Immune Unresponsiveness to Secondary Heterologous Bacterial Infection after Sepsis Induction Is TRAIL Dependent

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Sepsis is the leading cause of death in intensive care unit patients, taking >215,000 lives per year in the United States (1), and is classically defined as the body’s massive hyperinflammatory response to systemic infection. Not surprisingly, the majority of early studies on sepsis in humans and experimental animals focused on understanding the early hyperinflammatory phase, which is characterized by the increased production of a number of proinflammatory cytokines, including IFN-γ, IL-1β, IL-6, and TNF (2–4), and other proinflammatory mediators, such as HMGB1, MIF, TREM-1, and MRPS8/14 (5–9). Although the neutralization of IL-1β, TNF, or HMGB1 improved survival of septic mice and baboons (10–14), similar clinical attempts designed to neutralize IL-1β and/or TNF in septic patients failed to improve survival (15). Other anti-inflammatory–based therapeutic trials, such as antiendotoxin, steroids, anti–platelet-activating factor, also failed to produce a positive effect on the pathogenesis of sepsis (12, 15, 16).

The inability to decrease sepsis-induced mortality by dampening the hyperinflammation led many to question the idea that the early, massive inflammation in sepsis was the sole cause of mortality. It has since been shown that the initial hyperinflammation during sepsis is followed by a prolonged immunosuppressive phase that significantly increases morbidity and the chance of mortality caused by secondary (often nosocomial) infections (17). The increased susceptibility to secondary infection can be attributed to many things, but one hallmark of sepsis is the widespread apoptotic death of immune cells that provide protection. Adoptive transfer of apoptotic cells during sepsis increases mortality (18), whereas prevention of lymphocyte cell death using pharmaceutical agents (such as zVAD) or modified expression of pro- or antiapoptotic proteins (such as Bim−/− or Bcl-2 overexpressing mice) improves survival following sepsis (19–21). It is important to keep in mind that the sepsis-induced lymphopenia is not the only means by which the immune system is altered, because the function of the remaining immune cells is also significantly decreased. Using the well-defined cecal-ligation and puncture (CLP) mouse model (19, 20, 22), we recently found a clear relationship between sepsis-induced immune cell apoptosis and the ability to mount delayed-type hypersensitivity (DTH) (23). Moreover, this previous study showed that the lack of DTH responses during sepsis was dependent on TRAIL–mediated active immune suppression. Thus, the sepsis-induced hypoimmunological phase is likely the result of multiple mechanisms that together lead to the compromised overall health of the septic individual.

The present study continues our analysis of the role of TRAIL–mediated immune suppression during sepsis by modifying the CLP model to include a secondary (heterologous) bacterial infection with the Gram-positive, facultative intracellular bacterium Listeria
Bacterial preparation, infection, and titer

The attenuated L. monocytogenes strains DP-L1942 (attenuated L. monocytogenes) and OVA357-expressing (attenuated LM-OVA), which are ActA deficient, were grown, injected i.v., and quantified as previously described (35). Briefly, the bacteria were grown to log phase (OD600 0.06–0.1) in tryptic soy broth media. Bacteria were diluted to 10^7 CFU in 0.2 ml sterile PBS with 2% paraformaldehyde in PBS. mAbs used for surface staining were injected bacteria. Spleens and livers were harvested from infected mice on day 3 postinfection and homogenized in 0.2% IGEPA L buffer (Sigma-Aldrich, St. Louis, MO). The homogenized suspension was incubated at room temperature for 30 min, and serial dilutions were plated in streptomycin agar plates. Plates were cultured overnight at 37°C, and bacterial counts were determined.

Flow cytometry

For staining of surface markers, cells were incubated with fluorochrome-conjugated mAbs at 4°C for 30 min. The cells were then washed with FACS buffer (PBS containing 2% BCS and 0.2% NaN₃) and then fixed with 2% paraformaldehyde in PBS. mAbs used for surface staining were FITC-CD11a (clone M17/4; BioLegend), PerCP- or allophycocyanin-CD8 (clone 53-6.7; Biolegend), PE- or PerCP/Cy5.5-CD3 (clone 17A2 for PE and clone 145-C211 for PerCP/Cy5.5; BioLegend), PerCP- or allophycocyanin-CD4 (clone GK1.5; BioLegend), and PE-CD19 (clone 6D5; BioLegend).

For intracellular staining, 10^6 splenocytes were cultured at 37°C in the presence of OVA257 and brefeldin A (BD Biosciences) for 6 h. The cells were then washed and stained for surface markers as described above. The cells were then washed once with FACS buffer and fixed with 2% paraformaldehyde in PBS for 20 min at room temperature. After fixing, cells were washed and resuspended in saponin buffer at 30 min at 4°C. PE- or allophycocyanin–IFN-γ (clone XMG1.2; BioLegend) was added to the cells and incubated for 20 min. Cells were washed and resuspended in FACS buffer and analyzed using a Becton Dickinson FACS Calibur (BD Biosciences).

Statistical analysis

Significant differences between two groups were evaluated using a two-tailed Student t test (p < 0.05). When more than two groups were compared, one-way ANOVA with a Dunnett’s posttest was used (p < 0.05). All statistical tests were performed using GraphPad Prism 5 for Mac OS X (GraphPad, La Jolla, CA).
relevant animal models of sepsis (36, 37), and it has been suggested that this immune suppression is critical to the pathogenesis and subsequent morbidity and mortality in septic patients that acquire secondary infections. Thus, the current study examined the impact of sepsis-induced immunosuppression on the naive CD8 T cell response to the Gram-positive, facultative intracellular bacterium *L. monocytogenes*. Our version of the CLP model of sepsis involves ligation of the distal third of the cecum and a single puncture to permit release of the cecal contents into the peritoneum. This level of injury reproducibly resulted in the development of many clinical symptoms of sepsis, including a significant loss of weight compared with sham-treated wild-type (WT) B6 mice (Fig. 1A). Importantly, these CLP-treated mice regained all of the lost weight by 7 d after surgery. When we added the secondary infection with attenuated LM-OVA, the sham or untreated WT B6 mice displayed minimal morbidity (as measured by weight loss; Fig. 1B) and were able to control the LM-OVA infection (Fig. 1C). In contrast, CLP-treated WT B6 mice that received the subsequent attenuated LM-OVA infection demonstrated sustained weight loss compared with sham-treated mice that was not regained, and these mice were less able to control the attenuated LM-OVA infection (50- and 1400-fold increase in bacterial titer in the spleen and liver, respectively, compared with untreated or sham-treated mice). These results suggest that the induction of sepsis compromises overall health such that even a secondary heterologous infection with an attenuated bacterial strain cannot be adequately controlled.

Sepsis induces widespread immune cell apoptosis, and, consistent with previous studies (23), we observed a significant reduction in the number of CD8 T cells in WT B6 mice 2 d post-CLP compared with sham-treated mice (Fig. 2A). Similar significant reductions were also seen for CD3+CD4+, CD11c+, and CD19+ cells (Supplemental Fig. 1). We then specifically examined the primary CD8 T cell response 7 d after attenuated LM-OVA infection and found a significant decrease in total number of Ag-experienced [based on CD11a upregulation (38); Fig. 2B] and OVA257-specific CD8 T cells (based on IFN-γ production after in vitro OVA257 restimulation; Fig. 2C, 2D) in the spleens of CLP-treated WT B6 mice compared with sham-treated mice. Because CD8 T cells are essential for the control of many bacterial infections, including *L. monocytogenes*, we have concentrated our analyses on the Ag-specific CD8 T cell response in sham and CLP-treated mice. However, a vigorous Ag-specific CD4 T cell response is generated in B6 mice to residues 190–201 of the *L. monocytogenes* protein listeriolysin O190–201 presented on I-Ab (39, 40). Much like that for the Ag-specific CD8 T cell response, there was a significant decrease in number of listeriolysin O190-201-specific CD4 T cells in the spleens of LM-OVA–infected, CLP-treated WT B6 mice compared with sham-treated WT B6 mice.
(Supplemental Fig. 2). Together, these data suggest that sepsis significantly decreases the ability of WT B6 mice to control an attenuated LM-OVA infection and generate pathogen-specific T cell responses.

CLP-treated Trail−/− or Dr5−/− mice retain the ability to control a secondary L. monocytogenes infection and mount CD8 T cell immunity

We recently showed that sepsis-induced apoptosis resulted in the TRAIL-dependent suppression of DTH (23). To determine the extent to which the TRAIL-dependent immune suppression contributed to the sepsis-induced morbidity and inability to control the secondary L. monocytogenes infection, we first examined weight loss in sham- and CLP-treated WT, Trail−/−, and Dr5−/− B6 mice given a secondary infection with attenuated LM-OVA. As in Fig. 1, CLP-treated WT B6 mice showed sustained weight loss compared with sham-treated mice and were unable to control the attenuated LM-OVA infection as well as sham-treated mice (2200-fold increase in L. monocytogenes CFU in the spleen of CLP-treated mice; Fig. 3A, 3D). By comparison, the CLP-treated Trail−/− and Dr5−/− B6 mice were able to recover their body weight back to that of the sham-treated mice (Fig. 3B, 3C) postinfection. Moreover, the splenic LM-OVA burden in CLP-treated Trail−/− and Dr5−/− B6 mice was only slightly increased over sham-treated Trail−/− and Dr5−/− B6 mice (∼7- and 10-fold, respectively; Fig. 3E, 3F). Data presented in our previous report showed sepsis-induced lymphopenia was TRAIL independent (23), and similar findings were seen in the current study (Fig. 4A). However, there was no decrease in the total number of Ag-experienced CD11ahi (38) or OVA257-specific CD8 T cells in the spleens of CLP-treated Trail−/− and Dr5−/− mice compared with sham-treated mice (Fig. 4B, 4C). Thus, these data suggest that sepsis-induced alterations in morbidity, bacterial control, and CD8 T cell responses following a secondary infection with attenuated LM-OVA require an intact TRAIL/DR5 signaling pathway.

To investigate the extent to which the TRAIL-dependent decrease in ability to control a secondary bacterial infection after sepsis was mouse strain sensitive, we examined the ability of sham- and CLP-treated WT and Trail−/− BALB/c mice to control the secondary L. monocytogenes infection. There was no reduction of CD8 and CD4 T cells in CLP-treated WT and Trail−/− BALB/c mice compared with the sham-treated mice (Fig. 5A). Moreover, the CLP-treated WT BALB/c mice had increased splenic LM-OVA titers compared with sham-treated mice, but there were nearly identical LM-OVA titers in the spleens of the sham- and CLP-treated BALB/c Trail−/− CLP mice (Fig. 5B). Thus, these data suggest that there is no strain specificity for the observed TRAIL-dependent alterations in the ability to control a secondary bacterial infection during sepsis.

**Therapeutic use of a blocking anti-TRAIL mAb in septic mice decreases weight loss, improves the control of secondary bacterial infection, and restores CD8 T cell responses**

The data presented thus far suggest that an intact TRAIL/DR5 pathway correlates with increased morbidity, reduced control of a secondary bacterial infection, and decreased CD8 T cell response in CLP-treated mice. Because the genetic elimination of either TRAIL or DR5 in CLP-treated mice resulted in them behaving similar to sham-treated mice, we determined the extent to which the response of CLP-treated mice to secondary L. monocytogenes infection could be improved through the therapeutic disruption of the TRAIL/DR5 pathway. Thus, CLP-treated WT B6 mice were treated with a blocking anti-TRAIL mAb after the induction of sepsis, but before LM-OVA infection (Fig. 6). Using this approach, the anti-TRAIL mAb-treated mice lost more weight compared with the sham-treated mice, but not as much as the CLP-treated mice (Fig. 6A). However, there was a dramatic reduction in the splenic bacterial burden in the anti-TRAIL mAb-treated mice compared with the CLP-treated mice that did not receive the anti-TRIAL mAb (Fig. 6B). Similarly, the CD8 T cell response was restored in the anti-TRAIL mAb-treated mice (Fig. 6C, 6D). The magnitude of the Ag-specific CD8 T cell response in CLP-treated mice was similar to that seen in CLP-treated mice given an isotype control IgG (data not shown), which is consistent with other reports describing the in vivo use of the anti-TRAIL blocking mAb N2B2 and isotype control Ab 41–43. Together, these results suggest that mAb-mediated disruption of the TRAIL/DR5 pathway had a therapeutic benefit in the septic mice with regard to morbidity, bacterial control, and the CD8 T cell response after a secondary bacterial infection.

**Discussion**

Sepsis induces widespread immune cell apoptosis that is required for the subsequent immune suppression (23). Consequently, septic patients and animals become very susceptible to subsequent infection that can often result in death (44). In the current study, we used a modified version of the clinically relevant CLP sepsis...
model to include a secondary heterologous bacterial infection to study the role of TRAIL in sepsis-induced alterations in bacterial clearance and CD8 T cell immunity. Our results provide further evidence to suggest that TRAIL is a key molecular component in the establishment of sepsis-induced immune suppression. In this particular case, sepsis induced TRAIL-dependent immune suppression that limited the host’s ability to control a secondary bacterial infection and reduced the bacterial Ag-specific CD8 T cell response. Our data also suggest that TRAIL may be a potential therapeutic target during sepsis, because neutralization of TRAIL in septic mice restored the ability of these mice to clear the bacterial infection and mount a normal bacterial Ag-specific CD8 T cell response.

The CLP mouse model is considered the gold standard of sepsis models because it reproduces the pathophysiology of polymicrobial sepsis and intra-abdominal peritonitis seen in humans (34). Early after CLP, mice show many of the symptoms of sepsis that are seen in septic humans, such as hypothermia, tachycardia, and proinflammatory cytokine production. Depending on the severity of the sepsis induced (and the experimental interest of the investigator), death may occur within the first 48 h, or the mice will survive and develop immune suppression. This flexibility in disease severity and ability to study acute or chronic sepsis is simultaneously one of the biggest advantages and disadvantages of the CLP model. We reproducibly have a >95% animal survival rate in CLP-treated mice, which is similar to that reported by others examining the chronic effects of sepsis on the responsiveness of the immune system. A number of reports have combined secondary infection with CLP, and it is clear that sepsis alters the immune response to the infectious pathogen in the preclinical models much like that seen in the clinical situation. For example, CLP-treated mice are highly susceptible to pulmonary Pseudomonas aeruginosa infection and demonstrate increased mortality compared with sham-treated mice (2, 45, 46). One weakness in using P. aeruginosa as the secondary infections agent is that specific T cell responses are not as easily followed as they are when L. monocytogenes is used. The vast amount of information gathered over recent years regarding the T cell response to L. monocytogenes is one reason why we chose to use this bacterial pathogen in our system. L. monocytogenes normally induces a robust CD8 T cell response (25), so the observation that CLP-treated WT mice had a reduced ability to control a secondary attenuated L. monocytogenes infection and reduced CD8 T cell responses compared with sham-treated WT mice or CLP-treated Trail−/− or Dr5−/− mice was very intriguing. Interestingly, a recent report by Delano et al. (46) showed that CLP mice were more resistant to virulent L. monocytogenes infection when compared with sham-treated mice, resulting in increased survival. These data are in direct contrast with the data we show in this report. Possible explanations for these differences, compared with our data, include (but are not limited to): 1) use of attenuated versus virulent L. monocytogenes; 2) day of infection (day 2 versus day 3 postsurgery); 3) infectious dose (10^7 CFU attenuated LM-OVA; 2) Animal weight was measured daily beginning the day of surgery, and the percent weight loss with respect to the starting weight is shown. The dotted line represents the starting weight of the mice, normalized to 100%, and the arrow indicates the time of infection. C, The bacterial titer in the spleen was determined on day 3 postinfection. The dotted line represents the limit of detection (i.o.d.) for bacterial count in the spleen. On day 7 postinfection, the number of Ag-experienced (D) and OVA257-specific (E) CD8 T cells in the spleen was determined. There was no significant difference between the Sham and CLP + anti-TRAIL mAb groups. *p < 0.05 (ANOVA).
deficient such that it enters the cell and does not propagate; however, virulent L. monocytogenes replicates and propagates from one cell to another (48). The kinetics of bacterial burden and CD8 T cell responses elicited by attenuated and virulent L. monocytogenes are also considerably different (47); note that L. monocytogenes-specific CD8 T cells were not directly measured in the Delano et al. (46) study. Given these multiple differences, we are presently unable to reconcile the differences between the data in Delano et al. (46) and our data. Regardless, our study adds the important observation that bacterial Ag-specific CD8 T cell responses are suppressed in septic mice in a TRAIL-dependent manner.

We previously showed that sepsis-induced apoptosis led to suppression of DTH through a TRAIL-dependent mechanism (23), but the similar importance of TRAIL-dependent suppression of CD8 T cell responses during sepsis to a secondary heterologous bacterial infection had not been demonstrated until now. In our previous study, the suppression of DTH in septic mice resulted from the activity of TRAIL-expressing CD8 regulatory T (Treg) cells (23). We have had a long-standing interest in the tolerogenic nature of apoptotic cells, especially the ability of apoptotic cells to influence the induction of T cell-mediated immunity, and the induction of Ag-specific unresponsiveness (or tolerance) in an adult can be achieved experimentally through a variety of approaches (49–53). The use of several different experimental tolerance models has helped us demonstrate that one way the immune system reacts to the plethora of self-Ag derived from a large wave of apoptotic cells is the generation of a CD8 Treg population that models has helped us demonstrate that one way the immune cells (23). We have had a long-standing interest in the tolerogenic TRAIL-expressing CD8 Treg cells generated during sepsis (23), have any benefits during sepsis. We hypothesized the anti-TRAIL which therapeutic disruption of the TRAIL/DR5 pathway would

finds, especially for immunosuppressed sepsis patients that are susceptible to secondary infections. Recent studies have shown that therapies that block apoptosis of lymphocyte populations, either through administration of IL-7, IL-15, or anti-CD19 mAb, result in increased survival after sepsis induction in mice (55–57). Although these findings are exciting, these reports did not investigate the health of the immune system in regard to the ability to control subsequent heterologous infections. We included the use of a blocking anti-TRAIL mAb in the present series of experiments, not only as a complementary way to demonstrate the importance of TRAIL in the sepsis-induced unresponsiveness to a secondary heterologous bacterial infection, but also to test the extent to which therapeutic disruption of the TRAIL/DR5 pathway would have any benefits during sepsis. We hypothesized the anti-TRAIL mAb would inhibit the function of the immunosuppressive TRAIL-expressing CD8 Treg cells generated during sepsis (23), and the data showing the restored ability to control the LM-OVA infection and CD8 T cell responses would suggest this occurred. It is also possible that the anti-TRAIL mAb was having an effect outside of the immune system. For example, apoptosis of epithelial cells in the small and large intestine is increased in animals and human suffering from sepsis and is related to a poor prognosis (37, 56, 58, 59). Although the data presented in Fig. 6 investigated the potential impact of the anti-TRAIL mAb on immune system responses to a secondary heterologous bacterial infection after sepsis, we cannot exclude the possibility that the anti-TRAIL mAb was also inhibiting the death of cells outside of the immune system. Thus, anti-TRAIL mAb blockade of intestinal epithelial cell apoptosis may have contributed to the increased weight gain in this group of CLP-treated mice. Further investigation, which would also include analyses of CLP-treated Tail−/− and Dr5−/− mice, is needed to determine the likelihood of this. Regardless, the data presented in this study suggest TRAIL could be a potential therapeutic target in sepsis to help decrease the susceptibility to potentially life-threatening secondary heterologous infections.

Disclosures

The authors have no financial conflicts of interest.

References

Supplemental Figure 1. **CLP surgery results in a significant decrease in the number of CD4+ T cells, CD11c+ cells, and CD19+ cells in the spleen.** WT B6 mice underwent sham or CLP surgery. The total number of CD3+CD4+, CD11c+, and CD19+ cells in the spleen were determined 48 h after surgery. * p < 0.05 (Student's t-test).
Supplemental Figure 2. Suppressed Ag-specific CD4 T cell response in *L. monocytogenes*-infected, CLP-treated WT B6 mice. WT B6 mice underwent sham or CLP surgery. 48 h later, the mice were infected with 10⁷ CFU att LM-OVA i.v. Spleens were harvested on d 7 p.i., and the frequency and number of IFNγ-producing CD4 T cells were determined after *in vitro* stimulation with MHC II (I-Ab)-restricted epitope derived from the *L. monocytogenes* protein listerolysin O (LLO)190-201. * p < 0.05 (Student’s t-test).