How structural adaptability exists alongside HLA-A2 bias in the human alphabeta TCR repertoire

Sydney J. Blevins  
*University of Notre Dame*

Brian G. Pierce  
*University of Maryland*

Nishant K. Singh  
*University of Notre Dame*

*See next page for additional authors*

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Keywords
MHC bias, T-cell receptor, binding, peptide/MHC, structure

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How structural adaptability exists alongside HLA-A2 bias in the human αβ TCR repertoire

Sydney J. Blevins, Brian G. Pierce, Nishant K. Singh, Timothy P. Riley, Yuan Wang, Timothy T. Spear, Michael I. Nishimura, Zhiping Weng, and Brian M. Baker

*Department of Chemistry and Biochemistry, University of Notre Dame, Notre Dame, IN 46556; †Harper Cancer Research Institute, University of Notre Dame, Notre Dame, IN 46556; ‡University of Maryland Institute for Bioscience and Biotechnology Research, Rockville, MD 20850; §Department of Surgery, Loyola University Chicago, Maywood, IL 60153; †Cardinal Bernardin Cancer Center, Loyola University Chicago, Maywood, IL 60153; and 1Program in Bioinformatics and Integrative Biology, University of Massachusetts Medical School, Worcester, MA 01605

How T-cell receptors (TCRs) can be intrinsically biased toward MHC proteins while simultaneously display the structural adaptability required to engage diverse ligands remains a controversial puzzle. We addressed this by examining αβ TCR sequences and structures for evidence of physicochemical compatibility with MHC proteins. We found that human TCRs are enriched in the capacity to engage a polymorphic, positively charged “hot-spot” region that is almost exclusive to the α1-helix of the common human class I MHC protein, HLA-A^*0201 (HLA-A2). TCR binding necessitates hot-spot burial, yielding high energetic penalties that must be offset via complementary electrostatic interactions. Enrichment of negative charges in TCR binding loops, particularly the germ-line loops encoded by the TCR Vα and Vβ genes, provides this capacity and is correlated with restricted positioning of TCRs over HLA-A2. Notably, this enrichment is absent from antibody genes. The data suggest a built-in TCR compatibility with HLA-A2 that biases receptors toward, but does not compel, particular binding modes. Our findings provide an instructional example for how structurally pliant MHC biases can be encoded within TCRs.

MHC restriction is a hallmark of T-cell recognition (1). The first crystallographic structures of T-cell receptors (TCRs) in complex with antigen revealed the structural basis for MHC restriction, illustrating how TCRs bind a composite ligand consisting of the MHC protein and its presented peptide (pMHC) (2, 3). Around the same time, evidence began to mount that T cells, and by extension their TCRs, maintain a physical bias toward MHC proteins (4). The mechanism underlying this bias, and indeed its very existence, has remained controversial. On one hand, structural evidence has been presented that germ-line complementarity-determining region (CDR) loops incorporate evolved regions with intrinsic affinities toward MHC proteins (5). On the other hand, the requirement for coreceptor during thymic selection provides a mechanism for selecting TCRs that bind MHC (6–9).

Efforts to reconcile these positions have emphasized that they are not mutually exclusive (9–11). However, it is clear that any intrinsic bias TCRs have toward MHC proteins must exist alongside the need for TCRs to structurally adapt to different ligands or alterations in the TCR–pMHC interface (12). For example, changes to a peptide alone are sufficient to alter how the same TCR sits over the same MHC protein, altering TCR–MHC atomic contacts (13, 14). Similar results are seen with changes to TCR variable domains or hypervariable loops, or even MHC mutations (15–18). Perhaps not surprisingly then, there are no germ-line–based TCR–MHC contacts that are fully conserved at the atomic level when structures with TCRs sharing the same variable domain are compared. For example, TCRs sharing Vβ8.2 make similar contacts with the helices of the class II MHC protein I-A, but actual contacts are modulated by different peptides, hypervariable loops, and Vα domains (15, 19–21). Although such variances have been noted and even predicted (5, 22), they nonetheless make it difficult to clearly identify interactions encoding a TCR–MHC bias (12).

Furthermore, in addition to class I and class II MHC proteins, TCRs can bind a variety of nonclassical MHC molecules, non-MHC ligands (6, 23, 24), and as demonstrated very recently can even bind MHC molecules in orientations reverse from the “canonical” diagonal binding mode (25). Thus, whatever MHC biases actually do exist do not exempt a receptor from identifying alternate binding solutions or targets.

A possibility often overlooked in discussions of TCR binding is that an evolutionarily encoded MHC bias does not need to specify attractive (i.e., energetically favorable) interactions. A more fundamental feature is structural or physicochemical complementarity, or simply “compatibility.” A set of structurally/chemically compatible interactions whose formation is energetically weak, neutral, or even slightly unfavorable is better than a set of noncomplementary, unfavorable interactions. A well-understood example in protein chemistry is interactions between opposing charges in protein structures. Formation of such interactions require removal of the charges from bulk water, which comes with a substantial, unfavorable “desolvation” penalty (26, 27). The coulombic energy from the interaction between the charges is often insufficient to offset the desolvation penalty (28). However, a weak (or even unfavorable) charge–charge interaction is still energetically better than two uncompensated charges buried in a protein. In this way, charges can influence structural specificity even if they do not drive binding. Similar arguments can be made for shape complementarity: an energetically neutral but complementary set of interactions is better than a forced set of interactions that might result in steric hindrance or require costly conformational changes. This concept of compatibility is well understood in antibody–antigen interactions (29).

Significance

T-cell receptor (TCR) recognition of antigenic peptides presented by major histocompatibility complex (MHC) proteins defines specificity in cellular immunity. Evidence suggests that TCRs are intrinsically biased toward MHC proteins, yet how this bias coexists alongside the considerable structural variability that is necessary for TCRs to engage different ligands has been a longstanding puzzle. By examining structural and sequence data, we found evidence that human αβ TCRs have an inherent compatibility with structural and chemical properties of MHC proteins. This compatibility leads TCRs to an intrinsic MHC bias but does not compel the formation of particular modes of binding, providing a solution to how TCRs can be MHC-biased but still structurally adaptable.


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1To whom correspondence should be addressed. Email: brian-baker@nd.edu.

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Results

TCR Germ-Line Loops Are Diverse. We began examining TCR germ-line loops by generating sequence logos for each CDR1 and CDR2 loop, focusing on those VαVβ segments encoding the most common loop lengths (Fig. 1A; see Table S1 for loop statistics). Loop definitions and sequences were taken from the ImMunoGeneTics (IMGT) database, except that we used an extended definition for CDR2β that better accounts for loop structure in structures of TCRs bound to pMHC (Fig. S1A). We also separately calculated the Shannon entropy values for each position in each loop. Shannon entropies quantify diversity, with a value of zero indicating conservation of 1 aa and the maximum value of 4.32 indicating equal representation of all 20 aa. A previous analysis of TCR variable genes identified three general Shannon entropy categories: $H_0$ ($0 \leq H \leq 1$), $H_1$ ($1 < H \leq 2$), and $H_2$ ($H > 2$) (34). $H_0$ sites are highly conserved and associated with sites essential for fold or function. $H_1$ sites are semiconserved, and $H_2$ sites are highly variable with no obvious conservation pattern.

Only a single $H_0$ site in the TCR germ-line loops was identified, the histidine at position 29 in CDR1β, whose presence has been noted previously and is thought to be involved in loop organization (35). Five $H_1$ sites were identified, one each in CDR1α, CDR2α, and CDR1β, and two in CDR2β. The remaining sites are all $H_2$. This indicates that the majority of TCR germ-line loop positions are highly variable, with only a small fraction demonstrating sequence and presumably functional conservation.

There Is No Obvious Signal for Engaging HLA-A2 in Sequences of TCR Germ-Line Loops. We next asked whether binding a particular MHC protein dictates preferences in TCR germ-line loops. We assembled a set of structurally or biophysically characterized, natural human TCRs known to recognize peptides presented by the most common human class I MHC protein, HLA-A*0201 (A2) (Table S2). Complexes with HLA-A2. After accounting for duplicate genes, we used this set to compute CDR1/2 sequence logos and entropies (Fig. 1B). In all loops, diversity is reduced compared with the larger analysis of all sequences. To ask whether this result is attributable to

Fig. 1. There is no sequence signature for TCR binding HLA-A2. (A) Sequence logos for the most common germ-line loop lengths in human TCR VαVβ genes. The numbers at the top give the sequence number for the first amino acid in the loop. Numbers below give Shannon entropy values for each loop position. (B) Sequence logos for the set of structurally/physically characterized human TCRs that bind A2. Red entropy numbers indicate highly conserved $H_0/H_1$ sites. (C) Sequence logos for the set of structurally characterized human TCRs that bind human class I MHC proteins other than A2.

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restriction toward A2 or just reflective of a smaller sample size, we randomly generated 10 identically sized datasets of germ-line loop sequences from the larger set of all human germ-line loop sequences. The average entropies of the loops of the A2-binding TCRs were all within one SD of the averages of the randomly generated datasets, indicating that reduced diversity in the data in Fig. 1B is not likely a function of engaging A2 (Table S3).

Examining the entropy data for the A2-binding TCRs in more detail, there are at least two sites per CDR loop that are H0 or H1 (highly conserved or semiconserved; Shannon entropy values highlighted in red in Fig. 1B). For comparison, we computed sequence logos and entropies for a set of structurally characterized, natural human TCRs shown to bind human class I HLA proteins other than A2 (Fig. 1C; TCRs in Table S2. Complexes with other class I HLA-loops). Although these are notable similarities and differences, in every case, the most common amino acids in the A2-binding H0 or H1 sites are also present in the equivalent position in the non–A2-binding sequences. \( \chi^2 \) tests for independence indicated that the two sets of sequences are not statistically distinct. Thus, the available data indicate that there are no germ-line amino acids or amino acid sequences exclusively required for engaging A2.

**TCRs That Bind HLA-A2 Show No Conserved Pairwise Amino Acid Contacts with A2 but a Propensity for Engaging a Key Molecular Contact on the MHC \( \alpha \)1-Helix.** We next asked whether TCRs use H0 or H1 sites to form preferred contacts with particular MHC proteins. Within the set of A2-binding TCRs, excluding redundant contacts with altered peptides or mutants, there are 13 high-resolution crystal structures of naturally occurring human TCRs bound to peptide/A2 complexes (Table S2). Complexes with HLA-A2. We asked whether the most common amino acid in each H0/H1 position forms common interactions with A2. For example, does the strongly conserved serine at position 27 in CDR1α (\( H = 0.9 \)) commonly contact a certain residue on A2?

Of a total of 249 pairwise amino acid interactions between the germ-line loops and A2 in the entire dataset, 44 are made using amino acids in the H0/H1 positions. Of these 44, 26 are made using the most frequently occurring residues. Of these 26, although some contacts are repeated within different complexes, there are none that were common to every complex (Table 1). In some instances, the most conserved residues at the H0/H1 sites do not contact A2 at all.

The only pattern observed in the contact analysis was between the conserved N-terminal tyrosine of CDR2β (Tyr48β) and Arg65 on the A2 \( \alpha \)1-helix: these two residues contact each other in 6 of 13 complexes, although the numbers of contacts, their distances, and the native positioning of the two side chains differ. This observation is consistent with earlier studies indicating a potential role for this tyrosine (22, 36). None of the interactions between Tyr48β and Arg65 involves a hydrogen bond or other electrostatic interaction, and the interaction is not restricted to a certain Vβ gene use. When in contact, the shape complementarity between Arg65 and Tyr48β ranged from moderate to high. This was quantified using the Sc statistic (37), yielding values from 0.64 for Mel5 to 0.86 for 1G4 (a value of 1.0 would indicate perfect complementarity between interacting residues).

**A Correlation Between TCR Binding Position and Engagement of HLA-A2.** The observation demonstrating a propensity for TCRs contacting Arg65 on A2 with a conserved tyrosine is notable, as position 65 is a polymorphic site that in part distinguishes HLA-A from HLA-B: position 65 is arginine in 85% of HLA-A alleles, whereas it is glutamine in 95% of HLA-B alleles and 100% of HLA-C alleles. To follow up, we examined the relationships between positions 48β and 65 in structures of TCRs bound to human class I HLA proteins other than A2, using the dataset in Table S2 (Complexes with other class I HLA proteins). Eleven of the TCRs in these 16 complexes have a tyrosine at position 48 in CDR2β, and only one of the MHC proteins has an arginine at position 65. Of the 11 non–A2-binding TCRs with a tyrosine at 48β, only one used it to contact position 65. This analysis revealed a stark difference between the A2 and the non-A2 complexes: in the non-A2 complexes, position 48β is positioned across a broad stretch of the \( \alpha \)1-helix (Fig. 2B). This differs from the complexes with A2, in which Tyr48β is restricted to a much tighter region, even for those cases in which Tyr48β and Arg65 are not in contact. The difference in positioning is not due to TCR crossing (docking) angles: the average and SDs of the crossing angles of the A2-binding TCRs is 46 ± 14°, whereas for the non–A2-binding TCRs it is 49 ± 13° (Table S2). The variation also cannot be attributed to different loop conformations, as the CDR2β loops for all of the TCRs in Fig. 2 adopt similar conformations (Fig. S1B).

However, in examining the structures, we observed a greater variation in the global positioning of the TCRs over the MHC in the non-A2 complexes than the A2 complexes. To quantify this, we computed the center of mass of the V\( \alpha \)V\( \beta \) domains over the MHC. In the non-A2 complexes, the center of mass is broadly distributed over the pMHC (Fig. 2C). In contrast, the center of mass of the A2-binding TCRs is restricted to a tighter cluster. To quantify this difference, we computed the position of the average center of mass for the A2 and non-A2 datasets and tabulated its distance from each individual TCR’s center of mass. For the A2 complexes, the average distance was 3.5 ± 1.3 Å. For the non-A2 complexes, the average distance was 6.3 ± 4.4 Å. A two-tailed Mann–Whitney test indicated these differences were significant at \( P \leq 0.05 \) [We note that the values for the non-A2 structures include the SB47, SB27, and C55 TCRs, which engage a “superbudded” 13-mer presented by HLA-B*3508 (38)]. If these are excluded from the non-A2 data, the non-A2 average distance drops to a less significant 4.9 ± 2.5 Å, highlighting the need for more structural work on recognition of long peptides (39).

The **Interaction Between Tyr48β and Arg65 Does Not Drive TCR Binding to Peptide/HLA-A2 Complexes.** To assess the importance of the interaction between Tyr48β and Arg65 in TCR recognition of peptide/A2 complexes, we examined the impact of mutations at these positions. These were made in the interface between the TCR DMF5 and the MART1\(_{26-35}\) peptide presented by A2, a TCR–pMHC

**Table 1. Contacts to HLA-A2 made by the most conserved residues in the germ-line loops of A2-binding human \( \alpha \)β TCRs**

<table>
<thead>
<tr>
<th>Loop</th>
<th>H0/H1 residue</th>
<th>HLA-A2 contact</th>
<th>TCR (PDB)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CDR1α</td>
<td>D26</td>
<td>W167</td>
<td>Mel5 (3HG1)</td>
</tr>
<tr>
<td></td>
<td>D27</td>
<td>E58</td>
<td>DMF5 (3QDG)</td>
</tr>
<tr>
<td></td>
<td>D27</td>
<td>W167</td>
<td>B7 (1BD2)</td>
</tr>
<tr>
<td></td>
<td>E166</td>
<td>Q155</td>
<td>ASO1 (3O4L)</td>
</tr>
<tr>
<td></td>
<td>L156</td>
<td>Y159</td>
<td>ASO1 (3O4L)</td>
</tr>
<tr>
<td></td>
<td>Y155</td>
<td>E16</td>
<td>3UTT</td>
</tr>
<tr>
<td></td>
<td>Y155</td>
<td>B7</td>
<td>1BD2</td>
</tr>
<tr>
<td>CDR1β</td>
<td>N28</td>
<td>V76</td>
<td>1G4 (2BNR)</td>
</tr>
<tr>
<td></td>
<td>H29</td>
<td>V76</td>
<td>DMF4[10] (3QDM)</td>
</tr>
<tr>
<td></td>
<td>H29</td>
<td>V76</td>
<td>DMF4[9] (3QEQ)</td>
</tr>
<tr>
<td>CDR2β</td>
<td>Y48</td>
<td>R65</td>
<td>Mel5 (3HG1)</td>
</tr>
<tr>
<td></td>
<td>Y48</td>
<td>R65</td>
<td>DMF5 (3QDG)</td>
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<td>3UTT</td>
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<tr>
<td></td>
<td>Y48</td>
<td>R65</td>
<td>DMF4[9] (3QEQ)</td>
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<td>Y48</td>
<td>Q72</td>
<td>RA14 (3SGN)</td>
</tr>
<tr>
<td></td>
<td>V52</td>
<td>V56</td>
<td>1406 (42EZ)</td>
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<tr>
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<td></td>
<td>D56</td>
<td>K68</td>
<td>DMF4[9] (3QEQ)</td>
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</table>

Contacts measured with a 4.5-Å interatomic cutoff as described in Materials and Methods.
interaction we have previously studied in detail (13, 40). The shape complementarity between Tyr48β and Arg65 in the DMF5 interface is high, with an interresidue Sc statistic of 0.8. Mutation of Tyr48β to alanine reduced binding 40-fold (ΔΔG° = 2.1 kcal/mol) (Fig. 3A).

Mutation of Arg65 to alanine had a smaller but still significant effect, reducing binding eightfold (ΔΔG° = 1.2 kcal/mol). Tyr48β and Arg65 are thus clearly important for DMF5 recognition. These results are consistent with alanine mutations at these positions in other TCR–pMHC interfaces (31, 40), as well as the impact of mutations to Tyr48β on T-cell development (36).

However, the two alanine measurements do not report on the strength of the Tyr48β–Arg65 interaction. To assess this, we measured the interaction between the two alanine mutants, which when combined with the measurements for the wild type and two single mutants allowed us to construct a double-mutant cycle targeting the Tyr48β–Arg65 interaction. In a double-mutant cycle, the interaction free energy between two side chains (ΔGint) is equal to the difference between the ΔΔG° of the double mutant and the sum of the ΔΔG° values of the two single mutants (40, 41).

For the interaction between Tyr48 in DMF5 and Arg65 in A2, we measured a negligible ΔGint of 0.3 kcal/mol (Fig. 3A). This indicates that, in the interface between DMF5 and A2, although both Tyr48β and Arg65 are important, the interaction between them does not provide a driving force for binding. This result is consistent with structure, as despite their high shape complementarity in the DMF5 complex, Tyr48β and Arg65 form only three van der Waals interactions. As Tyr48β and Arg65 interact similarly in all other TCR complexes with A2 (Fig. 2A; average number of contacts is 3 ± 1), this result is likely to be generally applicable.

**TCRs That Bind HLA-A2 Form Electrostatic Interactions with Arg65.** We next asked whether other conservations exist between TCRs and A2 that could account for the more restricted positioning of TCRs over A2. For example, residues on the α1- or α2-helices may interact with different residues in TCR loops that nonetheless provide similar chemical complementarity. Using the set of TCR–peptide/A2 structures, we examined pairwise TCR–A2 interactions from the perspective of the MHC protein, asking which TCR amino acids...
Double-mutant cycles in the DMF5-MART1/HLA-A2 interface.

αB A H > was + Δ + to interact with Arg65, and sites for loops has been noted (22). Indeed, and and sites for loops has been noted (22). Indeed, Arg65 is not associated with variable gene use: only two of five A2-binding TCRs studied here, the average solvent accessibility of the position 65 side chain in the TCR-pMHC complex is 30%, compared with 82% in the free pMHC (Table S2). Complexes with HLA-A2). Notably, in A2, Arg65 is adjacent to another positively charged polyamino acid, Lys66. In A2, the solvent accessibility of Lys66 is reduced upon TCR binding from an average of 23% to 6%. Only HLA-A alleles have the Arg65/Lys66 combination, with A2 and its suballeles accounting for 93% of the sequences. The combination of these two amino acids results in a significant and distinctive positive charge density on the surface of A2 that is absent from other MHC proteins. This is shown in Fig. S4, which compares the electrostatic surface potentials of A2 (Arg5/Lys66) and HLA-A2.

Burial of charged amino acids in a protein interface is always associated with a penalty resulting from the removal of water molecules interacting with the charge (26, 27). We computed this desolvation penalty for Arg65 and Lys66 in each TCR interface with A2, using a continuum electrostatics approach that yields the desolvation and coulombic energies associated with charge burial (27, 43). We used this approach previously in studying TCR recognition of pMHC, validating it with mutational and binding studies (32). Across the 13 TCR–A2 interfaces, the average desolvation penalty for Arg65 was an unfavorable +2.0 kcal/mol, roughly -4.5 to +3.5 kcal/mol (Fig. 5B). The desolvation penalty was equally compensated by favorable coulombic interactions, which averaged -2.0 kcal/mol. We performed the same calculation for Lys66, which showed an average desolvation penalty of +1.7 kcal/mol (Fig. 5B).

These computed results are in good agreement with experimental measurements. For electrostatic interactions, the ΔGint from a double-mutant cycle reflects the interresidue coulombic interactions (28). With the A6 TCR binding Tax/A2, we previously used double-mutant cycles to measure the strength of the interaction between Arg65 and Asp99 of CDR3α (40). The experimental ΔGint was a highly favorable value of -2.8 kcal/mol. For comparison, in the A6-Tax/A2 interface, the continuum electrostatic calculations yielded a value of -3.2 kcal/mol for the intermolecular coulombic interactions with Arg65. As a second check, we performed a double-mutant cycle in the interface between Arg65 and Asp26 of CDR1α in the DMF5-MART1/A2 interface. Here, the ΔGint was -0.4 kcal/mol (Fig. 3B). For comparison, the computed intermolecular coulombic interactions of Arg65 with DMF5 amounted to 0.5 kcal/mol.

The Xenoreactive TCR AHIII Demonstrates Electrostatic Interactions with Arg65 and Lys66 Are Not Strictly Encoded. Our analysis so far indicates that the need to interact with and counteract a region of positive charge on the A2 α1-helix is reflected in the composition of TCR germline sequences, and doing so is correlated with more restricted TCR positioning over pMHC. However, the utilization of both hypervariable and germline loops in this capacity, even with TCRs sharing variable gene segments, indicates that the germline sequences do not obligate particular interactions with Arg65. In other words, although TCR germline loops are enriched in the capacity to interact with Arg65/Lys66, inherent structural adaptability and sequence variations allow charge complementarity to occur opportunistically via a variety of means.

As a test of this hypothesis, we examined the structure of the xenoreactive mouse TCR AHIII bound to the p1049 peptide

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**Fig. 3.** Double-mutant cycles in the DMF5-MART1/HLA-A2 interface. (A) Double-mutant cycle between Arg65 and Tyr48β. Mutation of either Arg65 or Tyr48β to alanine weakens TCR binding, although a double-mutant cycle shows that the interaction between the two side chains is negligible. This experiment was done in the background of the affinity-enhancing D26a/Y/L98/W mutations in DMF5 (65). (B) Double-mutant cycle between Arg65 and Asp26α. Both mutations alone have an impact on binding, although the double-mutant cycle analysis reveals a weak electrostatic interaction between the two side chains. This experiment was done in the background of the affinity-enhancing L98/W mutation in DMF5 (65).
presented by A2 (44), reasoning that strict genetic programming between germ-line loops and A2 would have diverged between mice and humans, altering how Arg65 is accommodated. In this structure, however, Arg65 interacts with Glu56 in CDR2β (Fig. 4). Tyr48 of the AHIII CDR2 structural model is wired to engage Arg65/Lys66 in predetermined ways, the ability to counteract these charges is nonetheless reflected in germ-line loop sequences. Has evolution imparted this as a way to promote—if not compel—MHC binding? We addressed this by comparing the sequences of human TCR and antibody germ-line CDR loops, using data for all functional genes from the IMGT database. Antibody and TCR genes share a common ancestral history, diverging more than 500 Mya (46). Unlike TCRs, antibodies are unrestricted in the ligands they bind, and we presumed that an imprint of evolution would be visible in the extent that TCR and antibody germ-line loops differ, particularly in the CDR1/CDR2 germ-line loops that in TCRs complement positive charges on the A2 α1-helix.

We first looked at the overall frequency of amino acids that comprise all four TCR and antibody germ-line loops. As shown in Fig. 6, the top five amino acids for antibodies are serine, glycine, tyrosine, threonine, and asparagine. The physicochemical basis for antibody enrichment in these amino acids is well understood (47, 48). The distribution in TCR germ-line loops resembles that in antibodies, but with some distinctions. The top five amino acids are serine, tyrosine, asparagine, glycine, and notably, glutamate. Indeed, TCR germ-line loops are twice as negatively charged than those of antibodies (14% Asp/Glu in TCRs, compared with 7% in antibodies). The negative charge difference between TCRs and antibodies is statistically significant as indicated by a χ² test (29).

**Evolution Has Enhanced the Ability of TCR Germ-Line Loops to Engage HLA-A2.** Although our analysis shows that TCRs are not hard-wired to engage Arg65/Lys66 in predetermined ways, the ability to

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**HLA-A2 α1 helix**

<table>
<thead>
<tr>
<th>TCR</th>
<th>Glu58</th>
<th>Asp61</th>
<th>Arg65</th>
<th>Lys66</th>
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<th>Ala69</th>
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**HLA-A2 α2 helix**

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**Fig. 4.** Hydrogen bonds and charge interactions between α1 TCRs and the HLA-A2 α1α2 helices in TCR-peptide/HLA-A2 structures. Red indicates charge-charge interactions, black indicates hydrogen bonds, and green indicates a water or ion bridge. Hydrogen bonds and charge interactions were identified as described in Materials and Methods. HLA-A2 amino acids not involved in electrostatic interactions are not shown. AHIII is a murine TCR bound to HLA-A2.
Studies have shown that differences between TCR and antibody gene sequences are not due to genetic drift (34).

As we have found, when using germ-line loops, TCRs that bind A2 use negative charges in CDR2β and CDR1α, in that order of preference, to offset the charge on the A2α1-helix. We thus compared TCR and antibody germ-line CDR loops. Previous antibody/TCR sequence comparisons indicate a VH = Vβ/VL = Vα equivalence (49). The antibody equivalents to CDR2β and CDR1α are accordingly CDR2-H and CDR1-L. The amino acid distributions for these TCR and antibody loops are noticeably different, particularly in their incorporation of negative charges (Fig. 6B and C). Negative charges account for 19% and 8% of the composition of TCR CDR2β and CDR1α loops, respectively, compared with 8% and 5% in antibody CDR2-H and CDR1-L loops. These differences remain if the domain equivalences are switched (i.e., VH = Vα and VL = Vβ), if alternative definitions are chosen for antibody CDR loops, or whether we use the classical IMGT definition of TCR CDR2β. The strategic enrichment in negative charges in TCR CDR loops compared with antibodies suggests evolution has imprinted A2 compatibility onto TCR germ-line loops.

**Discussion**

TCRs have long been hypothesized to be biased toward MHC proteins, but how such a bias can exist alongside TCR structural adaptability has remained a controversial puzzle. From a structural and energetic perspective, one challenge is that atomic contacts between germ-line regions of TCRs and MHC proteins are not conserved even when the same TCR variable regions and MHC proteins are compared (22). We expanded on this here by demonstrating that, in the structural database of TCRs that bind HLA-A2, not only are there no conserved TCR–MHC contacts, even those amino acids in TCR germ-line loops that are the least variable make different contacts or do not contact A2 at all. These results are consistent with findings that diversified TCRs can still bind MHC (35), and prompted us to search for a more fundamental basis for MHC bias based upon compatibility rather than simply contacts.
TCRs germ-line loops are enriched in negative charges compared with published online February 16, 2016 and antibody CDR2-H due to unique features in a ligand or is residues and CDR2 loops can also perform loop on the TCR binding is residues 48 Fig. S1 loop, one N-terminal residue and three C-terminal residues loop. Thus, evolution seems to not facilitates the cross-react has done so in a manner that allows structural adaptability and only have imparted MHC compatibility into the TCR repertoire, it indeed is not present in all structures with A2. However, in cases where it is present, it may act as a “check” on the TCR binding mode. The removal of such checks or other sites encoding compatibility from the repertoire would be expected to impact TCR recognition, explaining the negative impact on T-cell development seen with mutation of Tyr48β in mice (36).

Because our findings suggest a bias in the true sense of the word, they are broadly compatible with other results. For example, they do not exclude the possibility of TCRs binding structurally/chemically compatible non-MHC ligands, or instances in which an evolved bias is “overruled” due to unique features in a ligand or TCR. They do not rule out a role for coreceptor or thymic selection in shaping the repertoire to help select for TCR–MHC compatibility. Following this logic, it remains possible that the more restricted positioning of TCRs over A2 that emerges from charge complementarity may be functionally significant.

**Materials and Methods**

**TCR and Antibody Sequence Analysis** The sequences of all functional, naturally occurring, nonredundant human TCR and antibody genes were taken from the IMGT database (51). Germ-line CDR loops were selected based on the IMGT CDR definitions. For TCRs, TCR-pMHC crystallographic structures were used ensure CDR loop definitions adequately matched structural observations. For the TCR CDR2β loop, one N-terminal residue and three C-terminal residues were added to the loop definition to better fit structural observations as shown in Fig. S1A. Due to variations in the numbering of TCR residues, a uniform numbering was assigned to all HLA-A2-binding TCRs, using the B7 TCR (Protein Data Bank (PDB) ID code 1B02) as a template (52). The numbering scheme also applies to CDR loops of the most common length. The CDR1α loop is comprised of residues 26–31, CDR2α loop is residues 49–55, CDR1β is residues 27–31, and CDR2β is residues 48–57. TCRs recognizing human class I MHC proteins were identified via PDB and the IMGT database. For sequence logos, unique sequences matching the most commonly used loop length were used as shown in Table S1. Sequence logos were created using the online WebLogo server at weblogo.berkeley.edu (53).

![Fig. 6. TCR germ-line loops are enriched in negative charges compared with the corresponding antibody loops. (A) Distribution of all 20 aa in TCR (Left) and antibody (Right) germ-line loops. Total percent negative charges are shown. (B) Amino acid distributions in TCR CDR2β and antibody CDR2-H loops. (C) Amino acid distributions in TCR CDR1α and antibody CDR1-L loops.](image-url)
TCR–pMHC Structure Analysis. Structures of human αβ TCRs in complex with human class I MHC proteins were identified and downloaded from PDB. Conserved termolecular coulombic interactions between TCR and MHC were identified using ConPro (54), the PyMOL script DistancesRHS, and Accelrys Discovery Studio 4.1, using a 4.5-Å distance cutoff. We used this more liberal cutoff (compared with the more common 4 Å) to better account for coordinate error and the nonstatic nature of the protein interfaces (55, 56). TCR–pMHC complexes were superimposed by the PyMOL pair fit function, fitting the α carbon of residues 1–180 of the MHC protein. The two orientations of the DMF4 TCR over the boomer and decamer MART-1 peptides bound to HLA-A2 were analyzed separately (referred to as DMF4[9] and DMF4[10]). Hydrogen bonds were identified using Discovery Studio, with a 3.4-Å cutoff and a DNA base angle range of 90°–180°. Charge–charge interactions were identified using Discovery Studio with a maximum distance of 5.6 Å. This distance is greater than the 4.0 Å sometimes used for formal salt bridges, but allows for a better accounting of long-distance intermolecular interactions and helps account for coordinate error and protein dynamics. In the TCR contact analysis, the structure with the C7 TCR (S3) was omitted as electron density for many of the key side chains was missing. Center of mass calculations were performed for the TCR variable domains and MHC peptide-binding domains using the PyMOL center of mass script. Shape complementarity values (Sc statistic) were computed with the Sc program (37). Solvent-accessible surface areas were calculated using Discovery Studio with a 1.4-Å probe. Percent accessible surface areas in Table S2 are relative to the surface area of an arginine or lysine in an extended Ala-X-Ala tripeptide. TCR crossing and incident angles were calculated as described (58, 59). Literature references for each TCR–pMHC complex analyzed are listed in Table S4.

Continuum Electrostatics Calculations. Desolvation and electrostatic interaction energies for Arg65 and Lys66 of HLA-A2 were performed using finite-difference Poisson–Boltzmann methods as previously described (32), with minor modifications as listed below. Methods of computing electrostatic fields followed those of Sheinerman and Honig (43). Briefly, TCR structures were imported into Accelrys Discovery Studio. Hydrogen atoms were added and the structure’s energy minimized to optimize hydrogen placement, using 1,000 steps of steepest descent followed by 300 steps of conjugate gradient minimization using the CHARMM22 force field. Electrostatic potentials were calculated using Delphi 4.11 (26) as implemented in Discovery Studio. Solvent minimization using the CHARMM22 force field. Electrostatic potentials were calculated using Delphi 4.11 (26) as implemented in Discovery Studio. Solvent–dielectric was set to 80 and the interior dielectric set to 10. The value of 10 for an interior dielectric was chosen based on our previous work (32) and is consistent with values used to reproduce experimental observations in other systems (60). We note, however, that although absolute values will change, our overall conclusions will be unaffected by the use of other interior dielectrics (see ref. 32, table 4). Ionic strength was set at 0.15 M. Grid spacing was 0.5 Å per point. Focusing was used, moving from 50% to 90% grid occupancy in two steps. Calculations performed on TCR–pMHC complexes and free pMHC molecules used the same grid mapping.

Desolvation penalties, intermolecular coulombic interactions, and intramolecular coulombic interactions were calculated from electrostatic potentials computed with partial charges present only on the atoms of Arg65 or Lys66 (Fig. S8). Desolvation penalties were computed as the difference between the charging free energies of the TCR–pMHC complexes and the unbound pMHC. Intermolecular coulombic interaction energies were calculated similarly, except the calculation involved the full set of pMHC partial charges except those for Arg65 or Lys66, and is reported as the difference between calculations with pMHC potentials calculated for the free and TCR-bound states (43). Coulombic interaction energies reported in Fig. S8 are the sum of the intermolecular and intramolecular terms. Energies of 4 kcal/mol are reported to free energy values at 298 K. Interactions for the pMHC molecules in Fig. S4 were of the Tax peptide bound to HLA-A2 (61) and an HIV-8 binder bound to HLA-B*5101 (62), and electrostatic surface potentials in this figure were calculated using all formal charges.

Protein Expression and Double-Mutant Cycles. Soluble constructs for the αβ and DMF5 TCRs and HLA-A2 were generated from bacterially expressed inclusion bodies as previously described (63). TCRs used an engineered disulfide bridge connecting the constant domains to improve stability (64). DMF5 mutants were produced by site-directed mutagenesis and confirmed by sequencing. Peptides were purchased from Chi Scientific. Steady-state binding was measured with a Biacore 3000 instrument as previously described (63). Experiments were performed at 25 °C in 10 mM Hepes, 3 mM EDTA, 150 mM NaCl, and 0.005% surfactant P20 at pH 7.4. Refolded and purified TCR were coupled to the surface of a CMS sensor chip via amine linkage to a density of ~1,500 RU.

Double-mutant cycles were performed and analyzed as described previously (40). Briefly, soluble wild-type followed by mutant pMHC complexes were injected over wild-type or mutant TCR surfaces in a series of increasing concentrations of receptor points until steady-state binding was attained. Each injection series was repeated twice. In any one experiment, three flow cells were used: a blank, wild-type TCR, and mutant TCR. The output of one single experiment thus consisted of two sets of all four measurements that comprise a double-mutant cycle as shown in Fig. 3. Data were processed in BiaEvaluation 4.1, and all eight datasets were simultaneously analyzed in OriginPro 7 with a custom global fitting function. The wild-type and mutant TCR surface densities and the three Δ△G values that make up the cycle were global fitting parameters. Errors were propagated using standard statistical error propagation methods (63). High-affinity variants of the DMF5 TCR were used to facilitate the analysis (65). For analysis of Tyr48β–Arg65 pair, the D26βL/Tyr98W double mutant was used. For analysis of D26α–Arg65 pair, the L98β/W single mutant was used. We note that, excluding the sites of the two mutations, the structures of the high-affinity and wild-type DMF5 TCR complexes are essentially identical (13, 65). The utilization of affinity-enhancing mutations is unlikely to impact the double-mutant cycle experiments, owing to the structural similarities and the robust nature of double-mutant cycle analysis (40, 41).


