Activation of MDL-1 (CLEC5A) on immature myeloid cells triggers lethal shock in mice


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Systemic inflammatory response syndrome (SIRS) is a potentially lethal condition, as it can progress to shock, multi-organ failure, and death. It can be triggered by infection, tissue damage, or hemorrhage. The role of tissue injury in the progression from SIRS to shock is incompletely understood. Here, we show that treatment of mice with concanavalin A (ConA) to induce liver injury triggered a G-CSF–dependent hepatic infiltration of CD11b−Gr-1−Ly6G−Ly6C− immature myeloid cells that expressed the orphan receptor myeloid DAP12–associated lectin–1 (MDL-1; also known as CLEC5A). Activation of MDL-1 using dengue virus or an agonist MDL-1–specific antibody in the ConA-treated mice resulted in shock. The MDL-1+ cells were pathogenic, and in vivo depletion of MDL-1+ cells provided protection. Triggering MDL-1 on these cells induced production of NO and TNF-α, which were found to be elevated in the serum of treated mice and required for MDL-1–induced shock. Surprisingly, MDL-1–induced NO and TNF-α production required eNOS but not iNOS. Activation of DAP12, DAP10, Syk, PI3K, and Akt was critical for MDL-1–induced shock. In addition, Akt physically interacted with and activated eNOS. Therefore, triggering of MDL-1 on immature myeloid cells and production of NO and TNF-α may play a critical role in the pathogenesis of shock. Targeting the MDL-1/Syk/PI3K/Akt/eNOS pathway represents a potential new therapeutic strategy to prevent the progression of SIRS to shock.

Introduction

Activation of the innate immune system is a common feature of the systemic inflammatory response syndrome (SIRS), whether the initial trigger is infection or sterile tissue damage in trauma or hemorrhage. Activation of myeloid lineage cells, including monocytes, macrophages and neutrophils, leads to the production of proinflammatory cytokines as well as other mediators of tissue injury, such as ROS and reactive nitrogen species. Organ injury, in turn, induces the release of damage-associated molecular patterns (DAMPs) such as mitochondrial DNA, heat shock proteins (HSPs), and high-mobility group box 1 (HMGB1) that amplify the ongoing innate inflammatory response, which can progress to shock, multi-organ failure, and death (1). The progression to shock, defined as the systemic loss of blood pressure, has been attributed to cytokine-mediated capillary leakage and pathologic vasodilation, in which both TNF-α and NO have been implicated as critical mediators (2). Although the systemic release of TNF-α and NO may represent the catastrophic “tipping point” in the progression from SIRS to shock, many of the key cellular and molecular mechanisms involved in this pathophysiological decompensation remain to be elucidated, and these may represent key points of medical intervention.

Understanding the factors that drive the progression from dengue virus (DV) infection to lethal dengue shock syndrome (DSS) is of particular medical importance. DV infection is the most prevalent arboviral disease worldwide, with an estimated yearly incidence of 50 million cases. Although primary infection with one of the 4 DV serotypes usually results in mild disease, secondary infection with a second serotype conveys significant risk for the development of life-threatening DSS. In addition to the clear risks of previous exposure and production of non-neutralizing antibodies specific to the primary DV serotype, the progression from secondary dengue infection to DSS correlates with high levels of circulating TNF, young patient age, and the presence of tissue damage. In particular, liver injury has been implicated as one of the risk factors associated with the development of DSS, as elevated serum ALT and AST levels are a strong predictor for disease severity (3–5). However, the cellular and molecular mechanisms of progression to DSS remain largely unexplored. Recently, vascular leakage and shock were shown to be strictly dependent upon DV particles binding to and signaling through the myeloid-restricted cell surface receptor myeloid DAP12–associating lectin–1 (MDL-1) (6). Two recently published articles further highlight the importance of MDL-1 in DV-induced disease. One study reports that MDL-1 gene expression is a critical factor in differentiating dengue hemorrhagic fever (DHF) from dengue fever (DF) patients, while another article suggests blocking DV/MDL-1 interaction as a potential antiviral therapy (7, 8).

MDL-1, also known as C-type lectin domain family 5 member A (CLEC5A), is a type II transmembrane protein and a member of the C-type lectin superfamily. MDL-1 has a short cytoplasmic tail and lacks signaling motifs, therefore requiring association with the adaptor protein DAP12 to generate signals (9). However, the downstream signaling pathways triggered by MDL-1 are not well defined. Functionally, MDL-1 activation has been shown to induce production of cytokines (TNF-α, IL-1, IL-6, IL-8, IL-17A) and chemokines (MIP-1α, RANTES, IP-10, MDC) (6, 10, 11). Like triggering receptor expressed on myeloid cells–1 (TREM-1), which potentiates myeloid cell activation and cytokine release in response to TLR ligands and other pathogen-associated molecular patterns (PAMPs), MDL-1 appears to function as an amplifier of the innate immune response.

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The endogenous ligand for MDL-1 has yet to be identified. However, dengue viral particles can clearly function as a proinflammatory PAMP at the MDL-1 receptor to induce shock in the context of a productive DV infection. However, in our experience, systemic activation of MDL-1 in uninfected naïve mice results in no significant pathology or systemic cytokine production. Based on this, we hypothesized that an initial trigger of tissue injury was required to predispose the system to an MDL-1–induced shock response. To test this hypothesis, we employed a sublethal dose of concanavalin A (ConA) to induce nonlethal liver injury, and found that this injury did indeed sensitize mice to shock induced by triggering of MDL-1. In brief, we demonstrate that ConA induces a mobilization and hepatic accumulation of myeloid cells with an immature phenotype (CD11b+Gr1+Ly6G+Ly6C−) that express MDL-1 and are necessary to sensitize the mouse to MDL-1–induced shock. Furthermore, the MDL-1–mediated shock was surprisingly dependent on eNOS-induced, but not iNOS-induced, NO, as well as TNF-α production. This study for the first time to our knowledge delineates cellular and molecular mechanisms involved in the progression from tissue injury to shock that are driven by the pathologic expansion and activation of immature myeloid cells coexpressing MDL-1 and eNOS.

Results
Activation of MDL-1 induces shock. Intravenous administration of ConA causes liver injury (12). Using a novel bioluminescent inflammation probe (13) and in vivo imaging technology (Figure 1A), we confirmed that this ConA-induced inflammation was highly liver specific, while no inflammation signal was detected in naïve mice (data not shown). We also observed that MDL-1+ cells accumulated in the liver in response to ConA-induced liver inflammation in a time-dependent fashion, with maximal infiltration occurring at 4 hours after ConA treatment (Figure 1, B and C). Since the endogenous ligand for MDL-1 has not yet been identified, we activated MDL-1 in vivo by injecting DV, the only molecule known to interact with MDL-1. Activation of MDL-1 by intraperitoneal injection of DV 4 hours after ConA treatment resulted in lethal shock with onset at 12 hours. Almost all MDL-1+ mice were protected, thus confirming that death triggered by DV is mediated via MDL-1 (Figure 1D).

In order to avoid undesirable triggering of other signaling pathways, such as TLR, by the DV preparation, we also generated anti-mouse MDL-1 agonist mAb (10) and used it to activate MDL-1 in vivo. Interestingly, mice injected with anti–MDL-1 mAb also died of shock, albeit with a much earlier onset of approximately 15 minutes, and this rapid death was mediated via MDL-1, as all MDL-1+ mice were protected (Figure 1E). This rapid onset of MDL-1–triggered death could be delayed by titration of the dose of agonist mAb injected in a dose-dependent manner, and all mice injected with anti–MDL-1 antagonist mAb or IgG1 isotype control survived (Figure 1, F and G), further confirming that the observed shock response is mediated via activation of MDL-1. Of note, in the absence of ConA treatment, administration of DV or agonist mAb to mice resulted in no death (data not shown), indicating that prior liver injury is crucial in sensitizing the animal to shock triggered by MDL-1.

Hepatic infiltration of MDL-1+ cells is G-CSF dependent. To further understand the mechanism by which ConA initiates the infiltration of MDL-1+ cells to the liver, we measured the levels of 15 different chemokines and growth factors in both serum and liver homogenates of mice treated with ConA for 0–4 hours. Of the 15 chemokines and growth factors tested, we focused on G-CSF, GM-CSF, KC, MIP-2, and MCP-1, all of which have been implicated in the mobilization and/or maturation of myeloid precursors, neutrophils, and monocytes. The G-CSF level in both the serum and liver was increased by ConA in a time-dependent fashion (Figure 2A). To elucidate whether this growth factor plays a role in MDL-1–mediated shock, we neutralized G-CSF before initiation of MDL-1+ cell mobilization by ConA. As shown in Figure 2B, ablation of G-CSF significantly ameliorated MDL-1–triggered lethal shock. G-CSF level in the blood and liver of these mice was measured, and the results indicated that G-CSF was suppressed by 100% and 50%, respectively (Figure 2C). Liver sections of these mice were stained for MDL-1 and showed a 46% decrease in hepatic infiltration of MDL-1+ cells in mice subjected to G-CSF neutralization (Figure 2D). These results indicated that G-CSF is an important growth factor for the hepatic infiltration of MDL-1+ cells and that ablation of this growth factor confers protection against MDL-1–mediated lethal shock.

In addition to G-CSF, production of other growth factors and chemokines including GM-CSF, KC, MIP-2, and MCP-1 was also increased by ConA in a time-dependent manner, with slightly different kinetics (Supplemental Figure 1A; supplemental material available online with this article; doi:10.1172/JCI57682DS1). However, neutralization of GM-CSF, KC, or MIP-2 had no effect on survival (Supplemental Figure 1, B–D). MCP-1 is also not important for MDL-1–mediated shock, since mice that lack CCR2, the cognate receptor for MCP-1, showed survival similar to that of WT mice (Supplemental Figure 1E). Therefore, G-CSF seems to be the predominant factor driving recruitment of MDL-1+ cells to the liver. Intravenous administration of G-CSF also drove hepatic infiltration of MDL-1+ cells (Supplemental Figure 2, A and B), but subsequent administration of MDL-1 agonist mAb resulted in no death (data not shown). We therefore hypothesized that priming of MDL-1+ cells is required for these cells to be responsive to MDL-1 stimulation. In addition to chemokines, ConA also increased serum levels of multiple cytokines, including IFN-γ, TNF-α, IL-1β, and IL-6 (Supplemental Figure 2, C–F), all of which have been reported to be effective priming agents for immune cells (14, 15). To test the hypothesis that cytokine-induced activation is required for the priming of MDL-1+ triggered shock, we treated mice first with G-CSF to mobilize MDL-1+ cells, then IFN-γ, TNF-α, IL-1β, and IL-6. When agonist MDL-1 mAb or DV was administered, all primed mice died (Supplemental Figure 2, G and H), while all cytokine-primed mice treated with isotype control mAb and primed MDL-1+ mice triggered with DV survived.

We then asked whether other forms of liver damage may also predispose mice toward MDL-1–induced shock. As shown in Supplemental Figure 3A, intraperitoneal administration of a sublethal dose of acetaminophen (APAP) caused liver injury (assessed by serum ALT levels) in a time-dependent manner (16). Similar to ConA-induced liver inflammation, we also observed a time-dependent increase in hepatic infiltration of MDL-1+ cells in response to APAP treatment, with maximal recruitment occurring at 8 hours after APAP administration (Supplemental Figure 3, B and C). However, hepatic infiltration of MDL-1+ cells was 7-fold lower in response to APAP compared with ConA treatment (Figure 1, B and C). In vivo activation of MDL-1 by administration of anti–MDL-1 mAb 8 hours after APAP treatment caused no death, while all mice died within 45 minutes with prior ConA treatment (Supplemental Figure 3D). We also measured serum G-CSF levels in APAP-treated mice and observed a 30-fold lower...
induction compared with mice receiving ConA treatment (Supplemental Figure 3E). Therefore, there appears to be a threshold of cellular infiltration that needs to be reached before MDL-1 triggering results in shock. In addition to G-CSF, APAP-treated mice also showed markedly lower serum levels of cytokines including IFN-γ, TNF-α, IL-1β, and IL-6 (Supplemental Figure 3, F-I), which we have shown to be critical for priming.

MDL-1–expressing cells are CD11b+Gr-1+ immature myeloid cells. For identification of the cell type that expressed MDL-1, infiltrating leukocytes were isolated from ConA-treated livers, enriched by CD45 microbeads, and immunophenotyped by flow cytometry. As shown in Figure 3A, 88% of the CD45+ leukocytes infiltrating the liver in response to ConA were CD11b+, and more than 95% of the CD11b+ cells were also positive for Gr-1. CD11b+ myeloid cells are CD11b+Gr-1+ immature myeloid cells.
cells were further characterized with the lineage-specific markers Ly6G (neutrophils) and Ly6C (monocytes) (17, 18). When CD11b$^+$ cells were gated for Ly6G and Ly6C expression (Figure 3A), the majority (85.3%) of these cells were Ly6G$^+$Ly6C$^{lo}$ (red ellipsoid), with two smaller cell populations that were Ly6G$^-$Ly6C$^{hi}$ (green ellipsoid) and Ly6G$^-$Ly6C$^{lo}$ (blue ellipsoid). When these three cell populations were further analyzed for MDL-1 expression (Figure 3A), the predominant Ly6G$^+$Ly6C$^{lo}$ cell population (red curve) expressed the highest levels of MDL-1, followed by the Ly6G$^-$Ly6C$^{hi}$ (green curve) and Ly6G$^-$Ly6C$^{lo}$ cells (blue curve), suggesting that the majority of the MDL-1$^+$ cells were granulocytic in nature. Of note, MDL-1 was not primarily expressed on macrophages, as the majority (61%) of these cells were CD11b$^+$F4/80$^-$ and only a small population (5%) was double positive, as shown in the red and blue boxes, respectively, in Supplemental Figure 4A. When these two cell populations were further analyzed for MDL-1 expression, they both expressed similar levels of MDL-1. In addition, the F4/80 staining on livers isolated from mice treated with ConA showed a similar prevalence of F4/80$^+$ cells across all of the ConA time points (Supplemental Figure 4B). This also suggests that the F4/80 staining detected liver residual Kupffer cells and not the infiltrating MDL-1$^+$ cells shown in Figure 1B. Furthermore, the morphology of the F4/80-stained cells with long pseudopods is consistent with macrophages/Kupffer cells and is distinct from the round morphology of MDL-1$^+$-stained cells (high-magnification image shown in the inset of Figure 1B). Taken together, our results indicated that MDL-1 is primarily expressed on granulocytic myeloid cells. When comparing the total number and the percentage of MDL-1$^+$Ly6G$^+$Ly6C$^{lo}$ cells isolated from livers of naive and ConA-treated mice, there was a 40-fold increase in the percentage (0.096% to 3.8% of leukocytes/liver) and 46-fold increase in the number (0.02 to 1.49 million/liver) of MDL-1$^+$ cells in the liver in response to ConA treatment (Figure 3B).

Cytospin was performed next to visualize the morphology of these infiltrating cells. As shown in Figure 3C, the Gr-1$^+$-enriched cell population from the livers of ConA-treated mice showed a large number of morphologically heterogeneous cells. Many of these cells were relatively large (~10 μm), with ring-shaped nuclei (indicated by arrowheads), which is consistent with immature myeloid cells (19). The number of ring cells decreased significantly in the Cytospin preparation of cells isolated from naive mice (left panel), suggesting that the hepatic infiltration of these cells is ConA-dependent. In addition to the isolated and enriched cell preparation, immature myeloid cells were also found in the native liver tissue (Figure 3D). The ring cells could be observed primarily in the sinusoid area of ConA-treated liver (as indicated by arrows), which is consistent with immature myeloid cells (19). The number of ring cells decreased significantly in the Cytospin preparation of cells isolated from naive mice (left panel), suggesting that the hepatic infiltration of these cells is ConA-dependent. In addition to the isolated and enriched cell preparation, immature myeloid cells were also found in the native liver tissue (Figure 3D). The ring cells could be observed primarily in the sinusoid area of ConA-treated liver (as indicated by arrows), which is consistent with immature myeloid cells (19). The number of ring cells decreased significantly in the Cytospin preparation of cells isolated from naive mice (left panel), suggesting that the hepatic infiltration of these cells is ConA-dependent. In addition to the isolated and enriched cell preparation, immature myeloid cells were also found in the native liver tissue (Figure 3D). The ring cells could be observed primarily in the sinusoid area of ConA-treated liver (as indicated by arrows), which is consistent with immature myeloid cells (19).
that MDL-1 is expressed primarily on immature myeloid cells. G-CSFR (or CD114) was also highly expressed on MDL-1+ cells, which is consistent with our results demonstrating the importance of G-CSF in mobilizing these MDL-1+ cells.

As shown in Figure 3E, immunofluorescence staining with anti-mouse antibodies for CD11b and MDL-1 was performed on Gr-1-enriched cells isolated from livers of naive and ConA-treated mice. When the same number of cells was examined on Cytospin preparation (as indicated by equal DAPI staining), there was markedly more nuclei staining with ring-shaped morphology in the ConA-treated cell preparation. The same cell preparation also showed increased staining for CD11b and MDL-1. Furthermore, CD11b and MDL-1 were colocalized, in particular in cells with ring-shaped nuclei, as seen by the yellow staining in the merge image. The results together identified the MDL-1+ cells infiltrating the liver in response to ConA as immature myeloid cells with ring-shaped nuclei.

**MDL-1+ immature myeloid cells are pathogenic in lethal shock.** We set out to ascertain whether the MDL-1+ immature myeloid cells are the primary pathogenic cells in our model by performing both adoptive transfer and in vivo depletion experiments. Control mice that received CD11b+ cells (~85% pure) and isotype control mAb did not show any sign of shock (Figure 4A). However, injection of anti-mouse MDL-1 mAb triggered lethal shock. Shock was depen-
CD11b+Gr-1+ cells are pathogenic in MDL-1–mediated shock. (A) CD11b+ cells were isolated from livers of ConA-treated WT or MDL-1−/− mice and injected into naive WT recipient mice via tail vein (n = 10). Anti–MDL-1 mAbs were injected 30 minutes after transfer, and survival was monitored. **P < 0.01 compared with IgGα or transfer cells from MDL-1−/− mice. (B) Mice were pretreated with anti–Gr-1 mAb (n = 5) or IgGα (n = 4) prior to administration of ConA, followed by anti–MDL-1 mAb, and survival was monitored. ***P < 0.001 compared with IgGα. (C) Liver sections from B were immunostained with anti–MDL-1 mAb, and positively stained cells were quantitated (n = 5). **P < 0.01 compared with IgGα.
In addition, Tnfa−/− mice had a markedly improved survival rate compared with age-matched controls (Figure 7B). Furthermore, we ruled out defective hepatic infiltration of MDL-1+ cells or less severe liver injury as possible mechanisms of protection seen in Tnfa−/− mice, as they displayed liver MDL-1 staining and serum ALT levels comparable to those in WT mice (data not shown).

Interestingly, the elevated serum TNF-α level seen in WT mice was completely abolished in eNOS−/− mice (Figure 7C), suggesting that eNOS is an upstream regulator of TNF-α. Since NO has been shown to activate TACE, the enzyme responsible for the cleavage of the membrane-bound precursor to release the bioactive soluble TNF-α (29), we hypothesized that eNOS-induced NO can modulate TNF-α production by regulating TACE activity. When TACE activity of liver homogenates prepared from WT and eNOS−/− mice was measured, there was a modest but significant reduction in eNOS−/− mice (Figure 7D). To further demonstrate that regulating TACE plays an important role in MDL-1–induced shock, we treated mice with the TACE inhibitor TAPI-1 immediately after ConA administration. Inhibition of TACE markedly improved the survival rate (Figure 7E), correlating with attenuated release of TNF-α in the serum (Figure 7F).

To confirm that the MDL-1–expressing immature myeloid cells play a direct role in NO and TNF-α production in response to MDL-1 stimulation, we performed intracellular staining for eNOS and confirmed that they did not express iNOS protein (Supplemental Figure 6). Taken together, these results indicated that TNF-α- and eNOS-mediated NO production by MDL-1+ immature myeloid cells induces lethal shock.
Activation of DAP12, DAP10, Syk, PI3K, and Akt is important for MDL-1–mediated shock. We set out to define the downstream signaling pathway of MDL-1 that plays a role in MDL-1–triggered shock. MDL-1 has been reported to associate with adaptor protein DAP12 to generate signals (9). As expected, DAP12-deficient animals were resistant to lethal shock induced by MDL-1 (Figure 8A). Another adaptor protein, DAP10, has recently been reported to associate with MDL-1 in osteoclasts and to modulate bone remodeling in concert with DAP12 (30). As shown in Figure 8B, DAP10−/− mice were also protected, indicating that both DAP12 and DAP10 are important for lethal shock triggered by MDL-1.

In NK cells, stimulation of DAP12 and DAP10 leads to association and activation of the downstream protein kinase Syk (31, 32) and PI3K (33), respectively. To investigate the role of these two kinases on MDL-1–induced shock, we pretreated mice with inhibitors specific for Syk (BAY 61-3606) and PI3K (wortmannin) prior to initiation of shock. Blockade of Syk or PI3K resulted in complete protection from shock compared with pretreatment with control vehicle (Figure 8, C and D). Since Akt is an immediate downstream target of PI3K and has been shown to activate eNOS by phosphorylation and activation eNOS, resulting in NO production (34), membranes were stripped and reprobed to detect phosphorylated and total Akt. Akt phosphorylation was enhanced in response to MDL-1 stimulation, with an equal amount of total Akt detected. These data also demonstrated a direct physical interaction between the Akt and eNOS activated by MDL-1. The formation of this signaling complex is independent of MDL-1 activation, as the level of total eNOS and Akt detected was similar in control and MDL-1–stimulated cells. Our results clearly define the signaling pathway downstream of MDL-1, including activation of adaptor proteins DAP12 and DAP10, as well as kinases Syk, PI3K, and Akt, as critical for MDL-1–mediated lethal shock (as modeled in Figure 9).

Discussion

Based on our observation of the recruitment of MDL-1+ leukocytes following ConA-induced liver injury and the report that DV binds and activates MDL-1 (6), we set out to delineate the cellular and molecular mechanisms underlying the progression from tissue injury/SIRS to shock. In order to specifically isolate the MDL-1–mediated effects rather than those associated with a more complex infectious process, we employed inactivated DV and, even
more specifically, an agonist anti–MDL-1 antibody, to remove the effects of DV particles binding to other known binding partners such as DC-SIGN (6, 38, 39). Thus, our experimental system does not represent a model of DV infection but instead functions to specifically address the contribution of MDL-1 signaling in the progression from liver injury to shock. Using this system, we found that ConA-induced liver injury drives a hepatic infiltration of MDL-1 immature myeloid cells of the granulocyte lineage and that triggering of MDL-1 on these cells, either by inactivated DV or an agonist antibody, results in lethal shock. An increase in circulating immature neutrophils (“left shift”) is a common component of the clinical syndrome of SIRS/sepsis. This work suggests that, in the appropriate context such as liver injury, these immature neutrophils may contribute to the pathogenesis of shock.
In our model, in the absence of ConA treatment, very few MDL-1+ cells were detected in the liver (Figure 1B) and administration of DV or agonist mAb caused no overt response (data not shown). This fact highlights the importance of ConA-induced liver injury for the recruitment of immature myeloid cells. This is in agreement with two recent studies reporting that liver inflammation induced by high-fat diet or Th1 cells may drive the accumulation of immature myeloid cells in the liver (40, 41). The precise role of these infiltrating immature myeloid cells is not clear, as they have been reported to have a proinflammatory or antiinflammatory response. Interestingly, mice treated with ConA for 4 hours showed a modest, 1.5-fold increase in serum ALT (Supplemental Figure 3A, bottom panel), suggesting that only minor liver injury is sufficient to trigger the recruitment of these immature myeloid cells.

ConA-induced hepatic injury closely resembles the pathophysiology of T cell–mediated liver diseases; it therefore has been used extensively as an animal model for autoimmune and viral hepatitis (12, 42). DV-infected mice showed significant liver damage, which also correlated with T cell activation and hepatic cellular infiltrate (43). This is concordant with clinical data showing that in general more than 80% of dengue patients had elevated serum levels of liver enzymes (ALT, AST), and the mean levels of these enzymes were significantly higher in patients with DSS as compared with DF (44). Dengue patients also displayed increased lymphocyte infiltration to the portal track (45, 46). We therefore believe that ConA-induced, T cell–mediated hepatitis is a valid model for virus-induced liver injury.

IFN-γ, TNF-α, IL-1β, IL-6, and G-CSF have previously been reported to be elevated in serum of DV-infected patients (47, 48). We found that ConA treatment also elevated serum levels of these proinflammatory molecules; and we were able to recapitulate the ConA effect by treating mice with recombinant G-CSF to recruit the MDL-1+ cells, as well as a low dose of IFN-γ, TNF-α, IL-1β, and IL-6 to prime the pathogenic cells. Subsequent triggering by DV or agonist mAb resulted in mice dying of shock, mediated primarily by MDL-1 activation and not due to cytokine priming. Therefore, results from this in vivo reconstitution experiment may provide further insight into the important role these cytokines play in the recruitment and priming of the MDL-1+ pathogenic cells during DV infection.

Given the profound sensitizing effect of ConA-induced liver injury on MDL-1–mediated shock, we asked whether this effect is unique to ConA or if liver injury in general would trigger infiltration of these immature myeloid cells and sensitize mice to shock. To address this question, we used the APAP-induced liver injury model, since APAP overdose is currently the most frequent cause of acute liver failure in both the United States and the United Kingdom (49, 50) and thus has significant clinical implications. Although APAP treatment caused both liver injury and hepatic infiltration of MDL-1+ cells in a time-dependent manner, MDL-1 stimulation at the time of maximal recruitment failed to cause death. One possible explanation is that insufficient numbers of pathogenic cells were recruited to the liver, as there were 7-fold fewer MDL-1+ cells after APAP- versus ConA-induced injury. This rela-
The number of immature leukocytes in the blood of patients during sepsis is increased, which is in agreement with clinical data showing an increased influx of pathogenic cells are immature myeloid cells/promyelocytes. The expression of MDL-1 on the surfaces of human bone marrow cells was first reported; it would be of great interest to see whether the increased TACE activity. Both NO and TNF-α are important mediators for MDL-1-mediated lethal shock.

Our observation that liver injury induced by both ConA and APAP is capable of triggering hepatic infiltration of MDL-1+ cells, albeit with different efficiencies, led us to hypothesize that the association between liver injury and development of DSS may be attributed to the recruitment of pathogenic cells. Increased numbers of immature neutrophils in the blood of DSS patients have been reported; it would be of great interest to see whether these patients also have elevated liver enzyme levels in the blood.

Based on cell surface markers and morphology (19, 57), we have identified the pathogenic cells responsible for MDL-1-mediated lethal shock as immature myeloid cells. These cells also expressed the myeloid precursor marker CD33 (20, 21) and MHC class I, but not hematopoietic stem cell/progenitor cell marker CD34 (58) or MHC class II. This unique phenotype of CD33+CD34+ MHC class I cell class II is consistent with that of promyelocytes (59–62). We also observed strong G-CSFR staining on MDL-1+ cells, which is in accordance with two previous studies reporting that G-CSFR is highly expressed on CD33+CD34+ human bone marrow cells (63, 64) and provides further evidence that the MDL-1 expressing pathogenic cells are immature myeloid cells/promyelocytes. This is in agreement with clinical data showing an increased number of immature leukocytes in the blood of patients during DSS or septic shock (55, 56) and the detection of MDL-1+ cells in the spleen of septic patients (65). In mice, CD11b+Gr-1+ immature myeloid cells are also expanded in the spleen during sepsis (66). CD11b+Gr-1+ immature myeloid cells can be further characterized, based on cell surface markers Ly6G and Ly6C, into granulocytic (CD11b+Ly6G-Ly6C+) (67, 68) and mononuclear (CD11b+Ly6G Ly6Clo) (40) populations. The immature myeloid cells expanded in our model were primarily granulocytic, and they expressed higher levels of MDL-1 than the smaller monocytic population. Interestingly, the Ly6G/Ly6C+ granulocytic subset of the CD11b+Gr-1+ cells is also the predominant population expanded in tumor-bearing mice (69).

Immature myeloid cells have been reported to be mobilized from bone marrow into peripheral blood primarily by G-CSF (70–74), which corroborates our finding that G-CSF, but not GM-CSF, KC, MIP-2, or MCP-1, acts as a critical proinflammatory molecule in MDL-1–induced shock by promoting the mobilization (and possibly the generation, egression, and maturation) of the pathogenic cells to the liver. In addition to the liver, these ring cells are also found in peripheral blood in response to ConA treatment (Supplementary Figure 7A), supporting the notion that immature myeloid cells egress from the bone marrow into the circulatory system in response to inflammation. We also asked whether MDL-1 itself is involved in myeloid cell migration by comparing the number of ring cells in WT and MDL-1−/− mice treated with ConA. We observed similar ConA-induced migration of immature myeloid cells, in both Cyto spin preparation and IHC staining, between WT and MDL-1−/− mice (Supplementary Figure 7, A–D). Therefore, we concluded that ConA drives the recruitment of immature myeloid cells independent of MDL-1 and that the protection demonstrated in MDL-1−/− mice is not due to impaired hepatic migration of the pathogenic cells.

Overproduction of NO is known to be an important factor in the pathogenesis of shock of various etiologies in humans. Compared with healthy individuals, patients with septic or anaphylactic shock have an elevated NO level in blood or exhaled air, respectively (75, 76). In addition, DSS patients have significantly higher serum NO than patients with DHF (77). It is generally believed that during the early stage of shock, there is a transient release of low levels (nanomoles) of NO produced by eNOS, which is constitutively expressed primarily in endothelial cells and is activated by an increase in intracellular calcium. This is followed by sustained local production of a large quantity (micromoles) of NO via calcium-independent iNOS gene induction in immune cells, including macrophages, in response to immunological stimuli such as inflammatory cytokine production. The iNOS-mediated overproduction of NO is assumed to be responsible for the cardiovascular failure and mortality associated with different kinds of shock. However, results from our study clearly indicated that eNOS is the primary enzyme responsible for lethal shock triggered by MDL-1 and the associated increase in serum NO. This may seem surprising, although it is not without precedent: our results are consistent with a recent study showing the exclusive role eNOS plays in anaphylactic shock (78), as well as two reports implicating constitutive eNOS in septic and hemorrhagic shock (79, 80).

Although eNOS has originally been thought to be expressed primarily in endothelial cells, increasing evidence is revealing a much broader expression spectrum in leukocytes than previously thought. eNOS is also expressed in both mouse and human neutrophils, monocytes, and macrophages, as well as in human immature myeloid cells (81–87). In the mouse model, on the other...
hand, the production of NO by CD11b+Gr-1+ immature myeloid cells has only been reported to be mediated by iNOS (67, 88). Our study is the first to our knowledge to identify a unique population of NO-producing murine immature myeloid cells expressing only eNOS, as we demonstrated that these cells are iNOS- and that ConA treatment induces a time-dependent upregulation of eNOS mRNA in the liver, whereas iNOS transcript is undetectable (data not shown). The predominant role of eNOS in immature myeloid cells that we report is in agreement with a recent publication showing high eNOS expression in immature rat neutrophils, which is downregulated with maturation (89). Our results showing that these eNOS-expressing immature myeloid cells are also MDL-1- and are capable of producing NO with MDL-1 stimulation in vitro suggest a one-cell model scenario. The pathogenicity conferred by passive transfer and the protection achieved after in vivo depletion further highlight the importance of these cells. However, at this point we cannot eliminate the possibility of a two-cell model in which MDL-1–activated immature myeloid cells produce intermediate mediator(s) to stimulate endothelial cells to generate NO.

TNF-α has also been implicated as a crucial mediator for shock of different etiologies. In clinical data, elevated TNF-α levels were reported in blood of patients with septic, hemorrhagic, and anaphylactic shock (90–92). High levels of TNF-α were also observed in sera of all patients with dengue infection, with the highest values found in patients with DSS (93). Furthermore, the elevation of TNF-α in the serum has been reported to be strongly associated with clinical disease progression from DF to DSS (94, 95). Furthermore, anti–TNF-α antibody has been reported to be an effective treatment to reduce mortality associated with DV infection (96). Previously, macrophages were reported to be the primary cell type expressing MDL-1 that DV interacts with to trigger TNF-α release (6). The present study identifies immature myeloid cells as another MDL-1–expressing cell capable of releasing the inflammatory cytokine TNF-α in response to DV stimulation and playing a crucial role in DV-mediated pathobiology. Future studies measuring MDL-1 expression on the immature neutrophils that are increased in the blood of patients with DSS or septic shock, and the ability of these cells to produce TNF-α in response to MDL-1 stimuli, are expected to further establish the clinical relevance of these cells in shock. Our results showing that MDL-1+ cells expressed both eNOS and TNF-α led us to investigate the cross-regulation of these two mediators. In our MDL-1–mediated pathway, eNOS is upstream of TNF-α and is able to regulate TNF-α production by modulating TACE activity. This result fits into the paradigm of a previous study showing that NO activates TACE by nitrosation of the inhibitory cysteine switch motif in the TACE prodomain and cleaving the membrane-bound TNF-α (29). In addition to binding its cognate receptor to induce an inflammatory response, TNF-α can activate eNOS activity via an Akt-dependent pathway to initiate an amplification process (97, 98). TNF-α is also able to terminate or dampen the signal by downregulating eNOS mRNA by shortening its half-life as a negative feedback mechanism (99). Although the hypothesis has not been proven, it is likely that this complex network of interplay between NO and TNF-α is part of the MDL-1–mediated pathway to fine-tune the biological response.

In addition to NO and TNF-α, we also observed elevated levels of multiple cytokines (IFN-γ, IL-1β, IL-6, IL-10, MCP-1, MIP-1α, and IP-10) in the serum of mice that died of MDL-1–mediated shock (Supplemental Figure 8). This is in accordance with the results of 6 separate dengue patient studies done in Brazil, Cuba, India, Singapore, Thailand, and Vietnam that all showed increases in IFN-γ, IL-1β, IL-6, IL-10, MCP-1, MIP-1α, and IP-10 in the serum (48, 100–104). These data support the idea that a “cytokine storm” is involved in the pathogenesis of DSS (105). It also demonstrates that our MDL-1–mediated shock model resembles the cytokine profile observed in DV-induced human disease. However, the contribution of each individual cytokine or chemokine to the pathogenesis of DSS, and the role MDL-1 plays in modulating these mediators, are well beyond the scope of this study but will warrant separate detailed investigation in the future.

The MDL-1–mediated signaling pathway is not clearly defined. Current understanding of signaling events downstream of DAP12 and DAP10 are primarily based on in vitro data obtained by triggering of receptor TREM-1 and NKG2D, respectively (106, 107). Therefore, we decided to use both genetic knockout mice and biochemical inhibitors to interfere with the signaling pathways in vivo to identify the MDL-1–specific downstream signaling events that are relevant to this disease model. Our results strongly indicated that activation of both adaptor protein DAP12 and DAP10, as well as the protein kinase Syk, PI3K, and Akt, are critical for MDL-1–induced shock. Our results showing an absolute requirement for both DAP10 and DAP12 signaling is somewhat surprising, given that previous studies in NK cells have demonstrated at least partial redundancy between these two adaptor molecules (108, 109). However, it appears that the relative contribution of the two adaptor molecules to the downstream function is highly dependent on the examined receptor and cellular function. This requirement for signals generated from both adaptor molecules may also indicate that a critical “threshold” of signal, possibly at the level of PI3K (110), has to be reached to trigger shock. This hypothesis is supported by a recent study showing that both DAP10 and DAP12 are required for maximal TREM2-stimulated PI3K activity, with DAP10 mediating the recruitment of PI3K to DAP12 and the activation of downstream kinase Akt (111). In our model of MDL-1–induced shock, DAP10 may be similarly responsible for amplifying DAP12-mediated PI3K activation, leading to a pathogenic activation of the downstream Akt/eNOS signaling response.

This is the first report to our knowledge to establish eNOS as a target of MDL-1, the triggering of this receptor resulting in eNOS activation and NO release, which in turn modulates another downstream cytokine, TNF-α. It has been suggested that an increase in intracellular calcium alone is not sufficient to affect the enzymatic activity of eNOS and that protein phosphorylation is also critical in regulating eNOS function (112). Since Akt-mediated eNOS phosphorylation has been shown to play an important role in anaphylactic shock (78), we asked whether activation of MDL-1 can stimulate Akt to phosphorylate eNOS. Our results indicated that (a) triggering of MDL-1 results in phosphorylation of Akt and eNOS, (b) transduction of MDL-1 signal requires physical interaction between the two proteins to form a signaling complex, and (c) complex formation is independent of MDL-1 activation. In endothelial cells, HSP90 has been suggested to function as a scaffold to facilitate the proximity of and association between Akt and eNOS (113–116). As it is likely that such a scaffolding protein is involved in MDL-1–mediated signal transduction in immature myeloid cells, this should be further investigated.

The mortality rate for shock is high, with statistics associated with septic shock and DSS approximately 50% and 44%, respectively (117, 118). Volume replacement therapy is considered the only effective treatment to restore circulation. Several other treatment options...
have been tested and found not to be effective. Two clinical trials have been conducted using anti–TNF-α mAb for the treatment of septic shock, but the results were inconclusive, as one study showed reduced mortality, while the subsequent trial revealed no significant improvement in survival (119, 120). Another clinical trial using NOS inhibitor monomethyl-L-arginine (L-NMMA) treatment for septic shock patients showed improved resolution of shock with reduction in serum NO levels and increased vascular tone (121, 122). Despite a positive outcome on blood pressure, a phase III clinical trial had to be prematurely terminated due to increased mortality (123). Given the prominent role eNOS played in anaphylactic shock and the newfound importance of this enzyme in shock triggered by MDL-1 revealed by our study, it is plausible that a selective eNOS inhibitor could be used as a new therapy. TACE inhibitor is currently being tested in a clinical trial for the treatment of rheumatoid arthritis (124). Our results showing that TAPI-1 treatment significantly prolongs the survival of MDL-1–triggered shock suggest the prospect of using TACE inhibitor as an alternative treatment for shock. Furthermore, our study indicates the crucial role that the PI3K/Akt pathway plays in lethal shock mediated by MDL-1, suggesting the application of PI3K/Akt inhibitors for DSS patients, in addition to their use in anticancer therapy (125).

Our study suggests that this mechanism may play an important role in the progression from tissue injury/SIRS to shock in a variety of clinical settings where mobilization of immature granulocytic myeloid cells occurs, especially in the case of dengue infection, where progression to DSS has been associated with ongoing liver damage and the viral particle itself has been shown to activate MDL-1. Given that inhibitors of many components of this signaling pathway (MDL-1, Syk, PI3K, and Akt) are being developed as potential drugs in other therapeutic areas, it will be interesting to assess whether this mechanism contributes to the progression to shock in patients and whether inhibition of this pathway has therapeutic value.

**Methods**

Mouse. C57BL/6, eNOS−/−, iNOS−/−, and CCR2−/− mice were purchased from The Jackson Laboratory. MDL-1−/− (10), DAP12−/− (126), DAP10−/− (127), and Nfla−/− (128) mice were generated in-house. All knockout mice used were in a C57BL/6 background, and data were collected using female mice 6–10 weeks of age.

**Reagents.** ConA (Sigma-Aldrich) was diluted in saline and injected i.v. at a dose of 5 mg/kg. Rat anti–mouse MDL-1 agonist mAb (clone DX163, IgG2a, in-house) (10) or inactivated DV (type 2, Microbix) was injected i.p. at 0.5 mg/mouse 4 hours after ConA. BAY 61-3606 (EMD Chemicals Inc., 10 mg/kg in 10% DMSO), wortmannin (Sigma-Aldrich, 1.5 mg/kg in 1.5% DMSO), MK-2206 (Selleck Chemicals, 12.5 mg/kg in 5% DMSO), carboxy-PTIO (Tocris, 0.6 mg/kg in saline), L-NAME (EMD Chemicals, 30 mg/kg in saline), or L-NIO (Tocris, 20 mg/kg in saline) was administered i.p. at 1 hour before anti–MDL-1 mAb. TAPI-1 (EMD Chemicals Inc., 75 mg/kg in DMSO) was injected i.p. immediately after ConA. Survival was monitored up to 2 hours after anti–MDL-1 mAb or 24 hours after DV challenge.

APAP (Sigma-Aldrich) was diluted in PBS and injected i.p. at a dose of 500 mg/kg (16). Carrier- and endotoxin-free recombinant mouse cytokines were purchased from R&D Systems and diluted in sterile saline solution. G-CSF was injected i.v. at a dose of 4 μg/mouse 2.5 hours prior to MDL-1 activation. IFN-γ, TNF-α, IL-1β, and IL-6 were injected i.p. at doses of 50, 10, 2.5, and 0.5 μg/mouse, respectively, 0.5 hours after G-CSF administration.

In vivo and ex vivo bioluminescence imaging. To localize infiltration target of the inflamed cells, mice with shaved abdomen were anesthetized with isoflurane, injected i.p. with Xenolight Redject Inflammation Probe (Caliper Life Sciences) at 200 mg/kg 4 hours after ConA, and immediately imaged in an IVIS 200 Imaging System (Xenogen Corp.) for 5 minutes. Images were captured and analyzed with Living Image software version 2.6.2. Livers were removed from mice, incubated in inflammation probe for 1 minute, and imaged under the same conditions.

Quantitation of chemokines in mouse serum and livers. Blood and livers were isolated from mice treated with ConA for the indicated times. Serum was isolated from blood by centrifugation. Livers were weighed, homogenized in ice-cold PBS supplemented with protease inhibitor cocktail, and centrifuged at 14,000 g for 15 minutes at 4 °C. The supernatants were removed and kept at −80°C until use. Chemokines (G-CSF, GM-CSF, KC, and MIP-2) in serum and liver homogenates were quantified by using a custom Milliplex Mouse Cytokine/Chemokine Immunoassay Kit (Millipore) according to the manufacturer’s instructions. Data were acquired on a LumineX 100 System and analyzed by MasterPlex CT version 12.0.7 software (MiraBio).

In vivo depletion of chemokines, cytokines, and cells. Rat anti–mouse neutralizing mAbs for G-CSF (clone 67604, IgG1) or GM-CSF (clone MP122E9, IgG2a) were injected i.p. at doses of 0.25 mg/mouse 3 or 2.5 hours, respectively, prior to ConA treatment. Rat anti-mouse neutralizing mAbs for KC (clone 48B15, IgG2a) or MIP-2 (clone MAB452, IgG2a) were injected i.p. at doses of 0.05 mg/mouse 1 hour prior to ConA treatment. All neutralizing mAbs were from R&D Systems. Rat anti–mouse TNF-α neutralizing mAb (clone MP6-XT22, IgG1, in-house) (129) was administered i.p. at doses of 0.5 mg/mouse 1 hour prior to ConA treatment. Rat anti–mouse Gr-1 mAb (clone RB6-8C5, IgG2a, in-house) (130) was injected i.p. at doses of 0.1 mg/mouse 24 hours prior to ConA treatment. All rat isotype controls (IgG1 and IgG2a) were generated in-house. Peripheral blood from mice was collected by tail bleed and analyzed on an Advia 120 hematology system (Bayer Corp.). Immunohistochemistry. Livers were harvested immediately after death and either fixed in 10% parafformaldehyde, then embedded in paraffin, or snap-frozen in OCT. Consecutive sections of 5-μm thickness were cut and stained with H&E.

**Precision-cut liver slice preparation and culture.** Livers were isolated from ConA-treated WT or MDL-1−/− mice, 8-mm-diameter cores were obtained, and 250-μm-thick tissue slices were precision cut using a Brendel/Vitron tissue slicer (Vitron Inc.). Slices were incubated in oxygenated Aqix RS-1 solution supplemented with 2% FBS for 30 minutes before stimulation with anti–mouse MDL-1 agonist mAb, isotype control mAb, or DV at a final concentration of 10 μg/ml for the indicated time.

Cell isolation, flow cytometry, cytospin, cell culture, and adoptive transfer. Livers were removed from mice and cells were dissociated by gentleMACS Dissociator (Miltenyi Biotec) according to the manufacturer’s protocol. CD45+ or CD11b+ cells populations were enriched from mononuclear cells by antibody-conjugated microbeads, based on the manufacturer’s instructions, and isolated cells were counted by a ViCell XR Analyzer (Beckman Coulter). For immunophenotyping, cells were labeled with fluorescent-conjugated rat anti–mouse CD45 (clone 30-F11, IgG2a, eBioscience), CD11b (clone M1/70, IgG2b, eBioscience), Gr-1 (clone RB6-8C5, IgG2b, eBioscience), Ly6G (clone IA8, IgG2a, BD Biosciences), Ly6C (clone AL-2L, IgM, BD Biosciences), TNF-α (clone MP6-XT22, IgG1, eBioscience), F4/80 (clone BM8, IgG2b, eBioscience), MDL-1 (clone DX192, IgG1, in-house) mAbs, rabbit anti-human/mouse eNOS or iNOS (IgG, Santa Cruz Biotechnology Inc.) polyclonal Abs. For immunophenotyping of immature myeloid cells, cells were labeled with fluorescent-conjugated mouse anti–mouse MHC class I (H-2Kb) (clone AF6-88.5.3.5, IgG2a, eBioscience), MHC class II (I-Ab) (clone AF6-120.1, IgG2a, eBioscience), rat anti-mouse CD34 (clone RAM34, IgG2a, BD Biosciences) mAbs, goat anti–mouse CD3 or rabbit anti–mouse G-CSFR (IgG, Santa Cruz Biotechnology Inc.) polyclonal Ab. For intracellular staining, cells were fixed (Cytofix, BD Biosciences — Pharmingen) and permeabilized (PhosFlow Perm III, BD Biosciences — Pharmingen) prior to staining. Data were acquired on a FACSCan II flow cytometer (BD Biosciences) and analyzed by FlowJo version 7.6.1 software (TreeStar Inc.).
The isolated cells were assessed morphologically on Cytospin slide preparations stained with Diff-Quik (Siemens Healthcare Diagnostics Inc.) according to the product instructions and visualized using an upright light transmission microscope (Olympus BX51) at ×40 to ×100 magnification. Representative images were captured using a QImaging Retiga-2000R camera and analyzed with QCapture Pro 6.0 software (QImaging).

For immunocytochemistry, cells on Cytospin slides were stained with fluorescent-conjugated rat anti-mouse CD11b and MDL-1 mAbs and visualized with a Leica DM-RE fluorescence microscope at ×60 magnification. Representative images were captured with a Photometrics Cool-SNAP HQ camera (Roper Scientific) and analyzed using Image-Pro Plus 6.0 software (Media Cybernetics).

CD11b+ cells were resuspended in phenol red–free DMEM supplemented with 2% FBS and plated in 96-well plates at a density of 1 × 10^5 cells/100 μl in triplicate or quadruplicate. The following day, cells were stimulated for 24 hours with anti–mouse MDL-1 agonist mAb, isotype control mAb, or DV at a final concentration of 10 μg/ml. Cell culture media were collected and stored at −80°C for determination of NO and TNF-α levels.

For adoptive transfer, CD11b+ cells were washed, resuspended in PBS, and injected i.v. at 15 × 10^5 cells/mouse. Anti–mouse MDL-1 agonist mAb or isotype control mAb was injected i.p. at 0.5 mg/mouse 0.5 hours after transfer, and survival was monitored up to 16 hours after stimulation. Tissues and blood were collected immediately after death for IHC staining and for NO and TNF-α determination, respectively.

ELISA, Griess assay, and TACE activity assay. Conditioned media from liver slices or cell culture were collected at indicated times and spun at 10,000 g for 5 minutes to remove debris. G-CSF, TNF-α, and NO levels in serum or culture media were measured by mouse G-CSF, TNF-α ELISA (Invitrogen), and Total Nitric Oxide Assay Kit (Pierce), respectively. Absorbance was measured using a Spectramax Plus 384 plate reader (Molecular Devices). TACE activity in liver homogenates was quantitated using a fluorometric assay with a SensoLyte 520 TACE Activity Assay Kit (AnaSpec Inc.) according to the manufacturer’s instructions. The fluorescence intensity was measured in black micro-plates with a Modulus Microplate MultiMode Reader (Turner BioSystems).

Quantitation of ALT, chemokines, and cytokines in mouse serum. Blood was isolated from mice treated with APAP or ConA for the indicated times, or from WT and MDL-1−/− mice treated with ConA and triggered with anti–MDL-1 mAb. Serum was isolated from blood by centrifugation. Serum ALT levels was measured by the Stanford University Diagnostic Laboratory. TNF-α, IFN-γ, IL-1b, IL-6, IL-10, MCP-1, IP-10, and MIP-1α in serum were quantified by using Milliplex Mouse Cytokine/Chemokine Immunoassay Kit (Millipore).

Immunoprecipitation and immunoblot analysis. CD11b+ cells were stimulated for 15 minutes with anti–mouse MDL-1 agonist mAb or isotype control mAb at a final concentration of 10 μg/ml and solubilized in RIPA buffer containing protease and phosphatase inhibitors. Cell lysates (400 μg) were incubated with 7.5 μg anti-eNOS mAb (clone 3, IgG, BD Transduction Laboratories) for 3 hours at 4°C. Protein A/G beads were added and incubated overnight. Immunoprecipitates were washed three times with lysis buffer and boiled in Laemmli buffer. Cell lysates (50 μg) were also boiled in sample buffer. Proteins were resolved by 4–12% Bis-Tris NuPage gel and transferred to PVDF membranes. Conditions for blocking, washing, and dilution were based on instructions from antibody providers. To detect phosphorylation of eNOS and Akt, membranes were blocked with Tris-buffered saline with Tween 20 plus 5% BSA and incubated at 4°C overnight with rabbit mAb for anti–phospho-eNOS (Ser1177) (clone C03C1 1:1,000, Cell Signaling Technology) or anti–phospho-Akt (Ser473) (clone D9E, 1:2,000, Cell Signaling Technology), respectively, followed by incubation with HRP-conjugated anti-rabbit secondary antibody for 1 hour. The signal was detected with ECL (GE Healthcare) and autoradiographic films. Membranes were stripped with Restore Western Blot Stripping Buffer (Pierce) and reprobed with rabbit polyclonal Ab for anti-eNOS (1:1,000, BD Biosciences) or anti-Akt (1:1,000, Cell Signaling Technology).

Statistics. Data are presented as mean ± SEM. Statistical analysis was performed using Prism version 4.0 (GraphPad Software). Statistical significance was determined by 2-tailed Student’s t test for comparison of means and log-rank test to compare survival curves. P values less than 0.05 were considered statistically significant. Study approval. All animal procedures were approved by the IACUC of Merck.

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