A
verse left ventricular (LV) remodeling after myocardial infarction (MI) constitutes the structural basis for ischemic heart failure (HF) and comprised complex short- and long-term changes in LV size, shape, function, and cellular and molecular composition. Although multiple pathophysiological factors converge to remodel the heart after MI, the fundamental determinants of this process (and its progression to clinical HF) are the extent of the initial infarction and the
sufficiency of the post-MI reparative process. In clinical practice, limiting infarction extent is routinely addressed by timely coronary reperfusion. In contrast, therapeutic manipulation of the ensuing repair process, which is driven principally by robust tissue inflammation and subsequently by its active suppression and resolution, has proved much more challenging and elusive. Nonetheless, recent studies have suggested a large number of potential therapeutic targets that may favorably influence cardiac wound healing and repair. In this review, we will broadly consider the multiplicity of cellular and molecular factors that influence post-MI repair, highlighting the translational implications for these events in the amelioration of adverse remodeling and the development of ischemic HF.

**Phases of Cardiac Repair After MI**

Cardiac repair after MI results from a finely orchestrated and complex series of events, initiated by intense sterile inflammation and immune cell infiltration (inflammatory phase) that serve to digest and clear damaged cells and extracellular matrix tissue (∼3–4 d in mice), followed by a reparative phase with resolution of inflammation, (myo)fibroblast proliferation, scar formation, and neovascularization over the next several days (Figure 1).3,4 Early inflammatory activation is a necessary event for the transition to later reparative and proliferative programs. Appropriate and timely containment and resolution of inflammation are further determinants of the quality of wound healing; a proper physiological balance needs to be achieved between these 2 phases for optimal repair.5,6 An inflammatory phase that is disproportionately prolonged, of excessive magnitude, or insufficiently suppressed can lead to sustained tissue damage and improper healing, defective scar formation, and heightened cell loss and contractile dysfunction, thereby promoting infarct expansion, adverse remodeling, and chamber dilatation. To date, there has been no large-scale immunomodulatory or anti-inflammatory therapeutic strategy post MI that has been successfully translated into clinical practice, no doubt a reflection of both the exquisite complexity and our incomplete understanding of the healing process.

**Inflammatory Phase**

**Molecular Cascades Implicated in the Postinfarction Inflammatory Response**

Hypoxia during ischemia impairs vascular endothelial cell integrity and its barrier function thereby augmenting vessel permeability, facilitating leukocyte infiltration.7 If the ischemic period is sufficiently prolonged, parenchymal and cardiomyocyte cell death programs are activated, primarily because of cell necrosis, secondarily because of apoptosis and autophagic mechanisms.8,9 Restoration of blood flow may further augment tissue damage via reperfusion injury because of abrupt reoxygenation, reactive oxygen species (ROS) generation, and activation of the complement pathway.1,5,7-9 Necrotic and stressed/injured cells, and the damaged extracellular matrix, release substances that act as danger signals, termed danger-associated molecular patterns (DAMPs). DAMPs bind to cognate pattern recognition receptors (PRRs) of the innate immune system on surviving parenchymal cells and infiltrating leukocytes (and also activate the complement pathway) to robustly activate a cascade of inflammatory mediators, including inflammatory cytokines, chemokines, and cell adhesion molecules.8,10-14 In addition to being passively released...
on cell necrosis or matrix damage, select DAMPs may also be upregulated and secreted by stressed cardiomyocytes and fibroblasts, and by activated leukocytes.7,8,11,12,14 The PRRs are primarily the membrane-bound and secreted DAMPs, such as HMGB1, HSP, IL-1, IL-18, and RAGE. TLRs recognize several endogenous signals, including high mobility group box-1 (HMGB1), hyperglycemia, macrophage inflammatory protein-1α (MIP-1α), heat shock proteins, low molecular weight hyaluronic acid, calprotectin, and alarmins (e.g., high mobility group box-1, HMGB1, heat shock proteins, low molecular weight hyaluronic acid, ATP, uric acid, mitochondrial DNA, double-stranded RNA, single-stranded RNA, and complement, among others).8,10–12,14,15 The PRRs are primarily the membrane-bound toll-like receptor/IL-1 receptors (TLR/IL-1Rs), as well as cytosolic nucleotide-binding oligomerization domain–like receptors (NLRs) and the cell-surface receptor for advanced glycation end-products (RAGE). The signaling pathways downstream of these PRRs have been comprehensively detailed in recent reviews and briefly considered below. In the context of MI, downstream signaling converges on the activation of mitogen-activated protein kinases (MAPKs) and nuclear factor (NF)-κB. These pathways (NF-κB in particular) drive the expression of a large panel of proinflammatory genes including inflammatory cytokines (e.g., tumor necrosis factor-α [TNF], IL-1β, IL-6, and IL-18); CXC chemokines containing the glutamic acid-leucine-arginine motif that act predominantly as neutrophil chemoattractants; CC chemokines that attract monocytes and T-lymphocytes; cell adhesion molecules (e.g., vascular cell adhesion molecule, intercellular adhesion molecule, selectins), and complement factor B.14,20,23 Subsequent leukocyte recruitment further amplifies the inflammatory response, augments the production of DAMPs, and promotes both efferocytosis of dying cells and tissue digestion via the release of proteases and oxidases.1,2 Effcient efferocytosis of apoptotic cardiomyocytes is particularly important for transitioning to the phase of inflammation resolution and wound healing and is mediated, in part, by macrophages expressing the myeloid-epithelial-reproductive tyrosine kinase (Mertk).23

### Table. Select DAMPs and Corresponding Pattern Recognition Receptors

<table>
<thead>
<tr>
<th>DAMP</th>
<th>Receptor(s)</th>
<th>Reference(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HMGB1</td>
<td>TLR2, TLR4, TLR9, RAGE</td>
<td>8, 10–12, 14, 15, 25–40, 83</td>
</tr>
<tr>
<td>S100A8/S100A9</td>
<td>TLR4, NLRP3, RAGE</td>
<td>11, 14, 42–47, 83</td>
</tr>
<tr>
<td>S100A1</td>
<td>Endolysosomal TLR4</td>
<td>48</td>
</tr>
<tr>
<td>Fibronectin-EDA</td>
<td>TLR2, TLR4</td>
<td>8, 10, 11, 51–53</td>
</tr>
<tr>
<td>IL-1α</td>
<td>IL-1R</td>
<td>14, 54, 83</td>
</tr>
<tr>
<td>HSP-60, HSP-70</td>
<td>TLR2, TLR4/6</td>
<td>8, 10, 11, 83</td>
</tr>
<tr>
<td>LMW hyaluronic acid</td>
<td>TLR2, TLR4, NLRP3</td>
<td>8, 10, 11, 18, 83</td>
</tr>
<tr>
<td>ATP</td>
<td>P2X7/NLRP3</td>
<td>11, 14, 18, 83, 87, 88</td>
</tr>
<tr>
<td>Uric acid</td>
<td>TLR2, TLR4, NLRP3</td>
<td>11, 14, 18, 83</td>
</tr>
<tr>
<td>Mitochondrial DNA</td>
<td>TLR9, NLRP3</td>
<td>8, 10, 11, 14, 83</td>
</tr>
<tr>
<td>dsRNA</td>
<td>TLR3</td>
<td>8, 14, 83</td>
</tr>
<tr>
<td>ssRNA</td>
<td>TLR7, TLR8</td>
<td>8, 10, 11, 14</td>
</tr>
</tbody>
</table>

Some references are in-depth review articles. DAMP indicates danger-associated molecular pattern; ds, double stranded; EDA, extra domain A; HMGB, high mobility group box; HSP, heat shock protein; IL, interleukin; LMW, low molecular weight; NLR, nucleotide-binding oligomerization domain–like receptor; P2X7, purinergic P2X7 receptor; RAGE, receptor for advanced glycation end-products; ss, single-stranded; and TLR, toll-like receptor.

### Danger-Associated Molecular Patterns

HMGB1: HMGB1, a loosely associated chromatin protein involved in DNA stabilization and gene control,24 is a potent mediator of inflammation after tissue injury.25 HMGB1 is passively released from necrotic cells (but not from apoptotic cells),25 actively secreted by stimulated monocytes and macrophages,26 and induced by peroxynitrite and oxidative stress in ischemic cardiomyocytes.27 HMGB1 engages and activates several TLRs (including TLR2, TLR4, and TLR9) and RAGE,8,15,28,29 to induce NF-κB nuclear translocation and proinflammatory signaling. HMGB1 also promotes monocyte recruitment in a TLR- and RAGE-independent manner via direct binding to CXCL12 (stromal cell–derived factor-1) and the formation of HMGB1-CXCL12 heterocomplexes that synergistically enhance CXCR4 signaling in inflammatory cells.30

In humans with acute MI, serum HMGB1 levels are elevated and predictive of subsequent mortality, LV dysfunction, and effort intolerance.31–33 In rodents with reperfused15,34 and nonreperfused30 MI, serum levels and myocardial HMGB1 expression increase early after injury. In reperfused MI, HMGB1 plays a pivotal role in the activation of MAPK and NF-κB pathways, increasing leukocyte infiltration, and augmenting tissue injury, apoptosis, and infarct size, in part, via RAGE-dependent signaling.15,34 Interestingly and in contrast, however, in acute and chronic nonreperfused MI models, augmenting HMGB1 via either exogenous administration35–37 or cardiomyocyte-specific overexpression38,39 improved LV remodeling and function with augmented c-kit+ progenitor cell infiltration, reduced dendritic cell (DC) accumulation, less collagen deposition, and better tissue angiogenesis. Exogenous administration of HMGB1 before ischemia/reperfusion (I/R) also induces preconditioning and cardioprotection.40 Interestingly, antibody-mediated HMGB1 neutralization in nonreperfused MI reduced tissue inflammatory cytokine expression and macrophage infiltration at day 3, but induced scar thinning and more pronounced LV remodeling, underscoring the concept that inflammation, properly regulated and controlled, is essential for optimal wound healing in the heart.33 Hence, these results indicate that although HMGB1 is an inflammatory mediator, the ultimate effects of HMGB1 modulation depend on the underlying disease, its temporal context, and the degree of inflammatory response referable to the pathophysiology. Compared with nonreperfused MI hearts, I/R hearts exhibit greater magnitude but shorter duration of inflammatory cell infiltration.9,41 This profile of augmented inflammation may explain the beneficial results with HMGB1 inhibition in reperfused MI, and the divergence in response from nonreperfused MI in which angiogenic effects may predominate.

Other DAMPs: S100A8 (calgranulin A) and S100A9 (calgranulin B) are members of the calcium-binding S100 family expressed in phagocytic cells.42 S100A8 and S100A9 rapidly associate to form the S100A8/S100A9 heterodimer. S100A8/S100A9 complexes function as DAMPs secreted by neutrophils and monocytes/macrophages during inflammatory conditions and signal via RAGE and TLR4 receptors.43,44 Humans
with acute MI exhibit elevated serum S100A8/A9 levels that correlate with circulating neutrophil counts and the risk of cardiovascular death and subsequent MI. In mice with reperfused MI, S100A8/S100A9 is rapidly expressed and released after ischemia, primarily by inflammatory cells and fibroblasts, and induces proinflammatory signaling, leukocyte infiltration, and cardiac dysfunction in a RAGE-dependent manner, suggesting that these DAMPs are central to post-MI inflammation. Interestingly, S100A1, the S100 protein most abundant in cardiomyocytes, is also released from damaged cardiomyocytes in both humans and mice with acute MI. However, rather than promoting generalized inflammation, S100A1 is taken up by endocytosis in adjacent cardiac fibroblasts to transiently activate TLR4-endolysosomal signaling, resulting in an immunomodulatory and antifibrotic phenotype with beneficial effects on post-MI LV remodeling in vivo.

This suggests that specific DAMPs have unique cell targets and functional roles in the cardiac repair process that can be either pro- or anti-inflammatory. In this regard, the β-galactoside–binding lectin galectin-1 is expressed by hypoxic cardiomyocytes and infiltrating leukocytes after MI and also imparts anti-inflammatory and cardio-protective effects in the remodeling heart.

Fibronectin is an extracellular matrix protein secreted by fibroblasts in response to tissue injury and proinflammatory cytokines, and includes an alternatively spliced exon coding type III repeat extra domain A that binds to TLR-4 to activate mast cells and leukocytes. Mice with parenchymal myocardium-localized fibronectin-extra domain A deficiency exhibited improved LV remodeling and function, less monocyte recruitment, and reduced remote zone fibrosis after nonreperfused MI as compared with wild-type mice, indicating a critical role for fibronectin-extra domain A in tissue inflammation and remodeling. Conversely, recent studies have demonstrated that necrotic cardiomyocytes (but not fibroblasts) release IL-1α as a danger signal that activates proinflammatory MAPK and NF-κB signaling in cardiac fibroblasts in a myeloid differentiation factor 88 (MyD88)-dependent but NLRP3- and TLR-independent manner, via the activation of the IL-1R pathway. Hence, multiple danger signals act in a concerted fashion on parenchymal and inflammatory cells in the infarcted heart to drive and modulate inflammation. For a further discussion of DAMPs, the reader is referred to several comprehensive reviews.

**TLRs, NLRs, and RAGE**

**TLRs:** The TLRs comprise the major PRRs on mammalian cells. Expressed most prominently on leukocytes, TLRs are also expressed by parenchymal cells, including cardiomyocytes, fibroblasts, and endothelial cells. To date, 13 functional mammalian TLRs have been identified (10 in humans, TLRs 1–10), that recognize a variety of pathogen-associated molecular patterns and DAMPs to trigger innate immune responses. Of these, TLRs 1, 2, 4, 5, 6, and 11 are cell-surface receptors, whereas TLRs 3 and TLRs 7 to 10 are expressed in endolysosomes. Signal transduction by TLRs and IL-1Rs occurs through a conserved cytoplasmic Toll/IL-1R (TIR) domain that serves as the docking site for TIR-containing cytoplasmic adaptor proteins (Figure 2). Except for TLR3, all TLRs (and IL-1Rs) engage with the adaptor MyD88 either directly or, for TLR2 and TLR4, in combination with the adaptor TIR domain-containing adaptor protein to trigger receptor complex interactions with IL-1R–associated kinases 4, 1, and 2, TNF receptor–associated factor 6, and the MAPKKK transforming growth factor (TGF) activated kinase-1. As fully reviewed elsewhere, these signaling cascades ultimately activate NF-κB (p65 and p50) and MAPK pathways to upregulate a broad array of proinflammatory mediators (Figure 2). TLR4 is also endocytosed after ligand binding; endolysosomal TLR4 signals in a MyD88-independent manner via the cytoplasmic adaptor TIR domain-containing adaptor inducing interferon-β and the bridging adaptor TRIF-related adaptor molecule (TIR domain-containing adaptor inducing interferon-β-related adaptor molecule). This pathway results in NF-κB nuclear translocation, and the induction of type I interferon via activation of TANK-binding kinase and the transcription factor interferon-regulatory factor 3. In the heart, the most highly expressed TLRs are TLR4, TLR2, TLR3, and TLR5, with TLR4 and TLR2 the most studied in the context of myocardial injury.

Augmented TLR4 activation, and increased expression of proinflammatory mediators downstream of TLR4 signaling, has been demonstrated in circulating leukocytes from humans with acute MI and correlated with the development of HF. Similar finding has also been reported for TLR2 in circulating monocytes. Moreover, cardiac TLR4 expression increases both after acute MI and in chronic HF. Mice with genetic disruption or deficiency of TLR4, TLR2, MyD88, or TLR3 exhibit reduced infarct size after I/R and amelioration of pathological remodeling after nonreperfused MI. Moreover, pretreatment with eritoran, a specific TLR4 antagonist, in mice, or with an anti-TLR2 antibody in mice and pigs reduced infarct size after myocardial I/R. In both MI models, sustained TLR-mediated signaling generally augmented cell apoptosis, inflammation, interstitial fibrosis, oxidative stress, and leukocyte recruitment, indicating maladaptive responses triggered by TLR2, TLR4, and TLR3 after MI. Interestingly, and in contrast, beneficial effects were referable to TLR5 after I/R, as TLR5 deficiency increased infarct size, oxidant stress, inflammation, and LV dysfunction after reperfused MI.

Interestingly, short-term TLR2, TLR4, and TLR9 activation after I/R induces preconditioning and cardioprotection (with reductions in infarct size), in part, via TIR domain-containing adaptor protein- and PI3K/Akt-dependent mechanisms. Analogous short-term protective effects in cardiac myocytes have similarly been observed for several innate immune signaling mediators, including NF-κB, inflammatory cytokines, and chemokines. These observations suggest a paradigm whereby short-term activation of innate immune pathways, primarily localized to cardiomyocytes, yields cytoprotective and prosurvival effects via mitochondrial stabilization, whereas activation that is more prolonged or of greater magnitude and involving immune cells results in more robust inflammatory responses and leukocyte recruitment that induce tissue injury. In this regard, in vivo chimeric mouse models and ex vivo isolated perfused heart studies (in which circulating leukocytes are eliminated) have demonstrated that after I/R, leukocyte-localized TLR2 is responsible for inducing myocardial injury and determines infarct size, whereas parenchymal TLR2 signaling induces
contractile dysfunction without affecting infarct size. In contrast, both parenchymal and leukocytic TLR2 are needed to mediate endothelial injury and dysfunction after I/R.65 Interestingly, divergent effects of leukocyte vis-à-vis cardiomyocyte TLR4 signaling on cardiomyocyte impairment have also been shown in a model of systemic sepsis.85 Hence, the effects of TLR signaling, and proinflammatory mediators in general, are complex and graded, rather than all-or-none, and depend heavily on the cellular and disease context.

NLRs: The NLR family of intracellular PRRs responds to a variety of DAMPs (eg, ATP and uric acid) and include nucleotide-binding oligomerization domain receptors (nucleotide-binding oligomerization domain 1 and nucleotide-binding oligomerization domain 2) that activate NF-κB, and the NLRs (NLRP1, NLRP3/cryopyrin, NLRC4) that augment IL-1β and IL-18 secretion via the formation of multiprotein inflammasomes, comprised an activated NLR protein, the adaptor protein apoptosis speck-like protein containing a caspase-recruitment domain (ASC), and procaspase-1. One proposed model of NLRP3 inflammasome activation results from stimulation of the purinergic P2X7 ion channel by extracellular ATP, resulting in K+ efflux, recruitment of the pannexin-1 pore, DAMP entry into cytosol, and activation of NLRP3. This activates caspase-1, which then converts pro–IL-18 and pro–IL-1β to active IL-18 and IL-1β. As discussed in the text, cell-type–specific innate immune signaling can result in distinctive, and sometimes divergent, in vivo physiological responses during acute MI. Schema derived from Mann,13 Newton and Dixit,14 Schroder and Tschopp,18 Chao,19 and Mann20 (Illustration credit: Ben Smith).

Figure 2. Toll-like receptor (TLR) and nucleotide-binding oligomerization domain–like receptor (NLR) signaling. Danger-associated molecular patterns (DAMPs) released from necrotic and damaged cells and extracellular matrix bind to the TLRs, which comprised an extracellular leucine-rich repeat (LRR) domain, a transmembrane (TM) domain, and a conserved cytoplasmic Toll/interleukin (IL)-1R (TIR) domain, which serves as docking site for other TIR-containing cytoplasmic adaptor proteins (top left). The binding of DAMPs, and often coreceptors such as CD14 and MD2, to TLR4 engages the adaptor myeloid differentiation factor 88 (MyD88) via the adaptor TIR domain-containing adaptor protein (TIRAP). MyD88 recruits IL-1R–associated kinase (IRAK) 4 and the IRAK1/2 and TNF receptor associated factor (TRAF) 6 complex, which activates transforming growth factor activated kinase 1 (TAK1). TAK1, a mitogen-activated protein kinase (MAPK) KK, then activates the MAPK cascade and also phosphorylates IκB kinase (IKK), that leads to nuclear factor–κB (NF–κB) p65 and p50 nuclear translocation and the transcription of a panel of inflammatory genes, including cytokines, chemokines, cell adhesion molecules, and complement factor B. Furthermore, after endocytosis, TLR4 signals in a MyD88-independent manner via the cytoplasmic adaptor TRIF, in turn recruited through the bridging adaptor TRAM. This pathway results in noncanonical IKK and NF–κB activation, as well as the induction of type I interferon (IFN) via TANK-binding kinase (TBK) 1 and the transcription factor IFN-regulatory factor (IRF) 3. Except for TLR3, the other TLRs also signal, directly or indirectly as depicted, via MyD88. Endolysosomal TLR3 activates IRF3 signaling via TRIF and TBK1, whereas endolysosomal TLR7/8 and TLR9 also induce type I IFN via TRAF3 and IRF7 in a MyD88–dependent manner (not pictured). In addition to TLRs, intracellular NLRs respond to a variety of DAMPs via the formation of multiprotein inflammasomes, comprised an activated NLR protein, the adaptor protein apoptosis speck-like protein containing a caspase-recruitment domain (ASC), and procaspase-1. One proposed model of NLRP3 inflammasome activation results from stimulation of the purinergic P2X7 ion channel by extracellular ATP, resulting in K+ efflux, recruitment of the pannexin-1 pore, DAMP entry into cytosol, and activation of NLRP3. This activates caspase-1, which then converts pro–IL-18 and pro–IL-1β to active IL-18 and IL-1β. As discussed in the text, cell-type–specific innate immune signaling can result in distinctive, and sometimes divergent, in vivo physiological responses during acute MI. Schema derived from Mann,13 Newton and Dixit,14 Schroder and Tschopp,18 Chao,19 and Mann20 (Illustration credit: Ben Smith).
TLR pathways) to active IL-18 and IL-1β (Figure 2). One proposed model of activation of NLRP3 involves extracellular ATP stimulation of the purinergic P2X7 ion channel; this triggers K+ efflux, recruitment of the pannexin-1 membrane pore, and entry of DAMPs into cytosol to access NLRP3 (Figure 2).18

The major components of the NLRP3 inflammasome (apoptosis speck-like protein containing a caspase-recruitment domain, cryopyrin, caspase-1) are upregulated and activated early after MI in a variety of cell types in the heart, not only infiltrating leukocytes, fibroblasts, and endothelial cells but also border zone cardiomyocytes.86–88 IL-1β and IL-18, the cytokine end-products of inflammasome activation, are also increased early after MI.88–90 Inflammasome activation has been suggested to occur initially in cardiac fibroblasts during reperfused MI, in response to ROS production and K+ efflux.86 Global targeted genetic disruption of apoptosis speck-like protein containing a caspase-recruitment domain or caspase-1,88 as well as antibody neutralization of IL-18,89 has been shown to reduce infarct size in vivo after I/R in mice. Apoptosis speck-like protein containing a caspase-recruitment domain loss-of-function also improved post-MI cardiac remodeling and fibrosis and decreased leukocyte infiltration and the expression of proinflammatory cytokines and chemokines. Studies using chimeric mice indicate that inflammasome activation in leukocytes and resident cardiac cells both contribute to ischemic injury.86 Similarly, isolated perfused NLRP3−/− murine hearts exhibit reduced infarct size and improved contractile function during ex vivo I/R,89 whereas gene silencing of cryopyrin ameliorates cardiac remodeling and dysfunction in vivo after nonreperfused MI in mice.87 Hence, the NLRP3 inflammasome is a key mediator of the post-MI inflammatory response and tissue injury.

RAGE: RAGE is a PRR expressed by a variety of immune and parenchymal cell types that interacts with several DAMPs such as HMGB1 and S100A8/S100A9. RAGE activation triggers many intracellular signaling pathways, including NF-κB− and MAPK-dependent inflammatory genes.19 RAGE-deficient mice exhibited reduced infarct size, reduced leukocyte infiltration and inflammatory cytokine expression, and improved cardiac remodeling and function after reperfused MI.15,47 Studies of chimeric mice indicate that RAGE signaling in infiltrating leukocytes, rather than resident cardiac cells, is primarily responsible for these adverse proinflammatory and remodeling responses post MI.47 Thus, inflammatory cell-localized RAGE, in particular, amplifies and promotes tissue injury during MI.

Nuclear Factor-κB

NF-κB is a central transcriptional effector of inflammatory signaling. NF-κB activation and its subsequent nuclear translocation after MI trigger transcription of a large portfolio of genes including inflammatory cytokines, CXC and CC chemokines, and adhesion molecules. The spatial and temporal expression of these mediators in resident and infiltrating cells choreographs events that further amplify the inflammatory response (cytokines) and attract and recruit specific leukocyte populations (chemokines and adhesion molecules) to injured myocardium. The signaling pathways and outputs linked to NF-κB activation, as well as its effects in cardiac diseases, have been reviewed extensively.14,79,91,92 Five subunits—p65 (RelA), RelB, c-Rel, p50, and p52—comprise the NF-κB family; these subunits form homo- or heterodimers to modulate gene transcription. Classically, p65/p50 heterodimers are bound to inhibitor of κB (IκB) in the cytoplasm. On IκBα phosphorylation by IκB kinase, IκBα is rapidly ubiquitinated and degraded by the 26S proteasome, allowing for subunit nuclear translocation. Activation can also occur via IκBα-independent mechanisms to release p50/RelB or p52/RelB. Importantly, only p65, RelB, and c-Rel contain transactivation domains; hence, p50 and p52 homodimers can repress rather than activate gene transcription. Therefore, subunit-dependent differences in target gene specificity impact the transcriptional response and may contribute to the spectrum of effects observed on NF-κB activation, ranging from cardioprotection to injury and cell death.

In humans with acute MI, circulating leukocytes exhibit marked activation of NF-κB.77,93 In rodents, NF-κB is activated in the heart early after MI in the infarct zone,94–96 and later (after 24 hours) in the remote zone.95 Importantly, whereas there is nuclear translocation of both p65 and p50 in the first 24 hours after MI, the profile shifts near exclusively to p65 at later time points.95 Studies on a cardioprotective vis-à-vis detrimental role of NF-κB during MI have yielded conflicting results.79 Acute NF-κB activation is essential for late cardioprotection induced by ischemic preconditioning.96–97 However, mice with cardiomyocyte-restricted overexpression of phosphorylation-resistant IκBα,98 cardiomyocyte-specific p65 deletion,99 IκBα overexpression via gene transfer,100 NF-κB double-stranded decoy DNA transfection,101 and pharmacological blockade of IκBα102 or IκB kinase β103 have demonstrated that NF-κB inhibition (primarily in cardiomyocytes and perhaps more related to p65) during myocardial I/R decreases infarct size, reduces inflammatory responses including leukocyte infiltration, and improves cardiac function. Studies of nonreperfused MI in mice with cardiomyocyte-restricted overexpression of phosphorylation-resistant IκBα5 or A20 (NF-κB signaling inhibitor),104 and IκBα gene transfer105 have similarly shown that blocking NF-κB (mainly p65 based on time course studies105) attenuates long-term adverse cardiac remodeling, dysfunction, and inflammation.

The p50 subunit lacks a transactivation domain and thus can inhibit NF-κB transcriptional activity. A study using cardiac magnetic resonance imaging in p50−/− mice demonstrated that leukocyte p50 expression imparts beneficial effects on remodeling after nonreperfused MI, by improving scar stability and matrix remodeling, and attenuating leukocyte infiltration and cytokine expression.106 These results contrasted with prior I/R and permanent ligation studies of p50−/− mice that reported the opposite results.107,108 but were consistent with a more recent study showing no effects of myocardial p50 deficiency on infarct size during ex vivo I/R in the isolated perfused heart when the influence of circulating leukocytes was removed.109 Taken together, although further study is clearly required, the prevailing evidence underscores the importance of subunit-specificity and cellular localization as determinants of NF-κB-mediated responses after MI. One possible scenario is that cardiomyocyte p65 activation imparts tissue injurious effects, whereas leukocyte p50 may provide a counterbalance to temper excessive inflammation.
**Cytokines and Chemokines**

A variety of proinflammatory cytokines and chemokines are upregulated after MI as a result of innate immune activation. The effects of cytokines and chemokines in normal and injured hearts have been extensively reviewed, hence, only a few points will be highlighted in this review. Proinflammatory cytokines such as IL-1, TNF, IL-6, and IL-18 are upregulated and secreted early after MI and are key regulators and propagators of the inflammatory response. This occurs because of (1) downstream signaling that further amplifies the initial inflammatory responses via MAPK and NF-kB pathways, (2) spatial, paracrine extension of the inflammatory response to neighboring parenchymal and infiltrating cells that express cytokine receptors, and (3) recruitment of leukocytes via the upregulation of adhesion molecules in endothelial cells and chemokines in myocardium. Chemokines are broadly divided into CC, CXC, and CX3C subtypes. In general, the CC chemokines are strong attractants for mononuclear cells, whereas glutamic acid-leucine-arginine+ CXC chemokines are strong neutrophil chemoattractants. The chemokine expression portfolio then regulates the recruitment of leukocyte subpopulations to infarcted myocardium.

The central importance of specific cytokines and chemokines in the inflammatory response after MI is supported by multiple studies, including findings (among others) that (1) TNF-α−/− mice (or wild-type mice treated with anti-TNF antibody) exhibit smaller infarcts, attenuated leukocyte infiltration, and lower expression of chemokines and adhesion molecules after I/R, (2) IL-1R type 1 deficient mice exhibit less LV dilatation and dysfunction after reperfused MI, and similar reductions in cardiac neutrophil and macrophage infiltration and chemokine/cytokine expression, (3) mutant mice with augmented activation of gp130, the common receptor subunit for the IL-6 cytokine family, exhibit adverse remodeling and heightened myocardial inflammation, (4) wild-type mice treated with a competitive monocyte chemoattractant protein-1/chemokine (C-C motif) ligand 2 (MCP-1/CCCL2) inhibitor exhibit reduced infarct size and monocyte infiltration after I/R, whereas MCP-1−deficient mice have amelioration of adverse post-MI remodeling, (5) mice deficient in CCR2, the cognate receptor for MCP-1, also exhibit reduced infarct size and macrophage infiltration after I/R, and amelioration of post-MI remodeling.

Nonetheless, despite preclinical data suggesting that cytokines and chemokines serve to aggravate ischemic injury and remodeling, it should be recognized that several studies conflict with this paradigm, showing that these mediators engender cardioprotective responses and pleiotropic cellular effects on both immune and myocardial resident cells.

In mice, for example, dual TNF receptor deficiency exacerbated ischemic injury and myocyte apoptosis during I/R. IL-6 deficiency did not impact either infarct size or post-MI remodeling. Activation of signal transducer and activator of transcription 3 (signal transducer and activator of transcription 3, a signaling molecule downstream of gp130), either via IL-11 or constitutively, attenuated post-MI remodeling and fibrosis and improved neovascularization, and CCR5 deficiency resulted in attenuated recruitment of anti-inflammatory monocytes, impaired macrophage activation and aggravated post-MI cardiac remodeling. Moreover, clinical studies of anticytokine (anti-TNF biologics and IL-1R antagonists) and antichemokine strategies in humans with MI or HF have not proven clinical benefit (and in some cases suggested harm), suggesting that indiscriminate cytokine blockade eliminates both the beneficial and the detrimental effects of cytokines and chemokines, thereby yielding neutral responses.

Indeed, these and other studies indicate that proinflammatory cytokines and chemokines induce effects in the infarcted heart that are not simply gradations of “good” versus “bad,” but rather are complex and variable, depending on such factors as the temporal and disease context, the prevailing cellular composition in the microenvironment, and accompanying pleiotropic influences on multiple (immune and nonimmune) cell processes that include not only inflammatory responses but also events such as growth, differentiation, apoptosis, oxidative stress, and mitochondrial function. For example, studies in mice deficient for TNF receptor (TNFR) 1 or 2 have shown that after nonreperfused MI, TNF induces divergent TNFR-specific effects on remodeling, hypertrophy, NF-κB activity and inflammation, border zone fibrosis, and apoptosis such that TNFR1 exacerbates, whereas TNFR2 ameliorates, these events. This suggests that opposing receptor-specific myocardial responses in vivo may explain the negative clinical trial results with global TNF blockade. Also, although much of the current research focus is on the heart-localized effects of proinflammatory mediators, extracardiac effects may be of equal import to cardiac repair. In this regard, a recent study has demonstrated that circulating IL-1β induces the proliferation of bone marrow hematopoietic stem cells after MI, thereby enhancing circulating leukocytes and inflammation in the infarcted heart. As another example, the chemokine CXCL12/stromal cell–derived factor-1 may facilitate cardiac repair after MI by promoting homing and survival of stem cells and neovascularization. Finally, it is important to recognize that the inflammation is a required event for effective tissue repair, and as such suppression of inflammatory activation that is not dysregulated or excessive may not necessarily result in salubrious effects on cardiac remodeling after MI. Moreover, there is evidence that loss-of-function of select proinflammatory mediators (eg, MCP-1, IL-1, and myeloperoxidase) attenuate inflammation and adverse cardiac remodeling but do not impact cell death and infarct size during I/R. Hence, suppression of the inflammatory cascade during MI need not be accompanied by cardiomyocyte salvage. These caveats are important to consider when designing immunomodulatory therapeutic strategies to enhance post-MI cardiac repair.

**Cellular Effectors of the Inflammatory Response**

Cardiomyocytes, immune cells, vascular cells, and fibroblasts have been implicated as cellular effectors of the inflammatory reaction in the healing infract; their relative role in activation of specific inflammatory cascades remains unclear. Resident myocardial cells sense tissue necrosis and trigger the postinfarction inflammatory reaction leading to recruitment of circulating leukocyte subpopulations.
Cardiomyocytes
Necrotic cardiomyocytes provide the main stimulus for the postinfarction inflammatory reaction, by releasing DAMPs in the infarcted area. Surviving cardiomyocytes in the infarct border zone may also trigger inflammatory activation, by producing and secreting cytokines in response to activation with IL-1, TLR ligands, or ROS. Immunohistochemical studies and in situ hybridization experiments have suggested that viable cardiomyocytes in the infarct border zone express intercellular adhesion molecule-1 and may synthesize cytokines and chemokines. The relative contribution of cardiomyocyte-derived inflammatory mediators in progression and extension of postinfarction inflammation remains unknown.

Endothelial Cells
The heart is a highly vascular organ; in adult mammals, endothelial cells are the most abundant noncardiomyocytes. Extravasation of leukocytes into the infarcted area requires endothelial activation. Endothelial-specific activation of the transcription factor forkhead box O4 after infarction has been demonstrated to promote neutrophil infiltration in the infarcted heart. DAMPs released by dying cardiomyocytes induce rapid upregulation of endothelial adhesion molecules, triggering adhesive interactions with activated leukocytes. Preformed P-selectin is rapidly mobilized from Weibel-Palade bodies, and E-selectin is upregulated in the ischemic endothelium. Once expressed on the endothelial surface, selectins bind to their leukocyte ligands, capturing neutrophils and monocytes and mediating rolling along the venular endothelium. Moreover, activated endothelial cells in the infarct zone serve as an important source of cytokines and chemokines.

Neutrophils
Neutrophils are the first immune cell type to infiltrate the infarcted myocardium in response to such factors as DAMPs, cytokines and chemokines, endogenous lipid mediators (e.g., prostaglandin E, leukotriene B), histamine, and complement components. Infiltration of the infarct with neutrophils is predominantly localized in the border zone and is accelerated and accentuated by reperfusion. Neutrophil extravasation in the infarcted heart is dependent on activation of adhesive interactions between the leukocytes and the endothelial cells (Figure 3). Circulating neutrophils expressing selectin ligands are captured by the activated endothelium and roll along the endothelial layer. Rolling neutrophils sense chemokines bound to glycosaminoglycans on the endothelial surface. Interactions between CXC chemokines and the CXCR2 receptor expressed by the neutrophils induce conformational changes of leukocyte integrins, strengthening the adhesive interaction, and resulting in arrest and adhesion of the neutrophil to the endothelial surface. Extensive experimental evidence suggests that binding of neutrophil integrins, such as lymphocyte function-associated antigen 1 and macrophage-1 antigen (Mac1), with endothelial intercellular adhesion molecules is essential for firm adhesion. Neutrophil transmigration follows, as leukocytes actively crawl toward endothelial junctions, then migrate through basement membrane regions with low levels of matrix protein expression. These regions may overlap with gaps between pericytes that may increase in size in the inflamed myocardium, thus serving as exit points for extravasating neutrophils. Neutrophil extravasation across the microvasculature requires binding of leukocyte integrins to endothelial adhesion molecules and subsequent interactions between endothelial integrin ligands and functional proteins. Emigrated neutrophils release proteolytic enzymes and contribute to the clearance of the wound from dead cells and matrix debris. Infiltrating neutrophils may also amplify the immune response. Although both in vitro and in vivo experiments have suggested that neutrophils may exert direct cytotoxic actions on viable cardiomyocytes extending ischemic injury, the significance of such effects in the clinical context remains controversial.

Monocyte Subpopulations
Two distinct waves of monocyte recruitment have been identified in healing myocardial infarcts. Early recruitment of proinflammatory Ly6C monocytes is mediated through the activation of the MCP-1/CCR2 axis. At a later stage, anti-inflammatory monocyte subpopulations are selectively recruited and may participate in resolution of the postinfarction inflammatory response. During the first few hours after infarction, high levels of IL-1 in the infarct may stimulate a proinflammatory program in infarct monocytes. Monocytes infiltrating the infarcted myocardium originate not only from the bone marrow but also from the spleen, which may serve as a large reservoir of mononuclear cells that can be rapidly deployed to sites of inflammation.

Lymphocytes
Early infiltration of the infarcted heart with lymphocyte subsets has been extensively documented in both large animal and in rodent models of MI. Experiments in a rat model of MI suggested that cytotoxic T lymphocytes are activated after infarction; in vitro studies suggested that these cells may exert cytotoxic actions on healthy cardiomyocytes. Whether infiltrating T cells extend ischemic injury in vivo remains unknown. Emerging evidence suggests that lymphocyte subpopulations may play an important role as orchestrators of the inflammatory response. Using both genetic and antibody-mediated depletion strategies, Zouggari et al demonstrated that B cells promote mobilization of proinflammatory Ly6C monocytes, thus playing an important role in activation of the inflammatory cascade.

Fibroblasts
The adult mammalian myocardium contains abundant cardiac fibroblasts; in the absence of injury, these cells remain quiescent and may play a role in maintaining the extracellular matrix network. However, when stimulated with DAMPs, fibroblasts are capable of secreting large amounts of inflammatory cytokines and chemokines. In the infarcted myocardium, fibroblasts may respond to stimulation with ROS and IL-1, acquiring a proinflammatory phenotype, and serving as an important source of chemokines and cytokines. Because several other cell types are capable of proinflammatory activation during the early phase of infarct healing, the relative contribution of fibroblasts remains unknown. Activation of IL-1 signaling in cardiac fibroblasts during the inflammatory phase of cardiac repair inhibits α-smooth muscle actin expression and delays myofibroblast conversion, promoting a matrix-degrading phenotype (Figure 4). Thus, cytokine-driven
inflammatory activation of the fibroblasts may prevent premature acquisition of a synthetic myofibroblast phenotype, until the infarct is cleared of dead cells and matrix debris.

**Resident Mast Cells and Macrophages**

The heart contains resident populations of mast cells and macrophages that may play an important role in the activation of the inflammatory cascade. Mast cells are strategically located in perivascular areas and contain preformed stores of inflammatory mediators, such as TNF, histamine, and tryptase. Cytokine stimulation, adenosine, ROS, and activation of the complement cascade induce mast cell degranulation. TNF and histamine released by resident mast cells may play an important role in triggering the postinfarction inflammatory response.

Recent studies have characterized the resident macrophage population in mouse myocardium. Using flow cytometry and lineage tracing approaches, Epelman et al. found significant heterogeneity in macrophage populations in adult mouse hearts. At steady state, 2 distinct macrophage pools were identified: a CCR2-negative subset that represented an embryonically established lineage that originated from yolk sac macrophages and fetal monocytes and a second (much smaller) pool derived from circulating CCR2+ monocytes. The fate of these subpopulations after infarction and their contribution in regulation of the postinfarction inflammatory response remains unclear. Heidt et al. suggested that, at least in nonreperfused infarcts, resident cardiac macrophages die and may be replaced by monocyte-derived CCR2-expressing cells with potent proinflammatory properties. Reperfusion may protect resident macrophage subpopulations in the infarcted area; thus, in models of reperfused infarction, these cells may play an important role in activation of the inflammatory cascade. During progression of the inflammatory cascade, recruitment of large numbers of monocytes and proliferation of resident macrophage subsets results in marked expansion of the cardiac macrophage population. The abundant, dynamic, and highly plastic population of infarct macrophages plays an important role in regulation of the inflammatory and reparative response after MI.

**Extracellular Matrix**

Both cardiomyocytes and noncardiomyocytes are ensheathed in a network of extracellular matrix proteins. The cardiac interstitial matrix does not only simply serve as a structural scaffold but also transduce molecular signals and play an active role in regulation of inflammatory and reparative responses. Fragmentation of the extracellular matrix provides a key stimulus for activation of the inflammatory cascade after infarction. Generation and release of collagen and fibronectin fragments have been implicated in activation of proinflammatory signaling. Hyaluronan degradation may result in release of high molecular weight fragments with potent proinflammatory properties, capable of inducing cytokine and chemokine synthesis by endothelial and immune cells.

**Reparative and Proliferative Phase**

**Inhibition and Resolution of the Inflammatory Response**

**Cell Types Involved in Suppression of the Inflammatory Response**

Neutrophils: The transition from the inflammatory to the reparative and proliferative phase after MI is driven by changes...
in the cardiac microenvironment. Although their survival can be prolonged by DAMPs, proinflammatory cytokines, hypoxia, and acidosis, neutrophils are short-lived cells that rapidly undergo cell death, primarily by apoptosis but also secondarily by necrosis.\(^{139,170}\) In various models of acute inflammation, late-stage and apoptotic neutrophils are critical for ushering inflammation resolution by several mechanisms: (1) the release of mediators that promote inflammation resolution such as pro-resolving lipid mediators (eg, lipoxins and resolvins), annexin A1, and lactoferrin that dampen neutrophil transmigration and entry, and promote neutrophil apoptosis and the phagocytic uptake of apoptotic neutrophils by macrophages,\(^{139–141}\) (2) the expression of decoy and scavenging chemokine and cytokine receptors on apoptotic neutrophils that results in tissue depletion of these mediators,\(^{139,141}\) and (3) the expression of eat-me signals (eg, phosphatidylserine) that facilitate the ingestion of apoptotic neutrophils by macrophages.\(^{139,141}\) The subsequent phagocytic clearance of these apoptotic cells induces a pro-resolving M2 phenotype in macrophages and secretion of anti-inflammatory and profibrotic cytokines such as IL-10 and TGF-β that suppress inflammation and promote tissue repair. It should be noted that although these are fundamental aspects of inflammatory cell biology, they have not been widely tested in the infarcted heart. A recent study demonstrated that neutrophils, via secreted neutrophil gelatinase-associated lipocalin, polarize macrophages toward a reparative phenotype, thereby orchestrating tissue healing (Figure 4).\(^{171}\)

Monocytes, macrophages, and DCs: After the early appearance of neutrophils, monocytes and macrophages (Mo/Mϕ) comprise the most abundant cells in the infarcted heart.\(^3,4,41\) Seminal studies by Nahrendorf, Swirski, and co-workers\(^3,152,172–174\) demonstrated that Mo/Mϕ display phasic functional heterogeneity that serve to guide proper wound healing. The initial phase (peak day \(\approx 3–4\) post MI) promotes tissue digestion and is characterized by Ly6Chi monocytes and M1 macrophages that are proteolytic, with augmented expression of proteinases (eg, cathepsins and matrix metalloproteinases), and proinflammatory, with augmented TNF expression. The second phase (peak day \(\approx 7\) post MI) promotes tissue repair, with a predominance of Ly6C\(^{hi}\) monocytes and M1 macrophages that are profibrotic, with augmented expression of proteinases and profibrotic, and angiogenic factors (eg, IL-10, TGF-β, and vascular endothelial growth factor). It should be emphasized that in the healing infarct, macrophages cannot be simply categorized as polarized M1/M2 cells, but exhibit a wide range of nuanced phenotypes. Moreover, the repertoire of reparative...
monocytes/macrophages is not limited to traditional cytokines and growth factors. A recent investigation identified a novel secreted protein called myeloid-derived growth factor, as an essential monocyte-derived mediator that may promote repair of the infarcted heart.175

Initial studies4,112 suggested that the 2 phases resulted from separate waves of circulating monocyte infiltration—early recruitment of Ly6C<sup>+</sup>CCR2<sup>+</sup>CX,CR1<sup>+</sup> monocytes in response to augmented myocardial CCL-2/MCP-1 expression, and later recruitment of Ly6C<sup>+</sup>CCR2<sup>−</sup> CX,CR1<sup>+</sup> monocytes in response to augmented myocardial expression of fractalkine, the ligand for CX,CR1. However, more recent work177 using chimeric mice deficient for hematopoietic cell Nr4a1 (an orphan nuclear hormone receptor essential for patrolling Ly6C<sup>+</sup> monocyte development179) indicated that both phases derive from proinflammatory Ly6C<sup>+</sup> monocytes, and that during the reparative phase, recruited Ly6C<sup>+</sup> monocytes switch their phenotype to Ly-6C<sup>+</sup> anti-inflammatory macrophages that proliferate locally to effect inflammation resolution and wound healing. Although molecular regulators such as Nr4a1177 and interferon-on-regulator factor 5172 may serve as important modulators of inflammatory vs-<i>à-vis</i> reparative polarity in macrophages, the specific microenvironmental cues that induce this switch remain poorly defined.

In addition to Mo/Mϕ, CD11c<sup>+</sup> DCs infiltrate the infarcted heart, predominantly during the reparative phase.41,177 DCs are essential for proper inflammation resolution, scar formation, and angiogenesis post-MI, as DC ablation resulted in persistent cardiac accumulation of Ly6C<sup>+</sup> monocytes and CD206<sup>+</sup> macrophages, sustained proinflammatory cytokine expression, reduced endothelial cell proliferation, and deterioration of LV function post-MI.177

T-lymphocytes: T-lymphocytes, including CD4<sup>+</sup> and CD8<sup>+</sup> T-cells, Foxp<sub>3</sub> regulatory cells, invariant natural killer T cells, and γδT-cells, infiltrate the heart after MI, most robustly during the reparative phase.51,178–180 Studies using CD4<sup>+</sup> T-cell-deficient mice, and OT-II mice that exhibit defective T-cell antigen recognition, have demonstrated that CD4<sup>+</sup> helper T cells are activated after MI likely in response to released cardiac autoantigens, and that these T cells promote wound healing, resolution of inflammation and proinflammatory monocyte infiltration, and proper collagen matrix formation and scar formation, thereby limiting adverse remodeling.177 However, the specific identity of these autoantigens remain unclear. Notably, in a hindlimb ischemia model, CD4<sup>+</sup> T cells were also shown to be essential for the recruitment of proangiogenic macrophages and collateral artery formation.183 A recent study using both genetic and antibody-based approaches to modulate regulatory T cells early post MI showed that CD4<sup>+</sup>Foxp<sub>3</sub> regulatory T cells are also essential for favorable wound healing, scar formation, and inflammation resolution after MI, in part, by modulating macrophage differentiation toward an M2-like phenotype.184 Moreover, the activation of invariant natural killer cells after reperfused179 or nonreperfused MI180 has been shown to reduce leukocyte infiltration, myocardial injury, and adverse remodeling, in part, by enhancing the expression of anti-inflammatory cytokines such as IL-10. Hence, multiple T-lymphocyte subsets contribute to suppression of the inflammatory response. In contrast, CD4<sup>+</sup>γδT-cells seem to promote neutrophil and macrophage infiltration and impart detrimental effects on post-MI remodeling.182

Vascular cells: Tissue neovascularization is essential for supplying the healing infarct with nutrients and oxygen. A robust angiogenic response occurs after MI with rapid upregulation of VEGF in viable border zone cardiomyocytes, and upregulation of vascular endothelial growth factor receptors in border zone vasculature and in new vessels extending into the infarct zone.3,184 Initially, the neovessels are enlarged and lack a pericyte and smooth muscle cell mural coating; these features promote vessel hyperpermeability and inflammatory cell extravasation into the infarct tissue.185,186 During later phases of infarct healing, however, these neovessels mature and become invested with a mural coat. This process is dependent on endothelial cell platelet-derived growth factor (PDGF) and PDGF receptor-β signaling in pericytes and smooth muscle cells.186 Defects in the formation of the mural coat result in prolonged inflammatory cell infiltration in the infarct zone and reduced collagen deposition, suggesting that PDGF-β-mediated pericyte investment of neovessels is critical for the proper resolution of inflammation post MI. The importance of pericytes is further supported by the findings that in vivo human pericyte transplantation into the peri-infarct zone of mice attenuates vascular permeability, reduces tissue leukocyte infiltration, augments angiogenesis, and improves cardiac remodeling187,188

Cardiomyocytes: It is tempting to hypothesize that viable border zone cardiomyocytes may secrete mediators that limit extension of the inflammatory response, protecting noninfarcted myocardium from the unwanted effects of unrestrained inflammation.3,186 However, information on specific cardiomyocyte-derived signals that may contribute to containment of inflammation after infarction remains limited. Recent evidence suggested that, in the infarcted myocardium, cardiomyocytes may secrete regenerating islet-derived-3β, a mediator that regulates macrophage recruitment and inhibits inflammatory activation, preventing cardiac rupture and expansion of injury.190

**Molecular Signals Implicated in Resolution of Postinfarction Inflammation**

Timely suppression and spatial containment of the postinfarction inflammatory reaction is dependent on release of secreted anti-inflammatory mediators (such as IL-10, members of the TGF-β family, and lipid-derived proresolving mediators) and on activation of intracellular STOP signals that inhibit the innate immune response. Defects in the molecular pathways responsible for suppression and resolution of the inflammatory response may be involved in the pathogenesis of adverse remodeling and HF after MI.191

IL-10: IL-10 exerts potent anti-inflammatory actions, suppressing synthesis of proinflammatory cytokines and chemokines in macrophages192 through the activation of signal transducer and activator of transcription 3 signaling.195 IL-10 upregulation has been documented in both rodent and large animal models of MI.154,155 Although the late timing of IL-10 upregulation is consistent with a possible role in suppression of proinflammatory signaling, experiments using IL-10...
null animals have produced conflicting results. In a mouse model of coronary occlusion/reperfusion, genetic loss of IL-10 was associated with increased early mortality and accentuated expression of proinflammatory genes. However, another study with a much higher sample size did not confirm these observations, demonstrating comparable mortality and dilative remodeling in IL-10 null and WT animals undergoing reperfused infarction protocols, and suggesting that IL-10 loss is associated with relatively subtle alterations (including increased myocardial levels of TNF and MCP-1). Interestingly, in human patients, high plasma levels of IL-10 predict adverse outcome in patients with acute coronary syndromes and ST-segment–elevation MI. This observation may reflect a compensatory accentuation of anti-inflammatory cytokine synthesis in high-risk patients.

Members of the TGF-β family: Several members of the TGF-β family have been implicated in negative regulation of the inflammatory reaction. Unfortunately, dissection of the role of these mediators in postinfarction inflammation and repair has been hampered by the complex biology of their regulation and activation, by their pleiotropic and context-dependent actions on all cell types involved in infarct healing, and by the complexity of their downstream signaling effectors. Considering its actions on immune and reparative cells and the time course of its upregulation after MI, TGF-β1 may serve as the master switch regulating the transition from inflammation to fibrosis. Neutralization experiments using gene therapy with the extracellular domain of the type II TGF-β receptor in a model of MI suggested that early inhibition may worsen dysfunction accentuating the inflammatory response, whereas late disruption of TGF-β signaling may protect from interstitial fibrosis and hypertrophic remodeling. A recent study suggested that, although broad inhibition of TGF-β after infarction causes early mortality caused by cardiac rupture, cardiomyocyte-specific disruption of the TGF-β receptors was protective and stimulated a wide range of anti-inflammatory and cytoprotective signals. Thus, the detrimental actions of early TGF-β inhibition on the infarcted myocardium may not be because of direct actions on cardiomyocyte survival, but may reflect loss of anti-inflammatory actions on inflammatory cells, endothelial cells, or fibroblasts.

Growth differentiation factor-15, a member of the TGF-β family, is also implicated in suppression of the inflammatory response after infarction. Growth differentiation factor-15 exerts potent anti-inflammatory actions by countering chemokine-triggered leukocyte integrin activation. Thus, growth differentiation factor-15 loss in mice is associated with accentuated postinfarction inflammation and fatal cardiac rupture after MI. In patients with ST-segment–elevation MI, elevated plasma growth differentiation factor-15 levels are associated with increased mortality, likely reflecting activation of a protective anti-inflammatory pathway in patients with an accentuated postinfarction inflammatory reaction.

Lipid-derived proresolving mediators: Proresolving lipid mediators (including the lipoxins, resolvins, protectins, and maresins) have potent anti-inflammatory properties and may play an important role in resolution of the inflammatory infiltrate after infarction. Protective effects of exogenous resolvin E1 and resolvin D1 administration have been demonstrated in rodent models of I/R and nonreperfused MI; however, the potential role of endogenous proresolving lipid mediators in suppression and resolution of the postinfarction inflammatory response has not been investigated.

Do Chemokine-Mediated Effects Suppress Inflammation by Recruiting Anti-Inflammatory Leukocytes?

Although traditionally viewed as proinflammatory mediators, certain members of the chemokine family may suppress inflammation by recruiting anti-inflammatory monocyte and lymphocyte subsets to the infarcted myocardium. In a mouse model of reperfused MI, genetic disruption of the CC chemokine receptor CCR5 caused enhanced inflammation and accentuated dilative remodeling, associated with decreased infiltration of the infarct by regulatory T cells. Specific chemokine–chemokine receptor pairs may mediate recruitment of anti-inflammatory monocyte and lymphocyte subsets, thus protecting the infarcted myocardium from unrestrained inflammation.

Intracellular Pathways Involved in Negative Regulation of the Inflammatory Cascade

Activation of intracellular pathways that restrain the innate immune response may also play a crucial role in timely suppression of the postinfarction inflammatory response, protecting from adverse remodeling. Expression of IL-1R–associated kinase-M, a negative regulator of the innate immune response, is upregulated in infarct macrophages and fibroblasts and inhibits macrophage-derived cytokine expression, while promoting a matrix-preserving myofibroblast phenotype in cardiac fibroblasts.

Fibroblast Activation and Formation of the Scar

Myofibroblast Transdifferentiation and Acquisition of a Synthetic Phenotype

Expansion of the cardiac fibroblast population and conversion into synthetic myofibroblasts are hallmarks of the proliferative phase of cardiac repair. Myofibroblasts are phenotypically modulated fibroblasts that develop stress fibers and express contractile proteins, such as α-smooth muscle actin and the embryonal isoform of smooth muscle myosin. The origin of infarct myofibroblasts remains a debated issue. Experimental studies using bone marrow transplantation strategies have produced conflicting results, suggesting that either resident fibroblasts or circulating bone marrow progenitors may be the main source of myofibroblasts in the infarct. Endothelial cells undergoing mesenchymal transdifferentiation, epicardial epithelial cells, and pericytes may represent additional sources of myofibroblasts in the healing infarct. Recent studies using lineage tracing approaches in a model of MI have demonstrated that epicardial-derived cells that colonize the adult mammalian cardiac interstitium massively transdifferentiate into myofibroblasts in the infarcted heart. Thus, after MI, interstitial fibroblasts that survive the ischemic insult, or cells recruited from neighboring viable areas, may undergo myofibroblast transdifferentiation.
in response to increased levels of bioactive TGF-β and to the changes in the composition of the surrounding extracellular matrix. Moreover, in the healing infarct, marked induction of chemokines in response to extensive cardiomyocyte necrosis may result in recruitment and activation of additional subsets of reparative fibroblasts that may play an important role in scar formation.

**Mediators Involved in Myofibroblast Activation**

Conversion of fibroblasts into myofibroblasts requires the cooperation of both soluble mediators and specialized matrix components. TGF-β is induced and activated in the infarcted myocardium and is critically involved in myofibroblast transdifferentiation. In vitro studies have suggested that TGF-β1–induced myofibroblast conversion may be mediated through both canonical Smad-dependent218 and Smad-independent signaling pathways.219,220 Modulation of the extracellular matrix also contributes to myofibroblast conversion. TGF-β–mediated myofibroblast transdifferentiation requires activation of an outside-in signaling pathway transduced by polymerized fibronectin-extra domain A.53,221 Moreover, secretion and deposition of matricellular proteins, such as thrombospondin-1 and osteopontin family, may contribute to myofibroblast conversion, both by exerting direct actions on cellular phenotype and by accentuating growth factor-mediated responses.222–224

A growing body of evidence suggests that members of the transient receptor potential (TRP) family of ion channels play an essential role in regulating fibroblast to myofibroblast transition.225 TRP channels are ubiquitously expressed in all cell types, providing calcium entry pathways and regulating a wide range of Ca2+-dependent cell functions.226 Although in vitro studies have implicated TRPV4227 and TRPM7228 channels in cardiac myofibroblast transdifferentiation, their in vivo role is unclear. On the contrary, both in vitro and in vivo studies documented a critical role for TRPC6 in infarct myofibroblast conversion, demonstrating that TRPC6 absence is associated with impaired fibroblast function and increased mortality caused by cardiac rupture.229

Acquisition of a myofibroblast phenotype by infarct fibroblasts is associated with increased proliferative activity and stimulation of a matrix-preserving program. Extensive experimental evidence suggests that the activation of the renin–angiotensin–aldosterone system promotes myofibroblast proliferation and stimulates matrix synthesis. In addition to the well-described effects of circulating angiotensin II and aldosterone, local generation of angiotensin II in the infarct has also been implicated in fibroblast activation.230 Angiotensin II accentuates proliferative activity in cardiac fibroblasts and induces synthesis of extracellular matrix proteins and integrins,231 through effects that predominantly involve the AT1 receptor.232 Aldosterone also promotes cardiac fibroblast proliferation by stimulating Kirsten Ras-A (Ki-RasA) and MAPK1/2 signaling.233 Some actions of the renin–angiotensin–aldosterone system in cardiac fibroblasts may be mediated through activation of the TGF-β cascade. In addition to its critical effects on myofibroblast conversion, TGF-β also activates a matrix-preserving program in cardiac fibroblasts through Smad-dependent signaling.218,234 Other fibrogenic mediators, such as the PDGFs,235,236 members of the fibroblast growth factor family,237 and the mast cell–derived proteases tryptase238 and chymase239 are also released in the infarcted heart and may activate myofibroblasts.

**Extracellular Matrix During the Proliferative Phase of Infarct Healing**

The proliferative phase of infarct healing is characterized by dynamic alterations in the extracellular matrix network that directly regulate cellular phenotype and activity. As matrix fragments in the infarct zone are phagocytosed, a provisional matrix is formed, composed predominantly of fibrin and fibronectin.240 This highly plastic matrix network serves as a scaffold for migrating and proliferating cells, facilitating the dynamic changes that occur in the healing wound. The infarct matrix is also enriched through deposition of several members of the matricellular protein family. These structurally unrelated macromolecules are not present in normal myocardium, but are markedly upregulated in the infarcted and remodeling heart. Unlike structural matrix components (such as collagens and elastin), matricellular proteins do not provide mechanical support, but may bind to matrix proteins and cell receptors transducing signaling cascades. Thrombospondin-1,241 tenasin-C,242 secreted protein acidic and cysteine-rich,243 perimostin,244 osteopontin,245 osteoglycin,246 and members of the CCN family248 have been implicated in regulation of the inflammatory and reparative response after MI. Because matricellular proteins are capable of modulating behavior and function of all cells involved in cardiac repair, remodeling and fibrosis, dissection of specific molecular mechanisms responsible for the observed in vivo effects is particularly challenging. Modulation of growth factor activity and signaling231,240 or regulation of collagen fibrillogenesis and maturation246,247 has been suggested as potential mechanisms for specific matricellular actions.

**Maturation Phase**

The proliferative phase of cardiac repair is followed by scar maturation, as the extracellular matrix becomes cross-linked, and reparative cells are deactivated, and may undergo apoptosis. The molecular signals implicated in quiescence of infarct myofibroblasts remain unknown. Withdrawal of fibrogenic growth factors, activation of inhibitory STOP signals that terminate TGF-β and angiotensin II signaling, and clearance of matricellular proteins, may suppress proliferation and reduce the matrix-synthetic activity of the fibroblasts. Induction and secretion of antifibrotic mediators may also contribute to termination of the matrix-synthetic response. The CXC chemokine interferon-γ–inducible protein-10/CXCL10 inhibits fibroblast migration through proteoglycan-mediated actions, is upregulated in the infarcted heart, and contributes to spatial containment of the fibrogenic response in the infarcted region.240,245 However, because of the early timing of its induction in the infarcted myocardium, interferon-γ–inducible protein-10 is an unlikely candidate for a role in scar maturation. Although reduction in myofibroblast density during infarct maturation has been well documented,210,211 the fate of these cells remains unknown. Apoptotic death may mediate fibroblast loss in the scar and in the infarct border zone;252 the mediators responsible for fibroblast-specific activation of proapoptotic signaling are unknown.
Inflammatory Cells in the Late Phase of Post-MI Cardiac Remodeling

As detailed above and summarized in Figure 5, the 2 phases of healing after MI are acute inflammation with intense cellular infiltration, lasting up to 4 days in mice, followed by resolution and repair with active resolution of inflammation, quiescence of cell activity, and scar stabilization and maturation >14 days in mice. Although the time frame of these events is well defined in the murine model, larger animal models exhibit comparatively greater persistence of cellular infiltration and slower formation of granulation tissue after MI. After healing, in both humans and animal models with MI, a subset of those afflicted will exhibit late progressive ventricular dilation and HF, a state characterized by chronic inflammation (Figure 5). Among other variables, both larger infarcts and greater initial inflammatory activation are strong predictors of late cardiac remodeling and HF in humans. Moreover, histopathologic studies of human failing hearts with chronic ischemic cardiomyopathy have demonstrated augmented tissue macrophages and T-lymphocytes, and increased adhesion molecule expression in endothelial cells. One potential explanation for these findings is that late cardiac remodeling may be driven, in part, by incomplete or impaired resolution of myocardial inflammation with larger degrees of injury post-MI that amplifies over time. Indeed, the exogenous administration of the proresolving lipid mediator resolvin D1 post-MI that amplifies over time. Indeed, the exogenous administration of the proresolving lipid mediator resolvin D1 after nonreperfused MI hastened inflammation resolution and improved post-MI ventricular remodeling, suggesting that facilitation of active resolution may prevent persistent inflammation and ameliorate late HF.

Alternatively, chronic inflammation, and tissue inflammatory cell infiltration, in ischemic HF may represent late recrudescence of immune activation toward the heart in response to as-of-yet poorly identified factors or antigens. In support of this idea, Ismahil et al recently demonstrated that in chronic ischemic HF, there is local (and systemic) expansion of proinflammatory Mo/Mϕ, DCs, and T cells, together with heightened splenic expression of alarmins and proinflammatory mediators, and structural splenic remodeling consistent with heightened antigen processing. Moreover, activated mononuclear splenocytes trafficked to the failing heart to promote apoptosis, fibrosis, and dysfunction, suggesting that adverse LV remodeling was in part immune mediated, possibly in response to cardiac-derived alarmins. The role of particular immune cell populations in the pathogenesis of chronic remodeling and inflammation in HF requires further study, along with their organ-specific derivation (eg, local proliferation vis-à-vis infiltration from remote sites) and the potential antigens and molecular pathways responsible for their activation. As discussed above, these mechanisms may be separate and distinct from those that promote myocardial salvage after acute MI.

Targeting the Inflammatory Response in MI

Over the past 30 years, experimental work has revealed a crucial role for the inflammatory cascade in cardiac repair, remodeling, and fibrosis after MI. Unfortunately, this new knowledge has not yet translated into effective therapy. Because of the close link between inflammation and repair, nonselective inhibition of inflammation after MI (using corticosteroids or nonsteroidal anti-inflammatory drugs) may have detrimental effects on scar formation, promoting rupture and accentuating adverse remodeling. Thus, selective targeting of injurious proinflammatory signals is needed. Unfortunately, in clinical studies, approaches targeting several specific proinflammatory pathways have produced disappointing results. Despite promising experimental data in large animal models, CD11/CD18 integrin inhibition failed to reduce the size of the infarct in patients with MI. In a large clinical trial, complement inhibition did not reduce mortality and major adverse events in patients with ST-segment–elevation MI. P-selectin inhibition in patients with acute coronary syndromes seemed to attenuate cardiomyocyte necrosis, but was associated with trends toward worse clinical outcome. What are the causes for these translational failures?

First, inflammatory mediators are notoriously pleiotropic, exerting a wide range of actions on many different cell types. Thus, targeting a specific cytokine, growth factor, or inflammatory pathway may modulate several cellular responses; the clinical implications of these actions cannot always be predicted by investigating animal models. Second, temporal and spatial considerations are critical determinants of the effectiveness of an intervention, as described above. The reparative phase after MI is a highly dynamic process; the window of therapeutic opportunity is brief. Moreover, considering the spatial heterogeneity of the cellular environment in the remodeling infarcted heart, therapeutic interventions...
may have distinct effects on the infarct, the border zone, and the remote remodeling myocardium. Thus, a successful strategy requires careful design, optimally exploiting knowledge on the time course and topographical characteristics of the inflammatory response. Third, the pathophysiologic heterogeneity of postinfarction remodeling in humans complicates implementation of therapeutic strategies. The severity and characteristics of the remodeling response after infarction are not dependent only on the size of the acute infarct. Genetic background, concomitant conditions (such as hypertension or diabetes mellitus), age, and sex have major impact on the inflammatory response and profoundly affect post-MI remodeling and clinical outcome.

The pathophysiologic heterogeneity of patients with MI has important therapeutic implications. Certain patient subpopulations exhibit prolonged accentuation of proinflammatory signaling after infarction that may be associated with dilative remodeling and systolic dysfunction. These patients may benefit from interventions targeting the inflammatory cascade, such as IL-1 inhibition. Other patients do not exhibit significant postinfarction ventricular dilation, but develop a pronounced hypertrophic and fibrotic response, associated with diastolic dysfunction. This type of adverse remodeling is particularly common in diabetics and may be associated with an overactive TGF-β system. Identification of patient subpopulations with distinct pathophysiologic perturbations, using suitable biomarkers or molecular imaging modalities, is needed to design effective therapies to attenuate adverse remodeling in patients with MI.

The potential involvement of inflammatory signals in tissue regeneration adds a new perspective to the therapeutic potential of strategies targeting the postinfarction inflammatory response. Recently, neonatal macrophage subsets have been suggested to activate a regenerative program in the infarcted myocardium. Moreover, certain chemokines (such as stromal cell–derived factor-1/CXCL12), cytokines, and growth factors may regulate trafficking, activation, differentiation, and survival of progenitor cells. Clearly, this field is in its infancy. Whether modulation of the inflammatory response can contribute to activation of a regenerative program in adult mammalian myocardium is unknown.

**Concluding Remarks**

Our growing knowledge on the role of inflammatory cascades in injury, repair, and remodeling of the infarcted heart has revealed new therapeutic targets for patients surviving acute MI. Unfortunately, the pleiotropic actions of inflammatory mediators, and the remarkable pathophysiologic heterogeneity of cardiac remodeling in human patients, pose major challenges for clinical implementation of strategies targeting the inflammatory response. A concerted effort is needed to dissect the cellular actions and molecular signals activated by inflammatory mediators, and to identify the pathophysiologic perturbations that may be responsible for adverse remodeling in vulnerable patients. Strategies modulating the inflammatory cascade may not only hold promise as protective measures to prevent remodeling and HF but also may prove crucial in realizing the visionary goal of myocardial regeneration.

**Sources of Funding**

This study was supported by National Institutes of Health (NIH) R01 HL76246 and R01 HL85440 (to Dr Frangogiannis); NIH R01 HL125735 and VA Merit I01 BX002706 (to Dr Prabhu).

**Disclosures**

None.

**References**


S, Kubota I, Takeishi Y. High mobility group box SR, Salem HK, Brouilette SW, Yacoub MH, Suzuki K. Modulated inflam-


Xu H, Fei X, Su Z, Yang Y, Kao R, Martin CM, Rui T. Endogenous HMG1B1 contributes to ischemia-reperfusion-induced myocardial apoptosis by potentiating the effect of TNF-α/JNK.


Prabhu and Frangogiannis Repair After Myocardial Infarction 109


Frangogiannis NG, Mendoza LH, Lindsey ML, Ballantyne CM, Michael LH, Smith CW, Entman ML. IL-10 is induced in the reperfused myocardium and may modulate the reaction to injury. J Immunol. 2000;165:2798–2808.


Mylonas KJ, Jenkins SJ, Castellan RF, Rudin D, McGregor K, Phythian-Adams AM, Frohlich J, Hipson SM, MacDonald AS, Allen JE, Gray GA. The adult murine heart has a sparse, phagocytically active macrophage population that expands through monocyte recruitment and


228. McNaughton LJ, Koyjmcc.2011.06.023.


The Biological Basis for Cardiac Repair After Myocardial Infarction: From Inflammation to Fibrosis
Sumanth D. Prabhu and Nikolaos G. Frangogiannis

Circ Res. 2016;119:91-112
doi: 10.1161/CIRCRESAHA.116.303577

Circulation Research is published by the American Heart Association, 7272 Greenville Avenue, Dallas, TX 75231
Copyright © 2016 American Heart Association, Inc. All rights reserved.
Print ISSN: 0009-7330. Online ISSN: 1524-4571

The online version of this article, along with updated information and services, is located on the World Wide Web at:
http://circres.ahajournals.org/content/119/1/91

Permissions: Requests for permissions to reproduce figures, tables, or portions of articles originally published in Circulation Research can be obtained via RightsLink, a service of the Copyright Clearance Center, not the Editorial Office. Once the online version of the published article for which permission is being requested is located, click Request Permissions in the middle column of the Web page under Services. Further information about this process is available in the Permissions and Rights Question and Answer document.

Reprints: Information about reprints can be found online at:
http://www.lww.com/reprints

Subscriptions: Information about subscribing to Circulation Research is online at:
http://circres.ahajournals.org/subscriptions/