (1). Once activated by microbial products, macrophages acquire microbicidal competence that usually leads to effective immunity (2). However, several bacterial pathogens have evolved strategies to interfere with macrophage activation and to modulate host responses (3).

Macrophages are dynamic and heterogeneous cells; this is due to different mechanisms governing their differentiation, tissue distribution, and responsiveness to stimuli (4, 5). The heterogeneity of undifferentiated circulating monocytes may affect their polarization once they arrive in tissues (6, 7). In addition, the microenvironment, such as intestines, adipose tissue, or alveolar space, may also constrain the functional properties of macrophages (8, 9). Polarized macrophages have been broadly classified into two groups: M1 and M2 macrophages. During the 1970s, classically activated M1 macrophages were described as responsive to two signals, type 1 inflammatory cytokines and microbial products (2). More recently, M2 macrophages have been characterized by functional expression of alternative activation markers. M2 macrophages include at least three subsets: M2a, induced by IL-4 or IL-13; M2b, induced by immune complexes and agonists of TLRs or IL-1 receptors; and M2c, induced by IL-10 and glucocorticoid hormones (10). M1 and M2 macrophages differ in terms of receptors, cytokine and chemokine expression, and effector functions (Fig. 1). Whereas M1 macrophages are microbicidal and inflammatory (postinfec-tious pathogenesis), M2 macrophages are immunomodulators (M2a and M2c) and are poorly microbicidal. Thus, macrophage activation can be either pro-inflammatory or anti-inflammatory. However, these extreme and simplified polarization states (M1 vs M2) actually describe a complex process delineating a continuum of functional states. Recently, macrophage activation has been shown to be plastic, rapid, and fully reversible, suggesting that macrophage populations are dynamic and may first take part in inflammation and then participate in its resolution (11). Consequently, macrophages display progressive functional changes resulting from changes in the microenvironment (12). In this review, we will delineate the significance of macrophage polarization in the context of pathophysiology in acute and chronic infectious diseases.

Common macrophage responses to bacteria

Several studies suggest that host cells exposed to different groups of pathogens respond with common transcriptional activation programs, referred to as the core response to infection. A comparison of data collected from 32 published transcriptional-profiling studies show that a cluster of 511 genes, the “common host response,” is coregulated in innate immune cells in response to 77 pathogens, including bacteria, viruses, and fungi (13). In human peripheral leukocytes stimulated with Gram-negative and Gram-positive bacteria, some genes encoding inflammatory and cell-to-cell signaling molecules are also commonly regulated (14). Finally, Nau and colleagues have shown that human monocyte-derived macrophages respond with a robust and shared pattern of gene expression to a broad range of bacteria (15).

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Although these studies reveal a core reprogramming of the host transcriptome during infection, none focuses on macrophage polarization as a result of host-pathogen interactions. In this review, we collate and compare microarray data from 12 studies released into public databases (14–24) and from unpublished results (Gene Expression Omnibus record number: GSE5765). These studies represent transcriptional responses of mononuclear phagocytes to diverse bacteria and bacterial components. The data sets were processed by considering modulated genes involved in M1/M2 polarization. Together, 87 unique genes were extracted from these data and classified into four families: cytokine/chemokine receptors, chemokine/chemokine receptors, effector molecules, and pattern recognition receptor/costimulation molecules. To avoid comparison biases resulting from independent experiments performed on different platforms, we used a clustering analysis to permit the grouping of genes with a common expression pattern across samples. The resulting matrix displays color-coded gene expression ratios, where green represents down-regulated gene transcription and red represents up-regulated gene transcription.

The common response of macrophages to bacterial infections mainly involves the up-regulation of genes involved in M1 polarization (Fig. 2). These include genes encoding cytokines such as TNF, IL-6, IL-12, IL-1β, cytokine receptors such as IL-7R and IL-15RA, chemokines such as CCL2, CCL5, and CXCL8, and the chemokine receptor CCR7. Other M1-associated up-regulated genes encode the enzymes indoleamine-pyrrole 2,3 dioxygenase and NO synthase 2 (NOS2), which are involved in macrophage microbicidal activity, and costimulatory molecules such as CD80 and CD86. IL-1ra appears to be the only gene associated with M2 polarization that is expressed after bacterial challenge. It is likely that this robust M1-shifted activation corresponds to the common alarm signal against bacteria induced in macrophages, as most of these genes are induced independently of the bacterial species.

M1 polarization and control of acute infectious diseases

The M1 program of macrophages is usually associated with protection during acute infectious diseases. For instance, Listeria monocytogenes, which causes disease in immunocompromised patients and pregnant women, induces an M1 program, thus preventing bacterial phagosome escape and stimulating intracellular killing of bacteria in vitro and in vivo (25). Mice lacking IFN-γ and TNF, two canonical markers of M1 polarization, and their respective receptors die from L. monocytogenes infection (26). Similarly, Salmonella typhi, the agent of typhoid fever, and Salmonella typhimurium, a gastroenteritis agent, induce the M1 polarization of human and murine macrophages, and this induction is associated with the control of the infection. The protective role of M1 macrophages has been exemplified in mice deficient for components of the IL-12 pathway (27). The initial transcriptomic analysis of mouse macrophage responses to Mycobacterium tuberculosis reveals an overlap of genes modulated by mycobacteria and IFN-γ, which corresponds to an M1 program (28). In addition, during the early phase of M. tuberculosis infection, macrophages are polarized toward an M1 profile (29), which is in agreement with clinical data collected from patients with active tuberculosis. However, a small subset of tuberculosis patients is characterized by M2-type patterns, which can be reversed by antibiotic treatment (30). Other mycobacterial diseases such as Buruli disease (Mycobacterium ulcerans) and opportunistic infections (Mycobacterium avium) are also characterized and controlled by M1 polarization of macrophages (31, 32).

Similarly, the acute phase of chlamydial infections is characterized by protective M1 polarization as emphasized in IFN-γ+/−IFN-γR−/− mice or in mice treated with anti-IFN-γ Abs (33). NO is another feature of M1 polarization known to be important in Salinemona infections (34); however, a role for NO has not been confirmed in murine models of chlamydial infections.

Uncontrolled M1 polarization and infectious pathogenesis

As mentioned above, M1 polarization supports resistance to intracellular bacteria and controls the acute phase of infection. However, an excessive or prolonged M1 program is deleterious for the host, as demonstrated in acute infections with Escherichia coli or Streptococcus sp. E. coli causes many diseases, including gastroenteritis, urinary tract infections, neonatal meningitis, and sepsis. Sepsis couples systemic inflammatory response with immune dysregulation, leading to tissue damage and multiple organ failure (35). In vitro, E. coli induces a typical M1 profile through the recognition of LPS by TLR4 (36, 37). Signaling mechanisms include NF-κB activation, LPS-induced TNF-α factor up-regulation (38), and PI3K pathway stimulation (37). It has been demonstrated that M1 program induction and sepsis severity are related. In baboon experimental peritonitis caused by E. coli, the M1 phenotype is prominent in ba-boons that die from the infection; in contrast, surviving baboons display a mixed M1/M2 activation phenotype (39). In
FIGURE 2. Common transcriptional signature of macrophages in response to bacterial infections. Transcriptional data from 12 studies on the response of human and mouse macrophages to several bacteria and bacterial components were analyzed by hierarchical clustering analysis and represented by a color gradient from green (down-regulation) to red (up-regulation). Only genes involved in M1/M2 polarization that were modulated in at least one condition were included. Gray box represents unavailable data. Abbreviations/designations not defined elsewhere: BCG, Bacillus Calmette-Guérin; BCGhsp65, BCG heat shock protein 65; B. melitensis, Brucella melitensis; B. pertussis, Bordetella pertussis; C. pneumoniae, Chlamydia pneumoniae; EHEC, enterohemorrhagic E. coli; L. pneumophila, Legionella pneumophila; LPS E, E. coli LPS; LPS S, Salmonella LPS; LTA, lipoteichoic acid; MDP, muramyl dipeptide; M. leprae, Mycobacterium leprae; MPA, mycophenolic acid; S. aureus, Staphylococcus aureus; TBhsp70, tuberculosi heat shock protein 70.
patients with severe sepsis, high circulating concentrations of M1-type cytokines are highly correlated with mortality (40). Macrophages from these patients produce high levels of type I cytokines and chemokines that activate the endothelium and contribute to cardiac failure, loss of general organ perfusion, and death (41).

Streptococcus species can cause meningitis, pneumonia, endocarditis, erysipelas, and necrotizing fasciitis in humans and other animals. Host responses are generally characterized by an intense inflammatory reaction and an M1 polarization of macrophages involving the TLR2-dependent pathway (42). Human and murine macrophages differ in their responses to Streptococcus pyogenes. In humans, this pathogen induces a M1 profile characterized by enhanced mRNA expression of CCL2, CCL5, CXCL8, and CXCL10 (43). In mice, S. pyogenes stimulates an unusual activation program that combines M1 and M2 profiles (44). In a murine model of pneumonia caused by S. pneumoniae, mortality correlates with lung inflammation and the presence of M1-polarized macrophages (45).

**Bacteria-mediated interference with M1 polarization**

It is well established that intracellular bacteria subvert microbi- cidal effectors to survive in the hostile environment produced by macrophages. A growing number of studies show that some pathogens have evolved different strategies to interfere with M1 polarization. Some *Salmonella* or *Mycobacterium* species neutralize M1-related effectors. *S. typhimurium* SPI-2 encodes mediators that inhibit phagosome relocalization of NADPH oxidase, thus inhibiting the oxidative microbicidal activity of macrophages (46). Similarly, *Mycobacterium bovis* bacillus Calmette-Guérin interferes with NOS2 recruitment to phagosomes, inhibiting NO release (47). Other bacterial strategies include inhibition of M1 cytokine expression/secretion. *Salmo- nella dublin* suppresses IL-18 and IL-12p70 production (48). Through the membrane protein Omp25, *Brucella suis* inhibits the production of TNF in human macrophages, leading to reduced production of IL-12 (49). Mycobacteria interfere with M1 polarization through the secretion of virulence factors. Early secreted antigenic target protein-6 (ESAT-6) from *M. tuberculosis* directly inhibits the activation of NF-κB and IFN-γ regulatory factors downstream of TLR2 via Akt-dependent mechanisms (50). Mycobacteria also interfere with M1 activation via indirect mechanisms. Macrophages are unable to kill highly pathogenic strains of *M. tuberculosis* despite IFN-γ stimulation; this is thought to rely on the transcriptional inhibition of IFN-γ-targeted genes through a bystander effect involving IL-6 (51). Although IL-6 is classically associated with M1 polarization, it can inhibit the production of a subset of IFN-γ-responsive genes, including CXCL10 (52).

*Coxiella burnetii* is an obligate intracellular bacterium that causes Q fever, an acute disease with a risk of chronic evolution in immunocompromised patients, pregnant women, or patients with valve disease (53). It elicits an M1 program in monocytes (our unpublished data) and an atypical M2 profile in macrophages combining M1/M2 characteristics (24). *C. burnetii*-infected macrophages release the M2-associated molecules IL-10, TGFβ1, and CCL18 and express mannose receptor and the active form of arginase-1. They also secrete high levels of IL-6 and CXCL8, two molecules associated with M1 polarization (Fig. 3). However, *C. burnetii*-infected macrophages do not express other M1 molecules such as TNF, IL-12, CD80, and CCR7, and they fail to produce NO (24). As in mycobacterial infections, it is likely that IL-6 interferes with the IFN-γ pathway and contributes to chronic evolution of Q fever. Other pathogens stimulate a clear-cut M2 program in macrophages. For instance, *Yersinia enterocolitica* infection of susceptible BALB/c mice results in arginase-1 activation and TGFβ1 and IL-4 production (54). The M2 reprogramming of macrophages depends on yersinial virulence factors; the infection of murine macrophages with bacteria defective for the Yop-encoded type III secretion system results in M1 polarization (55). LcrV, another *Yersinia* sp. virulence factor, stimulates M2 polarization, probably via the induction of IL-10 (56).

**M2 polarization and chronic infectious diseases**

Chronic evolution of infectious diseases is thought to be associated with macrophage reprogramming toward an M2 profile. Chronic brucellosis is associated with IL-10-mediated M2 polarization. Neutralization of the M2-promoting cytokines

![Control of C. burnetii infection](http://www.jimmunol.org/)  
**Control of C. burnetii infection**
  
  - M1 polarization
    - + IFNγ
    - IL-12, TNF, IL-6
  
  - M2 polarization
    - IL-10, TGFβ1, arginase-1
  
  - Acute Q fever
  
  - Chronic Q fever

![Intense replication of C. burnetii](http://www.jimmunol.org/)  
**Intense replication of C. burnetii**
  
  - M1 polarization
    - + IFNγ
    - IL-12, TNF, IL-6
  
  - M2 polarization
    - IL-10, TGFβ1, arginase-1
  
  - Macrophages
    - Apoptotic cell
  
  - M2 reprogramming
    - C. burnetii
    - M1 and M2 profiles
The persistence of bacterial pathogens in tissues and the chronic nature of the infection are essential to understand the precise role of macrophage polarization in resistance/susceptibility to infection, clinical expression, and prognosis of infectious diseases. From public databases, it is possible to summarize a "common host response" of macrophages in different settings. Gene expression analysis in clinical situations will be of interest if uncontrolled. Some bacterial pathogens have evolved sophisticated strategies to prevent M1 polarization, neutralize macrobicidal effectors of macrophage, or promote M2 polarization. The persistence of bacterial pathogens in tissues and the chronic evolution of infectious diseases are linked to macrophage reprogramming toward heterogeneous M2 signatures. The development of gene expression analysis in clinical situations will be essential to understand the precise role of macrophage polarization in resistance/susceptibility to infection, clinical expression, and prognosis of infectious diseases.

**Conclusions**

Analysis of gene expression has revealed a continuum of activation signatures in macrophages. From public databases, it is possible to summarize a "common host response" of macrophages to bacterial infections with an M1 signature. Usually, the M1 signature is associated with the control of acute infections, but it may also be responsible for infectious pathogenesis if uncontrolled. Some bacterial pathogens have evolved sophisticated strategies to prevent M1 polarization, neutralize macrobicidal effectors of macrophage, or promote M2 polarization. The persistence of bacterial pathogens in tissues and the chronic evolution of infectious diseases are linked to macrophage reprogramming toward heterogeneous M2 signatures. The development of gene expression analysis in clinical situations will be essential to understand the precise role of macrophage polarization in resistance/susceptibility to infection, clinical expression, and prognosis of infectious diseases.
Disclosures
The authors have no financial conflict of interest.

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