Title: An Autoimmunity-associated allele of *PTPN22* enhances the innate immune response to

promote protection against acute coronavirus infection

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Abstract:

Allelic variation can impact viral clearance and disease severity, but the effect of the

autoimmunity-associated allelic variant of *Ptpn22* (PEP-R619W) on antiviral immunity remains

incomplete. This research defines how the loss of *Ptpn22* (PEP-null) and PEP-R619W changes

antiviral immunity during acute coronavirus infection. We address the hypothesis that

CRISPR/Cas9-generated PEP-null and PEP-R619W mice have enhanced antiviral immunity

over PEP-WT mice during coronavirus infection. Following Mouse Hepatitis Virus (MHV) A59

infection, we interrogated pathology, cytokine production, and cellular responses in the blood,

spleen, and liver of PEP-WT, PEP-null, and PEP-R619W mice. Key findings show that PEP-

R619W mice have reduced viral titer and weight loss, increased survival, and more mature NK

cells in the liver and spleen compared to PEP-WT mice. Interestingly, protection against disease

in PEP-null mice was inoculation-dose-dependent, whereas PEP-R619W conferred immunity

regardless of infection dose. Further, Rag1-/- PEP-R619W mice had increased survival and reduced viral titer over Rag1-/- PEP-WT mice. PEP-R619W mice also had higher concentrations of IFNγ and enhanced IFNγ production by mature NK cells in the liver at 3 days post-infection. Finally, NK cell depletion elevated PEP-R619W viral titer to similar levels as PEP-WT mice. This is one of the first studies investigating the role of *Ptpn22* within NK cells and demonstrates that the *Ptpn22* allelic variant augments NK cell function and is beneficial during coronavirus infection.

One Sentence Summary:

The *Ptpn22* autoimmunity-associated allele uniquely augments innate immunity to protect against acute coronavirus infection.

Main Text:

INTRODUCTION

Allelic variation in immune-regulatory genes is associated with protective or pathogenic immune responses during disease (*1, 2*). An example is *PTPN22* and its minor 1858C>T allele (rs2476601) (*1-10*). This *PTPN22* minor allele is strongly associated with multiple autoimmune diseases, has been cited as the highest non-HLA risk allele for autoimmunity, and is present in 5-15% of North Americans (*1-10*). The generational persistence of this *PTPN22* allele, despite its strong association with various severe autoimmune diseases, poses an evolutionary paradox. A theory is that the heightened immune responses it drives, though detrimental in autoimmunity, may offer protection against infections and cancer.

In humans, *PTPN22* encodes for the protein Lyp, and in mice, its ortholog, PEP, is predominantly expressed in immune cells (*3, 4*). The *PTPN22* 1858C>T allele results in an amino acid substitution of an arginine (R) to tryptophan (W) that alters immune-regulatory function in both human (Lyp-R620W) and murine ortholog (PEP-R619W) models (*3-6, 9, 11-21*) . To better understand the function of *Ptpn22*, prior studies have frequently utilized *Ptpn22* knockout (PEP-null) mice. The molecular function of PEP has been best characterized as a negative regulator of T-cell receptor (TCR) and B-cell receptor (BCR) signaling, but its role in other immune cells is less well understood (*3, 4, 11, 13, 16, 22-27*). Further, the Lyp-R620W and PEP-R619W mutations do not directly impact phosphatase activity but lead to a loss of binding capacity with other proteins, such as Csk, TRAF3, Vav, Grb2, SKAP-HOM, and NLRP3, resulting in altered immune function (*3, 11-13, 17, 24*). Studies have defined several mechanisms in which the *PTPN22* 1858C>T allele potentiates heightened immune responses (*3, 4, 11, 13, 16-21, 23, 24, 28*). These same mechanisms that are detrimental during autoimmunity, such as enhanced T cell function, are protective when combating chronic viral infection and cancer (*18, 19*).

Previous studies show that both PEP-null and PEP-R619W mice, unlike wildtype (PEP-WT) mice, can clear chronic lymphocytic choriomeningitis virus clone 13 (LCMV-cl13) infection, and this phenotype is attributed to their enhanced antiviral T cell effector function (*19, 29-31*). However, the role of PEP and its PEP-R619W variant in virus infection has mostly been studied in the context of LCMV infection and T cells (*19, 27, 29-32*). Consequently, much remains unknown regarding the impact of PEP and its PEP-R619W variant on 1) innate antiviral immunity, 2) non-LCMV infection models, and 3) whether PEP-null and PEP-R619W will consistently exert similar immune responses during infection. Despite the comparable

phenotypes of PEP-null and PEP-R619W defined in LCMV-cl13 immunity, other studies have

highlighted several cellular and molecular differences between these two strains. For example,

PEP-null mice have an increased amount of Tregs, and NLRP3-mediated IL-1β production in

PEP-R619W myeloid cells is increased (*20, 21, 26*). These findings provide additional rationale

to investigate differential responses between these strains, specifically within the context of viral

infection. Therefore, we investigated whether PEP-null mice, PEP-R619W mice, or both can

modulate innate antiviral immunity to confer protection during acute coronavirus infection.

In this study, we investigated the impact of *Ptpn22* (PEP) and its *Ptpn22* 1858C>T allele (PEP-

R619W variant) on the innate immune response following acute coronavirus infection using a

moribund highly liver-tropic mouse hepatitis virus (MHV) strain A59. Our findings show that

PEP-R619W enhances natural killer (NK) cell maturation and strengthens NK effector functions,

and that NK cells are necessary to restrict viral replication in the liver during innate time points

in PEP-R619W mice. The results of this research define new mechanisms by which the

autoimmunity-associated allele of *PTPN22* augments innate antiviral immunity and enhances

protection against coronavirus infection.

RESULTS

PEP-R619W reduces disease and viral titer during MHV A59 infection

To determine the impact of *Ptpn22* and its autoimmunity-associated minor allele (PEP-R619W)

during acute coronavirus infection, we infected wildtype (PEP-WT) and CRISPR-Cas9

generated *Ptpn22* knockout (PEP-null) and PEP-R619W mice with a common murine strain of

coronavirus, mouse hepatitis virus (MHV) strain A59, which primarily infects the liver.

Following 5e4 PFU MHV A59 infection, PEP-R619W mice had significantly reduced weight

loss at day 5 post-infection (dpi) and 3-8 dpi during 1e5 PFU infection (Fig. 1A and 1B)

compared to PEP-WT mice. This was paired with significantly enhanced survival at both doses

compared to PEP-WT mice (Fig. 1C and 1D). At 5e4 PFU infection, PEP-null mice phenocopy

PEP-R619W mice. However, during 1e5 PFU infection, PEP-null mice are no longer protected

from MHV A59 disease and phenocopy PEP-WT mice in weight loss and survival (Fig. 1A-D).

We also quantified the viral load of the whole liver, as it is the primary site of replication for

MHV A59, at 1-, 3-, 5-, and 7- dpi via plaque assay. PEP-R619W mice had significantly reduced

viral titer at 1-, 3-, and 5- dpi compared to PEP-WT mice (Fig. 1E). However, PEP-null mice

only demonstrated reduced titer at 5 dpi (Fig. 1F). Additionally, both PEP-R619W and PEP-null

mice had accelerated clearance compared to PEP-WT mice, as 7/7 PEP-R619W mice and 7/8

PEP-null mice had cleared the infection by 7 dpi, whereas only 2/7 PEP-WT mice had cleared

the infection at this time point (Fig. 1E and 1F). Splenic titers showed a low level of infection at

1-, 3-, and 5- dpi, regardless of genotype (Fig. S1A and S1B). All mice were able to clear the

MHV A59 infection from the spleen by 7 dpi (Fig. S1A and S1B).

To determine if the reduced viral titer observed in the livers of PEP-R619W and PEP-null mice

(Fig. 1E and 1F) was due to PEP-driven myeloid cell-intrinsic changes in these mice, resulting in

decreased viral replication, we differentiated bone-marrow-derived macrophages (BMMs) and

bone-marrow-derived dendritic cells (BMDCs). We infected them with MHV A59 *ex vivo*, as

they are both readily infected *in vivo* by MHV (Fig. S1C) (*33-35*). We did not detect any

significant differences in viral titer across the three genotypes in either BMMs (Fig. S1D) or

BMDCs (Fig. S1E), indicating that PEP-R619W and PEP-null do not mediate protection by

directly impacting viral replication through cell-intrinsic mechanisms. Histopathologic analysis

of liver sections at 3 dpi following 1e5 PFU infection demonstrated multifocal regions of marked

hepatocellular necrosis in PEP-WT mice, characterized by infiltration of inflammatory cells and

deposition of edema and fibrin (black arrow) (Fig. 1G and Fig. S1F). In comparison, PEP-

R619W and PEP-null mice exhibited markedly reduced hepatic injury, with mild necrosis and

inflammation (Fig. 1G and Fig. S1F). These combined results show that PEP-R619W mice have

improved disease outcomes and reduced viral burden, which includes accelerated clearance,

during MHV A59 infection.

Fig. 1

Figure 1: PEP-R619W mice have reduced disease during MHV A59 Infection.

C57BL/6J mice with *Ptpn22* wild type (PEP-WT, black circle), *Ptpn22* knockout (PEP-null, red square), or the *Ptpn22* autoimmune-associated allele (PEP-R619W, blue triangle), were infected with 5e4 PFU (A, C) or 1e5 PFU (B, D) MHV A59 (i.p). Mice are tracked by weight (A, B) and survival (C, D). Respective spider plots for individual mouse weights are shown below (A, B). To measure viral burden, liver homogenates from infected (5e2 PFU) PEP-WT, PEP-null, and PEP-R619W mice were used for plaque assay (E, F). Histopathology of the livers of mice at 3 dpi following 1e5 PFU MHV A59 infection, with representative photomicrographs of liver sections exhibiting areas of necrosis, inflammation, and edema/fibrin accumulation (black arrow) and cumulative pathology scores represented as mean + SEM. Scale bar = 500 μm (G). Weight loss and survival studies pooled from 3 individual experiments for each dose: Group sizes for 5e4 PFU infection (A, C) were PEP-WT n = 28, PEP-null n = 14, PEP-R619W n = 17. Group sizes for 1e5 PFU infection (B, D) were PEP-WT n = 31, PEP-null n = 27, PEP-R619W n = 31. For weight loss statistical analysis, significant p-values from One-way ANOVA with Tukey's Multiple Comparisons at each dpi are represented by #, comparing PEP-WT vs. PEP-R619W, * comparing PEP-null vs. PEP-R619W, or ∇ comparing PEP-WT vs. PEP-null. Log-rank Mantel-Cox Test (survival), *p<0.05, ***p<0.001. For whole liver titer (E, F), each symbol represents an individual mouse. The dashed line indicates the limit of detection (L.O.D.). Certain PEP-WT mice are represented in both graphs, as some experiments had all three genotypes, whereas others contained only PEP-WT vs PEP-null or PEP-R619W. Combined data from 2 independent experiments, multiple unpaired T-Tests, PEP-WT vs PEP-R619W, PEP-WT vs PEP-null, at each time point, *p<0.01, **p<0.01. 7 dpi was analyzed using Fisher's Exact Test, Cleared vs Not

142   Cleared, #p<0.05. For histopathological analysis, each dot represents an individual mouse, with

143   p-values from One-way ANOVA with Tukey's Multiple Comparisons shown, *p<0.05.

PEP-R619W prolongs the survival of infected mice in the absence of T and B cells

Due to the enhanced protection against disease conferred by PEP-R619W at early days post-infection (Fig. 1), we wanted to determine if a strengthened innate immune response was sufficient to fully protect these mice, or if T and B cells were necessary for survival during MHV A59 infection. To do this, we infected Rag1-/- PEP-WT, Rag1-/- PEP-null, and Rag1-/- PEP-R619W mice with 5e4 PFU or 1e5 PFU MHV A59. Like the immune-competent mice, Rag1-/- PEP-R619W mice had noticeably less weight loss throughout most of the early stages of the infection (Fig. 2A and 2B) and mice survived longer (Fig. 2C and 2D) compared to Rag1-/- PEP-WT mice at both 5e4 and 1e5 PFU MHV A59 infection. Rag1-/- PEP-null mice also have prolonged survival over Rag1-/- PEP-WT at 5e4 PFU infection (Fig. 2C). However, at 1e5 PFU infection, PEP-null mice no longer had prolonged survival (Fig. 2D). These data also show that T and B are necessary for overall survival, regardless of PEP- genotype or MHV A59 dose, as all mice on a Rag1-/- background eventually succumb to disease (Fig. 2C and 2D). Next, we measured viral load in the liver at 3- and 5-dpi. Rag1-/- PEP-R619W mice had reduced viral burden compared to Rag1-/- PEP-WT mice (Fig. 2E). No difference was detected between Rag1-/- PEP-WT and Rag1-/- PEP-null mice liver titers (Fig. 2F). There was no difference detected in splenic viral titers at 3 and 5 dpi between Rag1-/- PEP-WT and Rag1-/- PEP-R619W mice or Rag1-/- PEP-WT and Rag1-/- PEP-null mice (Fig. S2). Overall, this data suggests that PEP-null enhances the innate immune response during 5e4 PFU infection in both immune competent and Rag1-/- models to improve survival compared to PEP-WT mice, and these results are comparable to PEP-R619W mice (Figs. 1 and 2). However, only PEP-R619W mice showed enhanced protection following 1e5 PFU infection, suggesting that this autoimmune-associated

166   variant modifies the innate response through additional mechanisms compared to PEP-null, and

167   this confers increased resistance against MHV A59-associated disease (Figs. 1 and 2).

 Fig. 2

Figure 2: PEP-R619W innate cells provide some protection against disease, but T and B cells are necessary for survival.

Rag1-/- PEP-WT (black circle), Rag1-/- PEP-null (red square), or Rag1-/- PEP-R619W (blue triangle), mice were infected with 5e4 PFU (A, C) or 1e5 PFU (B, D) MHV A59 (i.p), and were tracked by weight (A, B) and survival (C, D). Respective spider plots for individual mouse weights are shown below (A, B). To measure viral burden, liver homogenates from infected (5e2 PFU) Rag1-/- PEP-WT, Rag1-/- PEP-null, and Rag1-/- PEP-R619W mice were used for plaque assay (E, F). Weight loss and survival studies pooled from 2 individual experiments for each dose: Group sizes for 5e4 PFU (A, C) were Rag1-/- PEP-WT n = 16, Rag1-/- PEP-null n = 6, Rag1-/- PEP-R619W n = 16. Group sizes for 1e5 PFU (B, D) were Rag1-/- PEP-WT n = 17, Rag1-/- PEP-null n = 13, Rag1-/- PEP-R619W n = 15. For weight loss statistical analysis, significant p-values from One-way ANOVA with Tukey's Multiple Comparisons at each dpi are represented by # comparing Rag1-/- PEP-WT vs. Rag1-/- PEP-R619W and * comparing Rag1-/- PEP-null vs. Rag1-/- PEP-R619W. Log-rank Mantel-Cox Test (survival), *p<0.05, **p<0.01. For whole liver titers (E, F), each symbol represents an individual mouse. The dashed line indicates the limit of detection (L.O.D.). Certain Rag1-/- PEP-WT mice are represented in both graphs, as some experiments had all three genotypes, whereas others contained only Rag1-/- PEP-WT vs Rag1-/- PEP-null or Rag1-/- PEP-R619W. Combined data from 2 independent experiments, multiple unpaired T-Tests, Rag1-/- PEP-WT vs Rag1-/- PEP-R619W, Rag1-/- PEP-WT vs Rag1-/- PEP-null, at each time point. *p<0.01, **p<0.01.

PEP-R619W mice have increased innate immune presence in the liver and spleen during MHV A59 infection

We next aimed to determine how the PEP-R619W variant augmented the innate immune response. We focused on 3 dpi because, 1) this is when we can consistently observe a divergence in weight loss between genotypes, 2) PEP-R619W mice have reduced liver titer and pathology at this time point, and 3) this is a time point that the innate response dominates, whereas, at 5 dpi, there could be some early T cell activity. As such, we investigated the innate cellular response after 5e4 PFU MHV A59 infection, and similar to the observed weight loss and survival results, PEP-R619W and PEP-null mice had comparable immune phenotypes at 3 dpi in the spleen (Fig. S3). There was no difference detected in the bulk number of splenocytes (Fig. S3B) or frequency of CD3e- CD19- (innate cells) of all live cells (Fig. S3C), regardless of infection or PEP genotype. However, PEP-R619W and PEP-null mice had significantly increased frequencies of NK cells and DCs compared to infected PEP-WT mice (Fig. S3D).

Interestingly, PEP-R619W mice had more splenic CD11b+ NK cells than PEP-WT, indicating PEP-R619W NK cells are significantly more mature than PEP-WT NK cells following infection (Fig. S3E) (*36, 37*). Further, there were no differences detected in the frequency of CD8α+ conventional dendritic cells (CD8α+ cDCs), which are likely type 1 conventional dendritic cells (cDC1s) (Fig. S3F) (*38*). While the expression of activation markers CD80 and CD86 was significantly upregulated post-infection in splenic CD8α+ cDCs, no significant difference was detected between infected genotypes (Fig. S3G and S3H, respectively). Similar results were seen in splenic CD8α- cDCs, which are likely type 2 conventional dendritic cells (cDC2s) (Fig. S3I-K), though there was a decrease in CD86 expression in PEP-null and PEP-R619W splenic CD8α- cDCs compared to PEP-WT post-infection (Fig. S3K) (*38*).

Next, we wanted to determine if, after 1e5 PFU MHV A59 infection, PEP-R619W mice had

enhanced antiviral immunity in the liver, as this is the main site of replication for MHV A59,

compared to PEP-WT and PEP-null mice. At 3 dpi, we did not detect significant differences in

the absolute number of liver cells (Fig. 3A) or in the frequency (%) of CD45+ cells (Fig. 3B)

between our mock mice (uninfected controls) and our infected PEP-WT, PEP-null, and PEP-

R619W mice. However, PEP-R619W mice have a higher proportion of CD3e- CD19- of CD45+

immune cells, which we define as an immune "innate subset," compared to PEP-WT mice (Fig.

3C). Delving further into this innate cell population, PEP-R619W mice had increased

proportions of natural killer (NK) cells, dendritic cells (DCs), and macrophages of CD45+ cells

over both PEP-WT and PEP-null mice (Fig. 3D). We did not detect any differences between

infected genotypes in plasmacytoid DCs (pDCs), monocytes, or neutrophils (Fig. 3D). We also

did not observe any differences in the proportion of or CD86 expression on Tim4+ macrophages,

which are likely Kupffer cells amongst infected PEP-WT, PEP-null, and PEP-R619W mice (Fig.

S4B-C) (*39-41*). Post infection, all genotypes increased CD86 expression on Tim4+

macrophages (Fig. S4C). Within the DC population, there was a decrease in both the frequency

and expression of MHC-II (Fig. S4D and S4E, respectively) in infected genotypes compared to

uninfected controls. Further, we did not identify any differences in the frequency and expression

of CD86 on DCs between infected genotypes (Fig. S4F and S4G).

MHV A59 infected PEP-R619W mice had more conventional NK cells compared to infected

PEP-WT and PEP-null mice, characterized as CD49b+ CD49a- of NK1.1+ cells, whereas the

inverse is considered tissue-resident type 1 innate lymphoid cells (ILC-1) (Fig. 3E) (*42, 43*).

Additionally, PEP-R619W conventional NK cells were more mature (CD11b+) compared to

PEP-WT (Fig. 3F), and overall, PEP-R619W mice had more mature conventional NK cells

(CD11b+ CD49b+ CD49a- NK1.1+) compared to both PEP-WT and PEP-null mice during

coronavirus infection (Fig. 3G). These mature NK cells are of particular interest because, as NK

cells mature, they enhance their effector function potential, including increased interferon-

gamma (IFNγ) production and elevated expression of cytotoxic molecules, such as perforin and

granzyme B (*36, 37*). Collectively, these data demonstrate that the PEP-R619W variant enhances

both splenic and liver innate antiviral immunity, specifically increasing the overall amount and

maturity of NK cells.

 Fig. 3

Figure 3: PEP-R619W mice have more innate immune and mature NK cells in the Liver.

Following PBS injection (Mock, white bar, circle) or 1e5 PFU MHV A59 infection (i.p) in PEP-WT (black bar, circle), PEP-null (red bar, square), and PEP-R619W (blue bar, triangle) mice, at 3 dpi the liver was perfused, harvested, and antibody stained for flow cytometric analysis. The absolute count of liver cells for all genotypes (A). Frequencies (%) of CD45+ cells of live cells (B) and of CD3e- CD19- of CD45+ Live (C). Frequency (%) of several innate cells of CD45+ cells is shown (D). Gating strategy for all innate subsets is: Lymphocytes> Single cell x2> autofluorescent-> Live> CD45+> CD3e- CD19-> Ly6G- Ly6C+/- (non-neutrophils). NK Cells: innate subsets> NK1.1+. DCs: innate subsets> NK1.1-> CD11c+ PDCA-1-. pDCs: innate subsets> NK1.1-> PDCA-1+ CD11c+/-. Monocytes: innate subsets> NK1.1-> Ly6C^{hi} CD11b+. Macrophage: innate subsets> NK1.1-> Ly6C- CD11b+/-> F4/80+ CD11b+. Neutrophils: Lymphocytes> Single cell x2> autofluorescent-> Live> CD3e- CD19-> Ly6G+ Ly6C+. Frequency (%) conventional NK cells of CD45+ (E). Frequency (%) mature conventional NK cells (F) of CD45+ cells (G). Gating strategy for NK subsets: Conventional NK Cells: innate subsets> NK1.1+> CD49b+ CD49a-. Mature Conventional NK Cells: Conventional NK Cells> CD11b+. Quantification of flow cytometric data was pooled from 6 independent experiments. Each symbol represents an individual mouse. Mock mice are a mixture of all 3 genotypes. p-values from One-way ANOVA with Tukey's Multiple Comparisons are shown for each panel. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

PEP-null splenic mature NK cell effector functions are changed depending on the MHV A59 inoculation dose

Since our data showed that PEP-R619W mice have significantly more mature NK cells in both the liver and spleen at 3 dpi, we next wanted to determine if the NK cells amongst our mice had changed functional properties. Again, we observed inoculation dose-dependent differences, where at 5e4 PFU, PEP-null and PEP-R619W mice had similar NK cell immune phenotypes in the spleen (Fig. S5A-F). Specifically, following 5e4 PFU infection, PEP-null and PEP-R619W mature splenic NK cells had less CD107a, a marker of degranulation (Fig. S5A and S5B), increased perforin (Fig. S5C and S5D), and no detectable difference in IFNγ (Fig. S5E and S5F) compared to PEP-WT mature splenic NK cells. Yet at 1e5 PFU, PEP-null and PEP-WT phenotypes were more similar in the spleen (Fig. S5G-L). With 1e5 PFU infection, PEP-R619W mature splenic NK cells had reduced degranulation marker CD107a (Fig. S5G and S5H), increased perforin (Fig. S5I and S5J), and an increase in frequency, but not expression, of IFNγ (Fig. S5K and S5L) compared to PEP-WT and PEP-null mature splenic NK cells. This data provides some insight into why PEP-null mice have differing phenotypes (survival) during different doses of MHV A59 infection, as differential immune activation at 1e5 PFU infection may be responsible for the previously described increase in morbidity (Figs. 1 and 2).

PEP-R619W enhances liver mature NK cell effector function and the overall production of IFNγ during virus infection

As only PEP-R619W mice, but not PEP-null, had more mature conventional NK (M-cNK) cells compared to PEP-WT mice at 3 dpi in the liver, we next investigated if PEP-R619W M-cNK cells have altered effector functions compared to PEP-WT M-cNK cells. Following 1e5 PFU infection, at 3 dpi in the liver, PEP-R619W M-cNK cells (CD11b+ CD49b+ CD49a- NK1.1+)

have higher expression of (i) IFNγ, (ii) T-bet, (iii) granzyme B, and (iv) perforin, compared to

PEP-WT M-cNK cells (Fig. 4A, i-iv). There was no difference detected in the expression of (v)

TNFα or (vi) CD107a between PEP-WT and PEP-R619W M-cNK cells (Fig. 4A, v-vi). Further,

PEP-R619W M-cNK cells were more poly-functional compared to PEP-WT, as there was an

increased proportion of IFNγ+ Perforin+ and IFNγ+ Perforin+ TNFα+ M-cNK cells in PEP-

R619W mice.

Next, we examined the magnitude of the cytokine/chemokine response both systemically and in

the whole liver at 3 dpi. Strikingly, out of the thirteen different cytokines and chemokines

paneled in the serum (Fig. 4C), only the concentration of IFNγ was significantly increased in

PEP-R619W mice (Fig. 4D), yet all other molecules, including interferon-alpha (IFNα) (Fig.

4E), which is necessary for protection against MHV A59 infection, were unchanged between

infected genotypes (*44*). Similar results were detected in the whole liver homogenate (Fig. 4F-

H). To corroborate these findings, we measured the levels of IFNβ in the liver at 3 dpi in our

PEP-WT, PEP-null, and PEP-R619W mice. We detected no difference between infected

genotypes (Fig. 4I).

Given the enhanced M-cNK IFNγ expression and the overall increased IFNγ concentration in our

PEP-R619W mice, we next wanted to determine if IFNγ and/or IFNγ-signaling was necessary

for survival and weight retention during MHV A59 infection. To test this, we infected WT, IFNγ

knockout (IFNγ KO), and IFNγ receptor knockout (IFNγR KO) mice with 5e4 PFU of MHV

A59. Both IFNγ KO and IFNγR KO mice had more severe weight loss (Fig. 4J) and nearly 100%

mortality (Fig. 4K) compared to WT mice, demonstrating the importance of IFNγ for protection

during MHV A59 infection.

Taken together, these data show that PEP-R619W liver M-cNK cells produce more IFNγ and are

more poly-functional than PEP-WT M-cNK cells, contributing to the increased levels of IFNγ in

both the serum and liver at 3 dpi. Further, IFNγ and IFNγ signaling are critical for survival. This

suggests that the protection conferred by PEP-R619W during MHV A59 infection may be

driven, in part, by enhanced NK cell IFNγ production.

Fig. 4

Figure 4: PEP-R619W augments mature conventional NK antiviral functions during coronavirus infection.

3 dpi liver M-cNK analysis following 1e5 PFU MHV A59 infection (i.p) in PEP-WT (black bar, circle) and PEP-R619W (blue bar, triangle) mice. Expression (gMFI) of IFNγ (i), T-bet (ii), Granzyme B (iii), Perforin (iv), TNFα (v), and CD107a (vi) in Mature Conventional NK cells, with representative histograms below (A). Proportion of IFNγ- (grey), IFNγ+ only (pink), IFNγ+ Perforin+ (teal), and IFNγ+ Perforin+ TNFα+ (purple) of Mature Conventional NK Cells (B). Expression of 13 different cytokines and chemokines were quantified using LEGENDplex. Radar plots showing the 13 different cytokines from the serum (C) and liver (F), with select cytokines, IFNγ (D, G) and IFNα (E, H), quantified to the right. IFNβ concentration in the liver at 3 dpi [ELISA] (I). C57BL/6 mice with wild type (PEP-WT, black circle), IFNγ knockout (IFNγ KO, purple triangle), or IFNγ Receptor knockout (IFNγR KO, orange square) were infected with 5e4 PFU MHV A59 (i.p). Mice are tracked by weight (J) and survival (K). Quantification of flow cytometric data is representative of 3 independent experiments. p-values from Welch's unpaired t test are shown, *p<0.05, **p<0.01, ***p<0.001. LEGENDplex assays are from 1 experiment. Each symbol represents an individual mouse. Mock mice are a mixture of all 3 genotypes. p-values from One-way ANOVA with Tukey's Multiple Comparisons are shown for each panel. *p<0.05, **p<0.01, ***p<0.001. Weight loss and survival studies pooled from 2 individual experiments. Group sizes were PEP-WT n = 19, IFNγ KO n = 4, and IFNγR KO n = 15. For weight loss statistical analysis, significant p-values from One-way ANOVA with Tukey's Multiple Comparisons at each dpi are represented by # comparing PEP-WT vs. IFNγ KO, or * PEP-WT vs. IFNγR KO. Log-rank Mantel-Cox Test (survival), ****p<0.0001.

NK Cell maturation is accelerated in PEP-null and PEP-R619W mice

Due to the increased presence of mature NK cells in the spleens (CD11b+ of NK1.1+) and liver (CD11b+ of CD49b+ CD49a- NK1.1+) of PEP-R619W mice post-infection (Fig. S3E, Fig. 3E-G), we examined if PEP-R619W NK cells had differential maturation states compared to PEP-WT at homeostasis. Previous studies have shown that murine NK cells follow a four-stage developmental program, defined by the subsequent acquisition and loss of surface receptors CD27 and CD11b, and these maturation states can be seen in the spleen (*36, 37*). The four stages, from least to most mature, are defined as; (i) CD27- CD11b- (Double Negative, DN), (ii) CD27+ CD11b-, (iii) CD27+ CD11b+ (Double Positive, DP), and (iv) CD27- CD11b+ (*36, 37*). This developmental program is associated with the stepwise acquisition of NK cell effector function, and the accumulation of terminally mature NK cells (CD27- CD11b+) plateaus at 8 weeks of age (*36, 37*). At 5 weeks of age, PEP-null and PEP-R619W splenic NK cells had differential maturation states compared to PEP-WT (Fig. 5). Specifically, of the NK cell repertoire, PEP-WT mice had more DP NK cells, but PEP-null and PEP-R619W had increased proportions of terminally mature (CD27- CD11b+) NK cells at 5 weeks of age (Fig. 5A, 5D, 5E). However, at 8 weeks of age, there were no differences detected in the proportion of DP or terminally mature NK cells between the three genotypes of mice. Collectively, this data indicates that PEP may negatively impact NK cell maturation at homeostasis, which could play a role in the observed differences in mature NK cell presence and function in PEP-R619W mice following MHV A59 infection.

Fig. 5

Figure 5: PEP-null and PEP-R619W splenic NK cell repertoires have higher proportions of terminally mature NK cells at 5 weeks of age.

Whole spleens were harvested and stained for flow cytometric analysis from 5-week-old or 8-week-old mice as indicated. Representative flow plots from 5-week-old mice are shown from CD3e- CD19- populations, pie charts represent the proportion of the NK1.1+ CD49b+ population that are: CD27- CD11b- (double negative, DN), CD27+ CD11b-, CD27+ CD11b+ (double positive, DP), or CD11b+ CD27- (A). Quantification for frequency (%) of CD27- CD11b- (double negative, DN) (B), CD27+ CD11b- (C), CD27+ CD11b+ (double positive, DP) (D), or CD11b+ CD27- (E) NK cells (NK1.1+ CD49b+). Gating strategy for examined NK cells: Lymphocytes> Single cell x2> autofluorescent-> Live> CD3e- CD19-> NK1.1+ CD49b+> CD27+/- CD11b+/-. Frequencies of flow cytometric data are combined from 5 independent experiments. Each symbol represents an individual mouse. p-values from Two-way ANOVA with Tukey's Multiple Comparisons are shown for each panel. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

PEP-R619W NK cells restrict viral replication and enhance IFNγ production during

coronavirus infection

Given our observation that NK cells are more mature and functional, and there are more of them

in PEP-R619W mice during infection, we next wanted to determine if NK cells were necessary

for driving disease protection during MHV A59 infection. To test this, we administered an anti-

NK1.1 (α-NK1.1) depleting antibody (clone PK136) or anti-IgG isotype control (α-Iso) two days

before MHV A59 infection. Subsequent injections were administered every four days after the

initial treatment (Fig. 6A). NK depletion was verified at all key time points, both within the

spleen and in the peripheral blood (Fig. S6A-E). Loss of NK cells in PEP-R619W mice resulted

in a decreased capacity to control virus infection, as viral burden in the liver at 3- and 5- dpi rose

to comparable levels of both α-NK1.1 PEP-WT and isotype-treated PEP-WT mice (Fig. 6B). In

addition, isotype-treated PEP-R619W mice maintained the reduced levels of viral titer in the

liver compared to isotype-treated PEP-WT mice at these time points (Fig. 6B). These data

indicate that PEP-R619W NK cells effectively reduce liver viral load, but PEP-WT NK cells

have minimal impact on combating viral replication within the liver. We again detected no

differences in the splenic titers, regardless of the presence of NK cells (Fig. S6F). This data

suggests that in PEP-R619W mice, the increased presence of NK cells in the liver is one of the

key innate cells responsible for combating viral replication during the early days of infection.

Our data support this conclusion, as all NK-sufficient PEP-R619W mice, including immune-

competent (Fig. 1E), Rag1-/- (Fig. 2E), and α-Iso (Fig. 6B) mice, had significantly reduced liver

viral titers at days 3 and 5 post-infection compared to PEP-WT counterpart mice. In contrast, this

protection was lost in α-NK1.1 PEP-R619W mice (Fig. 6B). Next, we wanted to determine if NK

cells were a critical source of IFNγ in our PEP-R619W mice. Upon depletion of NK cells, the

levels of IFNγ in liver homogenate at 3 dpi in α-NK1.1 PEP-R619W mice were significantly

reduced compared to α-Iso PEP-R619W mice (Fig. 6C). Further, α-Iso PEP-R619W had a

significantly higher concentration of IFNγ compared to α-Iso PEP-WT, recapitulating the

cytokine profiling data previously shown (Fig. 4G). In conclusion, this data highlights that PEP-

R619W enhances NK cell function to protect against MHV A59 viral replication in the liver

through, in part, boosting the production of NK cell-derived IFNγ.

PEP-R619W NK cells do not mediate weight loss, survival, or liver histopathology during

coronavirus infection

Since PEP-R619W NK cells mediate viral titer at early days post-infection and are a key source

of IFNγ, we next wanted to determine if they were necessary for mediating weight loss and

survival during MHV A59 infection. Following 1e5 PFU MHV A59 infection, NK cell depletion

in either PEP-WT or PEP-R619W mice did not result in changes in weight loss, survival, or in

liver histopathology compared to NK-sufficient PEP-WT and PEP-R619W counterparts (Fig.

6D-F and Fig. S6G).

Overall, this data indicates that NK cells in PEP-R619W mice play a specific role in combating

MHV A59 infection by restricting viral replication and are critical producers of IFNγ within the

primary site of replication, the liver. However, these NK cells are dispensable for protection

against weight loss, survival, and liver damage. While NK cell depletion in PEP-R619W mice

increased viral load and reduced liver IFNγ concentration, the same depletion in PEP-WT mice

did not affect liver viral titer or IFNγ production. This disparity can potentially be attributed to

the reduced number and impaired function of M-cNK cells in the livers of PEP-WT mice at 3 dpi

(Fig. 3D-G, Fig. 4A and 4B), making their absence less impactful on viral replication.

 Fig. 6

Figure 6: PEP-R619W NK Cells control viral burden and are key producers of IFNγ

during MHV A59 infection.

PEP-WT and PEP-R619W mice received Natural Killer cell depleting antibody (α-NK1.1, Clone

PK136) or non-depleting isotype control antibody (α-Iso) as indicated prior- and post-MHV A59

infection (i.p) (A). Following 5e2 PFU MHV A59 infection in α-Iso PEP-WT (black, black

circle), α-Iso PEP-R619W (blue, blue triangle), α-NK1.1 PEP-WT (clear, black circle) and α-

NK1.1 PEP-R619W (clear, blue triangle) mice, the whole liver was harvested at the indicated

dpi, homogenized, and viral titer was quantified via Plaque Assay (B). Mice were infected with

1e5 PFU MHV A59 infection (i.p), and at 3 dpi, the whole liver was harvested, homogenized,

and the levels of IFNγ were determined by ELISA (C). Following 1e5 PFU MHV A59 infection,

mice were tracked by weight (D) and survival (E). Respective spider plots for individual mouse

weights are shown below (D). Histopathology of the livers of mice at 3 dpi following 1e5 PFU

MHV A59 infection, with representative photomicrographs of liver sections exhibiting areas of

necrosis, inflammation, and edema/fibrin accumulation (black arrow) and cumulative pathology

scores represented as mean + SEM. Scale bar = 500 μm (F). Each symbol represents an

individual mouse for whole liver titer (B) and IFNγ ELISA (C). Viral titers are pooled data from

2 independent experiments at each time point, comparisons are shown from multiple unpaired T-

Tests, α-Iso PEP-WT vs α-Iso PEP-R619W, α-NK1.1 PEP-WT vs α-NK1.1 PEP-R619W,

*$p<0.01$, **$p<0.01$. The dashed line indicates the limit of detection (L.O.D.). IFNγ ELISA is

representative of two independent experiments, p-values from One-way ANOVA with Tukey's

Multiple Comparisons are shown, *$p<0.05$, **$p<0.01$, ***$p<0.001$, ****$p<0.0001$. Mock mice

are a mixture of both genotypes. Weight loss and survival studies were pooled from 2 individual

experiments. Group sizes were α-Iso PEP-WT n = 18, α-Iso PEP-R619W n = 17, α-NK1.1 PEP-

WT n = 19, and α-NK1.1 PEP-R619W n = 17. For weight loss statistical analysis (D), significant

p-values from One-way ANOVA with Tukey's Multiple Comparisons at each dpi are represented

by # comparing α-NK1.1 PEP-WT vs α-NK1.1 PEP-R619W, or * comparing α-Iso PEP-WT vs.

α-Iso PEP-R619W. Log-rank Mantel-Cox Test (survival) (E), ***$p<0.001$. For histopathological

analysis, each dot represents an individual mouse, with p-values from One-way ANOVA with

Tukey's Multiple Comparisons shown, *$p<0.05$.

DISCUSSION

Despite the strong genetic link between the minor allele of *PTPN22* and the development of various autoimmune diseases, this allele persists in the human population. A potential theory lies in the fact that the mechanisms driving heightened immune responses, while pathogenic in the context of autoimmunity, are likely protective when defending against infections and cancer. Previous studies support this reasoning, as PEP-R619W mice exhibit enhanced antiviral immunity during chronic LCMV-cl13 infection and increased antitumor immunity, resulting in reduced disease severity compared to PEP-WT mice (*18, 19*). Similar results in PEP-null mice have been reported during LCMV-cl13 infection (*29-31*). However, these diseases are chronic. Thus, we were interested in determining if PEP-null and/or PEP-R619W mice would also have improved disease outcomes during acute, moribund coronavirus infection, MHV A59.

Our results show that PEP-R619W and PEP-null do not always phenocopy each other. Regardless of whether PEP-null mice were fully immune-competent or on a Rag1-/- genetic background, their phenotypes were comparable to PEP-R619W mice after 5e4 PFU infection, but demonstrated increased susceptibility following 1e5 PFU infection and mirrored the outcomes observed in PEP-WT mice (Figs. 1 and 2). Despite similar splenic innate profiles and NK activation between PEP-null and PEP-R619W mice at 3 dpi following 5e4 PFU infection, after 1e5 PFU MHV A59 infection, PEP-null splenic NK cell phenotypes were comparable to PEP-WT (Fig. S3 and S5). These findings add to the current literature, highlighting that there are differences between PEP-null and PEP-R619W. While PEP-null and PEP-R619W mice may be similar in certain scenarios, such as in LCMV-cl13 antiviral immunity, there are other examples where they can differ (*19-21, 27, 29-31*). This may lie in cellular and/or molecular differences between these strains. For example, previous studies show that PEP-null mice have more Tregs

than PEP-WT and PEP-R619W mice, and that the PEP-R619W mutation does not directly

impact phosphatase activity (*3, 4, 9, 23, 24, 26-28*). Instead, the mutation disrupts molecular

interactions with other proteins, such as TRAF3 and Csk, leading to altered immune function (*3,*

4, 9, 23, 24, 26-28). The precise ways in which established molecular interactions and other

potential mechanisms that influence innate immune cell function diverge between PEP-null and

PEP-R619W mice are poorly understood. Further investigation into these mechanisms would

provide crucial insight into the varying outcomes observed between these strains during MHV

A59 infection.

Our data shows that PEP-R619W protects against murine coronavirus, MHV A59, associated

disease (Fig. 1). This is paired with reduced liver viral titer at early days post-infection, and

accelerated clearance compared to PEP-WT mice (Fig. 1). This protection in PEP-R619W mice

was partially mediated by an enhanced innate immune response. This is further strengthened by

the results of our studies using Rag1-/- models, as Rag1-/- PEP-R619W mice had reduced

disease compared to Rag1-/- PEP-WT mice (Fig. 2). These data indicate that PEP-R619W

differentially modulates the innate immune response to defend against acute MHV A59 infection

(Figs. 1 and 2). This data is further supported by the immune phenotyping of both the spleen and

liver at 3 dpi, where PEP-R619W mice had more innate immune cells compared to PEP-WT

mice (Fig. 3, Fig. S3 and S4).

We interrogated the immune response in the liver following 1e5 PFU infection to define how

PEP-R619W uniquely enhanced innate antiviral immunity. Notably, PEP-R619W mice had more

NK cells, DCs, and macrophages compared to PEP-WT and PEP-null mice (Fig. 3D). However,

we detected no differences in type-I interferon (IFN-I) production, which is necessary for

survival following MHV A59 infection (*44*). There were no changes in the pDC population,

which are critical producers of IFN-I (Fig. 3D), or in the systemic and liver homogenate levels of

IFNα and IFNβ (Fig. 4C, E, F, H, and I) between infected genotypes, indicating that PEP-

R619W protects through alternative mechanisms, such as enhancing NK cell function. NK cells

can directly lyse infected cells through the release of perforin and granzyme B, are the primary

producers of IFNγ during the innate immune response, and these functions are enhanced as NK

cells mature (*36, 37, 45, 46*). These effector functions are necessary for combating murine

cytomegalovirus (MCMV) disease and viral replication and have been specifically shown to be

vital in driving the innate immune response in the liver post-infection (*47-51*). As such, we more

closely interrogated the NK cell compartment in PEP-WT and PEP-R619W mice post-MHV

A59 infection.

We investigated the role of NK cells during MHV A59 infection and discovered that: 1) there

were more mature conventional NK (M-cNK) cells in the spleen and liver of PEP-R619W mice

(Fig. 3D-G and Fig. S3D, S3E), 2) PEP-R619W enhanced M-cNK effector function and

polyfunctionality compared to PEP-WT (Fig. 4A and 4B), and 3) PEP-R619W NK cells, but not

PEP-WT NK cells, are necessary for restricting viral replication in the liver at 3 and 5 dpi (Fig.

6B) and are a critical source of IFNγ (Fig. 6C). Taken together, these results indicate that PEP-

R619W augments M-cNK cell antiviral function in the liver during MHV A59 infection, leading

to reduced viral replication, but PEP-R619W M-cNK cells do not directly mediate weight loss,

survival, or liver pathology (Fig. 6D-F). These findings add to recent work and highlight the

protective role of NK cells at the primary site of coronavirus infection, as NK cells are critical

for combating SARS-CoV-2 replication in both human and non-human primate lungs (*52-54*).

However, our data also demonstrates that viral burden and disease symptoms are not always

directly correlated, and this is supported by other viral infection models. An example of this is

seen in chronic LCMV-cl13 infection, where weight loss is driven by CD8 T-cell

immunopathology (*55*).

We are one of the first groups to investigate the function of PEP in NK cells, yet the molecular

role of PEP in NK cells remains undefined, despite being the immune cells with the highest

Lyp/PEP expression in humans and mice (*56, 57*). Our results show that at 5 weeks of age, PEP-

R619W mice have more mature NK cells post-MHV A59 infection at 3 dpi in the spleen and

liver compared to PEP-WT (Fig. S3 and Fig. 3). This phenotype persists at homeostasis, where

both PEP-null and PEP-R619W mice had a higher proportion of terminally mature (CD11b+

CD27-) NK cells in the spleen compared to PEP-WT counterparts (Fig. 5). Despite these

findings, the molecular functions of PEP within NK cells, and how the PEP-R619W variant

accelerates maturity and enhances effector functions during infection, remains unknown. These

results warrant additional studies defining the molecular mechanisms by which PEP and PEP-

R619W regulate NK cell maturity and function at homeostasis and during disease.

In conclusion, our results indicate that the autoimmunity-associated allele of *PTPN22* enhances

innate antiviral immunity against acute murine coronavirus infection, MHV A59, and adds to the

growing literature supporting the protective role of this allele during viral and tumorigenic

challenges (*18, 19*). We have shown a divergence in protection against MHV A59 infection in

PEP-null mice in an inoculation dose-dependent manner, whereas PEP-R619W was protective

regardless of infection dose. Additionally, we showed that PEP-R619W boosts innate cell

infiltration, enhances NK cell maturation and function, and, overall, reduces disease following

murine coronavirus infection. This data highlights that PEP-R619W uniquely modifies immune

function through distinct mechanisms compared to both PEP-WT and PEP-null, especially in NK

cells. These findings provide further rationale for testing the protective capacity of PEP-R619W

in additional infection models and defining how PEP-R619W augments immunity in a context-

dependent manner.

MATERIALS AND METHODS

Study design

The primary objective of this study was to define how the loss of *Ptpn22* (PEP-null) and its

autoimmunity-associated allelic variant (PEP-R619W) impacts antiviral immune responses

during an acute coronavirus infection, MHV A59. Following MHV A59 infection, we assessed

the ability of MHV A59 to cause disease in our PEP-WT, PEP-null, and PEP-R619W mice. This

was achieved by measuring several different markers of pathogenesis (weight loss, survival, viral

titer, and histology), performing in-depth immune phenotyping in the spleen and liver (flow

cytometry), quantifying cytokine production (Legendplex), and testing if NK cells were

necessary for viral control and disease progression (NK depletion). Sample sizes were

determined based on prior experiments, and the number of independent experiments and

replicates was described in the figure legends. For most experiments, randomization and blinding

were not used as the results involved objective readouts. For liver histopathology, the manuscript

data were not shared, and the sample genotypes were blinded until the analysis was completed.

Ethics Statement

554 The University of Kansas (KU) Institutional Animal Care and Use Committee (IACUC)

555 reviewed and approved all animal studies under protocol number AUS 278-01.

Mice

Both male and female mice at 5 weeks of age were used in all studies unless otherwise noted.

We do not observe sex-based differences in these studies. C57BL/6J mice and C57BL/6 Rag1-/-

mice were originally purchased from Jackson Labs and then bred and maintained in the

University of Kansas Animal Care Unit (ACU) facilities. *Ptpn22* knockout (PEP-null) and

Ptpn22 R619W (PEP-R619W) mice were generated using CRISPR/Cas9 technology using

methods previously reported (*15, 18, 19*) (*58*). PEP-null Rag1-/- and PEP-R619W Rag1-/- mice

were derived as previously described (*18*). IFNγ KO (RRID: IMSR_JAX:002287) and IFNγR

KO (RRID: IMSR_JAX:003288) mice were purchased from Jackson Labs and were housed and

maintained in the University of Kansas ACU facilities as detailed above.

Cell Culture

<u>HeLa-MHVR and 17Cl-1 Cells:</u>

HeLa cells expressing the MHV receptor CEACAM1a (HeLa-MHVR) were cultured in

Advanced Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% FBS, 1% L-

glutamine, and 1% Penicillin/Streptomycin, and 17Cl-1 cells were grown in DMEM

supplemented with 5% FBS, 5% Tryptose Phosphate Broth, and 2% Penicillin/Streptomycin (*59*)

(*60*).

<u>Bone Marrow Dendritic Cells (BMDC) and Macrophages (BMM):</u>

To generate BMDCs, bone marrow cells were isolated from PEP-WT, PEP-null, and PEP-

R619W mouse femurs. Following isolation, cells were cultured in Advanced DMEM

supplemented with 10% FBS, 1% L-glutamine, 1% Penicillin/Streptomycin, and 100ng/mL

FLT3L (Stem Cell Technologies, Vancouver, CA). For BMMs, bone marrow cells were isolated

and cultured in Roswell Park Memorial Institute medium (RPMI) supplemented with 10% FBS,

1% L-glutamine, and 1% Penicillin/Streptomycin with 50ng/mL M-CSF (Stem Cell

Technologies, Vancouver, CA) for 8 days. An additional 10 mL of M-CSF-containing media was

added to BMM cultures on day 3 (*61*), and on day 8, differentiated cells were harvested, counted,

and replated for further assays.

MHV A59 Production, Titer, and Infections

MHV A59 stocks were grown in 17Cl-1 cells, and viral titers were determined on HeLa cells

expressing the MHV receptor CEACAM1a (HeLa-MHVR), as previously described (*59, 60, 62-*

64). Briefly, HeLa-MHVRs were seeded in 12-well plates the day before infection. The

following day, once the HeLa-MHVRs were grown to 90-95% confluency, 10-fold dilutions of

titer samples were prepared, and the HeLa-MHVRs were inoculated for a 45-to-60-minute

adsorption phase, followed by 1 mL overlay per well of 1:1 mixture of 1.2% Agarose and 2x

DMEM (10% FBS, 1% L-Gln, 1% Pen/Strep). Once solidified, 500 µL D2 media (DMEM, 2%

FBS, 1% L-Gln, 1% Pen/Strep) was added to the overlay. The plaques were counted and

recorded 48 hours later for viral titer (PFU/sample) calculation.

For *in vivo* infections, mice were inoculated with 500 PFU, 5e4 PFU, or 1e5 PFU MHV A59 in a

final volume of 200 µL sterile PBS via intraperitoneal (i.p.) injection. Throughout all infections,

mice were weighed daily and euthanized if weight loss was greater than 20% of the original

starting weight. To determine viral load, the whole liver and spleen were harvested and

homogenized in 5 mL or 1 mL sterile DMEM, respectively, centrifuged to remove cellular

debris, and stored at -80^{0}C. The viral titer was determined on HeLa-MHVR cells as detailed

above.

For *ex vivo* Bone Marrow Dendritic Cell (BMDC) and Bone Marrow Macrophage (BMM)

infections, cells were inoculated at a multiplicity of infection (MOI) of 0.1 with a 45-to-60-

minute adsorption phase. The viral inoculum was aspirated, and 1 mL of advanced DMEM

supplemented with 10% FBS, 1% L-glutamine, 1% Penicillin/Streptomycin or RPMI

supplemented with 10% FBS, 1% L-glutamine, and 1% Penicillin/Streptomycin, for BMDC or

BMM, respectively, was added per well and incubated for 24 hours. At 24 hours post-infection,

the cells were scraped and resuspended before being placed in the -80^0C freezer overnight.

Following freeze-thaw, the virus from the supernatant and cells was combined and tittered on

HeLa-MHVRs as described above.

Leukocyte Isolation and Flow Cytometry

Mice were euthanized at indicated time points in line with AVMA and KU IACUC guidelines by

CO2 inhalation followed by cervical dislocation before tissue harvest.

The spleen was excised at indicated days post-infection, smashed over 40 μm filters, rinsed with

DMEM, and centrifuged to remove debris. The cell pellet was resuspended in 2 mL ACK red

cell lysis buffer, incubated at RT for 2 minutes, quenched with 10 mL DMEM, and centrifuged.

The resultant pellet was resuspended in 2 mL advanced DMEM supplemented with 10% FBS,

1% L-glutamine, 1% Penicillin/Streptomycin to generate a single cell suspension.

Whole livers were harvested following cardiac perfusion with 15-20 mL sterile PBS and placed

in 3 mL DMEM supplemented with 10% FBS on ice. Livers were digested and processed using a

murine liver dissociation kit (Miltenyi Biotec, Bergisch Gladbach, North Rhine-Westphalia,

Germany) per the manufacturer's protocol. Following centrifugation, the cell pellet was

resuspended in 1 mL sterile DMEM (1% L-glutamine), gently overlaid onto a 20 mL 33%

percoll gradient in PBS, and centrifuged at 800xg for 25 minutes at room temperature (RT) (*65*).

After aspiration, the cell pellet was resuspended in 2 mL Advanced DMEM (supplemented with

10% FBS, 1% L-glutamine, 1% Penicillin/Streptomycin) to generate a single cell suspension.

To harvest peripheral blood for NK Depletion verification, 50 µL of blood was acquired via

retro-orbital (r.o.) bleeds using heparinized capillary tubes. 10 µL of blood was plated in a 96-

well plate for each sample. 100 µL of ACK red cell lysis buffer was added and incubated at RT

for 2 minutes, quenched with 100 µL Advanced DMEM (supplemented with 10% FBS, 1% L-

glutamine, 1% Penicillin/Streptomycin), centrifuged, and resuspended in 200 µL of media to

generate a single cell suspension.

All single cell suspensions were counted using Vi-CELL BLU (Beckman Coulter, Brea, CA).

The concentration of each sample was adjusted to plate 2e6 cells/well in round-bottom 96-well

plates for antibody staining and flow cytometric analysis.

All flow cytometry was performed on the Cytek Aurora 5 laser system (355 nm [UV], 405 nm

[Vio], 488 nm [Blue], 561 nm [YG], and 640 nm [Red]) spectral flow cytometer (Fremont, CA,

US). Single stain control Biolegend Compensation Beads were used for unmixing (San Diego,

California, U.S). Unmixed files were analyzed using FlowJo Software (BD Biosciences, San

Diego, California). Antibodies used in varying combinations (depending upon the experiment)

are shown below in the Supplementary Materials (Table S1).

All samples were incubated with diluted Fc block (Biolegend) for 10 minutes and then stained

for 30 minutes at 4^0C in the dark for surface marker staining in serum-free PBS. For intracellular

cytokine staining, cells were incubated with brefeldin A (BFA, Thermo Scientific) for four hours

at 37^0C before surface staining. BD Cytofix and Permwash kit or Tonbo Foxp3 Fix/Perm kit

were used according to manufacturers' protocols for intracellular cytokine or intranuclear

transcription factor staining, respectively.

Cytokine and Chemokine Quantification

500 µL of blood was acquired via retro-orbital (r.o.) bleeds using non-heparinized capillary tubes before euthanasia. After incubating at RT for 30 minutes, the blood was centrifuged at 13,000 RPM for 10 minutes at RT, and the serum supernatant was collected and stored at -80^0C for future analysis. As described above, the whole liver was homogenized in 5 mL DMEM, centrifuged to remove cellular debris, and stored at -80^0C for future analysis. Serum and liver homogenate antiviral cytokines and chemokines were quantified using a LEGENDplex assay (Biolegend), with the serum being diluted 1:2 as described in the manufacturer protocol. In a separate experiment, a portion of the left lateral liver lobe was harvested, weighed, homogenized, and the concentration of IFNβ was determined using the Mouse IFN-Beta ELISA Kit (PBL Assay Science). The levels of IFNγ were determined using LEGEND MAX™ Mouse IFNγ ELISA Kit (Biolegend) in NK cell depletion experiments following whole liver harvest and homogenization at indicated time points.

Natural Killer (NK) cell depletion

Depletion of NK cells was achieved through i.p. injection of 100 µg anti-NK1.1 monoclonal antibodies (clone PK136) two days before infection and followed by 25 µg anti-NK1.1 injections every four days to sustain depletion (Bio-X-Cell). In parallel, separate mice were administered control IgG injections at the same dosage and timings as detailed above (Bio-X-Cell). The experimental outline is shown in Supplementary Figure 6.

Histopathology

Whole livers were harvested following cardiac perfusion with 15-20 mL sterile PBS, followed by 10-15 mL of 4% PFA diluted in PBS, and placed in 20 mL of 10% PFA diluted in PBS

(minimum ratio of 1 gram tissue:10 mL 10% PFA). After 72 hours at 4^0C in the dark, a

representative section from each lateral and medial (right and left) lobe was cut and processed

for routine hematoxylin and eosin (H&E) staining. The liver lesions were blindly scored by an

American College of Veterinary Pathology Board-certified pathologist. The lesions scored were

inflammation, necrosis, and edema/fibrin on a scale of 0–10% (score 1), 10–40% (score 2), 40–

70% (score 3), and >70% (score 4). Cumulative scores were obtained for each mouse and

presented as total pathology score.

Statistical Analysis and Graphing

All graphs and appropriate statistical analysis for data were done in GraphPad Prism (La Jolla,

CA). The type of statistical tests used are listed in each figure legend. Data was considered

statistically significant if the p-value<0.05. Data with a p-value>0.05 was determined non-

significant, and pairwise comparisons were either not labeled or represented with "ns." Figure

legends indicate if data are from pooled experiments or are representative of multiple studies.

Most graphs display mean + SEM, unless otherwise stated.

Supplementary Materials

Figure S1: PEP-R619W does not impact splenic titer or restrict viral replication in myeloid cells.

Figure S2: Splenic titers are unchanged in Rag1-/- mice regardless of PEP genotype.

Figure S3: PEP-R619W increases the splenic innate immune population.

Figure S4: Representative gating strategy for different liver immune cell populations and

additional quantification of immune cells.

Figure S5: Infection dose-dependent impact on splenic mature NK function.

Figure S6: NK depletion protocol and NK-depleted spleen titer and histopathology scores.

Table S1: Flow Cytometry Antibodies

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ACKNOWLEDGMENTS:

848 We thank the KU Flow Cytometry Core, KU Animal Care Unit, and all members of the Orozco
849 lab for their discussions and assistance. We also thank Dr. Hans Dalton for his edits on this
850 manuscript.

Funding Sources:

NIH T32 Chemical Biology T32 Training Grant GM13206 (AB)
KU Chemical Biology of Infectious Disease (COBRE) National Institute of General Medical
Sciences (NIGMS) of the National Institutes of Health under award number P20GM113117
(RCO, ARF)
KU Center for Genomics Seed Grant (RCO)
Funds from the University of Kansas (RCO)
NIGMS R35GM138029 (ARF)
NIH T34 GM062232 (KJLHR)

Author contributions:

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Funding acquisition: AMB, KJLHR, SM???, RCO

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Writing – original draft: AMB, SM, ARF, RCO

Writing – review & editing: AMB, KJLHR, NS, TRC, CMK, SM, ARF, RCO

871 **Competing interests:**

872 Authors declare that they have no competing interests.

873 **Data and materials availability:**

874 All data are available in the main text or the supplementary materials. Raw data is available upon
875 request.

Supplementary Materials

Fig. S1

Figure S1: PEP-R619W does not impact splenic titer or restrict viral replication in myeloid cells.

To measure viral burden, spleen homogenates from infected (5e2 PFU MHV A59) PEP-WT, PEP-null, and PEP-R619W mice were used for plaque assay (A, B). Experimental schematic for deriving bone marrow-derived macrophages (BMMs) and bone marrow-derived dendritic cells (BMDCs) (C). The viral titer was quantified via Plaque Assay for BMMs (D) and BMDCs (E). Liver histopathology scores of individual parameters (inflammation, necrosis, and edema/fibrin) at 3 dpi following 1e5 PFU MHV A59 infection are shown (F). For whole spleen titer (A, B), each symbol represents an individual mouse. The dashed line indicates the limit of detection (L.O.D.). Certain PEP-WT mice are represented in both graphs, as some experiments had all three genotypes, whereas others contained only PEP-WT vs. PEP-null or PEP-R619W. Combined data from 2 independent experiments, multiple unpaired T-Tests, PEP-WT vs PEP-R619W, PEP-WT vs PEP-null, at each time point. For BMM and BMDC titer, each MHV A59 infection was performed at MOI = 0.1. Data are shown from two independent experiments with 3 technical replicates per experiment. For histopathological analysis, each dot represents an individual mouse, with p-values from One-way ANOVA with Tukey's Multiple Comparisons shown, $*p<0.05$, $**p<0.01$.

 Fig. S2

Figure S2: Splenic titers are unchanged in Rag1-/- mice regardless of PEP

genotype.

To measure viral burden, liver homogenates from infected (5e2 PFU) Rag1-/- PEP-

WT (black), Rag1-/- PEP-null (red), and Rag1-/- PEP-R619W (blue) mice were

used for plaque assay (A, B). Each symbol represents an individual mouse. The

dashed line indicates the limit of detection (L.O.D.). Certain Rag1-/- PEP-WT

mice are represented in both graphs, as some experiments had all three genotypes,

whereas others contained only Rag1-/- PEP-WT vs Rag1-/- PEP-null or Rag1-/-

PEP-R619W. Multiple unpaired T-Tests, PEP-WT vs PEP-R619W, PEP-WT vs

PEP-null, at each time point.

Fig. S3

Figure S3: PEP-R619W increases the splenic innate immune population.

Representative gating strategies to identify splenic immune cell populations of

interest (A). Populations are labeled on flow cytometry plots, where black arrows

indicate the down-gating of the population from which they are drawn from, and

red arrows indicate the down-gating from one population to multiple populations.

Following PBS injection (Mock, white bar, circle) or 5e4 PFU MHV A59 infection

(i.p) in PEP-WT (black bar, circle), PEP-null (red bar, square), PEP-R619W (blue

bar, triangle) mice, at 3 dpi the spleen was harvested and antibody stained for flow

cytometric analysis. The absolute count of splenocytes for all genotypes (B).

Frequencies (%) of CD3e- CD19- of Live cells (C). Frequency (%) of several

innate cells of Live cells is shown (D). The gating strategy for all innate subsets is:

Lymphocytes> Single cell x2> autofluorescent-> Live> CD3e- CD19-> Ly6G-

Ly6C+/- (non-neutrophils). NK Cells: innate subsets> NK1.1+. DCs: innate

subsets> CD11c+ PDCA-1-. pDCs: innate subsets> PDCA-1+ CD11c+/-.

Monocytes: innate subsets> Ly6Chi CD11b+. Macrophage: innate subsets> Ly6C-

CD11b+/-> CD11b+> F4/80+. Neutrophils: Lymphocytes> Single cell x2>

autofluorescent-> Live> CD3e- CD19-> Ly6G+ Ly6C+. Frequency (%) of

CD11b+ (mature) NK cells (E). Frequency (%) Splenic CD8α+ cDCs (F) and

expression (gMFI) of CD80 (G) and CD86 (H) with representative histograms to

the right. Frequency (%) CD8α- cDCs (I) and expression (gMFI) of CD80 (J) and

55   CD86 (K) with representative histograms to the right. Quantification of flow

56   cytometric data was pooled from 3 independent experiments. Each symbol

57   represents an individual mouse. Mock mice are a mixture of all 3 genotypes. p-

58   values from One-way ANOVA with Tukey's Multiple Comparisons are shown for

59   each panel. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

Fig. S4

Figure S4: Representative gating strategy for different liver immune cell populations and additional quantification of immune cells.

Representative gating strategies to identify liver immune cell populations of interest presented in Figure 3 (A). Populations are labeled on flow cytometry plots, where black arrows indicate the down-gating of the population from which they are drawn from, and red arrows indicate the down-gating from one population to multiple populations. Following PBS injection (Mock, white bar, circle) or 1e5 PFU MHV A59 infection (i.p) in PEP-WT (black bar, circle), PEP-null (red bar, square), PEP-R619W (blue bar, triangle) mice, at 3 dpi the liver was perfused, harvested, and antibody stained for flow cytometric analysis. Tim4+ Macrophages (Kupffer-like cells) frequency (%) (B) and expression of CD86 (gMFI) in Tim4+ Macrophages (C), with representative histograms below. The first plot (left) comparing Mock, PEP-WT, and PEP-R619W and the second plot (right) comparing Mock, PEP-WT, and PEP-null are representative of two separate independent experiments. The gating strategy for Kupffer-like (Tim4+ macrophages) is: Lymphocytes> Single cell x2> autofluorescent-> Live> CD45+> CD3e- CD19-> Ly6G- Ly6C+/- (non-neutrophils)> NK1.1-> Ly6C- CD11b+/-> F4/80+ CD11b+> Tim4+. MHC-II+ DCs frequency (%) (D) and expression of MHC-II (gMFI) in DCs (E) with a representative histogram below. CD86+ DCs frequency (%) (F) and expression of CD86 (gMFI) in DCs (G) with a

81 representative histogram below. The gating strategy for MHC-II+ DCs or CD86+

82 DCs is: Lymphocytes> Single cell x2> autofluorescent-> Live> CD45+> CD3e-

83 CD19-> Ly6G- Ly6C+/- (non-neutrophils)> NK1.1-> CD11c+ PDCA-1-> MHC-

84 II+ or CD86+. Quantification of flow cytometric data was pooled from 2

85 independent experiments. Each symbol represents an individual mouse. Mock mice

86 are a mixture of all 3 genotypes. p-values from One-way ANOVA with Tukey's

87 Multiple Comparisons are shown for each panel. *p<0.05, **p<0.01, ***p<0.001,

88 ****p<0.0001.

Fig. S5

Mature NK Cell

50,000 PFU

100,000 PFU

Figure S5: Infection dose-dependent impact on splenic mature NK function.

Following PBS injection (Mock, white bar, circle) or 5e4 PFU (A-F) or 1e5 PFU (G-L) MHV A59 infection (i.p) in PEP-WT (black bar, circle), PEP-null (red bar, square), and PEP-R619W (blue bar, triangle) mice, at 3 dpi the spleen was harvested, surface and intracellularly antibody stained for flow cytometric analysis. Frequency (%), expression (gMFI), and representative histogram to the right of CD107a (A-B, G-H), Perforin (C-D, I-J), and IFNγ (E-F, K-L) in Mature NK cells, for 5e4 PFU and 1e5 PFU MHV A59 infections, respectively. The gating strategy for Mature NK cells and effector markers was: Lymphocytes> Single cell x2> autofluorescent-> Live> CD3e- CD19-> Ly6G- Ly6C+/- (non-neutrophils)> NK1.1+> CD11b+> CD107a+ or Perforin+ or IFNγ+. Frequencies of flow cytometric data are combined from 2 independent experiments, gMFI's are representative images from 2 independent experiments at each dose. Each symbol represents an individual mouse. Mock mice are a mixture of all 3 genotypes. p-values from One-way ANOVA with Tukey's Multiple Comparisons are shown for each panel. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

 Fig. S6

Figure S6: NK depletion protocol and NK-depleted spleen titer and histopathology scores.

Experimental timeline detailing the concentration of α-NK1.1 antibody (Clone PK136) and frequency of doses (A). NK cell depletion representative flow plots and absolute counts of NK1.1+ cells (per 10^6 cells) are shown for the spleen and peripheral blood at day 2 (B) and day 4 (C) post-100μg α-NK1.1 or α-Iso injection (i.p). Alternatively, mice were administered 100μg α-NK1.1 or α-Iso injection (i.p), and on day 4, an additional dose of 25μg α-NK1.1 or α-Iso injection was given. NK cell depletion representative flow plots and absolute counts of NK1.1+ cells (per 10^6 cells) are shown for the spleen and peripheral blood at day 8 (D). NK depletion at 3 dpi following 1e5 PFU MHV A59 infection using the timeline depicted in Figure 6A (E). Following 5e2 PFU MHV A59 infection (i.p), spleens were harvested and tittered at the indicated days post-infection with NK depletion (α-NK1.1) or non-depleting isotype control (α-Iso), with timeline depicted in Figure 6A (F). Liver histopathology scores of individual parameters (inflammation, necrosis and edema/fibrin) are shown (G). PEP-WT mice were used to verify NK cell depletion. The gating strategy to identify splenic and peripheral blood NK cells was: Lymphocytes> Single cell x2> autofluorescent-> Live> CD45+> CD3e- CD19-> NK1.1+. Representative flow plots are shown from CD3e- CD19. Each dot represents an individual mouse. p-values from Welch's unpaired t test are

shown for NK cell counts, *p<0.05, **p<0.01. Viral titers are pooled data from 2

independent experiments at each time point; comparisons are shown from multiple

unpaired T-Tests, α-Iso PEP-WT vs α-Iso PEP-R619W, α-NK1.1 PEP-WT vs α-

NK1.1 PEP-R619W. For histopathological analysis, each dot represents an

individual mouse, with p-values from One-way ANOVA with Tukey's Multiple

Comparisons shown, *p<0.05, **p<0.01.

Table S1: Flow Cytometry Antibodies

Antigen	Fluorophore	Dilution (1:x)	Company	Clone	CAT / REF	LOT
Ghost Viability	Violet510	1000	TONBO Biosciences	N/A	13-0870-T100	D0870120221133
CD45	Spark+ BUV395	200	BioLegend	30-F11	103192	B428503
CD45	BUV395	200	BD Biosciences	30-F11	564279	3205129
CD3e	PECy5	250	BioLegend	145-2C11	100309	B359890
CD19	BV711	400	BioLegend	6D5	115555	B287454
CD19	APC	250	BioLegend	6D5	115512	B371440
CD19	AF700	250	BioLegend	6D5	115512	B371440
Ly6C	BV785	400	BioLegend	HK1.4	128041	B386418
Ly6G	PE610	200	Invitrogen	1AB-Ly6g	61-9668-80	2445867
Ly6G	BV570	200	BioLegend	1AB	127629	B418454
CD11c	PECy5.5	200	Invitrogen	N418	35-0114-82	2286398
CD11c	APC-Cy7	200	BioLegend	N418	117324	B391502
CD8a	R710	200	TONBO Biosciences	53-6.7	80-0081-U100	C0081010722803
CD8a	AF700	200	BioLegend	53-6.7	100730	B401541
PDCA-1 (CD317)	Pacific Blue	200	BioLegend	927	127108	B302820
PDCA-1 (CD317)	BV421	200	BioLegend	927	127023	B365891
PDCA-1 (CD317)	BV650	200	BioLegend	927	127019	B365769
CD80	BV421	200	BioLegend	16-10A1	104725	B366741
CD86	APC/Cy7	200	BioLegend	GL-1	105029	B349514
CD86	BV605	200	BioLegend	GL-1	105037	B373866
F4/80	Pacific Orange	100	Invitrogen	BM8	MF48030	2209625
F4/80	PE	200	BioLegend	BM8	123109	B223149
F4/80	FITC	200	BioLegend	BM8	123108	B407719
F4/80	APC/Fire 810	200	BioLegend	BM8	123166	B431884
Tim4	PE	150	BioLegend	RMT4-54	130006	B428998
CD11b	PerCPCy5.5	200	TONBO Biosciences	M1/70	65-0112-U100	C0112121919653
CD11b	PerCPCy5.5	200	BioLegend	M1/70	101228	B423267
CD206	PEcy7	200	BioLegend	C068C2	141719	B239603
CD206	APC	150	Invitrogen	MR6F3	17-2061-80	1956852
MHC-II	FITC	150	BioLegend	M5/114.15.2	107606	B398140
NK1.1	FITC	200	BioLegend	PK136	108705	B376169
NK1.1	BV711	200	BioLegend	PK136	108745	B423146
CD49b	FITC	200	eBioscience	DX5	11-5971-82	E023186
CD49b	PE/Dazzle 594	200	BioLegend	DX5	108924	B396304
CD49b	PE	200	BioLegend	DX5	108908	B391901
CD49a	APC/Fire 750	200	BioLegend	HMα1	142610	B420608
CD107a	PEcy7	200	BioLegend	1D4B	121619	B348898
CD107a	BV650	200	BioLegend	1D4B	121645	B424309
CD27	BV605	200	BioLegend	LG.3A10	124249	B408891
CD27	AF700	200	BioLegend	LG.3A10	124240	B329641
IFNg	BV650	100	BioLegend	XMG1.2	505832	B361629
IFNg	PE	100	BioLegend	XMG1.2	505807	B366833
Perforin	Pacific Blue	100	BioLegend	S160009A	154311	B356368
Granzyme B	PE	100	Invitrogen	GB11	12-8899-41	2682463
Granzyme B	FITC	100	BioLegend	GB11	515403	B397296
TNFa	BV605	100	BioLegend	MP6-XT22	506329	B422381
TNFa	PE-Cy7	100	BioLegend	MP6-XT22	506324	B424713
T-bet	BV605	100	BioLegend	4B10	644817	B387805

List of antibodies used in various combinations throughout all experiments.

Antigen, fluorophore, dilution (1:x), company, clone, catalog/reference number,

and lot number listed.