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The Specificity of Trimming of MHC Class I-Presented Peptides in the Endoplasmic Reticulum

Arron Hearn,* Ian A. York, † and Kenneth L. Rock2*

Aminopeptidases in the endoplasmic reticulum (ER) can cleave antigenic peptides and in so doing either create or destroy MHC class I-presented epitopes. However, the specificity of this trimming process overall and of the major ER aminopeptidase ERAP1 in particular is not well understood. This issue is important because peptide trimming influences the magnitude and specificity of CD8+ T cell responses. By systematically varying the N-terminal flanking sequences of peptides in a cell-free biochemical system and in intact cells, we elucidated the specificity of ERAP1 and of ER trimming overall. ERAP1 can cleave after many amino acids on the N terminus of epitope precursors but does so at markedly different rates. The specificity seen with purified ERAP1 is similar to that observed for trimming and presentation of epitopes in the ER of intact cells. We define N-terminal sequences that are favorable or unfavorable for Ag presentation in ways that are independent from the epitopes core sequence. When databases of known presented peptides were analyzed, the residues that were preferred for the trimming of model peptide precursors were found to be overrepresented in N-terminal flanking sequences of epitopes generally. These data define key determinants in the specificity of Ag processing. The Journal of Immunology, 2009, 183: 5526–5536.

Peptides capable of binding MHC class I (MHC I) molecules are generated during intracellular protein degradation. These can then be presented on the cell surface and nonnative peptides (e.g., from viral proteins) recognized by circulating CTL (1–5).

A single type of MHC I molecule can bind to a large repertoire of different peptides in the ER. This is due to the fact that the MHC binding groove interacts with main chain atoms plus a few amino acid side chains of the peptide (6). However, the groove also interacts with the amino (N) and carboxy (C) terminal groups of the epitope, thus limiting antigenic peptides to a length of 8, 9, or 10 residues, depending on the particular MHC I molecule (6). Despite the promiscuity of peptide binding, MHC I molecules typically present only a small fraction of potential peptides encoded by viral genomes, and even fewer peptides trigger a potent T cell response; for example, of the five potential H-2Kb-binding peptides in OVA, genomes, and even fewer peptides trigger a potent T cell response; for example, of the five potential H-2Kb-binding peptides in OVA, only one (SINFEKL (S-L)) stimulates a strong immune response (7). The reasons for this phenomenon (“immunodominance”) are unclear and probably complex (reviewed in Ref. 8), but Ag processing and ultimately epitope abundance at the cell surface can be a major factor (9–11).

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2 Abbreviations used in this paper: MHC I, MHC class I; ER, endoplasmic reticulum; ERAP1, endoplasmic reticulum aminopeptidase I; MFI, mean fluorescence intensity; siRNA, small interfering RNA.

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N terminus (11, 25, 26, 29, 30). In addition, mice lacking ERAP1 had markedly different presentation of a variety of epitopes (11, 29–31), leading to differences in immunodominance hierarchies (11, 31). These results suggest that ability of ERAP1 to remove N-terminal amino acids from epitope precursors is a key determinant of the amount of epitope displayed on the cell surface and the specificity of the immune response to invading pathogens. This led us to initiate the present study to systematically examine the trimming of N-terminal sequences from antigenic precursors in the ER and the role ERAP1 plays in this process.

Materials and Methods

Peptide trimming assays

Peptides were synthesized by Sigma-Aldrich and were >80% by MS analysis. Peptides (100 μM) were incubated with purified recombinant human ERAP1 (3.5 μg/ml) (a gift from T. Nguyen and L. J. Stern, University of Massachusetts Medical School, Worcester, MA) at 37°C in 50 mM Tris-HCl (pH 7.8) and 0.5 μg/ml protease-free BSA (Sigma-Aldrich). Reactions were terminated by adding 0.6% trifluoroacetic acid. The peptide-containing supernatant was analyzed by reversed phase-HPLC on a 4.6 x 250 mm C18 column (Vydac) and eluted with a 7–50% acetonitrile gradient in 10 mM sodium phosphate buffer (pH 6.8) or a gradient of 7% acetonitrile in 0.06% trifluoroacetic acid to 41% acetonitrile in 0.06% trifluoroacetic acid. The amount of each peptide was calculated by integration of the area under the peak.

Plasmids

N-terminal S-L (OVAV Asp-26) precursors were targeted to the ER using a signal sequence (ss) derived from the adenoviral E3/19k protein (32). To ensure efficient cleavage by the signal peptidase an alanine residue was encoded between the signal sequence and the C-terminally fused peptide. Synthetic complementary oligonucleotides encoding N-terminal extended epitope precursors were annealed and inserted into pBluescriptSK− (pSt and Xbal). The oligonucleotides used were as follows: for pBS-ss-XXS-L, 5′-CTGCAGCGCT GCT XXX AGT ATA ATC AAC TTG GAA AAA CTG TAGTTCCTTAGA-3′; for pBS-ss-XXYY S-L, 5′-CTGCAGCGCT GCT XXX XXX AGT AGA CTG GGA AAA CTG TAC TAT AGT ATA ATC AAC TTT GAA AAA CTG TAGTTCCTTAGA-3′; for pBS-ss-XXY Y S-L, 5′-CTGCAGCGCT GCT XXX XXX AGT ACT GAT AGA CTG GGA AAA CTG TAC TAT AGT ATA ATC AAC TTT GAA AAA CTG TAGTTCCTTAGA-3′; for pBS-ss-XXF-L (Sendai NP321–332), 5′-CTGCAG CGCT GCT XXX XXX TTC GCC CCC GCC AAC TAC CCC GCC CCT GTG TAGTTCCTTAGA-3′; and for pBS-ss-XXX-R (HCV NS5B2588 –2596), 5′-CTGCAG CGCT GCT XXX XXX CCC CCC GCC AAC TAC CCC GCC CCT GTG TAGTTCCTTAGA-3′. These were subcloned into pTracer-CMV2 (Invitrogen Life Technologies) a plasmid containing a GFP/zeocin resistance cassette, using oligofectamine (Invitrogen) as described previously (26). Cells were transfected with siRNA for both ERAP1 and control mTOP.

Cells

HeLa-Kb and HeLa-Kb-ICP47 (HeLa-Kb-A3–47 cells) were transfected with pBS-ss-X-S-L, pBS-ss-X-XF-L, and pBS-ss-X-XYY S-L, pBS-ss-X-XXF-L (Sendai NP321–332), 5′-CTGCAGCGCT GCT XXX XXX AGT ACT GAT AGA CTG GGA AAA CTG TAC TAT AGT ATA ATC AAC TTT GAA AAA CTG TAGTTCCTTAGA-3′; for pBS-ss-X-XXS-L, 5′-CTGCAGCGCT GCT XXX AGT AGA CTG GGA AAA CTG TAC TAT AGT ATA ATC AAC TTT GAA AAA CTG TAGTTCCTTAGA-3′; for pBS-ss-X-XXY Y S-L, 5′-CTGCAGCGCT GCT XXX XXX AGT ACT GAT AGA CTG GGA AAA CTG TAC TAT AGT ATA ATC AAC TTT GAA AAA CTG TAGTTCCTTAGA-3′; for pBS-ss-X-XXF-L (Sendai NP321–332), 5′-CTGCAG CGCT GCT XXX XXX TTC GCC CCC GCC AAC TAC CCC GCC CCT GTG TAGTTCCTTAGA-3′; and for pBS-ss-X-XXX-R (HCV NS5B2588 –2596), 5′-CTGCAG CGCT GCT XXX XXX CCC CCC GCC AAC TAC CCC GCC CCT GTG TAGTTCCTTAGA-3′. These were subcloned into pTracer-CMV2 (Invitrogen Life Technologies) a plasmid containing a GFP/zeocin resistance cassette, using oligofectamine (Invitrogen) as described previously (26). Cells were transfected with siRNA for both ERAP1 and control mTOP.

Abs and flow cytometry

Cells were transiently transfected with plasmid (1 μg) using TransIT HeLa Transfection Reagent (InVitrogen Life Technologies) at 37°C in 50 mM Tris-HCl (pH 7.8) and 0.5 μg/ml protease-free BSA (Sigma-Aldrich). Reactions were terminated by adding 0.6% trifluoroacetic acid. The peptide-containing supernatant was analyzed by reversed phase-HPLC on a 4.6 × 250 mm C18 column (Vydac) and eluted with a 7–50% acetonitrile gradient in 10 mM sodium phosphate buffer (pH 6.8) or a gradient of 7% acetonitrile in 0.06% trifluoroacetic acid to 41% acetonitrile in 0.06% trifluoroacetic acid. The amount of each peptide was calculated by integration of the area under the peak.

Online databases and epitope analysis

A total of 4934 naturally presented MHC I epitopes from SYFPEITHI (www.syfpeithi.de) and The Internet Epitope Database (IEDB) (www.immuneepitope.org) were selected in April 2009 (MHC II epitopes in these databases were excluded from analysis) and the sequences of the proteins from which they originated were obtained from GenBank. The 15 aa immediately N-terminal to each epitope sequence (or, if the epitope was <15 aa from the origin of the protein, as many as possible) were identified and stored in a SQLite database. The epitopes, the MHC I alleles to which they bind, and the upstream sequences are listed in Supplemental Table I. Python scripts were used to calculate the frequency of each amino acid in each position N-terminal of the epitope. As a control, the protein precursors were pooled, and 4934 15-aa-long peptides were randomly selected from this pool and analyzed in the same way; random selection and analysis was repeated 500 times, and the average frequency and SD of each amino acid was calculated.

Results

In vivo ERAP1 specificity

The observation that the loss of ERAP1 reduces the presentation of many peptides indicates that these epitopes must be initially produced as longer precursors that are subsequently trimmed in the ER. Moreover, the finding that ERAP1 deficiency affects the presentation of different epitopes in different ways suggests that either some peptides are made as precursors while others are not (and hence manifest a differential requirement for trimming) or that ERAP1 has specificity and trims some precursors better than others (or both). Microsome preparations have previously been shown to be capable of trimming some precursor peptide epitopes (37, 38). However, because the specificity of ERAP1 for trimming polypeptide substrates has not yet been well defined, we sought to initially test the second possibility in vitro using recombinant human ERAP1.

To systematically examine the specificity of trimming of N-extended precursors of MHC I-presented peptides we synthesized a series of peptides containing the model epitope S-L (the immunodominant H-2Kb-restricted epitope SIINFEKL from chicken OVA) and compared the rates of degradation. Each peptide was generated with a single amino acid extension on the N terminus of SIINFEKL. In total, the rates of removal of 16 aa were analyzed (four of the possible twenty were excluded due to imperfections or insufficient resolution). Time courses of peptide degradation were evaluated (Fig. 1A). As shown previously the mature epitope SIINFEKL is a very poor substrate for ERAP1 and is not degraded further (27). On the other hand, LSIINFEKL is trimmed very rapidly to SIINFEKL (Fig. 1B). The amount of mature eight-residue peptide steadily increased over time and the trimming process stopped when the nine-residue peptide was converted to SIINFEKL. The rates of degradation of all 16 N-terminal extended peptides are shown in Fig. 1B arranged from highest to lowest, left to right. This analysis revealed that the N-terminal flanking residue had a marked and highly reproducible influence on the rate of mature epitope generation, e.g., leucine and methionine were both efficiently removed from the N terminus, in comparison aspartic acid and glutamic acid were poorly removed.

4 The online version of this article contains supplemental material.
**N-terminal flanking amino acids affect presentation from ER-targeted precursors**

ERAP1 is localized in the ER. We next wanted to determine whether the N terminus of epitope precursors, specifically targeted to the compartment where ERAP1 resides, would affect the amount of peptide seen on the cell surface in vivo.

To do this systematically, we generated a series of minigene constructs containing S-L. Each minigene was constructed with an N terminus containing one of the possible 20 aa. To amplify any differences between constructs in the rate of removal of their flanking residues, they were expressed with two identical amino acids upstream of the epitope (XXS-L), where “X” represents any amino acid. These sequences were then fused to an N-terminal signal sequence derived from the adenoviral E3/19K protein (MRYMGLLALAAVCSAAXXSIINFEKL) so that they would be cotranslationally transported by Sec61 into the ER and the signal sequence removed during this process (these constructs will be referred to as ss XXS-L). To ensure equal trimming by signal peptidase, an alanine residue was encoded between the signal sequence and the C-terminally fused peptide. The ss XXS-L constructs were transiently transfected into HeLa-Kb cells stably transfected with the TAP blocker ICP47 to specifically analyze ER processing. The presence of S-L-Kb complexes on the cell surface of transfected (GFP/H11001) cells was quantified by staining with the mAb 25.D1.16. This assay gave highly reproducible results between replicate groups and independent experiments. This analysis revealed that N-terminal flanking amino acids had a marked influence on the levels of presented peptide detected on the cell surface (Fig. 2A). N-terminal amino acids such as methionine, leucine and tyrosine appear to be efficiently removed from precursors to generate mature S-L epitope. On the other hand residues such as arginine and proline were processed inefficiently by ER resident aminopeptidases resulting in presentation that was \(<1\%\) of that observed with ss YYS-L (the construct leading to the greatest presentation). The effects of other amino acids on presentation fell between these two extremes resulting in a hierarchy of presentation among the 20 constructs tested that was highly reproducible (Fig. 2A). In fact 14 of the 20 aa were associated with presentation that was \(\approx 50\%\) of that observed with ss YYS-L demonstrating that many amino acids are removed rather inefficiently in the ER. Although amino acids with acidic, amide and basic side chains appear to be processed poorly there is a broad range of efficiencies of presentation within each group when amino acids are grouped by the chemical nature of their side chain.

We next examined whether a single amino acid showed the same effect as the corresponding doublet when targeted to the ER. To this end we generated a subset of ss XS-L constructs which encoded amino acids which were processed efficiently (L, M, and Y) and inefficiently in the ER (D, E, K, P, R, V, and W) as well as amino acids which lie in between these two extremes (S and T). The data obtained with these constructs are largely consistent with those obtained with the corresponding doublet (Fig. 2B). To test whether the efficiency of amino acid removal was length-dependent, we measured processing of constructs in which Leu (efficiently processed), Arg, Asp, or Lys (poorly processed), or His or Gly (moderately processed) amino acids were present at the N terminus of a 12-mer (ss XXYYS-L, since YYS-L is efficiently processed) rather than a 10-mer (ss XXS-L). Again, removal of XX from XXYYS-L was consistent with the efficiency of removal of XX from XSS-L (Fig. 2C).

It was important to determine whether the results we obtained with HeLa cells were generalizable to another cell type. Moreover, the HeLa cells used in our analyses express ERAP1 but not the homologous peptidase ERAP2, which may also trim peptides in the ER. Of importance, ERAP2 has a different specificity than ERAP1 and is more active in removing basic...
residues, at least in cell-free systems (40). Therefore, to test the
generality of the results obtained with HeLa, we performed a
similar analysis using a second cell line (COS 7) that expresses
both ERAP1 and ERAP2 (Supplemental Fig. 1). All 20 of the
ss XXS-L constructs were transfected into COS-Kb cells and
the generation of SIINFEKL-Kb complexes quantified with
25D1. The results of this analysis correlated extremely well
(correlation coefficient of 0.74) with those obtained with HeLa
cells, even for charged residues that were potential substrates
for ERAP2 (correlation between Hela-Kb and COS-Kb for
charged residues /H110050.995) (Fig. 2D).

Analysis of the trimming of ss XXS-L in the ER by ERAP1
For presentation of S-L precursors with the natural N-terminal
flanking sequence from OVA (LEQLE), ERAP1 appears to be
the only important peptide-trimming enzymatic activity in the
ER (25, 26). We therefore examined whether this enzyme was
vital for epitope liberation from the various ss XXS-L con-
structs. In these experiments, the ER-targeted precursors were
transfected into HeLa-Kb ICP47 cells that were treated with
control or ERAP1-specific siRNA under conditions where
ERAP1 protein expression is reduced by at least 90% (26).

The loss of ERAP1 reduced the presentation of all 20 constructs,
most of them to little more than background levels (Fig. 3). The
presentation of a few of the best presented constructs was inhibited
by 70 – 80%, leaving significant presentation of H-2Kb-S-L (e.g.,
ss YYS-L and ss MMS-L); whether the remaining presentation is
due to residual amounts of ERAP1, or whether another peptidase
can contribute to processing of these peptides, remains to be de-
termined. The construct that was least dependent on ERAP1 was ss
AAS-L; this may be because the signal peptidase cleaves prefer-
entially after small, uncharged residues such as alanine and there-
fore may be able to generate the mature epitope from this con-
struct. In any case, this analysis clearly shows that ERAP1 is
required for the bulk of presentation of all 20 constructs. Therefore
the differences in trimming and presentation of the various con-
structs must be due to the specificity of ERAP1, allowing us to
define the specificity of ERAP1 as it functions in intact cells.
We next investigated how incorporating different residues directly upstream of S-L in a subset of longer precursor peptides, LEQLXS-L (variable residue underlined), influenced liberation of the mature epitope, compared with the natural context in chicken OVA of LEQLES-L (Fig. 4A). The ER-targeted constructs LEQLLS-L, LEQLMS-L, and LEQLYS-L were presented very efficiently, whereas epitope generation from LEQLKS-L and LEQLRS-L was lower than that from LEQLES-L. The data obtained with these constructs are highly consistent with those obtained with simpler constructs where the residue was expressed as a doublet (Fig. 4B) or a single residue (Fig. 4C) upstream of S-L.

Poorly cleaved residues are dominant in a doublet

We next investigated the effect of juxtaposing, in different orientations, residues that were efficiently removed from precursors in the ER and those that were not. We generated a series of constructs expressing XZS-L and ZXS-L in the ER (where X and Z are two different amino acids which were efficiently (Leu, Met and Tyr) or poorly (Lys, Arg and Val) trimmed from S-L and compared Ag presentation to that observed with the single amino acid counterparts (XS-L and ZS-L). Juxtaposing lysine and valine, both of which are poorly removed, leads to low epitope generation. On the other hand when the N-terminal flanking doublet is composed of leucine and methionine, which are both efficiently removed, S-L presentation on the cell surface is high (Fig. 5). We next tested constructs that had an efficiently trimmed residue juxtaposed with a poorly trimmed one. When methionine and lysine or tyrosine and arginine were juxtaposed in either orientation, presentation is significantly lower than that of the single methionine or tyrosine residue precursors. However, epitope generation from these constructs was not reduced to the level of the corresponding single poor residue (Lys or Arg). The difference in presentation between these constructs and the corresponding single efficiently trimmed residue was statistically significant (p < 0.05, Student’s t test). This suggests that poorly removed amino acids have a large impact on the efficiency of presentation when located at either the P1 or P2 position. Interestingly, we found one exception to this rule. Although the level of presentation from the LVS-L construct was consistent with the above observations in that it was significantly lower than that of the single leucine precursor, presentation from the VLS-L construct was almost as high as that of the LS-L construct (Fig. 5). These results suggest that not only the identity of the amino acid, but also adjacent residues may sometimes be important in determining the efficiency of removal.

Comparison of in vitro and in vivo ERAP1 specificity

Given that the specificity of N-terminal amino acid removal from epitope precursors observed in vitro appears to dependent on ERAP1 (Fig. 3) we next compared these observations to that seen in vitro with recombinant ERAP1 (Fig. 1). There is a good correlation between presentations from ER targeted XSS-L and the specificity of recombinant ERAP1 (Fig. 6A) again suggesting that
ERAP1 is the major aminopeptidase within the ER responsible for epitope liberation and that its specificity determines which epitopes are generated from precursors with N-terminal extensions. This finding is also mirrored when comparing ERAP1 specificity to presentation from ER targeted XS-L (Fig. 6B).

The influence of upstream amino acids is the same on multiple epitopes

When precursors are expressed in the ER the residues upstream of the model epitope S-L have a marked impact on presentation by MHC I molecules. Given this result we next wanted to broaden the observation and determine whether the same amino acids upstream of other epitopes had a similar effect on presentation. The two epitopes chosen for this analysis were FAPGNYPAL (F-L), a H-2Kb-restricted epitope derived from Sendai virus nucleoprotein, and RVCEKMALY (R-Y), a HLA-A3-restricted epitope derived from the hepatitis C virus NS5b. We generated signal sequence fusion constructs which allowed expression of X XF-L and XXR-Y in the ER, where the N-terminal doublet (XX) consisted of amino acids which were efficiently removed from S-L in the ER (Leu, Met, and Tyr) and those which were not (Lys, Arg, and Val).

We were unable to measure the presentation of these Sendai and hepatitis virus epitopes using the same approach used for S-L because there are no Abs available that are specific for F-L/H2-Kb or R-Y/HLA-A3 complexes. We therefore developed an alternate quantitative assay. In HeLa Kb cells stably transfected with ICP47, endogenous peptides are prevented from gaining access into the ER (39). In the absence of peptides, most H-2Kb and HLA-A3 molecules are retained in the ER and very few are transported to the cell surface. However, if binding peptides are delivered into the ER via Sec61, the MHC I molecules are then transported to the cell surface. Quantitation of cell surface MHC I levels, by staining with anti-H-2Kb- or anti-HLA-A3-specific Abs, is therefore a measure of peptide supply to the molecules in the ER and of precursor N-terminal trimming. Transfecting the HeLa K b-A3–47 cells with ER-targeted MMS-L, SSS-L, and KKS-L increased H-2Kb expression on the cell surface, and the amount of this increase paralleled the level of H-2Kb/S-L complexes (measured with 25.D1.16) (Fig. 7A). Similarly, the ER-targeted R-Y peptide increased the surface expression of HLA-A3 in HeLa K b-A3–47 cells (Fig. 7B). In contrast, S-L (which does not bind HLA-A3), when targeted into the ER, did not restore surface expression.

Using this system we then tested the effect of different N-terminal amino acids on presentation of F-L (Fig. 7C) and R-Y (Fig. 7D). For 9 of the 10 constructs, the effects of the various N-terminal residues were the same as those observed with S-L. This led to a highly significant correlation between presentation from ss X XS-L and ss XXF-L (Fig. 7C, inset). Methionine and tyrosine (which are efficiently removed from S-L) led to high presentation of both F-L and R-Y, whereas lysine and arginine led to poor presentation of the two alternate epitopes. Valine in the flanking doublet also led to poor presentation of F-L as it had done for S-L. However, in contrast with S-L, valine was efficiently removed from the N terminus of R-Y, leading to good presentation. Valine was also efficiently processed in the context of a long peptide, ss-VVYYS-L (data not shown), suggesting that amino acid or length context may be particularly important for trimming of this amino acid. Interestingly, the natural flanking residue of R-Y is valine, suggesting that the context of the amino acids to be removed may occasionally also play a role in determining efficient cleavage.

Efficiently removed amino acids are overrepresented upstream of natural epitopes

We reasoned that if the findings with model epitopes are broadly applicable, then residues that permit high-level expression of epitopes should be overrepresented upstream of naturally-presented epitopes, and those that were associated with poor presentation should be underrepresented. This issue has previously been investigated by Schatz et al. (38), but it was worth revisiting using a larger number of epitopes (4394 vs 1543) from the IEDB as well as SYFPEITHI databases allowing an analysis with substantially more statistical power. Therefore, we selected 4394 naturally processed epitopes from the SYFPEITHI and IEDB on-line databases, and identified the 15-aa N-terminal to the epitopes in their precursor proteins. At each position (where “1” represents the amino acid adjacent to the epitope, and “15” the most distal amino acids).
acid) we calculated the frequency of each amino acid. As controls, we also selected 4394 random nonepitope peptides of the same size from the pool of precursor proteins and analyzed their N-terminal flanking residues. This random selection was repeated 500 times, and the average and SDs of these “background” frequencies were calculated. Comparison of sample to background frequencies shows that amino acids in positions 1 and (to a lesser extent) 2 and 3 diverge furthest from background frequencies, consistent with previous observations that MHC I epitopes presented on MHC I are often imported into the ER with 1, 2, or 3-amino acid extensions (23); the probability of this variation being due to chance ($\chi^2$ test) is $< 10^{-17}$ (Fig. 8A). The amino acids most responsible for this skewed distribution are indicated in Fig. 8B. Ala, Cys, Leu, Met, Ser, and Tyr are all >2 SDs greater than “background” frequency, and Val and (especially) Pro are >2 SDs lower than background. Charged residues (Asp, Glu, His, Lys, and Arg) all showed a strong trend toward being underrepresented, although this trend was not statistically significant for any of these residues when analyzed individually. However, when analyzed as a group, charged residues were >2 SDs lower than background frequency. Other groups of amino acids (aromatic, hydrophobic, nucleophilic) did not differ significantly from their respective background frequencies. These results, particularly for charged residues, differ somewhat from an earlier study (38) presumably because the present analysis analyzed a much larger set of peptides and was therefore more highly powered.

Thus the residues that we find empirically to lead to high-level Ag presentation (Tyr, Met, Leu, and Cys) are all overrepresented residues N-terminal to natural epitopes in our analysis and that of Shatz et al. (38) (although in the latter study Tyr and Met are more abundant than background frequency but do not reach a significant difference). Ala is also overrepresented and better presented, however, as discussed some of its trimming in our in vivo system is not due to ERAP1. In our experiments,
charged residues were processed poorly, correlating to some extent with the overall underrepresentation of charged residues immediately adjacent to natural epitopes.

The bond upstream of the most under-represented residue, proline, is poorly trimmed by ERAP1 (Fig. 1 and 2A) and cannot be trimmed by many other aminopeptidases (41); therefore, we expect that constraints of aminopeptidase trimming would select against proline being in the P1 and P2 position. In our experiments, Val showed evidence of context-dependent trimming: when immediately adjacent to the epitope Val was generally processed poorly, but when separated from the epitope by one or more residues, Val was processed relatively well. Similarly, in natural epitopes Val is under-represented immediately adjacent to epitopes (P1; >2 SD less than background) but is present at background frequency at P2 and more distant positions (data not shown).

Similar results were obtained when we performed an analysis only of epitopes presented on human MHC I molecules (Supplemental Table II). This is not surprising because they account for 85% of the sequences in the databases we have analyzed (4231 of 4934 total). It should be noted that the epitopes presented on human MHC I molecules are primarily (~90%) longer than 8 aa, meaning that in some cases they could be further trimmed by ERAP1.

Discussion

MHC I epitopes are generated through a complex pathway that is influenced by proteasomes, peptidases, TAP, and tapasin as well as physical binding of mature epitopes to MHC I alleles. The efficiencies by which potential epitopes are generated from precursor proteins influence epitope abundance and recognition, which is important in vaccine design and the development of immunodominance hierarchies. Although some steps in the pathway are relatively well understood (e.g., TAP translocation, proteasome processing) the importance and direction of some other steps (e.g., peptidase processing) have not been as well studied.

N-terminally extended epitopes, generated by the proteasome (16), can be trimmed by aminopeptidases to generate peptides of the correct length for MHC I binding (24). However, only a small fraction of the peptide pool bind MHC I molecules and even fewer trigger a significant T cell response. This immunodominance can be a result of Ag processing and ultimately epitope abundance at the cell (9–11). In cells lacking the ER-resident aminopeptidase ERAP1, ER-targeted precursors are presented poorly if at all and ERAP1-deficient mice have markedly different presentation of many MHC I epitopes (11, 29–31). Previous studies have also shown that this aminopeptidase can contribute to the pattern of immunodominance (11, 42). ERAP1 is a unique aminopeptidase in that its substrate preferences are guided in part by the C terminus of the recognized peptide (28). However, its specificity is not otherwise well characterized. Most previous analyses of the N-terminal sequence specificity of ERAP1 have been done with nonphysiological substrates (such as dipeptides), and it has been clear that in some cases such substrates don’t model ERAP1’s behavior with longer “physiological” epitope precursors (43). Moreover, these analyses have been primarily performed in cell-free systems with purified enzymes or microsomes and it is not clear whether these assays replicate what occurs in living cells. Because ERAP1 is such a key player in the Ag presentation pathway, we set out to understand its specificity for N-terminal amino acids on N-extended epitopes and how this specificity could influence peptide delivery to MHC I molecules.

Using purified ERAP1, we showed that this aminopeptidase was capable of removing many different amino acids from the N terminus of an epitope precursor. This broad activity is of obvious biological importance in allowing ERAP1 to trim the panoply of MHC I-presented epitopes. However, the rates at which N-terminal residues were cleaved varied considerably and reproducibly between different amino acids. This suggests that ERAP1’s specificity could limit peptide supply from ER precursors if epitopes are extended on the N terminus by unfavorable amino acids. Conversely, more efficient trimming by ERAP1 of other amino acids could lead to greater epitope production for competition and presentation to the immune system. Previous studies characterizing ERAP1 or microsomal extracts, using a limited set of simple single amino acid fluorogenic substrates (X-AMC) (38, 44) have shown activity primarily for cleaving Leu and Met residues. This is consistent with our results that show that these amino acids are the most rapidly removed from the XS-L peptides and presumably reflects the higher affinity of Leu and Met for the ERAP1 active site. However, it is clear from our work that ERAP1 can remove many other amino acids, although more slowly. Our results are largely consistent with an analysis of the trimming of a limited number of peptide precursors by microsomes in vitro (38, 44); the few variations between these studies, particularly for charged amino acids, may reflect differences between our using a pure enzyme vs the earlier study using crude microsome preparations (potentially contaminated with cytosolic peptidases).

Another finding of interest was that regardless of the N-terminal flanking residues, purified ERAP1 virtually stopped trimming when the mature S-L epitope was generated. This is consistent with our previous findings, that ERAP1 trims with a molecular ruler down to a peptide of eight or nine residues in length (27), and indicates that this ruler is not influenced by the identity of the P1 residue. This unique function may contribute to the dominant role ERAP1 plays in Ag presentation and epitope generation due to the fact that trimming ceases once
peptides capable of MHC I binding are generated. Kanaseki et al. (45) recently suggested that ERAP1 does not have a molecular ruler because it hydrolyzed and destroyed a mature antigenic epitope; however, this epitope was a 9-mer and we have previously established that ERAP hydrolyzes ~50% of 9- to 8-mers (27). In other words, the concept of a molecular ruler is that ERAP1 trims down to a final core size (which can be eight or nine residues) and this core may or may not result in a mature epitope. This explains why ERAP1 can help to both create and destroy epitopes (11, 26). Importantly, the specificity of ERAP1 for N-terminal residues was not just seen at the 9- to 8-mer conversion but also at sequences further upstream of the epitope (e.g., the conversion of 12-mers to 11-mers to 10-mers). To determine the relevance of these findings to the in vivo situation we transfected cells with minigenes encoding ER-targeted (signal sequence) epitope precursors. The amino acid in the P1 or P2 positions strongly influenced the amount of MHC class I presentation from precursors in the ER. The same trends were seen whether the residue upstream of the epitope was present as a single amino acid or as a doublet, when the residue was preceded by a longer sequence (e.g., LEQLYXS-L), when the precursor peptide was a 10-mer or a 12-mer, and when different unrelated epitopes were used including 8-mers and 9-mers (S-L, F-L, or R-Y). When residues that were efficiently or poorly removed were paired in either orientation, the poor residue usually dominated and led to low presentation, as expected since trimming of the N-terminal extension would be affected whether it is the first or second residue that is removed slowly. Taken together, these results demonstrate that in vivo the amino acids in the P1 or P2 positions of both long and short precursors are critical determinants of the amount of epitope presented on MHC I molecules.

The specificity of trimming of the ER-targeted precursors was similar in both HeLa and COS7 cells. This suggests that our findings are not cell type specific but more general, although additional cell types need to be examined to fully evaluate this issue. Another point is that because COS7 cells express ERAP1 and ERAP2, our findings suggest that ERAP1 is the dominant ER-trimming enzyme; of note this is true even for charged residues that ERAP2 could potentially trim. Nevertheless, it is possible that the few differences in presentation that were observed between HeLa and COS7 cells were due to the presence or absence of ERAP2. Moreover, it remains possible that ERAP2 plays a more important role for other sequences and/or in different cells.

We were not able to identify any simple chemical feature that determined whether an amino acid is a good substrate or not. In general, charged residues are processed slowly, but the large hydrophobic Trp, the polar noncharged Asn, and the small nonpolar Gly are each also processed slowly. Thus, although there is clear specificity in the trimming process, it is not simply defined by the chemical class of amino acid side chains.

In almost all cases when two amino acids from either end of the presentation hierarchy were combined the inefficient residue was dominant and led to poor presentation. One exception suggests that context (i.e., adjacent amino acids or peptide length) may also influence processing of some residues. When valine was immediately adjacent to S-L or F-L, the precursors were slowly trimmed, whereas when Val was separated from S-L by one residue (e.g., VLS-L) or in the peptide VR-Y, processing was efficient. It is also interesting that even when the presentation of epitopes preceded by an efficient/inefficient or inefficient/efficient pair was low, it was better than was observed with the inefficient residue alone, suggesting that the rate of trimming in vivo is also influenced to some extent by adjacent amino acids or peptide length. Similarly, presentation of the long XXXYS-L peptides was generally higher than for the same residue as an XXS-L peptide. Nevertheless, it is important to emphasize that while context may influence trimming (particularly of valine), there clearly are definable rules of efficiency and these rules apply with different epitopes.

Knocking down ERAP1 strongly inhibited presentation from the vast majority of ER targeted epitope precursors, suggesting a major role in trimming. We interpret the difference in presentation between the different precursors as reflecting the specificity of ERAP1 trimming. This conclusion makes the assumption that the various XX residues do not influence cleavage by the signal peptidase (which liberates the epitope precursor from the signal peptide). Two pieces of data support this assumption. The first is that we have observed essentially the same results for sequences that are adjacent (sS X-S-L) or six residues away (ss LEQLXS-L) from the signal sequence cleavage site. The second is that the results with the presentation from minigenes and trimming of the same sequences by purified ERAP1 correlates well with one another. Nevertheless, it should be noted that this in vitro to in vivo correlation is not 100%. Where concordance is not perfect there must be other factors that influence peptide trimming in vivo. In these situations we can’t exclude a minor contribution from the signal peptidase although the difference could equally well reflect the participation of other ER molecules (chaperones, other peptidases) or that the conditions in the ER and cell-free buffer system are not identical and this somehow influences ERAP1’s properties. A complete understanding of ERAP1’s specificity will require further study and may be aided when its crystal structure is solved.

We believe our results are potentially contributory to helping to define some of the specificity of Ag processing. The power of current algorithms to predict presented peptides from the sequence of an Ag is limited presumably because they do not take into account all of the events, such as peptide trimming, that are needed to generate (or destroy) epitopes. Consistent with these idea that peptide trimming is an important factor in determining the repertoire of MHC I-presented peptides (the presented “peptidome”) we find that the residues that empirically lead to high-level Ag presentation in our system (Tyr, Met, Leu, Ala, and Cys) are all overrepresented N-terminal to natural epitopes by at least 2 SDs above background frequency; while residues that are underrepresented adjacent to natural epitopes (Pro and Val, and charged residues as a group) are poorly processed in our system. Overall these results are mostly similar qualitatively to the earlier analysis of a smaller set of sequences by Schatz et al. (38). It should be noted that one limitation of the databases used for these analyses is that the majority of the epitopes were defined based of their ability to optimally stimulate specific CD8 T cells and because of this some may not be identical to the naturally processed peptides. However, it is thought that only a small minority of epitopes are incorrectly assigned and therefore this should have a minimal effect on such analyses. Therefore, nonrandom frequencies of various amino acids are almost certainly due to differences in Ag processing.

Although it is possible that the upstream residues also affect proteasome cleavage or TAP transport, the residues that are consistently associated with high-level presentation of our model epitopes are not particularly preferred for proteasomal cleavage (46, 47) or TAP translocation (23, 48). This implies that aminopeptidase specificities, specifically ERAP1, play an important role in vivo in determining the generation of presented peptides, and that our system accurately defines at least some of these specificities. It is in fact remarkable that correlations are seen between ERAP1’s specificity and the presented peptidome because there
are other peptidases (e.g., cytosolic ones) that can contribute to trimming N-terminal residues.

Presumably other peptidases do contribute to the trimming of the sequences that are poorly trimmed by ERAP1; this may especially be the case for epitopes flanked by charged residues. Such flanking residues show only a modest reduction in frequency in the databases of presented peptides yet are very poorly trimmed by ERAP1 in vitro and in vivo. This might be because cytosolic aminopeptidases such as leucine aminopeptidase can remove charged residues (15). Alternatively, the proteasome’s trypptic active site, which cleaves preferentially on the carboxylxylic side of basic residues and its caspase-like site, which cleaves after acid residues, might remove these charged residues. Consistent with this later idea, the presentation from OVA of SIINFEKL (which is flanked on its N-terminus with a charged E residue) is not affected in ERAP1 deficient cells. Interestingly, although ERAP2 can hydrolyze basic residues (40), we find that precursors with charged flanking residues are still poorly presented in ERAP2-expressing cells.

In summary, our findings reveal that the amount of MHC-peptide complex presented to the immune system is determined in part by the amino acids upstream of epitope precursors and the ability of ERAP1 to remove these. The specificity of this trimming process for ERAP1 in vivo and in vitro for multiple epitopes is defined and reveals that that ERAP1 influences the extent of presentation in predictable ways.

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References


