Cutting Edge: Impaired MHC Class I Expression in Mice Deficient for Nlrc5/Class I Transactivator

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Cutting Edge: Impaired MHC Class I Expression in Mice Deficient for Nlrc5/Class I Transactivator

Amlan Biswas, Torsten B. Meissner, and Koichi S. Kobayashi

MHC class I and class II are crucial for the adaptive immune system. Although regulation of MHC class II expression by CIITA has long been recognized, the mechanism of MHC class I transactivation has been largely unknown until the recent discovery of NLRC5/class I transactivator. In this study, we show using Nlrc5-deficient mice that NLRC5 is required for both constitutive and inducible MHC class I expression. Loss of Nlrc5 resulted in severe reduction in the expression of MHC class I and related genes such as β2-microglobulin, Tap1, or Lmp2, but did not affect MHC class II levels. IFN-γ stimulation could not overcome the impaired MHC class I expression in Nlrc5-deficient cells. Upon infection with Listeria monocytogenes, Nlrc5-deficient mice displayed impaired CD8+ T cell activation, accompanied with increased bacterial loads. These findings illustrate critical roles of NLRC5/class I transactivator in MHC class I gene regulation and host defense by CD8+ T cell responses. The Journal of Immunology, 2012, 189: 000–000.
infection with *Listeria monocytogenes*, as highlighted by impaired CD8+ T cell activation and increased bacterial burden in the infected organs, indicating a critical role of Nlrc5/CITA in MHC class I-dependent CD8+ T cell responses.

Materials and Methods

**Mice**

Nlrc5-deficient mice were provided by T. Kawai and S. Akira (Osaka University, Osaka, Japan) (22). Wild-type mice (F1 mice from 129SvEv and C57BL/6 mice) were obtained from Taconic. OT-1 TCR transgenic mice were a gift of H. Cantor (Dana-Farber Cancer Institute, Boston, MA). Mice were maintained under specific pathogen-free conditions and used in accordance with institutional and National Institutes of Health guidelines.

**Cell culture and reagents**

Generation and stimulation of bone marrow-derived macrophages and dendritic cells have been described previously (23). Splenocytes and thymocytes were cultured in RPMI 1640 supplemented with 10% FBS, 55 μM 2-ME (Life Technologies), and penicillin/streptomycin (Life Technologies). Murine rIFN-γ was from BioLegend. Peritoneal cells were isolated without pretreatment with thioglycollate.

**RNA isolation and quantitative PCR**

RNA isolation and quantitative PCR were performed, as previously described (13). Primer sequences are listed in Supplemental Table I.

**Western blot analysis**

Western blot analysis was performed, as described previously (13), using the following Abs: anti-H2-Kb, anti-β2m (gifts of T. Hansen, Washington University), and anti-heat shock protein (Hsp) 90 Ab (F-8; Santa Cruz Biotechnology).

**Flow cytometric analysis**

FACS analysis was performed, as previously described (13), using the following Abs: FITC anti-mouse B220, FITC anti-mouse CD11c, allophycocyanin anti-mouse CD4, PE/Cy5 anti-mouse CD8, allophycocyanin anti-mouse F4/80, PE anti-mouse I-AI/A2 (eBioscience), PE anti-mouse H2, and allophycocyanin anti-mouse IFN-γ (BioLegend).

**OT-1 cell coculture assay**

MACS-sorted CD8+ T cells from OT-1 mice with CD45.1 background were CFSE labeled and cocultured with SIINFEKL (1 μM) pulsed irradiated splenic B220+ cells from either Nlrc5+/+ or Nlrc5−/− mice at a ratio of 1:25 (B:T) for 72 h. Proliferation of OT-1 T cells was determined by FACS analysis of the CFSE dilution in CD45.1 gated cells.

**L. monocytogenes infection**

*L. monocytogenes* (strain 10403s, provided by D. Portnoy at University of California, Berkeley) was grown to midlog phase (A600, 0.1), and injected into mice via the lateral tail vein. The bacterial burden in the spleen and liver of infected mice was determined by CFU count of serial dilution of lysates.

**Statistical analysis**

Data were subjected to one-way ANOVA for analysis of statistical significance using Prism (GraphPad). Results are given as the mean ± SEM. A p value <0.05 was considered to be significant.

Results and Discussion

To clarify the role of NLRC5 in MHC class I gene expression in vivo, we analyzed Nlrc5-deficient mice. Heterozygous littermates (+/−) and F1 mice from a C57BL/6×129SvEv breeding (+/+ × +/−) with a similar mixed genetic background to the knockout mice (−/−) were used as controls. As can be seen in Fig. 1A, MHC class I (H2-Kb) transcript levels in the thymus, spleen, kidney, and ileum were significantly reduced in Nlrc5-deficient mice compared to that of wild-type or heterozygous mice, confirming that MHC class I expression is indeed largely dependent on Nlrc5. The expression of MHC class I-related genes, β2m, Tap1, Lmp2, and H2-Aa, as well as the nonclassical MHC class I gene, H2-M3, was impaired in the thymus and spleen of Nlrc5-deficient mice (Fig. 1B). In contrast, Nlrc5 deficiency did not affect the expression of MHC class II (H2-Ab) and CITA gene expression in splenocytes, as determined by qPCR. β2m expression was also reduced in the spleen and thymus from mice with the indicated genotype. The expression of Hsp90 is shown as a loading control. *p < 0.05, **p < 0.01; ns, not significant.

FIGURE 1. Nlrc5 is required for the constitutive expression of MHC class I in various organs. (A) Expression of MHC class I (H2-Kb) in the indicated organs of wild-type mice (+/+ , n = 3), or mice heterozygous (+/−, n = 4) or homozygous (−/−, n = 3) for the targeted disruption of the Nlrc5 gene, as determined by quantitative PCR (qPCR) analysis using gene-specific primers. Error bars represent ±SEM. (B) Expression of β2m, Tap1, Lmp2, and H2-M3 in the spleen and thymus of Nlrc5+/+ (n = 3) and Nlrc5−/− mice (n = 3) was analyzed by qPCR using the indicated gene-specific primers. Error bars represent ±SEM. (C) Analysis of Nlrc5, MHC class II (H2-Ab), and CITA gene expression in splenocytes, as determined by qPCR, n = 3. Error bars represent ±SEM. ns, Not significant. (D) Western blot analysis of MHC class I (H2-Kb) and β2m protein expression in the spleen and thymus from mice with the indicated genotype. The expression of Hsp90 is shown as a loading control. *p < 0.05, **p < 0.01; ns, not significant.

We observed a reduction of MHC class I levels in the thymus and spleen, we further investigated the cell type-specific expression of MHC class I in those organs by flow cytometry. The surface expression of MHC class I (H2-D, -K, -L) was severely reduced in CD4+ and CD8+ T cells in the spleen, thymus, and lymph nodes from Nlrc5-deficient mice (Fig. 2A–C). Furthermore, MHC class I expression was reduced in Nlrc5-deficient B cells from the spleen, lymph nodes, peritoneal cavity, splenic F4/80+ macrophages, and CD11c+ dendritic cells, although they retained significant levels of MHC class I on their surface (Fig. 2A–C, Supplemental Fig. 1A). Also, the transcript levels of MHC class I in bone marrow-derived macrophages and dendritic cells were significantly reduced (Supplemental Fig. 1B), indicating that Nlrc5 is important for the induction of MHC class I genes in macrophages and dendritic cells, whether they are of tissue...
origin or bone marrow derived. Interestingly, the surface expression of MHC class I on these bone marrow-derived cells was largely unaffected (Supplemental Fig. 1A), suggesting that there appears to be a compensatory posttranscriptional mechanism to rescue the MHC class I deficiency in cultured cells. Together, these findings suggest that Nlrc5 plays a major role in the regulation of MHC class I gene expression, albeit the degree of the requirement for Nlrc5 in MHC class I expression varies between different cell types.

We have previously demonstrated that NLRC5 is required for MHC class I gene expression upon IFN-γ stimulation (13). Therefore, we examined the impact of Nlrc5 deficiency on IFN-γ–inducible MHC class I expression by stimulating splenocytes from Nlrc5−/− mice with IFN-γ. As previously shown (13, 15, 20, 21), IFN-γ treatment resulted in the upregulation of Nlrc5 transcript, which correlated with the induction of MHC class I gene (H2-Kb) expression in both wild-type and heterozygous splenocytes (Fig. 3A) (13). In Nlrc5-deficient splenocytes, however, IFN-γ stimulation could not rescue the impairment of MHC class I expression, when compared with the levels of MHC class I observed in the controls (Fig. 3A). β2m expression was also only partially rescued (Fig. 3A). In contrast, upregulation of Stat1 transcripts, which is induced by IFN-γ stimulation in a Nlrc5-independent manner (13), was comparable among the three genotypes, indicating that the JAK/STAT signaling cascade downstream of the IFN-γ receptor is intact in Nlrc5-deficient cells. Interestingly, there was a small, but distinct, induction of MHC class I expression in Nlrc5−/− splenocytes upon IFN-γ stimulation, supporting the existence of a Nlrc5-independent mechanism(s) of MHC class I expression (Fig. 3A).

To address whether the impaired MHC class I expression caused by Nlrc5 deficiency has an impact on immune responses, OT-1 CD8+ T cells were cocultured with peptide-loaded B cells. OT-1 T cells stimulated with Nlrc5-deficient B cells displayed impaired proliferation, indicating that NLRC5 is indeed required for Ag-specific stimulation of CD8+ T cells (Fig. 4A). The role of NLRC5 in MHC class I-

![FIGURE 2. Reduced MHC class I expression in various cell types of Nlrc5-deficient mice. Single-cell suspension of spleen (A, left panel; D), thymus (B, left panel), and lymph node (C, left panel) from Nlrc5−/− (gray line) and Nlrc5−/− (black line) mice was analyzed by flow cytometry for the expression of MHC class I [H2-K/D/L, in (A), (B), and (C), left panel] or MHC class II (D) molecules (I-Ab/I-Ad), gated on CD8+, CD4+, B220+, F4/80+, or CD11c+ cells. Shaded region represents the isotype control. Data are representative of two independent experiments. Bar graphs (A–C, right panel) present the mean and SEM of the corresponding mean fluorescence intensity (n = 3 for each genotype). *p < 0.05, **p < 0.01.](http://www.jimmunol.org/doi/abs/10.4049/jimmunol.1700214)
mediated immune responses was further investigated by infection studies using an intracellular bacterium, *L. monocytogenes*, because a CD8+ T cell response is critical for the host defense against this bacterium. Although *Listeria* infection clearly induced Ag-specific CD8+ T cell activation in the spleen and liver of wild-type mice, as demonstrated by increased numbers of IFN-γ-positive cells after ex vivo stimulation with heat-killed bacteria (Fig. 4B, Supplemental Fig. 1C), in *Nlrc5*-deficient mice, Ag-specific CD8+ T cell activation was impaired and the mice harbored increased numbers of the bacterium in both spleen and liver (Fig. 4B, 4C). Furthermore, we show that NLRC5 is required for CD8+ T cell responses in an Ag-specific manner. Ag peptide-loaded *Nlrc5*-deficient B cells failed to activate OT-1 T cells efficiently. Strikingly, our *Listeria* infection study demonstrated that CD8+ T cells obtained from *Nlrc5*-deficient mice displayed impaired Ag-specific activation, and the mice had increased bacterial loads in the spleen and liver. Therefore, we conclude that NLRC5 plays a critical role in MHC class I-mediated immune responses in vivo. This study also reveals that the requirement for NLRC5 in MHC class I gene expression varies between different cell types. The reduced MHC class I phenotype was most prominent in CD4+ and CD8+ T cells and less prominent in B cells (Fig. 2A–C). Also, macrophages and dendritic cells retained residual MHC class I expression (Fig. 2A). This may suggest that an alternative, NLRC5-independent mechanism of MHC class I transactivation exists. Interestingly, similar residual expression of MHC class II genes has been reported in CIITA-deficient mice; CIITA-deficient dendritic cells retained MHC class II expression, although expression levels were significantly reduced (12). These observations indicate that although NLRC5/CIITA and CIITA are critical for the expression of MHC class I and class II, respectively, APCs may possess alternative mechanisms to ensure the efficient presentation of

**FIGURE 3.** IFN-γ stimulation does not rescue the reduced MHC class I expression observed in *Nlrc5*-deficient mice. (A) Splenocytes from *Nlrc5*+/+, *Nlrc5*−/−, and *Nlrc5*−/+ mice (*n* = 3 for each genotype) were stimulated for 18 h with IFN-γ (100 U/ml), and transcript levels were analyzed by qPCR using the indicated gene-specific primers. Error bars represent ±SEM. (B) MHC class I (H2-Kb) and β2m protein expression in splenocytes and thymocytes from mice with the indicated genotype. Cell extracts were prepared 18 h poststimulation with IFN-γ and analyzed by Western blotting. Hsp90 levels determined by flow cytometric analysis of CFSE dilution. Data are representative of two independent experiments (*n* = 3). Bar graphs (*B*, right panel) present the mean and SEM of the percentage of CD8+ IFN-γ+ cells (*n* = 3 for each genotype). (C) Bacterial load in the spleen and liver of *L. monocytogenes*-infected *Nlrc5*+/+, *Nlrc5*−/−, or *Nlrc5*−/+ mice at day 6 postinfection were cultured with heat-killed *L. monocytogenes* for 16 h and analyzed by flow cytometry for the expression of IFN-γ on CD8+ cells. Numbers indicate percentage of cells. Data are representative of two independent experiments; *p < 0.05, **p < 0.01.

In addition to our previous study in which we used human lymphoid and epithelial cell lines (13), the current study compellingly demonstrates the critical role of NLRC5 in both constitutive and inducible MHC class I expression in vivo using *Nlrc5*-deficient mice. Moreover, we show that NLRC5 is required for CD8+ T cell responses in an Ag-specific manner. Ag peptide-loaded *Nlrc5*-deficient B cells failed to activate OT-1 T cells efficiently. Strikingly, our *Listeria* infection study demonstrated that CD8+ T cells obtained from *Nlrc5*-deficient mice displayed impaired Ag-specific activation, and the mice had increased bacterial loads in the spleen and liver. Therefore, we conclude that NLRC5 plays a critical role in MHC class I-mediated immune responses in vivo. This study also reveals that the requirement for NLRC5 in MHC class I gene expression varies between different cell types. The reduced MHC class I phenotype was most prominent in CD4+ and CD8+ T cells and less prominent in B cells (Fig. 2A–C). Also, macrophages and dendritic cells retained residual MHC class I expression (Fig. 2A). This may suggest that an alternative, NLRC5-independent mechanism of MHC class I transactivation exists. Interestingly, similar residual expression of MHC class II genes has been reported in CIITA-deficient mice; CIITA-deficient dendritic cells retained MHC class II expression, although expression levels were significantly reduced (12). These observations indicate that although NLRC5/CIITA and CIITA are critical for the expression of MHC class I and class II, respectively, APCs may possess alternative mechanisms to ensure the efficient presentation of...
Ags to T cells. In summary, we demonstrated the critical role of NLRC5/CITA in MHC class I expression and CD8+ T cell responses in vivo. Further analysis of Nlrc5-deficient mice will certainly extend our understanding of MHC class I biology, and, hence, may improve therapeutic interventions in the field of infectious diseases, transplantation, and cancer immunotherapy.

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Disclosures
The authors have no financial conflicts of interest.

References
5. Nlrc5-deficient mice lack the MHC class II transactivator (CITA).
### Supplemental Table 1

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Primer sequence</th>
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| **H2-Kb** | 5'-GTGATCTCTGGCTGTGAAGT-3’ (forward)  
5'-GTCTCCACAAGCTCCATGTC-3’ (reverse) |
| **Nlrc5** | 5'-CTTCCCCGCCTCTCCTCCACAAT-3’ (forward)  
5'-CTCCACCTGCCCACATCCTACCA-3’ (reverse) |
| **Ciita** | 5'-CCCTGCGTGTGATGGATGTC-3’ (forward)  
5'-ATCTCAGACTGATCCTGGCAT-3’ (reverse) |
| **H2-α**  | 5'-CAACCGTGACTATTCCCTTC-3’ (forward)  
5'-CCACAGTCTCTGTGACT-3’ (reverse) |
| **Stat1** | 5'-TCACAGTGTTTCGAGCTTCAG-3’ (forward)  
5'-GCAAACGAGACATTAGGCA-3’ (reverse) |
| **β-Actin** | 5'-GCTGTGCTCTTTGATGCCTCT-3’ (forward)  
5'-ITTCTCAGCTGTGGTGCTAGAAGC-3’ (reverse) |
| **β2m**  | 5'-CCCAACTGAGACTGATACACG-3’ (forward)  
5'-CGATCCCAGTAGACGGTCTTG-3’ (reverse) |
| **Tap1** | 5'-GGACTTTGCTTTCCAGAG-3’ (forward)  
5'-GCTGCCCACATACTGAGCGA-3’ (reverse) |
| **Lmp2**  | 5'-CATGAAACCAGATGGCTCTGAG-3’ (forward)  
5'-TCATCGTAGAATTTTGGCAGCTC-3’ (reverse) |
| **H2-M3** | 5'-ACTATCAGGGCTCGATAGG-3’ (forward)  
5'-ACTCTAAACGGCTTGTAAGGC-3’ (reverse) |
| **IL-6**  | 5'-CCAGAAACCGCTATGAAGTTCC-3’ (forward)  
5'-TTGTCACCAGCATCAGTCCC-3’ (reverse) |
| **TNF-α** | 5'-ACAGAAACGATGGGCTCTGAGG-3’ (forward)  
5'-GCCCCCACTCTTTGGA-3’ (reverse) |
| **IL-1β** | 5'-AAGGAGGACCAAAGCAACGACAAA -3’ (forward)  
5'-TGAGGGAACCTCTCACTGCTGA-3’ (reverse) |
| **IL-12p40** | 5'-TGGTTTCCATGTTTCTG-3’ (forward)  
5'-ACAGGTGAGGTTTCACTGTTTCT-3’ (reverse) |

Gene-specific primers used for amplification in qRT-PCR.
SUPPLEMENTAL FIGURE 1. Nlrc5 plays critical roles in MHC class I expression and host defense against L. monocytogenes infection but not TLR responses. (A) Peritoneal cavity cells, bone marrow-derived dendritic cells (BMDC) and macrophages (BMDM) from Nlrc5 +/- (grey line) and Nlrc5-/- (black line) mice were analyzed by flow cytometry for the expression of MHC class I (H2-K/D/L) gated on B220+, F4/80+ or CD11c+ cells (left panel). Shaded regions represent the isotype control. Bar graphs (right panel) represent the mean and SEM of the corresponding MFI (n = 3 for each indicated genotype). *p < 0.05; ns, not significant. (B) Expression of MHC class I (H2-Kb) in BMDC and BMDM of Nlrc5+/+, Nlrc5+/- and Nlrc5-/- mice were determined by qPCR analysis using gene-specific primers. n = 3 for each indicated genotype. Error bars represent ± SEM. *p < 0.05. (C) Nlrc5+/+ and Nlrc5-/- mice were infected with L. monocytogenes (1 X 10^4 CFU). Untreated splenocytes and hepatic leukocytes isolated from Nlrc5+/+ and Nlrc5-/- mice at day 6 after infection were analyzed by flow cytometry for the expression of IFN-γ gated on CD8+ cells. Data are representative of two independent experiments. (D) BMDM from Nlrc5 +/- (n=3) and Nlrc5-/- mice (n=3) were stimulated with LPS (10 ng/ml) for 16 hours. Transcript levels of IL-6, TNF-α, IL-12p40 and IL-1β were analyzed by qPCR using the indicated gene-specific primers. Error bars represent ± SEM. ns, not significant. (E) BMDM from Nlrc5 +/- (n=3) and Nlrc5-/- mice (n=3) were stimulated with LPS, CpG DNA (10 μM) or poly(I:C) (50 μg/ml) for 16 hours. Cell free supernatants were analyzed for the level of IL-6 and TNF-α by ELISA. Error bars represent ± SEM. ns: not significant.