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Peptide Presentation to an Alloreactive CTL Clone Is Modulated Through Multiple Mechanisms Involving Polymorphic and Conserved Residues in HLA-B27

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This study addressed the mechanisms by which HLA class I polymorphism modulates allore cognition. CTL 27S69 is an alloreactive clone raised against HLA-B*2705, with a known peptide epitope. This CTL cross-reacts with B*2702, which differs from B*2705 in the D77N, T80I, and L81A changes, but not with B*2701, which has D74Y, D77N, and L81A changes. To explain this differential recognition, B*2705 mutants mimicking subtype changes were used. The A81 mutant was not recognized, despite binding the natural epitope in vivo, suggesting that, when bound to this mutant, this peptide adopts an inappropriate conformation. The N77 and I80 mutations restored recognition in the N77A81 or I80A81 mutants. These compensatory effects explain the cross-reaction with B*2702. The Y74 and the Y74N77 mutants were weakly recognized or not recognized by CTL 27S69. This correlated with the absence or marginal presence of the peptide epitope in the Y74N77-bound pool. As with B*2701, exogenous addition of the peptide epitope sensitized Y74 and Y74N77 targets for lysis, indicating that failure to cross-react with B*2701 or these mutants was due to poor binding of the peptide in vivo and not to inappropriate presentation. The abrogating effect of Y74 was critically dependent upon the K70 residue, conserved among subtypes, as demonstrated with mutants at this position. Thus, HLA polymorphism affects allore cognition by modulating peptide binding or the conformation of bound peptides. Compensatory mutations and indirect effects of a polymorphic residue on residues conserved play a critical role. The Journal of Immunology, 1999, 163: 6060–6064.

Major histocompatibility complex class I molecules constitutively bind and present at the cell surface a large repertoire of endogenous peptides that can be recognized by CTLs. During ontogeny, T cells are selected to respond against foreign peptides complexed with self-MHC proteins. However, a large fraction of these T cells can be stimulated by allelogeneic MHC molecules. This extraordinarily strong response is a basis for the acute rejection of allogeneic transplants.

The clonal diversity of alloreactive T cell responses is a consequence of the large number of peptides that are presented by the allo-MHC (1–4). Most alloreactive T cells recognize epitopes whose structure involves both the nonself presenting molecule and specific peptides. However, alloreactive T cells are heterogeneous in their degree of peptide specificity, and a minor set may recognize common motifs shared by many peptides or be peptide-independent (5–7).

To understand the molecular basis for alloreactivity, critical issues are the nature of the peptides involved and the contribution of the allo-MHC molecule to the epitope. Only a few natural ligands recognized by alloreactive CTL have been identified (8–14). Some alloreactive CTL clones recognize different peptides complexed with different MHC class I molecules (15–17). It may be assumed that the various epitopes recognized by a single CTL share structural features, but this similarity may not be obvious from the primary structure of the peptides involved. The molecular mimicry model, proposed for explaining T cell cross-reactivity, suggests that different class I/peptide complexes may form antigenic surfaces that are similar in shape, charge, or both (18–20). A modified model, in which a critical local charge mimicry formed by two residues contributes to the recognition of self- and allo-class I/peptide complexes, has also been suggested (21). However, a recent report has demonstrated that the TCR footprint regions of two complexes recognized by a single TCR are significantly different in shape and charge (22).

Alloreactive CTLs can also cross-react with the same peptide bound to both allo- and self-class I molecules (23, 24) or to several different alloantigens (25). In a recent report from our laboratory (14), the peptide epitope recognized by the HLA-B27-specific CTL clone 27S69 was identified as the RRFFPYYV octamer. This CTL was raised against B*2705, and recognized the same peptide also in the context of B*2702, and B*2703, which differ from B*2705 by three (D77N, T80I, L81A) amino acid changes and one (Y59H) amino acid change, respectively. The same clone was unable to recognize B*2704, B*2706, and B*2710 despite efficient binding of the peptide to these subtypes. CTL 27S69 also failed to lyse B*2701 targets, but this was due to absence of constitutive binding of the peptide epitope to this subtype in vivo, because B*2701 efficiently presented the exogenous peptide to the CTL clone. B*2701 differs from B*2705 in the D74Y, D77N, and L81A changes and differs from B*2702 only by the D74Y and T80I changes. All of the changes in B*2701 and B*2702 are located in the α1-helix and are spatially close.

The differential presentation of a peptide epitope to an alloreactive CTL by closely related class I alloantigens provided the opportunity to analyze the mechanisms by which single changes in
the MHC molecule modulate allorecognition, and the interactive effects of multiple changes on peptide binding and presentation. Thus, the present work determined the basis for the differential recognition of B*2701 and B*2702 by CTL 27S69 by analyzing the recognition of single and double mutants mimicking subtype changes and the effects of these mutations on the binding and presentation of the natural peptide epitope.

Materials and Methods

CTL 27S69

CTL 27S69 was raised against B*2705. Its culture conditions and fine specificity with other HLA-B27 subtypes have been described previously (26). The natural peptide epitope recognized by this clone in the context of B*2705 and other subtypes has also been determined (14).

HLA-B27 mutants and transfectant cells

Hmy2.C1R (CIR1) transfectants expressing B*2701, B*2702, B*2705, and various HLA-B27 mutants were used (Fig. 1). B*2705 mutants were designated with the one-letter code of the amino acid(s) introduced followed by the number(s) of the position(s) changed. A B*2701 mutant carrying the K70A mutation was designated as A70-B*2701. The generation and expression levels of these mutants on transfected cells have been described previously for most of them (27–30). The I80A81 construct was generated by site-directed mutagenesis from I80 genomic DNA and transfected into C1R cells using previously described procedures (27, 31). HLA-B27 subtypes and mutants were expressed at high and similar levels on C1R transfectants (27). RMA-S is a murine TAP-deficient cell line (32). HLA-B27 subtypes and mutants were expressed at high and similar levels on C1R transfectants (27). RMA-S is a murine TAP-deficient cell line (32).

Isolation and analysis of HLA-B27 mutant-bound peptides

The peptide pools bound to the Y74N77 and A81 mutants were purified from 1–1.5 × 10⁶ C1R transfectant cells and fractionated by HPLC as described for B*2705 (14). The peptide composition of individual HPLC fractions was determined by matrix-assisted laser desorption/ionization time of flight (MALDI-TOF) mass spectrometry (MS), using a Reflex instrument (Bruker-Franzen Analytik, Bremen, Germany) as described previously (14). Peptide sequencing was conducted with an LCQ electrospray ion trap mass spectrometer (Finnigan, MAT, San Jose, CA), as described previously (14).

Peptide synthesis

The RRFFPYVV octamer was synthesized using standard fluorenylcarbonylmethyl chemistry and purified by HPLC. Its quantification was conducted by amino acid analysis and its correct composition was verified by MALDI-TOF and electrospray/ion trap MS.

Epitope stabilization assay

The quantitative procedure used has been described previously (34). Briefly, RNA-S transfected cells were incubated at 26°C for 24 h. Next, the synthetic peptide was added at 10⁻⁴ to 10⁻⁹ M. Cells were incubated for 1 h at 26°C, transferred to 37°C, and collected for flow microcytometry analysis after 2 h. Binding of the RRFFPYVV octamer was expressed as the C50, which is the molar concentration of peptide at 50% of the maximum fluorescence obtained in the concentration range used. Values of C50 of ≥10 μM were considered to reflect high affinity. C50 values of ≥50 μM indicated low affinity.

Cytotoxicity assays

When exogenous peptide was not added, a standard 4-h ⁵¹Cr release assay was conducted. In peptide sensitization assays, labeled targets were incubated for 30 min at room temperature with synthetic RRFFPYVV peptide or aliquots of HPLC fractions in RPMI 1640 medium (Life Technologies) with 1% FCS. Effector cells were then added and incubated at 37°C for 5 h. The procedures have been described in detail elsewhere (14).

RESULTS

Differential and compensatory effects of mutations mimicking HLA-B27 polymorphism on recognition by CTL 27S69

A set of CIR transfectants expressing single and double B*2705 mutants mimicking B*2701 and B*2702 polymorphism was tested for recognition by CTL 27S69 (Fig. 1A). Among the mutants with single changes, A81 abrogated lysis, Y74 targets were lysed with significantly decreased efficiency (36% relative lysis), and N77 and I80 did not affect recognition by the CTL clone. Among the double mutants, Y74N77 was not recognized, but N77A81 was recognized equally as B*2705 by CTL 27S69. Thus, the N77 change has a compensatory effect on A81, but not on Y74. In addition, the I80A81 mutant was also recognized nearly as B*2705 (79% relative lysis), indicating that I80 also has a compensatory effect on A81. Finally, N77I80 was well recognized by the CTL clone.

These results explain the differential recognition of B*2701 and B*2702 by CTL 27S69. Thus, a lack of recognition of B*2701 is accounted for by the combined effect of the Y74N77 changes, despite the compensatory effect of N77 on A81. Recognition of B*2702 is explained by the compensatory effect of both N77 and I80 on A81.

A key role of Lys70 in allorecognition by CTL 27S69

Previous experiments demonstrate an influence of the D74Y change on recognition by CTL 27S69. In B*2705, D74 forms a salt bridge with K70. This interaction restricts the conformational freedom of the K70 side chain and keeps it away from the B pocket (35). The Y74 mutation results in a conformational rearrangement of the K70 side chain, which is dependent upon the peptide residue at position 2 (30). Thus, to address the possibility that the effect of the Y74 change could be an indirect one mediated through


K70, we tested two mutants at this position for recognition by CTL 27S69. One was Q70, a B*2705 mutant carrying the K70Q change. The second was a B*2701 mutant carrying the K70A change, designated A70-B*2701 (Fig. 1B). Q70 targets were lysed with low efficiency (27% relative lysis), and similarly to Y74 targets. In contrast, the K70A mutation on the B*2701 background had the opposite effect, because A70-B*2701 targets were lysed similarly to B*2705.

These results demonstrate that K70 plays a key role in the allospecificity of CTL 27S69, and strongly suggest that the effect of the D74Y change on recognition by this CTL is mediated through K70.

The RRFFPYYV epitope binds in vitro HLA-B27 mutants not recognized by CTL 27S69

To test whether lack of recognition by CTL 27S69 could be explained by lack of binding of the corresponding peptide epitope, we tested the RRFFPYYV octamer with some cell surface-expressed mutants that abrogated or did not abrogate recognition by this CTL. As shown in Table I, this peptide efficiently bound (C50 of <10 μM) the mutants tested, regardless of whether they were recognized or not by CTL 27S69. These results indicate that there is no correlation between the binding efficiency of the octamer to these mutants in vitro and their recognition by CTL 27S69.

Differential presentation of exogenous peptide epitope by HLA-B27 mutants

Because four mutants abrogated or significantly reduced the recognition by CTL 27S69 (Fig. 1), the octamer epitope was tested for its capacity to sensitize C1R transfectants expressing these mutants for lysis (Fig. 2). The clone efficiently killed Y74 and Y74N77 targets in the presence of exogenously added octamer (half-maximal lysis was 2.3 × 10^{-13} M for Y74 and 4.4 × 10^{-13} M for Y74N77). This behavior is similar to that observed for B*2701 (14) and strongly suggests that the weak cross-reaction with Y74-C1R in the absence of exogenous peptide is due to a low amount of the peptide epitope bound to this mutant in vivo. The results also suggest that failure to kill Y74N77 targets in the absence of exogenous peptide is due to lack of constitutive binding of the octamer to this mutant in vivo.

The octamer also sensitized Q70-C1R targets, but the peptide was recognized much less efficiently (half-maximal lysis at 1.3 × 10^{-9} M) in the context of this mutant. This was not due to lower binding, relative to Y74 or Y74N77 (Table I). Because Q70 differs from Y74 at two positions (K70Q and Y74D), its less efficient presentation of the octamer was probably due to direct involvement of these residues in the alloantigenic epitope or to effects on peptide conformation.

Significant lysis of A81-C1R cells was only obtained when the concentration of this octamer was ≥1 μM, indicating inefficient presentation of the exogenous peptide epitope to CTL 27S69 by this mutant.

A81, but not Y74N77, binds the CTL 27S69 epitope in vivo

Because Y74N77 and A81-C1R cells were differentially sensitized by the octamer, the presence of this peptide in the corresponding mutant-bound peptide pools was analyzed. These pools were obtained from immunopurified mutant molecules on C1R transfectants and fractionated by HPLC; next, the fractions corresponding to the elution position of the octamer were analyzed by MALDI-TOF MS (Table II). Fractions 209 and 210 from A81-bound peptides revealed a species with the appropriate molecular mass of this peptide (mass/charge: 1149 Da). Its correct amino acid sequence was confirmed by electrospray/ion trap MS. This finding demonstrates that a lack of cross-reaction of CTL 27S69 with A81 is not due to absence of the octamer epitope in the peptide pool bound to this mutant in vivo.

The amount of the octamer relative to the related RRFFPYVVY nonamer was estimated to be 1:5.6 in A81 by MALDI-TOF analysis. This ratio is only slightly lower than the 1:4.5 ratio reported for B*2705 (14), further suggesting that the A81 mutation has little effect on the binding of the octamer epitope. Analysis of the corresponding fractions from the Y74N77-bound peptide pool by MALDI-TOF MS revealed a species whose molecular mass was compatible with the octamer (mass/charge: 1148.44 Da) in HPLC fraction 206. The sequence of this peptide could not be determined. Other peptides coeluting with the octamer in both B*2705-bound (14) and A81-bound peptide pools were found and sequenced from the fractions analyzed from Y74N77 (Table II), demonstrating that fraction 206 is the one that should contain the octamer. This result is compatible with the presence of low amounts of the octamer bound to Y74N77 in vivo.

In an additional attempt to determine the presence of the octamer in the Y74N77-bound peptide pool, individual HPLC fractions from this pool were incubated with B*2701-C1R targets and tested for lysis by CTL 27S69 (Fig. 3). HPLC fractions 202–221 failed to sensitize these targets for lysis. In contrast, significant

Table I. Binding of RRFFPYYV to HLA-B27 mutants on RMA-S transfectant cells*

<table>
<thead>
<tr>
<th>RMA-S Transfectants</th>
<th>C50</th>
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<tbody>
<tr>
<td>B*2705</td>
<td>5</td>
</tr>
<tr>
<td>Q70</td>
<td>7</td>
</tr>
<tr>
<td>Y74</td>
<td>7</td>
</tr>
<tr>
<td>N74I80</td>
<td>4</td>
</tr>
<tr>
<td>A81</td>
<td>6</td>
</tr>
<tr>
<td>B*2705Q70I80</td>
<td>4</td>
</tr>
</tbody>
</table>

* Binding to each HLA-B27 variant is expressed as the micromolar concentration of peptide required to obtain half the maximum fluorescence in the concentration range used (C50; see Materials and Methods). Data are the mean of two experiments.
lysis was detected in fraction 209 of the A81-bound peptide pool (used as a positive control). This result confirms that Y74N77 either fails to bind the octamer epitope in vivo or binds it in a very low amount. Thus, the lack of cross-reaction of CTL 27S69 with Y74N77 with the Y74N77 mutant is probably due to a lack of or a marginal presence of the octamer in the mutant-bound peptide pool.

In the peptide pools used in these experiments, which were obtained from similar cell numbers, the total amount of peptides recovered from the A81 mutant was ~20% higher than for Y74N77, as estimated by the total absorbance of HPLC fractions at 210 nm. However, this was not reflected equally in individual peptide yields. For instance, among the peptides in Table II, RRFFPYYV was obtained from both mutants with similar yields, GRHGVFLEL was 2.5-fold more abundant in A81, as estimated by MALDI-TOF analysis. It is obvious that different mutations may affect the binding in vivo of different peptides in distinct ways. Thus, peptide pools extracted from different mutants cannot be normalized for a given natural ligand. However, these data suggest that failure to detect the octamer epitope in Y74N77 is not simply due to a globally low yield of the peptide pool extract relative to A81.

### Discussion

A molecular understanding of how alloreactivity is modulated by HLA class I polymorphism can be achieved with CTL clones of well-characterized fine specificity and known peptide epitopes. In a previous report (14), identification of the peptide epitope recognized by CTL 27S69 allowed explanation of its fine specificity with HLA-B27 subtypes on the basis of three mechanisms. First, cross-reaction of this CTL with B*2705, B*2702, and B*2703 was through recognition of the same peptide in the context of the three subtypes. Second, lack of cross-reaction with B*2704, B*2706, and B*2710 occurred despite efficient binding of the epitope to these subtypes, and was very likely due to direct impairment of the V152E change, common to these three subtypes, on TCR interaction. Third, failure to cross-react with B*2701 was due to absence of the peptide epitope in the B*2701-bound pool in vivo, but not to an inability of the subtype to present the peptide, as shown by exogenous peptide sensitization of B*2701 targets.

Our results now explain the role of HLA-B27 polymorphism in the differential recognition of B*2701 and B*2702. A striking result was that the L81A change, common to B*2701 and B*2702, abrogated allorecognition, but not binding of the peptide epitope both in vitro and in vivo. A direct impairment of TCR interactions, as proposed for the V152E change (14, 36), is unlikely in this case because residue 81 is pointing into the F pocket of HLA-B27 (35, 37). The most likely explanation for the effect of the L81A change is that the conformation of the RRFFPYYV epitope bound to this mutant is different from that in B*2705. The decreased hydrophobicity of the F pocket and its enlarged size as a result of the L81A change should destabilize the interaction with the C-terminal Val residue of the peptide and promote side chain rearrangements to compensate for this effect. Recognition of B*2702, despite the A81 change, is explained by the compensatory effects of the two other changes in this subtype, D77N and T80I. The latter one is likely to compensate, especially in terms of increased hydrophobicity, the corresponding decrease due to the L81A change. The mechanism by which the D77N change restores peptide presentation is not obvious.

Lack of recognition of B*2701 is not accounted for by the L81A change, due to the compensatory effect of the concurrent D77N change. Rather, it is explained by the Y74 mutation, unique to this subtype, especially together with N77. In contrast to A81, the effect of Y74 and Y74N77, like that of B*2701 (14), was to impair the binding of the peptide epitope in vivo, but not its presentation when added exogenously. These effects are probably not limited to the particular peptide epitope in this study, because multiple alloreactive CTL clones recognizing B*2702 but not B*2701 were affected by the Y74 and/or Y74N77 changes (27).

A previous study demonstrated that the influence of the D74Y change on the peptide specificity of HLA-B27 is largely mediated through the K70 residue (30). That this was also the case for the RRFFPYYV epitope reveals a novel mechanism by which HLA class I polymorphism affects allorecognition: the long-range effect of a polymorphic residue on the conformation of a conserved one.

### Table II. Molecular species detected in HPLC fractions from the A81- and Y74N77-bound peptide pools by MALDI-TOF MS

<table>
<thead>
<tr>
<th>Fraction No.</th>
<th>m/z</th>
<th>Sequence</th>
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</thead>
<tbody>
<tr>
<td>209</td>
<td>1084.24</td>
<td>RRFFPYYV</td>
</tr>
<tr>
<td></td>
<td>1149.01</td>
<td>RRLPIFSRL</td>
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<td></td>
<td>1159.36</td>
<td>GRHGVFLEL</td>
</tr>
<tr>
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<td>RLRPIFSRL</td>
</tr>
<tr>
<td></td>
<td>1148.84</td>
<td>RRFPPYYV</td>
</tr>
<tr>
<td></td>
<td>1159.84</td>
<td>RRLPIFSRL</td>
</tr>
<tr>
<td></td>
<td>1269.86</td>
<td>GRHGVFLEL</td>
</tr>
<tr>
<td></td>
<td>1029</td>
<td>RRLPIFSRL</td>
</tr>
<tr>
<td></td>
<td>1051</td>
<td>RRLPIFSRL</td>
</tr>
<tr>
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<td>1312.8</td>
<td>RRFFPYYV</td>
</tr>
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<td>206</td>
<td>1084.87</td>
<td>RRLPIFSRL</td>
</tr>
<tr>
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<td>1159.77</td>
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<td></td>
<td>1326.57</td>
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</tr>
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<tr>
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<td>1029</td>
<td>GRHGVFLEL</td>
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</tr>
<tr>
<td></td>
<td>1348</td>
<td>RRFFPYYV</td>
</tr>
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</table>

* Those peptides whose amino acid sequence was determined by electrospray/ion trap MS are indicated. m/z, mass/charge.
In conclusion, modulation of allore cognition by HLA-B27 class I polymorphism occurs through various mechanisms, including direct impairment of TCR interactions (14, 36), impairment of peptide binding, inappropriate peptide presentation (presumably through conformational alteration of the bound peptide), and long-range effects affecting a residue conserved among differentially recognized alloantigens. In addition, interactive effects among concomitant mutations allow recognition of an HLA alloantigen carrying a change that by itself would be abrogating.

The multiple mechanisms by which HLA class I polymorphism modulates allore cognition and the subtleties of the interactive effects involving polymorphic residues have implications concerning the relationship between the structure and peptide-presenting properties of the class I molecules. First, there is no strict correlation between structural and peptide-presenting similarity. For HLA-B27, the best example is B*2710, a subtype differing from B*2705 by a single amino acid residue, but showing very low cross-reactivity at the T cell level (36). This was well illustrated in the present study by the compensatory effects of additional mutations on A81. Second, there is no strict correlation between peptide-binding specificity and antigenic similarity. T cells specific for a given peptide in a particular HLA context may not recognize that peptide in complex with a different restriction element, as seen in this study with A81. Thus, when considering the role of HLA-B27 subtypes as restriction elements in T cell responses or as risk factors for spondyloarthropathy (38), their peptide-binding properties are not sufficient to understand their differential behavior, as their structural differences may modulate in various ways the antigenicity of bound peptides.

Acknowledgments

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