T Cell Epitope Specificity and Pathogenesis of Mouse Hepatitis Virus-1–Induced Disease in Susceptible and Resistant Hosts

Aaruni Khanolkar, Ross B. Fulton, Lecia L. Epping, Nhat-Long Pham, Dilea Tifrea, Steven M. Varga and John T. Harty

*J Immunol* 2010; 185:1132-1141; Prepublished online 16 June 2010;
doi: 10.4049/jimmunol.0902749
http://www.jimmunol.org/content/185/2/1132

**References**
This article cites 34 articles, 14 of which you can access for free at:
http://www.jimmunol.org/content/185/2/1132.full#ref-list-1

**Subscription**
Information about subscribing to *The Journal of Immunology* is online at:
http://jimmunol.org/subscription

**Permissions**
Submit copyright permission requests at:
http://www.aai.org/About/Publications/JI/copyright.html

**Email Alerts**
Receive free email-alerts when new articles cite this article. Sign up at:
http://jimmunol.org/alerts
Intranasal mouse hepatitis virus-1 (MHV-1) infection of susceptible mouse strains mimics some important pathologic features observed in the lungs of severe acute respiratory syndrome (SARS)-coronavirus–infected humans. The pathogenesis of SARS remains poorly understood, although increasing evidence suggests that immunopathology could play an important role. We previously reported that the adaptive immune response plays an important protective role in MHV-1–infected resistant B6 mice and that both CD4 and CD8 T cells play a significant role in the development of morbidity and lung pathology following intranasal MHV-1 infection of susceptible C3H/HeJ and A/J mice. In this study, we have identified novel CD4 and CD8 epitopes in MHV-1–infected susceptible and resistant strains of mice. Susceptible C3H/HeJ mice mount robust and broad MHV-1–specific CD4 T cell responses, whereas in resistant B6 mice, Ag-specific CD8 T cell responses dominate. We also show that previously immunized susceptible C3H/HeJ mice do not develop any morbidity and are completely protected following a lethal-dose MHV-1 challenge despite mounting only a modest secondary T cell response. Finally, we demonstrate that the resistance displayed by B6 mice is not solely accounted for by the elaboration of a broad and vigorous MHV-1–specific CD8 T cell response, as MHV-1 infection of C3SW-H2b/SnJ mice, which mount an equally robust CD8 T cell response of the same specificity, is still associated with significant morbidity. Thus, identification of novel CD4 and CD8 T cell epitopes for MHV-1 permitted high-resolution analyses of pulmonary T cell responses in a mouse model of SARS. 

T Cell EpitopeSpecificity and Pathogenesis of Mouse Hepatitis Virus-1–Induced Disease in Susceptible and Resistant Hosts

Aaruni Khanolkar,* Ross B. Fulton,* Lecia L. Epping,* Nhat-Long Pham,† Dilea Tifrea,* Steven M. Varga,*† and John T. Harty*,†

Intranasal mouse hepatitis virus-1 (MHV-1) infection of susceptible mouse strains mimics some important pathologic features observed in the lungs of severe acute respiratory syndrome (SARS)-coronavirus–infected humans. The pathogenesis of SARS remains poorly understood, although increasing evidence suggests that immunopathology could play an important role. We previously reported that the adaptive immune response plays an important protective role in MHV-1–infected resistant B6 mice and that both CD4 and CD8 T cells play a significant role in the development of morbidity and lung pathology following intranasal MHV-1 infection of susceptible C3H/HeJ and A/J mice. In this study, we have identified novel CD4 and CD8 epitopes in MHV-1–infected susceptible and resistant strains of mice. Susceptible C3H/HeJ mice mount robust and broad MHV-1–specific CD4 T cell responses, whereas in resistant B6 mice, Ag-specific CD8 T cell responses dominate. We also show that previously immunized susceptible C3H/HeJ mice do not develop any morbidity and are completely protected following a lethal-dose MHV-1 challenge despite mounting only a modest secondary T cell response. Finally, we demonstrate that the resistance displayed by B6 mice is not solely accounted for by the elaboration of a broad and vigorous MHV-1–specific CD8 T cell response, as MHV-1 infection of C3SW-H2b/SnJ mice, which mount an equally robust CD8 T cell response of the same specificity, is still associated with significant morbidity. Thus, identification of novel CD4 and CD8 T cell epitopes for MHV-1 permitted high-resolution analyses of pulmonary T cell responses in a mouse model of SARS. The Journal of Immunology, 2010, 185: 1132–1141.

Severe acute respiratory syndrome (SARS) is a clinical manifestation of infection by a human respiratory coronavirus (CoV) (1). Although the virus is capable of establishing a systemic infection, the most striking pathology is observed in the lungs (1). There appears to be an emerging consensus that immunopathology may play an important role in mediating the morbidity and mortality associated with SARS-CoV infection (2–4). The early phase of SARS-CoV infection is associated with elevated levels of proinflammatory cytokines (2, 3), however, the exact role of specific components of the immune response to SARS-CoV infection that could be involved in the development of pathology is still unclear and remains an area of active investigation. Although some reports have suggested a link between the severity of disease and an inability of the host to mount an optimal adaptive immune response following infection, others have reported a correlation between increased disease severity and robust Ag-specific CD4 and CD8 T cell responses (2, 3). In addition, one of the major limitations of human studies is their restriction to analyzing responses in PBMCs and the inability to sample immune responses occurring in the tissue of interest.

SARS-CoV infection is associated with elevated levels of proinflammatory cytokines (2, 3), however, the exact role of specific components of the immune response to SARS-CoV infection that could be involved in the development of pathology is still unclear and remains an area of active investigation. Although some reports have suggested a link between the severity of disease and an inability of the host to mount an optimal adaptive immune response following infection, others have reported a correlation between increased disease severity and robust Ag-specific CD4 and CD8 T cell responses (2, 3). In addition, one of the major limitations of human studies is their restriction to analyzing responses in PBMCs and the inability to sample immune responses occurring in the tissue of interest.

Materials and Methods

Peptide library

A total of 420 peptides encompassing the spike (S), nucleocapsid (N), membrane (M), and envelope (E) were synthesized by Mimotopes (Victoria, Australia) based on the MHV-1 structural protein sequence obtained from the
National Center for Biotechnology Information database (accession number EF862498). Each peptide was a 15-mer with an overlap of 10 aa and an offset of 5 aa. The crude peptides (>65% pure by HPLC) were reconstituted using 100% sterile DMSO (Sigma-Aldrich, St. Louis, MO) to a concentration of 2 mM. A substock was prepared that was diluted to a concentration of 25 µM using sterile 1× Dulbecco’s PBS (Life Technologies, Grand Island, NY). Peptides were screened for potential epitopes by performing standard intracellular cytokine staining for IFN-γ production from splenocytes obtained from mice 7 d after i.p. infection with MHV-1 (described below). Following identification of the relevant epitopes, independent synthesis of candidate peptides was undertaken (Biosynthesis, Lewisville, TX).

Mice

Five- to 7-wk-old female A/J (H-2^d), C3H/HeJ (H-2^b), BALB/c (H-2^d), and C57BL/6 (H-2^b) were purchased from the National Cancer Institute (Frederick, MD). C3.5W-H2^b/SnJ mice were obtained from The Jackson Laboratory (Bar Harbor, ME). Infected with MHV-1 (described below), all mice were housed under specific pathogen-free conditions at the University of Iowa (Iowa City, IA) animal care unit until the time of infection, at which point the mice were transferred to housing at the appropriate biosafety level. All animals were maintained in accredited facilities at the University of Iowa and used in accordance with the guidelines established by the University of Iowa animal care and use committee. Mice were infected at 8 to 9 wk of age.

Virus

Parent stock of MHV-1 was obtained from the American Type Culture Collection, (Manassas, VA). The virus was propagated and titrated as previously described (6).

Virus infection of mice

For intranasal infections, mice were anesthetized with avetin (2,2,2-tribromoethanol; Aldrich, Milwaukee, WI) i.p. and administered a subdental dose of MHV-1 intranasally in a volume of 50 µl. The subdental dose used for infecting C3H/HeJ mice was 5 × 10^4 PFU/mouse and 10^5 PFU/mouse for B6 mice. This dosing was based on morbidity and mortality patterns described for susceptible and resistant strains previously (6). For screening the peptide library, splenocytes were obtained from mice that had been previously infected with 2 × 10^5 PFU MHV-1 i.p.

Analysis of FoxP3^+ CD4^+ T cells

Single-cell suspensions obtained from spleens, lungs, and draining lymph nodes of naive B6 and C3H/HeJ control mice and B6 and C3H/HeJ mice infected intranasally with MHV-1 were stained for Foxp3 using the mouse regulatory T cell staining buffer kit (eBioscience, San Diego, CA) according to the manufacturer’s instructions. Briefly, following cell surface staining and fixation, cells were stained with optimal concentrations of mAb specific to Foxp3 (clone FJK-16s; eBioscience). Cells were then washed twice with 1× permeabilization buffer and resuspended in staining buffer.

Intracellular cytokine staining

Intracellular cytokine staining was performed as previously described (12, 13). For the peptide library screen and analysis of Kb^-/- mOva mice, single-cell suspensions from the spleens of MHV-1-infected mice were either left untreated or stimulated with MHV-1–derived peptide epitopes at a concentration of 1 µM for 5 h at 37 °C. The intracellular accumulation of IFN-γ was facilitated by the addition of brefeldin A (GolgiPlug; BD Pharmingen, San Jose, CA). Infected mice were perfused with 10 ml PBS, and explanted lungs were treated with collagenase (100 U/ml) (Life Technologies)/DNAse I (1 mg/ml) (Sigma-Aldrich) for 45 min. Single-cell suspensions were prepared using wire mesh screens, and erythrocytes were removed by treatment with ACK lysis buffer and counted using 0.1% trypan blue. APCs were left either untreated or incubated with appropriate MHV-1–derived peptides at a concentration of 1 µM for CD8 peptide epitopes and 10 µg/ml for CD4 peptide epitopes at 37 °C for 1 h, washed, and added to each tube along with the lung cell suspensions followed by incubation for 5 h at 37 °C. For B6 mice, the mouse B cell line CHB3 was used as APC. In the case of C3H/HeJ mice, APCs were derived from splenocytes of naive syngeneic mice that were left either untreated or incubated with appropriate MHV-1 peptide epitopes at 37 °C for 1 h, washed, and then labeled with 2 µM CFSE for 10 min at 37 °C in PBS to facilitate discrimination from lung cells during flow cytometric analysis. For assays describing the identification of MHC restriction element for CD8 peptide epitopes in B6 mice, APCs used were either P815 cells (H-2^d MHC) or P815 cells transfected with cDNA encoding either the D^d or K^b molecules. Total numbers of Ag-specific CD4 and CD8 T cells in the spleens and lungs were determined by multiplying the frequency of IFN-γ^+ cells with total numbers of CD4 or CD8 T cells present in that tissue. Surface and intracellular staining was performed using the following mAbs: anti-CD8 (clone 53-6.7), anti-CD4 (clone RM4-5), and anti-CD90.2 (clone 30-H12), anti-IFN-γ (clone XMG1.2), anti–TNF-α (clone MP6-XT2), and anti–IL-2 (clone JS65-5H4). Samples were acquired using FACSCalibur and FACSCanto (BD Biosciences, San Jose, CA) and analyzed using FlowJo software (Tree Star, Ashland, OR).

Evaluation of morbidity and mortality

For the evaluation of weight loss postinfection, the weight of each mouse was normalized to 100% at the time they were infected (day 0), and subsequent weight measurements were recorded at defined time points postinfection. Weight data are presented as the mean percentage of the starting weight ± SEM. Survival data for mice are represented by Kaplan-Meier curves indicating the percentage of mice that survived the viral challenge.

Lung function

Baseline airway resistance as determined by the measurement of the parameter enhanced pause (Penh) was evaluated using a whole-body plethysmograph from Buxco Electronics (Troy, NY).

Statistical analyses

All statistical analyses were performed using GraphPad software (GraphPad, San Diego, CA). For weight loss and cytokine analysis data, statistical significance was determined using an unpaired Student t test. A p value <0.05 was considered statistically significant. For survival data, statistical significance was determined using a two-tailed Fisher’s exact test. Once again, a p value <0.05 was considered statistically significant.

Results

Identification of MHV-1–specific CD4 and CD8 T cell epitopes in susceptible and resistant mice

Previously published data from our laboratory showed that T cells contribute to morbidity and lung pathology observed in MHV-1–susceptible strains of mice (6). We have also demonstrated that resistance to MHV-1–induced disease is compromised in B6-Rag1-KO mice, indicating the importance of the adaptive immune response in infection control (6). Based on these data, we wanted to examine Ag-specific T cell responses to MHV-1 in susceptible and resistant strains of mice. T cell epitopes in other CoVs have been primarily localized to structural proteins (3, 14–20), thus we obtained protein sequence information for the S, N, M, and E structural proteins of MHV-1 from the National Center for Biotechnology Information database (accession number EF682498) to screen a peptide library consisting of 420 overlapping peptides encompassing the four proteins mentioned above. Each peptide was a 15-mer with an overlap of 10 aa and an offset of 5 aa. To identify MHV-1–specific T cell epitopes, each peptide was individually screened in an intracellular cytokine staining assay to determine IFN-γ production by peptide-pulsed splenocytes harvested and pooled from mice 7 d after i.p. MHV-1 infection. The large number of peptides to be screened necessitated the use of splenocytes instead of lung cells in our initial analysis. Responses to peptide stimulation that resulted in IFN-γ production at least 2.5-fold over that observed in no-peptide controls were considered positive. We were able to identify several novel CD4 and CD8 T cell epitopes in both susceptible (C3H/HeJ) and resistant (B6) mice (Fig. 1, Table I). In the susceptible C3H/HeJ strain of mice, we identified six novel CD4 epitopes, three of which mapped to the S protein, two to the N protein, and one to the M protein. The screen revealed a single CD8 epitope in these susceptible mice, and it was localized in the N protein. Based on the analysis of the peptide library screen for the resistant B6 mice, we identified four CD8 epitopes and three CD4 epitopes. Once again, the majority of CD4 and CD8 epitopes were found in the S protein. None of the epitopes identified in the resistant B6 mice mapped to the N protein. In addition, we also
identified several novel MHV-1–specific CD4 and CD8 T cell epitopes in susceptible A/J mice and BALB/c mice that display a broader virus-specific CD4 T cell response in the lungs of C3H/HeJ mice. Between days 8 and 11 postinfection, roughly 16–19% of the total CD4 T cells in the lungs of these mice were specific for MHV-1. The response to all six CD4 epitopes was similar in magnitude, and we did not observe any significant difference in the numbers of Ag-specific CD4 T cells in the lungs of susceptible C3H/HeJ mice and resistant B6 mice.

**Kinetics of MHV-1–specific CD4 and CD8 T cell responses in the lungs of susceptible C3H/HeJ and resistant B6 mice**

As mentioned above, our analysis of the peptide library was performed using splenocytes from mice infected i.p. with MHV-1. Intraperitoneal MHV-1 infection of mice is asymptomatic, whereas intranasal infection is associated with pulmonary pathology and morbidity that is most severe in susceptible C3H/HeJ mice and minimal in the resistant B6 mice (6, 7). Given these differences in morbidity after intranasal MHV-1 infection, we were interested in determining Ag-specific T cell responses in the lungs of both susceptible and resistant strains of mice after sublethal infections, as previously defined for each mouse strain (6). Virus-specific CD4 and CD8 T cell responses in the lungs of C3H/HeJ mice (Fig. 3) and B6 mice (Fig. 4) were determined by intracellular cytokine staining following peptide stimulation at the indicated time points after MHV-1 infection, and total numbers of Ag-specific T cells in the lungs were also enumerated. MHV-1 infection induced a broad virus-specific CD4 T cell response in the lungs of C3H/HeJ mice. Between days 8 and 11 postinfection, roughly 16–19% of the total CD4 T cells in the lungs of these mice were specific for MHV-1. The response to all six CD4 epitopes was similar in magnitude, and we did not observe any significant difference in the numbers of Ag-specific CD4 T cells between days 8 and 11 postinfection. A slight reduction in numbers was discernible by day 15 postinfection, and these numbers continued to decline up to day 66 postinfection, the last time point measured for this analysis. The CD8 T cell response in the lungs of the C3H/HeJ mice was more narrowly focused targeting the N421 epitope. This response peaked at day 11 postinfection, after which there was a clearly defined contraction phase, and thereafter, similar to the CD4 T cells, the numbers of N421-specific CD8 T cells displayed a downward trend.

Clearly measurable responses to all three CD4 epitopes identified in the peptide library scan were also detected in the lungs of the resistant B6 mice, with ~5% of the total CD4 T cells in the
Table 1. Identification of MHV-1–specific T cell epitopes in susceptible C3H/HeJ and resistant B6 mice

<table>
<thead>
<tr>
<th>15-mer</th>
<th>CD4 or CD8 Epitope</th>
<th>Predicted 8-mer</th>
<th>Predicted MHC Restriction</th>
<th>Confirmed MHC Restriction</th>
</tr>
</thead>
<tbody>
<tr>
<td>C3H/HeJ</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>M196–210</td>
<td>CD4</td>
<td></td>
<td>I-E^k</td>
<td></td>
</tr>
<tr>
<td>S171–185</td>
<td>CD4</td>
<td></td>
<td>I-E^k</td>
<td></td>
</tr>
<tr>
<td>S881–895</td>
<td>CD4</td>
<td></td>
<td>I-E^k</td>
<td></td>
</tr>
<tr>
<td>S921–935</td>
<td>CD4</td>
<td></td>
<td>I-E^k</td>
<td></td>
</tr>
<tr>
<td>N346–360</td>
<td>CD4</td>
<td></td>
<td>I-E^k</td>
<td></td>
</tr>
<tr>
<td>N376–390</td>
<td>CD4</td>
<td></td>
<td>I-E^k</td>
<td></td>
</tr>
<tr>
<td>N421–435</td>
<td>CD8</td>
<td>N421–428</td>
<td>D^b</td>
<td></td>
</tr>
<tr>
<td>C57BL/6</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>M131–145</td>
<td>CD4</td>
<td></td>
<td>I-A^b</td>
<td></td>
</tr>
<tr>
<td>S361–375</td>
<td>CD4</td>
<td></td>
<td>I-A^b</td>
<td></td>
</tr>
<tr>
<td>S766–780</td>
<td>CD4</td>
<td></td>
<td>I-A^b</td>
<td></td>
</tr>
<tr>
<td>M184–198</td>
<td>CD8</td>
<td>M184–191</td>
<td>K^b</td>
<td></td>
</tr>
<tr>
<td>S317–331</td>
<td>CD8</td>
<td>S317–324</td>
<td>K^b</td>
<td></td>
</tr>
<tr>
<td>S532–546</td>
<td>CD8</td>
<td>S532–539</td>
<td>K^b</td>
<td></td>
</tr>
<tr>
<td>S887–895</td>
<td>CD8</td>
<td>S887–955</td>
<td>K^b</td>
<td></td>
</tr>
</tbody>
</table>

lungs of these mice being specific for MHV-1 at day 8 postinfection (Fig. 4). Calculation of total numbers revealed that B6 mice had ~4.3-fold lower numbers of Ag-specific CD4 T cells (~7 × 10^5 cells) in the lungs compared with C3H/HeJ mice (~3 × 10^5 cells) at the peak of the response. The magnitude of the responses of all three CD4 epitopes in B6 mice were similar to each other, and their numbers peaked at day 8 postinfection, after which they declined and by day 58 postinfection were at levels similar to those observed in the lungs of C3H/HeJ mice. B6 mice also mounted broad and strong MHV-1–specific CD8 T cell responses with the S587-specific response being clearly immunodominant, accounting for 72% of the total Ag-specific CD8 T cell response in the lungs of these mice. The responses directed against the other three CD8 epitopes were similar to each other in magnitude and ~8-fold lower than that measured for the S587 epitope. Overall, the MHV-1–specific CD8 T cell response in the B6 mice (~7.4 × 10^5 cells) was ~11-fold greater than the corresponding CD8 T cell response measured in the lungs of the susceptible C3H/HeJ mice (~7 × 10^5 cells). The CD8 T cell response also peaked at day 8 postinfection, after which it contracted and gradually declined. However, the S587-specific CD8 T cells were maintained at higher levels in the lungs of infected B6 mice than the other specificities.

Collectively, these data suggest that either qualitative (ratios of CD4/CD8 T cells) or quantitative (absolute numbers of CD4 or CD8 T cells) differences in the MHV-1–specific T cell response could dictate the development of lung disease and morbidity following intranasal MHV-1 infection of mice.

Evaluation of cytokine production by Ag-specific T cells and determining FoxP3^+ CD4^+ T cell responses in MHV-1–infected B6 and C3H/HeJ mice

To expand on the results of the kinetics of the MHV-1–specific T cell responses described above, we wanted to determine if differences in cytokine production by MHV-1–specific T cells might also account for some of the differences in morbidity between MHV-1–infected B6 and C3H/HeJ mice. To address this possibility, we used intracellular cytokine staining to analyze the ability of MHV-1–specific CD8 and CD4 T cells to coproduce IFN-γ and TNF-α following MHV-1 infection of B6 and C3H/HeJ mice (Fig. 5A, 5B). We observed a significant reduction in the frequency of N421-specific CD8 T cells (C3H/HeJ) coproducing IFN-γ and TNF-α in comparison with S587-specific CD8 T cells (B6) in the lungs. No differences were observed in the spleens and draining lymph nodes of the infected mice. CD4 T cell responses were analyzed using pooled APCs separately pulsed with M131, S361, and S766 peptides (B6) or M196, S171, and S921 peptides (C3H/HeJ). In contrast to the CD8 T cell data, we observed a significantly greater fraction of IFN-γ–TNF-α–coproducing CD4 T cells in all
three tissues analyzed in the susceptible C3H/HeJ mice versus the resistant B6 mice.

In addition to looking at TNF-α production, a preliminary examination of IL-2 production by MHV-1–specific CD4 T cells showed that although the C3H/HeJ mice had a higher fraction of IFN-γ–IL-2 coproducers in the spleens and draining lymph nodes versus the B6 mice, this trend was reversed in the lungs (data not shown).

In an effort to further dissect the qualitative properties of the immune response to MHV-1 in the resistant B6 and susceptible C3H/HeJ mice, we also analyzed FoxP3+CD4+ regulatory T cells. Published evidence from animal models and human studies of viral infections suggest a crucial role for FoxP3+CD4+ T cells in the development of symptomatic disease (23, 24). Therefore, we wanted to determine if differences in FoxP3+CD4+ T cell responses might account for the difference in morbidity between the resistant B6 and susceptible C3H/HeJ mice following intranasal MHV-1 infection. We examined the spleens, draining lymph nodes, and lungs of infected B6 and C3H/HeJ mice for the presence of FoxP3+CD4+ T cells at day 8 postinfection, a time point at which morbidity differences between the two strains are clearly evident (Fig. 5C).

Our data revealed no significant differences in the total numbers of FoxP3+CD4+ T cells detected in all three of the tissues examined between the two strains of mice.

Overall, these results demonstrate the presence of subtle yet significant differences in the cytokine profiles of MHV-1–specific CD8 and CD4 T cells that might potentially influence development of symptomatic disease in the susceptible C3H/HeJ mice following intranasal MHV-1 infection. Furthermore, MHV-1–induced lung disease in susceptible C3H/HeJ mice is not due to numerical deficiencies in FoxP3+ regulatory CD4 T cells.

Previously immunized C3H/HeJ mice display no morbidity and are completely protected following a lethal MHV-1 challenge

Intranasal MHV-1 infection of naive C3H/HeJ mice induces vigorous Ag-specific T cell responses in the lungs as well as significant morbidity (6). Additionally, we have previously shown that naive C3H/HeJ mice adoptively transferred with memory CD4 or CD8 T cells obtained from previously MHV-1–immunized syngeneic donors display enhanced morbidity and mortality following intranasal MHV-1 infection (6). Given these data, we were also interested in determining the outcome of an MHV-1 challenge in previously immunized C3H/HeJ mice that have an established pool of memory T cells. Significant lethality is observed in naive
C3H/HeJ mice at doses >5 × 10^3 PFU/mouse of MHV-1 administered intranasally (6, 7). Thus, we administered a 10-fold higher dose to C3H/HeJ mice that had previously been immunized with a sublethal dose of MHV-1. As controls, we also included naive C3H/HeJ mice that also received the same high-dose challenge as the immunized mice. Both sets of mice were followed for the development of morbidity following infection. As expected, naive controls progressively lost weight following infection, and all mice in this group died by day 8 postinfection. In contrast, previously immunized mice experienced no morbidity, and all mice survived the lethal MHV-1 challenge (Fig. 6). This result was noteworthy considering the propensity of adoptively transferred memory T cell responses to enhance morbidity and pathology in naive mice following exposure to MHV-1 and prompted us to examine secondary T cell responses in previously immunized C3H/HeJ mice following a lethal MHV-1 challenge.

Suboptimal expansion of secondary T cell responses in lethally challenged immune C3H/HeJ mice

Our data from the lethal MHV-1 challenge of previously immunized C3H/HeJ mice showed that these mice experienced no morbidity and mortality, leading us to speculate that the memory T cells in these mice were unable to exert their pathologic effects. To examine this issue, we evaluated Ag-specific T cell responses in the lungs of previously immunized C3H/HeJ following rechallenge with a lethal dose (5 × 10^4 PFU/mouse) of MHV-1. As controls, we included naive C3H/HeJ mice that received a sublethal dose of MHV-1 (5 × 10^3 PFU/mouse). This difference in viral input doses was necessary to ensure survival of naive mice to allow us to evaluate T cell responses in their lungs at day 8 postinfection. Analysis of the secondary S171-specific CD4 and N421-specific CD8 T cell responses revealed that their numbers remained fairly static between days 5 and 8 postrechallenge, whereas enumeration of cells participating in a primary response in naive control mice that received a 10-fold lower dose of MHV-1 displayed a marked expansion in numbers between days 5 and 8 postinfection (Fig. 7). In addition, the control mice developed characteristic signs and symptoms of MHV-1–induced disease (weight loss, ruffled fur, hunched posture, reduced activity), whereas no morbidity was observed in the rechallenged mice.
Elaboration of a broad and vigorous Ag-specific CD8 T cell response to MHV-1 does not prevent the development of morbidity in susceptible C3.SW-H2b/SnJ mice

One of the key differences we observed between the susceptible C3H/HeJ mice and the resistant B6 mice was that MHV-1 infection elicited a broad and vigorous virus-specific CD8 T cell response in the lungs of the resistant B6 mice. Thus, we were interested in determining if elaboration of a similarly broad and vigorous virus-specific CD8 T cell response in susceptible background mice would minimize morbidity. Hence, we examined morbidity and Ag-specific T cell responses in the lungs of congenic C3.SW-H2b/SnJ mice that express the H-2b MHC-haplotype of the B6 mice (25) following infection with a sublethal dose of MHV-1 (5 × 10^3 PFU/mouse). As controls, we included wild-type B6 mice that were similarly infected. Analysis of the Ag-specific T cell responses in the lungs of the congenic C3.SW-H2b/SnJ mice at day 8 postinfection demonstrated that they elaborated strong Ag-specific CD8 and CD4 T cell responses that were not significantly different from the responses observed in the lungs of similarly infected control B6 mice (Fig. 8A–C). Interestingly, however, development of morbidity assessed in terms of weight loss and development of airway resistance revealed that, despite elaboration of Ag-specific T cell responses similar to those observed in the resistant B6 mice, the C3.SW-H2b/SnJ mice nonetheless lost a significant amount of weight and showed significantly elevated airway resistance compared with controls following intranasal MHV-1 infection (Fig. 8D, 8E). These data demonstrate that
elaboration of vigorous Ag-specific CD8 T cell responses on their own are insufficient to confer a resistant phenotype following intranasal MHV-1 infection.

**Discussion**

In this report, we have expanded on the findings of our previous study in which we examined the protective and pathologic roles of the immune response to MHV-1 in resistant and susceptible strains of mice (6). In the previous report, we had demonstrated that the adaptive immune response plays a protective role in the resistant B6 mice, whereas conversely, both CD4 and CD8 T cells contributed significantly to the development of lung pathology following intranasal MHV-1 infection of susceptible C3H/HeJ mice (6). Given these contrasting roles of the adaptive immune response to MHV-1 infection, we were interested in carrying out a more comprehensive examination of the T cell response to MHV-1. Screening of an overlapping peptide library encompassing the four main structural MHV-1 proteins led to the identification of several novel CD4 and CD8 T cell epitopes in both susceptible and resistant strains of mice. Identification of these epitopes allowed us to examine the kinetics of the Ag-specific T cell responses in the lungs of these mice following both a primary as well as a secondary infection. One of the differences between the susceptible and resistant strains was the fact that MHV-1 infection induced robust and broad Ag-specific CD4 T cell responses in the susceptible mice, whereas the Ag-specific CD8 T cell responses dominated in terms of magnitude and breadth in the resistant B6 mice. Although primary MHV-1 infection was associated with significant morbidity and T cell-mediated immunopathology in susceptible strains (6), re-exposure to lethal doses of MHV-1 following recovery from primary infection was marked by the complete absence of any morbidity. The rechallenged mice were fully protected, and analysis of the secondary T cell responses in these mice revealed a lack of robust expansion of these cells. Finally, we also demonstrate that vigorous expansion and elaboration of a broad set of MHV-1–specific CD8 T cells, which is the hallmark of the resistant B6 mice, fail to induce a similar resistant phenotype in C3H mice engineered to express the B6 haplotype.

The limited availability of genomic and T cell epitope information for MHV-1 necessitated the generation and screening of a peptide library encompassing the four main viral structural proteins, S, M, E, and N. The reason to exclude analysis of the nonstructural proteins at this juncture was based on historical data suggesting that T cell epitopes for coronaviruses reside primarily in structural proteins (3, 14–20). This also appears to be the case for SARS-CoV, as a recently published report showed 70% of the responses were localized to the four main structural proteins, with the S protein being highly immunogenic and accounting for 41% of the total Ag-specific T cell response (3). In contrast, the nonstructural replicase protein that spans two-thirds of the viral proteome accounted for only 13% of the total Ag-specific response (3). Screening of our peptide library revealed that resistant B6 mice had a broader MHV-1–specific CD8 T cell response, whereas the susceptible C3H/HeJ mice had a broader MHV-1–specific CD4 T cell response with a majority of the epitopes mapping to the S protein. Following the identification of the epitopes, we ran the sequences of the specific 15-mers through the SYFPEITHI epitope-prediction software program (21) to identify the minimal CD8 epitopes as well as the MHC restriction element for the particular epitope. MHC restriction element binding was also separately confirmed as described in the Results. Overall, these results seem consistent with those observed for SARS-CoV in which analysis of PBMC samples from SARS-CoV–infected patients revealed that patients that had more severe disease, like the susceptible C3H/HeJ mice in our analysis, tended to have stronger CD4 T cell responses that were primarily directed against epitopes identified in the S protein (3).

As T cell-mediated immunopathology in the lungs is an important feature of intranasal MHV-1 infection of mice (6), we were interested in examining the magnitude and kinetics of the Ag-specific T cell responses in the lungs of the infected mice. Although a number of studies have examined T cell responses to SARS both in human and murine systems, they are beset with certain limitations (2, 3, 14, 26–31). One of the major limitations of human studies is that they are often restricted to analyzing immune responses from PBMC samples that may not reflect the quality and magnitude of the immune response occurring in situ at the primary site of infection or pathology, and the limitation of a majority of small animal studies examining immune responses to SARS is the fact that the human SARS-CoV infection of mice does not recapitulate all of the pathologic features of the disease observed in humans (1, 32). Hence, measurement of immune responses in the lungs of mice following human SARS-CoV infection may not provide a complete picture of the immunopathology that is believed to play an important role in the pathogenesis of the disease. However, the use of MHV-1 infection of susceptible and resistant mouse strains (5–7) and the availability now of mouse-adapted SARS-CoV (33) provide a useful tool to carry out rapid throughput analyses to examine pathology and the role of the immune response in the pathogenesis of respiratory coronaviral diseases such as SARS. Our analysis revealed that intranasal MHV-1 infection of susceptible C3H/HeJ mice resulted in the induction of a robust Ag-specific CD4 T cell response in the lungs of these mice and between days 8 and 11 postinfection. Overall, based on the available epitope information, the total numbers of Ag-specific CD4 T cells (~3 × 10^6) far outnumbered the Ag-specific CD8 T cells (7 × 10^5) in the lungs of the C3H/HeJ mice. In contrast to this picture, intranasal MHV-1 infection of the resistant B6 mice induced a very strong and multi-epitope specific CD8 T cell response in the lungs of these mice, with S887–594 clearly emerging as the immunodominant epitope. The S587–specific CD8 T cells also had a significantly greater proportion of IFN-γ–TNF-α coproducers in the lungs versus the N421–specific CD8 T cell response elaborated in the lungs of the susceptible C3H/HeJ mice. This trend was reversed for the CD4 T cells in which the susceptible C3H/HeJ mice had a significantly greater proportion of IFN-γ–TNF-α coproducers in the lungs, spleen, and mediastinal lymph nodes in comparison with the resistant B6 mice. Our preliminary data also indicate the presence of fewer IFN-γ–IL-2–coproducing CD4 T cells in the lungs of the susceptible C3H/HeJ mice. We also examined the role of FoxP3^+CD4^+ T cells in regulating MHV-1 infection-associated morbidity in the susceptible and resistant strains. We had speculated that susceptible strains would mount a suboptimal regulatory T cell response, thereby allowing the development of immunopathology, whereas the resistant strains of mice would mount an optimal regulatory T cell response that keeps T cell-mediated immunopathology in check. However, our data reveal no difference in the magnitude of the FoxP3^+CD4^+ T cell response in the spleens, lungs, or mediastinal lymph nodes measured at day 8 postinfection, indicating that MHV-1 infection-associated disease in susceptible mouse strains is not due to decreased regulatory CD4 T cell responses. The data up until this point suggested that differences in magnitude and cytokine profile of the Ag-specific CD4 and CD8 T cell responses to MHV-1 might account for the differences in morbidity observed between the susceptible and resistant mouse strains.

We have previously reported that both CD4 and CD8 T cells play an important role in mediating acute disease and lung pathology observed in the susceptible C3H/HeJ mice following primary intranasal infection (6). Moreover, these T cells retain their pathologic
properties as they differentiate into memory T cells (6). Adoptive transfer of these memory T cells into naive syngeneic hosts that are subsequently intranasally infected with MHV-1 results in greater morbidity and mortality than that observed during primary MHV-1 infection (6). These findings suggested that re-exposure to the virus could potentially amplify the pathologic behavior of the MHV-1–specific T cells. To examine this issue in a system that would be more representative of what would occur in a natural setting, we rechallenged C3H/HeJ mice that had been previously immunized with MHV-1 at least 3–6 mo previously with a lethal dose of MHV-1 and assessed morbidity and mortality at various time points following reinfection. In contrast to what we had observed in the adoptive transfer experiment, interestingly, the rechallenged mice did not develop any morbidity, and all of the mice survived the lethal dose challenge. We have previously shown that primary MHV-1 infection of susceptible C3H/HeJ mice induces robust neutralizing Ab responses by days 15–20 postinfection, and adoptive transfer of immune serum into naive syngeneic recipients is very effective at minimizing systemic viral burden and morbidity following MHV-1 challenge (6). Neutralizing Abs would also be present in previously immunized C3H/HeJ that were subsequently rechallenged with MHV-1. Given this information, we wanted to closely examine the magnitude of the secondary T cell response in the rechallenged mice. One of the hallmarks of a secondary T cell response is to respond very vigorously and rapidly following re-exposure to the pathogen (34). Our analysis of the secondary T cell response in the lungs of the rechallenged mice at days 5 and 8 postinfection revealed that the memory T cells failed to expand optimally, and their numbers remained unchanged between these two time points. Overall, these findings suggested a putative link between that the absence of morbidity in the previously immunized C3H/HeJ mice that were rechallenged with a lethal dose of MHV-1 and the blunted secondary T cell response. Although it is formally possible that the secondary T cell response may have peaked prior to day 5, the pathologic properties of these T cells and the failure to detect any morbidity during the course of this analysis argue more in favor of a weak secondary T cell response. It is likely that neutralizing Ab responses dominate the recall response in previously immunized C3H/HeJ mice after re-exposure to the virus, effectively and rapidly controlling the rechallenge inoculum, thereby reducing the numbers of memory T cells that get recruited into the secondary response. This could be a mechanism to try and curb T cell-mediated immunopathology in susceptible hosts that survive primary MHV-1 infection-induced disease.

Our data show that C3H/HeJ mice that are highly susceptible to MHV-1–induced disease mount a vigorous and Ag-specific CD4 T cell response directed against at least six epitopes in the lungs, whereas B6 mice that are resistant to MHV-1–induced disease generate a strong and multiepitope-specific CD8 T cell response in the lungs following intranasal MHV-1 infection. These findings led us to ask the question if the susceptible phenotype could be modulated by inducing a strong, multiepitope-specific CD8 T cell response similar to that observed in the resistant B6 mice. We addressed this question by analyzing T cell responses in the lungs of C3.SW-H2^b/SnJ mice following intranasal MHV-1 infection. This congenic strain of mice expresses the H-2^b MHC haplotype similar to the B6 mice instead of the H-2^a haplotype of the parent strain, C3H/HeSnJ, which is also shared by the susceptible C3H/HeJ mice (25). As we expected, the C3.SW-H2^b/SnJ mounted an Ag-specific T cell response very similar in magnitude to that of wild-type B6 controls characterized by a strong and broadly defined Ag-specific CD8 T cell response that was dominated by the SS87-specific CD8 T cells. However, these mice did experience morbidity, as evidenced by weight loss and development of airway resistance following primary MHV-1 infection. These results suggest that the fine specificity of the Ag-specific T cell response does not control disease phenotype in the context of MHV-1 infection. In the larger context, these findings additionally suggest that host background genes play a significant role in determining host resistance/susceptibility to disease. It is formally possible that qualitative differences in innate immune responses and functional properties of FoxP3^+CD4^+ T cells influenced by host background genes could affect development of disease following MHV-1 infection. The cross-talk between background genes and the immune response genes may be crucial in programming the host immune response into one that induces pathology and morbidity (as observed in the C3H/HeJ mice and C3.SW-H2^b/SnJ mice versus one that does not (as observed in the B6 mice).

In conclusion, in this report, we have identified novel CD4 and CD8 T cell epitopes specific to MHV-1 in both susceptible and resistant strains of mice. Our data demonstrate the divergence in the quality and quantity of the Ag-specific T cell response between susceptible and resistant hosts following primary MHV-1 infection. This report also shows that re-exposure to MHV-1 in susceptible hosts will most likely be associated with minimal morbidity and a favorable outcome for the host. Reduced morbidity in this setting will most likely be due to a dominant neutralizing Ab response that reduces viral burden and curtails an overwhelming and potentially lethal secondary T cell response. Finally, our data also highlight the potentially important contribution that host background genes make in shaping the host response to infection that alters the balance between disease and lack thereof. Overall, these findings have important implications for trying to understand the complex, multifactorial nature of coronaviral disease pathogenesis and suggest the importance of focusing on an Ab-based versus a T cell-based vaccine approach to combat respiratory coronaviral infections.

Acknowledgments

We thank Stanley Perlman for critical review of the manuscript.

Disclosures

The authors have no financial conflicts of interest.

References


