ERAAP and Tapasin Independently Edit the Amino and Carboxyl Termini of MHC Class I Peptides

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Transient contacts with APCs, effective CD8+ T cell responses are generated and loaded peptides with appropriate consensus motifs onto MHC I. In this article, we show that both tapasin (Tpn), a key component of the peptide loading complex, and the endoplasmic reticulum aminopeptidase associated with Ag processing (ERAAP) are quintessential editors of distinct structural features of the peptide repertoire. We carried out reciprocal immunization of wild-type mice with cells from Tpn- or ERAAP-deficient mice. Specificity analysis of T cell responses showed that absence of Tpn or ERAAP independently altered the peptide repertoire by causing loss as well as gain of new pMHC I. Changes in amino acid sequences of MHC-bound peptides revealed that ERAAP and Tpn, respectively, defined the characteristic amino and carboxy termini of canonical MHC I peptides. Thus, the optimal pMHC I repertoire is produced by two distinct peptide editing steps in the endoplasmic reticulum. The Journal of Immunology, 2013, 191: 1547–1555.

Presentation of endogenous peptides by MHC class I (MHC I; peptide–MHC I complexes [pMHC I]) on the cell surface enables the immune system to detect and eliminate infected or transformed cells. The peptides are generated from intracellular proteins and loaded onto MHC I by the Ag processing pathway (1, 2). The pathway begins in the cytoplasm where antigenic precursors are fragmented to produce a pool of intermediate peptide fragments. The fragments are transported into the endoplasmic reticulum (ER) where they are loaded onto MHC I molecules. The resulting pMHC I are exported to the cell surface to serve as potential ligands for recognition by the CD8+ T cell Ag receptors. Because circulating CD8+ T cells make only transient contacts with APCs, effective CD8+ T cell responses are critically dependent on presentation of an optimally stable pMHC I repertoire.

To elicit robust CD8+ T cell responses, we selected peptides entering the Ag presentation pathway to yield high-affinity pMHC I that will persist on the cell surface. In addition to a characteristic length of 8–10 aa, the peptides presented by MHC I on the cell surface are uniquely defined by the presence of conserved consensus motifs. The set of peptides bound by a given MHC I molecule shares conserved amino acids located at discrete positions, called anchor residues, that allow peptide binding to the MHC I (3). Amino acid substitutions at these anchor positions resulted in loss of stable interactions between peptides and MHC I that, in turn, inhibited CD8+ T cell responses.

The pool of peptides for MHC I presentation is produced from endogenously synthesized proteins fragmented mainly by the multicatalytic proteasome (4), as well as other proteasomes (5, 6). These models suggest that cytoplasmic proteolysis is primarily responsible for generating the canonical C termini of antigenic peptides. The intermediate peptide fragments are transported into the ER by the TAP (7). Upon entering the ER, the peptides encounter the peptide loading complex (PLC) that facilitates loading of optimal peptide onto MHC I (8, 9). The PLC consists of TAP, the aminopeptidase (Tpn) and calreticulin, the thiol oxidoreductase ERAp57, β2-microglobulin, and the MHC I H chain. Among these components, Tpn is critical for the formation and function of the PLC (8–10). Tpn interacts directly with TAP, the MHC I H chain, and ERAp57, thereby bringing the PLC components together and keeping the empty MHC I close to the source of incoming peptides (9–15). Consistent with its central function in the PLC, surface expression of MHC I molecules is profoundly diminished in Tpn-deficient mice (16, 17) and in several MHC I molecules in human cells (9, 18). Furthermore, the loss of Tpn results in presentation of suboptimal pMHC I (9, 11, 17, 19–22). Thus, Tpn is the key mediator of peptide loading in the PLC. Nevertheless, the molecular features of the peptide cargo affected by Tpn remain unknown.

The ER aminopeptidase associated with Ag processing (ERAAP) has emerged as yet another editor of the pMHC I repertoire in the ER (23, 24). The loss of ERAAP caused profound changes in the
pMHC I repertoire relative to wild-type (WT) mice (25–29). Analysis of CD8+ T cell responses elicited in WT mice by ERAAP-deficient cells showed that classical as well as nonclassical MHC I presented a distinct, highly immunogenic peptide repertoire (26, 27, 30, 31). Furthermore, examination of the sequence of presented peptides in ERAAP-deficient cells by mass spectrometry revealed that the peptides were longer, often because of extra N-terminal residues (30). How ERAAP edits peptides presented by MHC I and whether editing occurs within the PL C is not known. Because Tpn physically brings together PLC components, cells without Tpn lack a functional PLC. We reasoned that the peptide editing events in the PLC might be evident in cells lacking Tpn or ERAAP.

In this study, we analyzed the peptide editing functions of Tpn and ERAAP required for generating the optimal pMHC I repertoire. We examined peptide editing events in cells lacking Tpn or ERAAP. By immunological, biochemical, and molecular analyses, we find that ERAAP and Tpn independently edited the N and C termini of the peptide repertoire presented by MHC I on the cell surface.

Materials and Methods

Mice

ERAAP-deficient (25), Tpn-deficient (16), TAP1-deficient (32), and Kβ and Dβ double-deficient (KβDβ dko) mice (33) have been described elsewhere (25, 31). Activation of T cell hybridomas was determined by manual spectral validation (36). To analyze the amino acid conservation of groups of more than seven peptides, we used WebLogo program (http://weblogo.berkeley.edu/).

Peptide extraction and reverse-phase HPLC analysis

The preparation, fractionation, and detection of the peptide extracts has been described previously (34). In brief, the peptides were eluted from the cells by 10% formic acid, fractionated by reverse-phase HPLC, treated with trypsin, and assayed as described previously. Synthetic peptides were prepared by D. King (University of California at Berkeley).

Antibodies

The following Abs used for flow cytometry analysis were purchased from BD Biosciences: anti-H-2Kβ (AF6-88.5), anti-H-2Aβ (25-9-17), anti-CD8α (53-6.7), anti-CD4 (RM4-5), and anti–IFN-γ (XMG1.2). Abs CD16/32 (Fc receptor, clone 93) and anti–H-2Dβ (28-14-8) were purchased from eBiosciences. For in vivo depletions, purified anti-NK1.1 Ab (PK136) from Bio-Xcell was used. To block presentation by MHC I to T cell lines, we used the following culture supernatants: anti–H-2Kβ (SFL5), anti–H-2Dβ (B22.249), or anti–H-2Aβ (MS/114). In the immunofluorescence purification of pMHC I for mass spectrometry, anti–H-2Kβ (Y3) and anti–H-2Dβ (B22.249) were used.

Results

ERAAP and Tpn differentially influence pMHC I repertoire

ERAAP and Tpn are both ER-resident editors of the peptide repertoire in vitro. Cultures contained 20 U/ml (first two restimulations) or 50 U/ml (subsequent restimulations) hIL-2 (BD Biosciences) and irradiated spleen cells from female mice of the same genotype used for immunization. Additional restimulations were done every 7–10 d.

Peptide extraction and reverse-phase HPLC analysis

The preparation, fractionation, and detection of the peptide extracts has been described previously (34). In brief, the peptides were eluted from the cells by 10% formic acid, fractionated by reverse-phase HPLC, treated with trypsin, and assayed as described previously. Synthetic peptides were prepared by D. King (University of California at Berkeley).

Immunizations and CTL lines

To generate T cell lines, we immunized female Tpn-deficient or WT mice i.p. with 2 × 107 spleen cells from male WT or Tpn-deficient mice, respectively. Ten days after immunization, spleen cells were restimulated in vitro. Cultures contained 20 U/ml (first two restimulations) or 50 U/ml (subsequent restimulations) hIL-2 (BD Biosciences) and irradiated spleen cells from female mice of the same genotype used for immunization. Additional restimulations were done every 7–10 d.

Measurement of intracellular IFN-γ production by CTLs

The CD8+ T cell responses of the immunized mice were measured by intracellular IFN-γ production. Spleen cell APCs were treated with 200 ng/ml LPS (Sigma) overnight, and CD4+ and CD8+ cells were depleted using magnetic beads (Dynal Biotech, Invitrogen) before incubation with restimulated CD8+ T cells. A total of 1 µl/ml brefeldin A (BFA; GolgiPlug [BD Biosciences]) was added after 1 h, and total incubation of CD8+ T cells and APCs was 5 h. Cells were stained for surface markers followed by intracellular staining for IFN-γ. Cells were analyzed by flow cytometry using an LSR II (BD) and with FlowJo Software (TreeStar). All plots were first gated on live cells based on forward/side scatter, followed by gating on CD8+ and IFN-γ.

In vivo cytotoxicity assay

WT female mice, depleted of NK cells at least 36 h before every immunization, were primed i.p. with 2 × 107 male WT, ERAAP−/−, or Tpn−/− splenocytes. Mice were challenged on day 27 with a 1:1:1 mix of labeled ERAAP−/−, Tpn−/−, and WT female APCs. Target cell labels were ERAAP−/− labeled with 20 µM CellTracker Blue CMAC (7-amino-4-chloromethylcoumarin; Invitrogen), Tpn−/− targets labeled with 0.125 µM CFSE (low dose), and WT targets labeled with 1.25 µM CFSE (high dose; Invitrogen). Twenty hours after challenge with labeled cells, host mice were sacrificed and splenocytes analyzed by flow cytometry to determine percentage of cells remaining. Plots were gated on live cells before analysis of target populations. Percent specific lysis was calculated as follows: 100 × (1 − [ratio of target output]/[ratio of target input]), where input is determined before injection of targets and output represents targets recovered after challenge. To calculate ratios, (% population of interest)/ (%(ERAAP−/− + %Tpn−/− + %WT).

Large-scale peptide sequencing by tandem mass spectrometry

Peptide sequencing using immunofluorescence purification of pMHC complexes from detergent-solubilized spleen lysates was performed as reported previously (35). In brief, freshly isolated spleen cells from 25 C57BL/6 and 50 Tpn-deficient mice were lysed and pMHC I was immuno-purified using mAbs Y3 (anti–H-2Kβ) and B22.249 (anti–H-2Dβ). Samples were subject to fast protein liquid chromatography–HPLC fractionation, and sequence identification by nanochip electrospray ionization-quadrupole time of flight mass spectrometer. Peptides were identified with high confidence using an initial search with Spectrum Mill algorithm followed by expert manual spectral validation (36). To analyze the amino acid conservation of groups of more than seven peptides, we used WebLogo program (http://weblogo.berkeley.edu/).
or ERAAP-deficient (ERAAP−/−) mice (Fig. 2). The absence of ERAAP affected pMHC I presentation differentially (23, 25, 31), ranging from no detectable change in the pKb ligand recognized by the 27.5Z hybridoma to an almost complete loss of the pMHC I ligands recognized by the LPAZ and 11p9Z hybridomas. In contrast, presentation of pMHC I ligands recognized by 1AZ, 30NXZ, and BEko8Z hybridomas was markedly enhanced on surface of ERAAP-deficient cells. In contrast, loss of Tpn was generally deleterious for all the pMHC I tested. Taken together, these observations show that normal expression of pMHC I was influenced by ERAAP and even more so by Tpn.

Absence of Tpn causes selective loss of pMHC I ligands

To further define the specific changes that occurred in the pMHC I repertoire because of loss of Tpn, we took advantage of the immune systems’ ability to detect differences between self and nonself. If certain pMHC I were absent in Tpn-deficient mice, specific CD8+ T cells would not be tolerized to them and would respond to the novel pMHC I expressed by WT cells. We immunized Tpn−/− mice with WT spleen cells expressing the normally diverse pMHC I repertoire. After 10 d, splenocytes from recipient mice were restimulated for a week with WT spleen cells. The cultures were then analyzed for presence of CD8+ T cells that produced IFN-γ when stimulated with spleen cell APCs of the indicated genotype. The Tpn−/− anti-WT CD8+ T cells responded strongly to WT APCs but not to self APCs (Fig. 3A, 3B), showing that Tpn-deficient mice perceived normal pMHC I as foreign in WT cells. We infer that Tpn deficiency caused the loss of many pMHC I normally present in WT cells. Typical of peptides presented by MHC I, these pMHC I required TAP for their presentation (Fig. 3B).

To establish the ligand specificity of the responding CD8+ T cells, we used spleen cells from KβDb dko mice as APCs. The Tpn−/−
anti-WT T cells did not respond to K\textsuperscript{b}D\textsuperscript{b} dko spleen cells, indicating that Tpn-dependent peptides were presented by K\textsuperscript{b} and D\textsuperscript{b} MHC I in WT cells, rather than nonclassical MHC I molecules (Fig. 3B).

**Tpn-deficient cells also express novel immunogenic pMHC I**

To determine whether loss of Tpn editing also resulted in presentation of novel pMHC I, we immunized WT mice with Tpn\textsuperscript{-/-} cells. The recipient T cells were restimulated in vitro and analyzed for responses to WT or Tpn\textsuperscript{-/-} APCs. WT anti-Tpn\textsuperscript{-/-} T cells produced IFN-\gamma in response to Tpn\textsuperscript{-/-}, but not to self WT APCs, indicating presence of novel pMHC I in Tpn\textsuperscript{-/-} cells (Fig. 4A, 4B).

Tpn expression appears to affect TAP stability and could thus influence peptide transport into the ER (37). Therefore, it was possible that the peptides presented in the absence of Tpn could be independent of TAP transport (38, 39). However, when we used TAP\textsuperscript{-/-} cells as APCs, WT anti-Tpn\textsuperscript{-/-} T cells did not produce IFN-\gamma (Fig. 4B), indicating that peptide transport is required for presentation of these pMHC I, and that this presentation is not a consequence of TAP deficiency. Furthermore, although blocking the A\textsuperscript{b} MHC II molecule or the K\textsuperscript{b} MHC I molecule did not inhibit IFN-\gamma production in any of the five lines tested, blocking with the anti-D\textsuperscript{b} Ab inhibited T cell responses more effectively than blocking with anti-K\textsuperscript{b} (Fig. 4C). The possible contribution of CD8\textsuperscript{+} T cells restricted by other nonclassical MHC I to the overall CD8\textsuperscript{+} T cell response is presently unclear. Alternatively, some ligands may represent novel pMHC I conformations that are not recognized by conventional anti-MHC I Abs. Together, these results show that loss of Tpn not only caused a profound loss of pMHC I, it also allowed generation of new and immunologically distinct pMHC I.

In Tpn\textsuperscript{-/-} mice, many K\textsuperscript{b} and D\textsuperscript{b} are less stable on the cell surface than in their WT counterparts (16). To test the stability of the immunogenic pMHC I in Tpn\textsuperscript{-/-} cells, we used WT or Tpn\textsuperscript{-/-} splenocytes as APCs after treatment with BFA, an inhibitor of ER-Golgi transport, for either 2 or 4 h (Fig. 4D). Although BFA treatment of WT APCs did not affect expression of pMHC I recognized by the Tpn\textsuperscript{-/-} anti-WT T cells, treatment of Tpn\textsuperscript{-/-} APCs caused a dramatic loss of WT-anti-Tpn\textsuperscript{-/-}-stimulating ligands. Thus, even though pMHC I expressed by Tpn\textsuperscript{-/-} cells were markedly less stable than those expressed by WT cells, they were nevertheless highly immunogenic.

**PLC components TAP and Tpn are not required for peptide trimming by ERAAP**

The loss and gain of novel pMHC I in either Tpn or ERAAP-deficient cells suggested the function of these two editors may be linked. For example, peptide trimming could be more effective if ERAAP interacted with the PLC that could provide ERAAP with access to incoming peptides and empty MHC I. To directly assess the role of PLC in determining ERAAP function, we analyzed peptide processing in cells lacking the key PLC components TAP or Tpn (Fig. 5A, 5B). We transfected ERAAP\textsuperscript{-/-}TAP\textsuperscript{-/-} or ERAAP\textsuperscript{-/-}Tpn\textsuperscript{-/-} fibroblasts with N-terminally extended SHL8 precursors in the presence or absence of WT ERAAP. The peptides extracted from transfected cells were fractionated by HPLC to separate the untrimmed precursor from the trimmed peptide products. The HPLC fractions were assayed for presence of antigenic peptides containing SHL8 with or without the N-terminal extension using the SHL8/K\textsuperscript{b}-specific B3Z hybridoma as described earlier (34). In ERAAP\textsuperscript{-/-}TAP\textsuperscript{-/-} cells without ERAAP (vector alone), the N-terminally extended precursor peptide was the predominant peptide species (Fig. 5A, upper panel). Upon coexpression of ERAAP, the precursor peptide was no longer detected, and two peaks corresponding to the precisely cleaved SHL8 octapeptide and the KSHL8 nonapeptide were found (Fig. 5A, lower panel). The SHL8 and KSHL8 peptides, respectively, represent the final products presented by the K\textsuperscript{b} and D\textsuperscript{b} MHC I present in these cells. Likewise, the same precursor and processed peptides were detected in presence or absence of ERAAP in Tpn-deficient cells (Fig. 5B). Thus, in the ER, ERAAP could trim antigenic precursors to their final products in the absence of TAP or Tpn. The results show directly that expression of either TAP or Tpn, and therefore an intact PLC, is not required for N-terminal trimming of antigenic precursors by ERAAP.

**Tpn- and ERAAP-deficient cells express unique, nonoverlapping pMHC I**

To further assess the relationship between peptide editing by ERAAP and Tpn, we examined the potential overlap between novel peptides generated in the absence of Tpn or ERAAP. T cell lines generated in WT mice by immunization with Tpn or ERAAP-deficient cells were tested for responses to various APCs. The Tpn\textsuperscript{-/-} anti-WT CD8\textsuperscript{+} T cell lines responded to both WT and ERAAP\textsuperscript{-/-} APCs equally well, suggesting that both cells presented the unique pMHC I that were lost in Tpn\textsuperscript{-/-} mice (Fig. 6A). In contrast, the WT anti-Tpn\textsuperscript{-/-} lines recognized only Tpn-deficient cells but did not recognize either WT or ERAAP\textsuperscript{-/-} cells (Fig. 6B). Likewise, WT-anti-ERAAP\textsuperscript{-/-} lines recognized ERAAP\textsuperscript{-/-} APCs but did not respond to either WT or Tpn\textsuperscript{-/-} APCs (Fig. 6C). The lack of cross-reactivity between T cells specific for Tpn\textsuperscript{-/-} or ERAAP\textsuperscript{-/-} APCs showed that ERAAP and Tpn have distinct and nonoverlapping roles in editing peptides for presentation on MHC I.

To further rigorously establish the distinction between the immunologically distinct Tpn or ERAAP-dependent ligands, we

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**FIGURE 3.** Tpn-deficient mice elicit CD8\textsuperscript{+} T cell response to pMHC I expressed by WT cells. (A) Intracellular IFN-\gamma\textsuperscript{+} produced by Tpn\textsuperscript{-/-} anti-WT CD8\textsuperscript{+} T cell lines in response to WT or Tpn\textsuperscript{-/-} APCs. (B) Tpn\textsuperscript{-/-} anti-WT CD8\textsuperscript{+} T cell IFN-\gamma\textsuperscript{+} response against WT, Tpn\textsuperscript{-/-}, TAP\textsuperscript{-/-}, or K\textsuperscript{b}D\textsuperscript{b} dko APCs. Each point represents an individual mouse. Data are from one of two independent experiments (A) or pooled from two independent experiments (B). (A and B) Numbers represent percent IFN-\gamma\textsuperscript{+} cells in the CD8\textsuperscript{+} T cell gate.
assessed the ability of WT mice to eliminate ERAAP−/− or Tpn−/− target cells in vivo (Fig. 7). We primed WT mice with splenocytes from ERAAP−/−, Tpn−/−, or WT mice as a negative control. Seven days later, the mice were challenged with a cell mixture containing an equal number of WT, ERAAP−/−, and Tpn−/− spleen cells as targets (Fig. 7A, 7B). We depleted NK cells in host mice before immunization and challenge to obviate the possible effect of these cells in targeting Tpn−/− or ERAAP−/− cells with lower MHC I expression (17, 40). To distinguish the three populations of donor cells recovered from host animals in vivo, we labeled each target cell population with a different fluorescent dye as shown schematically (Fig. 7A). After 20 h, spleens from host WT mice were analyzed for the presence of each labeled cell population (Fig. 7B, output). A decrease in the percentage of cells recovered relative to the WT (self) targets indicates elimination of individual populations by the immune system of WT hosts.

FIGURE 4. Tpn-deficient cells elicit CD8+ T cell responses in WT mice. (A) IFN-γ+ response of WT anti-Tpn−/− CD8+ T cell lines against WT or Tpn−/− APCs. Numbers indicate percent IFN-γ+ cells of total CD8+ T cells. (B) WT anti-Tpn−/− CD8+ T cell responses against WT, Tpn−/−, or TAP−/− APCs. (A and B) Numbers indicate percent IFN-γ+ cells in the CD8+ T cell gate. (C) WT anti-Tpn−/− CD8+ T cell responses against WT APCs previously treated with blocking Abs to MHC I Kb (α-Kb) or Db (α_Db), or to MHC II Ab (α-Ab). Percentages of CD8+ IFN-γ+ cells were normalized to no Ab control (No Ab). (D) IFN-γ+ production by WT anti-Tpn−/− (left) and Tpn−/− anti-WT (right) CD8+ T cell lines against splenocyte APCs treated with BFA for 2 or 4 h before coculture with T cells. Percent of CD8+ IFN-γ+ was normalized to untreated (−). Data are representative of three independent experiments (A, B) or are pooled from two independent experiments (C, D).

FIGURE 5. Peptide trimming by ERAAP does not require Tpn or TAP. (A and B) The ES-X9[SHL8] construct was cotransfected with ERAAP cDNA or with empty vector into (A) ERAAP−/− TAP−/− or (B) ERAAP−/− Tpn−/− fibroblasts. Cell lysates were fractionated by RP-HPLC and trypsinized to release SHL8 peptides before detection with B3Z hybridoma in the presence of L cells expressing H-2Kb. Synthetic SHL8 and KSHL8 peptide run under identical conditions verified the HPLC fraction numbers. Data are representative of three independent experiments.
Mice primed with ERAAP<sup>−/−</sup> cells efficiently eliminated ERAAP<sup>−/−</sup> targets but did not influence the recovery of Tpn-deficient or self-WT cells (Fig. 7C). In contrast, WT mice primed with Tpn<sup>−/−</sup> splenocytes eliminated Tpn<sup>−/−</sup> targets, but not ERAAP<sup>−/−</sup> or WT targets. Finally, there was no specific loss of any of these target cells in mice primed with self-WT cells. Furthermore, the requirement for prior immunization for the in vivo elimination of ERAAP<sup>−/−</sup> or Tpn<sup>−/−</sup> targets suggests that these responses are mediated by the adaptive immune system. The in vitro and in vivo assessment of WT anti-Tpn<sup>2/2</sup> and WT-anti ERAAP<sup>2/2</sup> T cell lines demonstrates that the unedited peptide repertoires in cells deficient in ERAAP versus Tpn were distinct without any detectable overlap.

**Tpν-deficient cells present peptides lacking canonical consensus motif**

The earlier findings showed that loss of Tpn results in the presentation of a novel set of peptides on the cell surface that are immunogenic to WT T cells and are distinct from the unedited peptides presented by ERAAP-deficient cells. Our previous analysis of the unedited peptides in ERAAP<sup>−/−</sup> spleen cells had found that the novel peptides were longer in length and varied at their N termini (30). Whether specific structural changes also occurred in peptides produced in absence of Tpn is not known. To define the Tpn-dependent changes in the peptide repertoire, we isolated K<sub>b</sub> and D<sub>b</sub> pMHC I from WT as well as Tpn<sup>−/−</sup> splenocytes, eluted the bound peptides, and determined their amino acid sequences by tandem mass spectrometry. From WT cells, we identified 210 and 163 peptides bound to D<sub>b</sub> and K<sub>b</sub>, respectively. In contrast, the lower pMHC I expression in Tpn-deficient cells allowed recovery of fewer peptides; 63 and 22 peptides bound to D<sub>b</sub> and K<sub>b</sub>, respectively. We did not find any obvious differences in the intracellular localization of the source proteins for these peptides (data not shown). Many peptides in Tpn<sup>−/−</sup>-deficient splenocytes were also found in WT mice (Fig. 8A, Supplemental Fig. 1A, Supplemental Tables I, II). Remarkably, comparison of the unique...

**FIGURE 6.** Immunogenic pMHC I expressed by Tpn or ERAAP-deficient cells do not overlap. T cell responses against indicated splenocyte APCs. (A) Tpn<sup>−/−</sup> anti-WT T cell response, (B) WT anti-Tpn<sup>−/−</sup> T cell response, and (C) WT anti-ERAAP<sup>−/−</sup> T cell response against spleen cell APCs derived from WT, Tpn<sup>−/−</sup>, or ERAAP<sup>−/−</sup> mice. Immunizations to induce specific CD8<sup>+</sup> T cells and intracellular cytokine staining to detect IFN-γ production are described earlier. The p values were calculated by Mann–Whitney U test. **p < 0.01, ***p < 0.001. Data are pooled from two (C) or three (A, B) independent experiments.

**FIGURE 7.** Different ligands are used for rejection of Tpn- or ERAAP-deficient cells by WT mice in vivo. T cells from WT mice primed 7 d earlier with male WT, Tpn<sup>−/−</sup>, or ERAAP<sup>−/−</sup> splenocytes were assessed for their ability to specifically eliminate WT, Tpn<sup>−/−</sup>, or ERAAP<sup>−/−</sup> female targets in vivo. Targets were given distinct labels so they could be compared in the same host mouse: WT = CFSE (high dose); Tpn<sup>−/−</sup> = CFSE (low dose); ERAAP<sup>−/−</sup> = CMAC. (A) Schematic indicating the populations that represent ERAAP<sup>−/−</sup>, Tpn<sup>−/−</sup>, and WT. (B) Representative FACS plots of labeled targets before (input) and after (output) challenge. Input refers to proportions of each labeled cell type before challenge, whereas output refers to the labeled populations identified 20 h posttransfer. (C) Summary of in vivo killing assay from (B). Negative loss (gain) is plotted as zero. Data are representative of two independent experiments (B) or are pooled from two independent experiments (C).
peptides in Tpn<sup>−/−</sup> cells with their WT counterparts revealed significant differences. First, peptides in Tpn<sup>−/−</sup> cells were markedly longer than those in WT cells (Fig. 8B, Supplemental Fig. 1B). Second, the canonical asparagine (N) residue at the p5 position of D<sup>b</sup> bound peptides was consistently absent in peptides produced in absence of Tpn (Fig. 8C, 8D). A loss of the conserved phenylalanine or tyrosine residues (F/Y) at the p5 anchor position was less obvious in peptides bound to K<sup>b</sup> (Supplemental Fig. 1C, 1D).

The most striking difference in the amino acid sequences was found in the C-terminal (P<sub>V</sub>) position of K<sup>b</sup> and D<sup>b</sup> peptides eluted from Tpn<sup>−/−</sup> samples. Typically, the C-terminal position is occupied by an aliphatic amino acid: Met (M), Ile (I), Leu (L), or Val (V), as seen in peptides found in WT cells (Fig. 8C, 8D, Supplemental Fig. 1C, 1D). However, in the Tpn<sup>−/−</sup> samples, a higher frequency of abnormal amino acids was identified at PΩ. These included Lys (K), Ser (S), Asn (N), Pro (P), and Ala (A) for D<sup>b</sup> (Fig. 8C, 8D), and Thr (T) and Pro (P) for K<sup>b</sup> (Supplemental Fig. 1C, 1D). Thus, the ability to choose the appropriate C-terminal amino acid, a key determinant of pMHC I stability, was lost in the absence of Tpn.

We verified the MHC I binding characteristics of a few representative peptides by assessing their ability to stabilize D<sup>b</sup> or K<sup>b</sup> on the surface of TAP-deficient RMA/s cells. Each peptide bound to the respective MHC I, although the binding was lower and the decay was faster than the canonical K<sup>b</sup> and D<sup>b</sup> binding peptides (Supplemental Fig. 2A–D). From Tpn-deficient mice, even the peptides that contained both anchor residues, such as FSPLNPVRV (D<sup>b</sup>) and SLNRFIPL (K<sup>b</sup>), were suboptimal binders even the peptides that contained both anchor residues, such as FSPLNPVRV (D<sup>b</sup>) and SLNRFIPL (K<sup>b</sup>), were suboptimal binders.

Discussion
We show in this article that generation of the optimal pMHC I repertoire required independent editing by Tpn and ERAAP. The absence of Tpn profoundly altered the pMHC I repertoire, causing loss of many pMHC I normally expressed in WT cells, as well as gain of other novel pMHC I. Interestingly, the new pMHC I in Tpn<sup>−/−</sup> cells were immunologically distinct from those found in cells lacking the N-terminal peptide editor, ERAAP. The CD8<sup>+</sup> T cells in WT mice elicited by either ERAAP<sup>−/−</sup> or Tpn<sup>−/−</sup> cells were highly specific and did not cross-react. Amino acid sequences of unedited peptides revealed that differences between the peptides in ERAAP versus Tpn-deficient cells were in their N- and C-terminal anchor residues, respectively. Thus, Tpn defines the C terminus, whereas ERAAP shapes the N terminus of canonical MHC I peptides.

The MHC I molecules present an extraordinarily diverse set of peptides to allow effective immune surveillance of virtually all endogenous proteins (3). Nevertheless, the canonical peptides presented by a given MHC I molecule share certain key features: a length of 8–10 aa, and the presence of conserved residues at the C terminus and at an internal p2 or p5 position (41). These conserved amino acids are called anchor residues because their presence determines the stability of the pMHC I (42). Editing of the available peptide repertoire is crucial to ensure that only the stable pMHC I reach the surface that are capable of triggering CD8<sup>+</sup> T cell responses. To generate the optimal pMHC I repertoire thus requires the editing mechanisms to determine the appropriate C termini, the length, as well as the internal conserved residues. The extent to which these choices are determined by the shape of the peptide binding groove of the MHC I itself versus other key players in the pathway has remained unclear.

![FIGURE 8. MHC I in WT and Tpn-deficient cells present unique peptides. The H-2D<sup>b</sup> MHC I were immunoprecipitated from WT and Tpn-deficient spleen cells. Eluted peptides were sequenced by mass spectrometry and manually validated. (A) Numbers of distinct or shared peptides found in pMHC I expressed by WT or Tpn-deficient cells. (B–D) Analysis of the unique peptides from WT and Tpn-deficient cells. (B) The average lengths of peptides recovered from WT or Tpn-deficient cells. The indicated p value was calculated by two-tailed t test. (C) Conservation of p5 and C-terminal anchor residues (PΩ). Plots represent frequency of Asn (N) at P4–6 or the frequency of indicated amino acids at PΩ of H-2D<sup>b</sup> peptides. (D) Logo representation of H-2D<sup>b</sup> peptides eluted from WT or Tpn-deficient cells. Peptides are grouped according to their lengths, and the numbers of peptides in each group are indicated. The height of each bar is proportional to the degree of amino acid conservation, and the height of each letter composing the column is proportional to its frequency at the given position. Amino acids are colored as follows: hydrophobic (black), aromatic (purple), acidic (red), basic (blue), neutral (green), and the others (orange).](http://www.jimmunol.org/DownloadedFrom)
The MHC I molecules are loaded with their peptide cargo in the ER within the PLC (8). The crucial role of the PLC in peptide loading has been demonstrated by the severe loss of peptide-loaded MHC in cells without Tpn (16, 17). Tpn is the key element that holds the PLC together and retains the MHC I molecules in the ER until loaded with appropriate peptides (43). When various antigenic peptides were assessed for binding MHC I in the ER and subsequent display on the cell surface, presentation efficiency was determined by peptide affinity in presence of Tpn, but not other PLC components (20). Likewise, through in vitro reconstitution in microsomes, Tpn mediated the binding of high-affinity peptide to MHC I (44). Taken together with the severe reduction of pMHC I expression on the surface when Tpn was lost, these observations suggest that most peptides require editing in the PLC. Which structural aspects of the canonical MHC I-bound peptides determined the appropriate affinity threshold remained unclear.

We first used an immunological approach to characterize the changes in the peptide repertoire caused by loss of Tpn. We elicited CD8+ T cell responses in WT mice immunized with spleen cells from Tpn-deficient mice and vice versa. Because the immune response has evolved to distinguish nonself from self, the CD8+ T cell responses are exquisitely specific for nonself pMHC I. Importantly, the T cell can reveal changes in the pMHC I repertoire caused by alterations in Tpn expression that are not readily detected by any other assay. The specificity of the CD8+ T cell responses showed that the absence of Tpn, like that of ERAAP described earlier (26), caused the loss of many WT pMHC I, as well as gain of other immunogenic pMHC I. As in ERAAP-deficient cells, the new pMHC I expressed by Tpn-deficient cells were also less stable, suggesting that the presented peptides were structurally distinct from their WT counterparts.

Interestingly, different structural changes in the pMHC I repertoire were caused by the loss of Tpn rather than by loss of ERAAP. We compared the effects of ERAAP versus Tpn deficiency to determine whether there were similarities in their editing functions. To examine a broad set of endogenous pMHC I, we compared the potential cross-reactivity of WT CD8+ T cells responses elicited by Tpn versus ERAAP-deficient cells. We did not detect cross-reactivity of WT CD8+ T cells responses, showing that the absence of Tpn, like that of ERAAP or Tpn was also found in vivo, ruling out potential overlapping, it should be interesting to determine why Tpn or ERAAP are differentially targeted for immune evasion by viruses (49–51) and in cancer (40, 52).

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Disclosures

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References