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Posttranslational Modification of Gluten Shapes TCR Usage in Celiac Disease

Shuo-Wang Qiao,* Melinda Ráki,†,1 Kristin S. Gunnarsen,‡,1 Geir-Åge Løset,‡ Knut E.A. Lundin,†,§ Inger Sandlie,‡ and Ludvig M. Sollid,*†

Posttranslational modification of Ag is a key element of the pathogenesis of celiac disease, and posttranslational modifications of Ags have been similarly implicated in several other autoimmune diseases (1–5). Celiac disease is a human inflammatory condition of the small intestine precipitated by the ingestion of cereal gluten proteins in wheat that consist of gliadin and glutenin subcomponents. The disease has a very strong HLA association, and T cells of celiac lesions recognize gluten epitopes presented by disease-associated HLA-DQ2 (DQA1*05:01/DQB1*02:01) or HLA-DQ8 (DQA1*03/DQB1*03:02) molecules (6, 7). These gluten-reactive CD4+ T cells appear to be essential for the development of the disease, and they can be readily cultured from intestinal lesions of diseased patients but not control subjects (6, 8). Over the years, a number of gluten T cell epitopes, each recognized by distinct T cell clones derived from celiac disease patients, have been identified (9–14). For most of these epitopes, the notable conservation of a non-germline-encoded Arg residue in the CDR3β loop. Functional testing of a prototype DQ2-α-II–reactive TCR by analysis of TCR transfectants and soluble single-chain TCRs indicate that the deamidated residue in the DQ2-α-II epitope poses constraints on the TCR structure in which the conserved Arg residue is a critical element.

The findings have implications for understanding T cell responses to posttranslationally modified Ags. The Journal of Immunology, 2011, 187: 3064–3071.

Posttranslational modification of Ag is implicated in several autoimmune diseases. In celiac disease, a cereal gluten-induced enteropathy with several autoimmune features, T cell recognition of the gluten Ag is heavily dependent on the posttranslational conversion of Glu to Glu residues. Evidence suggests that the enhanced recognition of deamidated gluten peptides results from improved peptide binding to the MHC and TCR interaction with the peptide–MHC complex. In this study, we report that there is a biased usage of TCR Vβ6.7 chain among TCRs reactive to the immunodominant DQ2-α-II gliadin epitope. We isolated Vβ6.7 and DQ2-α-II tetramer-positive CD4+ T cells from peripheral blood of gluten-challenged celiac patients and sequenced the TCRs of a large number of single T cells. TCR sequence analysis revealed in vivo clonal expansion, convergent recombination, semipublic response, and the notable conservation of a non-germline-encoded Arg residue in the CDR3β loop. Functional testing of a prototype DQ2-α-II–reactive TCR by analysis of TCR transfectants and soluble single-chain TCRs indicate that the deamidated residue in the DQ2-α-II peptide poses constraints on the TCR structure in which the conserved Arg residue is a critical element.

In the current study, we found a biased usage of TCR Vβ6.7 chain encoded by the TRBV7-2 gene segment among TCRs reactive to the DQ2-α-II gliadin epitope. Based on this knowledge, we performed single-cell TCR cloning of a large number of Vβ6.7-positive, DQ2-α-II tetramer-positive CD4+ T cells sorted from peripheral blood of gluten-challenged celiac patients. Analysis of the TCR sequences revealed in vivo clonal expansion, convergent recombination, semipublic response, and the notable conservation of a non-germline-encoded Arg residue in the CDR3β loop. Sequencing and functional data support the notion that the deamidated residue in the DQ2-α-II peptide poses constraints on the TCR structure in which the conserved Arg residue is a critical element.

Materials and Methods

T cell culture, tetramer staining, and FACS sorting

Biological material was obtained from celiac disease patients according to protocols approved by the regional ethics committee, and subjects donating material gave written informed consent. Polyclonal T cell lines and T cell clones (TCCs) were established from intestinal biopsies of celiac disease patients as previously described (18). T cells were expanded with anti-
CD3/anti-CD28 beads (Invitrogen) for at least 7 d before mRNA isolation and TCR cloning.

Tetramerized recombinant HLA-DQ2 tethered with glutathione peptides containing the T cell epitopes DQ2-α1 (QLQPFQPPELPY, underlined 9mer core sequence), DQ2-α2-IP (QPQPFQPPELPY), and the control peptide CLIP2 (MATPLIMALPMGAL) were generated as previously described (19, 20). Likewise, the DQ-γ-2 tetramer was generated with the same protocol where the DQ-γ-1 peptide (QGHPQEPQGL), and the control peptide QGHPQEPQGL were covalently coupled to HLA-DQ2. Circulating tetramer-positive T cells in peripheral blood of celiac patients 6 d after a 3-d gluten challenge were stained according to a previously established protocol (21).

Single, Vβ6.7-positive (FTTC-OT145 from Endogen), DQ2-α1I tetramer-positive cells were sorted by a FACSAria sorter (BD) into 96-well PCR plates (Bio-Rad) with 10 μl ice cold lysis reverse-transcription buffer containing 50 mM Tris-HCl pH 8.2, 7.5 mM DTT, 0.5% Nonidet P-40, 2 mM deoxyribonucleotide triphosphate 10 mM DTT, 800 nM TRBC_rev primer 5′-TTACCCACAGCTGACCTC-3′, 800 nM TRAC_rev primer 5′-AGTCAGATTTGTTGCTCCAGGCC-3′, 12 U RNasin (Promega), and 30 U SuperScript II reverse transcriptase (Invitrogen) in each well.

### TCR cloning and sequencing

The TCR was cloned using a seminested PCR approach performed with Phusion DNA polymerase (Finnzymes). mRNA of in-vitro-cultured T cells was isolated with RNeasy Mini kit (Qiagen) and TRB gene-specific first-strand cDNA was synthesized from mRNA with TRAC_rev and TRB_rev primers and SuperScript II reverse transcriptase. After RNase H digestion (Rnasin Plus; Promega), the cDNA was precipitated with Pellet Paint (Novagen), and a poly-C-tail was added to the 3′-end with rTerminal transferase (Roche). The cDNA was reprecipitated, and the TRA and TRB genes were PCR amplified with forward poly-G-NoT primer (5′-ATACTGGCGCCGGCCGGGGGGGGGGGGGGGG-3′) and reverse TRAC_mild rev (5′-5'ATAACCGTTCCTCCTACGTTAAGACG-3′) or TRBC_mild rev (5′-ATAACCGTATAGTCTCCTCTGATTG-3′) primers in 35 cycles (98°C for 10 s, 53°C for 30 s, 72°C for 15 s). The PCR product was ligated into the pHOG21-pHOx cloning vector and subjected to sequencing.

From sorted single cells, TCR-specific first-strand cDNA was synthesized by reverse transcription by incubation of the PCR plate at 4^°C overnight. The virus supernatant was then removed and hybridoma cells were pelleted and resuspended in 400 ml ice-cold periplasmic extraction YTAG medium to an OD600nm of 0.025. At OD600nm 0.6–0.8, the bacteria were pelleted and resuspended in 400 ml ice-cold periplasmic extraction YTAG medium to an OD600nm of 0.025. At OD600nm 0.6–0.8, the bacteria were pelleted and resuspended in 400 ml ice-cold periplasmic extraction solution (50 mM Tris-Cl, 20% sucrose, 1 mM EDTA, pH 8) supplemented with 1 mg/ml lysozyme and 100 μg/ml RNaseA (Sigma-Aldrich) before incubation for 1 h at 4°C with rotation. The mixture was then centrifuged, and the supernatant was collected as the soluble periplasmic fraction. After filtration through an 0.2-μm sterile filter, the soluble periplasmic fractions were then purified on immobilized metal affinity chromatography spin columns (Qiagen) with a procedure modified from the manufacturer’s protocol such that the salt concentration was increased to 1 M NaCl and the pH was adjusted to 7. The immobilized metal affinity chromatography fractions were concentrated to 140 μl with Amicon Ultra-4 centrifugal filter devices (Millipore) and dialyzed against HBS-EP buffer (GE Healthcare) supplemented with 0.5 M NaCl. Protein concentrations were determined at A280 nm on a NanoDrop ND-1000 apparatus (Thermo Scientific) and found to be 12.6 mg/ml for wt.β109R, 16.5 mg/ml for s.β109R, 27 mg/ml for s.β109A, and 5.7 mg/ml for s.β109E. Size-exclusion chromatography on a Superdex 200 10/300 GL column was performed on an automated ÄKTA 900 chromatography system (GE Healthcare). The monomeric fractions were pooled, concentrated to equal volumes, and protein concentrations were determined as described earlier.

### Surface plasmon resonance binding assays

A BiaCore T100 instrument was used together with a CM3 chip (GE Healthcare). All experiments were performed in HBS-EP buffer. Neut...
travavidin was immobilized by amine coupling to ~4500 resonance units (RU) followed by capture of ~3500 RU biotinylated DQ2-αI or DQ2-CLIP2. Samples of s.β109R and s.β109A at concentrations from 0.32 to 1 μM were then injected over each surface, as well as a negative reference cell with Neutravidin only, at a flow rate of 30 μl/min at 25˚C. In all experiments, data were zero-adjusted and the Neutravidin reference cell value subtracted.

**Results**

**Overusage of Vβ6.7 (TRBV-7-2) in DQ2-αII-reactive T cells**

Systematic TCR sequencing of 40 in vitro-generated gluten-reactive TCCs derived from 14 celiac disease patients produced 29 unique TRBV sequences encoded by 14 different V-gene segments. Notably, one of the V-gene segments, TRBV7-2, was used in 10 of the 29 unique TRBV sequences encoded by 14 different V-gene segments. Closer examination revealed that 9 of the 10 TCCs that used this particular V-gene segment were reactive to either the DQ2-αI or DQ2-αII epitopes (Table I). No other V-gene segment was overrepresented.

To probe how frequently Vβ6.7 was used by Ag-specific T cells in in vitro-expanded polyclonal lines, T cell lines cultured from celiac lesions were co-stained with various DQ2-tetramers and a Vβ6.7 (28) specific mAb, OT145. Although this Ab was previously reported to specifically bind Vβ-chain encoded by the TRBV7-2*01 allele only (29), we found that CD4+ T cells from TRBV7-2*02 homozygous individuals bound OT145 as well (Supplemental Fig. 1). We observed overusage of Vβ6.7 among DQ2-αII tetramer-positive T cells in several polyclonal lines (Supplemental Fig. 2), whereas few or none of the DQ2-αI or DQ2-γI tetramer-positive T cells used Vβ6.7.

Extended in vitro culture may introduce bias. Therefore, we looked at the Vβ6.7 usage in peripheral blood T cells of nine celiac patients where the T cells were directly stained with tetramers. Oral gluten challenge for 3 d of celiac disease patients in remission leads to egress of gluten-reactive T cells into the peripheral blood on day 6, and such cells can be detected by IFN-γ ELISPOT assay (30) or by HLA-DQ2 tetramer staining (21). We found that significantly more DQ2-αII tetramer-positive T cells were Vβ6.7 positive compared with all CD4+ T cells (p < 0.01, paired Wilcoxon rank test), whereas a slight increase for DQ2-αI tetramer-positive cells did not reach statistical significance (p = 0.10) (Fig. 1).

**In vivo clonal expansion of DQ2-αI and DQ2-αII tetramer-positive cells**

The knowledge of overusage of the TRBV7-2 gene segment among DQ2-αI- or DQ2-αII-reactive T cells allowed us to sequence TRBV gene segments from sorted single cells that were double positive for Vβ6.7 and either tetramer. We successfully sequenced TRBV genes of 23–108 sorted single cells from peripheral blood of each of the four gluten-challenged celiac disease patients (Fig. 2). All cells were Vβ6.7-positive and either DQ2-αI tetramer-positive, DQ2-αII tetramer-positive, or DQ2-αII–tetramer-negative. Within both DQ2-αI and DQ2-αII tetramer-positive cells, we found clonal dominance as a result of in vivo clonal expansion. This was particularly evident for the DQ2-αI tetramer-positive cells, in which 32 of 33 (patient CD757) or 36 of 37 (patient CD823) sequences obtained represented one clone in each of the two patients (Fig. 2). In comparison, the TCR repertoire in Vβ6.7-positive, DQ2-αII tetramer-positive cells was more diverse. Between 5 and 19 unique TRBV sequences were retrieved from each patient of which more than half of the cells expressed the two most frequently used sequences (Fig. 3), indicating a considerable clonal expansion in the DQ2-αII tetramer-positive cells as well. In contrast, we found no identical sequences among tetramer-negative cells.

**Public response as a result of convergent recombination in Vβ6.7 and DQ2-αII tetramer double-positive cells**

In the TRBV7-2 sequences we obtained from both ex vivo DQ2-αII tetramer-positive single-cell sequencing and in vitro-cultured

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**Table I. The usage of TRBV7-2 by in vitro-expanded TCCs sorted according to epitope recognition**

<table>
<thead>
<tr>
<th>Epitope</th>
<th>HLA Restriction</th>
<th>9-aa Core Sequence</th>
<th>TRBV7-2</th>
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</thead>
<tbody>
<tr>
<td>DQ2-αI</td>
<td>DQ2</td>
<td>P P P Q P E L P Y</td>
<td>3/4*</td>
</tr>
<tr>
<td>DQ2-αII</td>
<td>DQ2</td>
<td>P Q Q P E L P Y P P</td>
<td>6/9</td>
</tr>
<tr>
<td>DQ2-αIII</td>
<td>DQ2</td>
<td>P Y P Q P E L P Y</td>
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<td>Q P Q E Q P F P Q</td>
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<td>Q P Q Q S F P E Q Q</td>
<td>0/2</td>
</tr>
<tr>
<td>DQ2-αII</td>
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<td>DQ2</td>
<td>Q P Q Q S F P E Q Q</td>
<td>0/1</td>
</tr>
<tr>
<td>DQ2-αI</td>
<td>DQ2</td>
<td>Q P Q Q S F P E Q Q</td>
<td>0/1</td>
</tr>
<tr>
<td>DQ2-αII</td>
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<tr>
<td>DQ2-αV</td>
<td>DQ2</td>
<td>Q P Q Q S F P E Q Q</td>
<td>0/1</td>
</tr>
</tbody>
</table>

*3/4 indicates that of the total of four TCCs cloned, three used the TRBV7-2 gene segment.

**FIGURE 1. Overusage of TRBV7-2 encoding the Vβ6.7 chain in DQ2-αII tetramer-positive cells analyzed directly ex vivo.** Peripheral blood cells from treated celiac disease patients after gluten challenge were stained with Vβ6.7 Ab and DQ2 tetramers containing an irrelevant control peptide (CLIP2) or the DQ2-αI or DQ2-αII gliadin epitopes. A, CD4-gated T cells are shown. In a representative patient, ~5% of tetramer-negative cells were Vβ6.7-positive compared with 16% among DQ2-αI-positive and 50% among DQ2-αII-positive cells. B, The percentage of cells staining positive for Vβ6.7 of all CD4+ T cells and of DQ2-αI or DQ2-αII tetramer-positive cells in nine celiac patients is shown. The p values were calculated with Wilcoxon paired rank test.
A high throughput of ex vivo single-cell sequencing generated a large body of sequence data that revealed interesting molecular features of the CDR3β loops in Vb6.7-positive DQ2-αII tetramer-binding T cells. The vast majority (78%) of the CDR3β loops were of the same length of 11 aa, a fact that would have led to the assumption of oligoclonality if the cells had been subjected to CDR3 length analysis only. However, single-cell TCR sequencing revealed a number of different clones on the nucleotide level underscoring the importance of TCR sequencing.

The most striking finding from the single-cell TCR data was the conservation of an Arg residue in position 5 of the CDR3β loop. Of the total 143 DQ2-αII cells from which we obtained TRBV7-2 sequences by single-cell sequencing, 132 (92%) expressed CDR3β loops with an Arg in position 5. On the clonal level, 35 of 41 (85%) unique TRBV7-2 sequences from DQ2-αII tetramer-positive cells contained Arg in this position. In comparison, only 1 of 70 (1%) DQ2-αI positive and 4 of 49 (8%) DQ2-αII tetramer-negative cells showed this Arg signature (Fig. 2).

Examination of the nucleotide sequences revealed that 73% (30 of 41) of the Arg residues in our data set were non-germline encoded (Supplemental Fig. 3). The fact that most of the Arg residues in our data set were non-germline encoded indicated that
The conserved Arg residue in position 5 of CDR3 is crucial for DQ2-α-II epitope recognition

To probe the functional importance of Arg in position 5 of CDR3, we made transfectants with the TCR of the TCC TCC364.1.0.14 (i.e., TCR 364.14). The wild-type 364.14 TCR expressing the conserved Arg residue in a prototypic CDR3 loop, ASSI-RSTDTQY, and mutant 364.14 TCRs were retrovirally transduced into a murine hybridoma cell line, BW5147, which was devoid of endogenous TCR (23). Human CD4 was introduced into the hybridoma cells by stable transfection for coreceptor binding to HLA-DQ2. Despite similar levels of CD3ε and TCR surface expression in the wild-type and mutant transfectants (Supplemental Fig. 4), only hybridoma cells expressing the wild-type TCR were reactive to the DQ2-α-II ligand (Fig. 5A). None of the mutants in which the Arg residue in position 5 of the CDR3β (position 109 of the TCR β-chain according to IMGT V-gene alignment) was mutated to Ala (β109A), Lys (β109K), or Glu (β109E), responded to deamidated (Fig. 5A) or native peptides containing the gliadin DQ2-α-II epitope (Table II). The cell signaling machineries in the transfectants were intact as anti-CD3ε stimulation elicited similar levels of murine IL-2 secretion in both wild-type and mutants (Fig. 5B). Additional experiments confirmed that the wild-type transfectant responded to Ag in the same way as the corresponding TCC from which the TCR sequence originated. This included DQ2 restriction (Fig. 5C), deamidation dependence (Fig. 5D), epitope specificity, as well as ability to recognize the DQ2-α-II peptide presented by the closely related DQ2.2 molecule.

The importance of the Arg residue in DQ2-α-II recognition was independently confirmed in a set of experiments using soluble recombinant TCRs. The variable domains of 364.14 TCR were expressed recombinantly as single-chain constructs either with the wild-type sequence (wt.β109R), a stabilized version of the wild type (s.β109R), or with mutants where the Arg residue was mutated to Ala (s.β109A), Lys (s.β109K), or Glu (s.β109E) residues. Initial surface plasmon resonance (SPR) binding experiments demonstrated poor functional yields of wt.β109R, and therefore, point mutations were introduced at the V domain interface to increase intrinsic molecular stability as described (27). The mutants s.β109K and s.β109E could not be produced in functional yields that allowed SPR measurements. A dramatic reduction in binding to DQ2-αII was observed in the s.β109A mutant compared with s.β109R, which expressed the wild-type CDR3β sequence (Fig. 6A, 6B). Neither s.β109R nor s.β109A bound the DQ2-CLIP2 molecule that displayed an irrelevant peptide, demonstrating the specificity of binding to DQ2-αII (Fig. 6C, 6D).

Combined, consistent functional data from 364.14 TCR transfectants and binding data from soluble 364.14 TCRs showed that
FIGURE 5. Arginine residue in position 5 of CDR3β is important for DQ2-α-II recognition by TCR 364.14. A, WT, wild-type. B, the same TCR transfectants were stimulated with plate-bound anti-CD3ε Abs. Untransfected cells (*). C, Activation of wild-type 364.14 TCR transfectant by 1 μM 33mer peptide was blocked by 10 μg/ml anti-DQ Ab but not by anti-DP or anti-DR Abs. D, The wild-type 364.14 TCR transfectant was tested with either deamidated 33mer (solid circle), native 33mer (open circle), deamidated 14mer DQ2-α-II peptide (solid triangle), or native 14mer (open triangle). The arrows indicate peptide concentrations needed to elicit 18 pg/ml mouse IL-2 secretion. None of the mutant transfectants were activated by native 33mer peptide. E, Two-log stronger activation of wild-type 364.14 TCR transfectant by anti–HLA-DP Abs (Troybodies) engineered to contain deamidated (solid circle) 33mer compared with those containing native 33mer (open circle). F, Two-log stronger activation of wild-type 364.14 TCR transfectant by streptavidin-immobilized biotinylated soluble deamidated DQ2-αII molecules (solid triangle) compared with native DQ2-αII (open triangle) molecules. For all panels, the experiments were repeated at least two times, and the error bars indicate SEM of each triplicate. The dotted lines indicate the detection limit of mouse IL-2 ELISA. WT, wild-type.

The TCR interacts with the posttranslationally modified Glu residue of the DQ2-α-II epitope

Data thus far showed in vivo Ag-driven TCR selection of DQ2-α-II-reactive T cells in celiac patients that resulted in biased Vβ usage, in vivo clonal expansion, convergent recombination, semi-public response, and the notable conservation of an Arg residue at position 5 of CDR3β. We next asked which part of the DQ2-α-II complex was interacting with the Arg residue and thus participated in the selection of Vβ6.7 chains containing the signature Arg in the CDR3β loop.

Table II. Recognition of variants of the DQ2-α-II epitope by TCR transfectants expressing wild-type or mutant 364.14 TCR

<table>
<thead>
<tr>
<th>Peptide Ag</th>
<th>TCR Transfectant</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 2 3 4 5 6 7 8 9</td>
<td>WT β109A β109K β109E</td>
</tr>
<tr>
<td>P Q P E L P Y P Q E</td>
<td>+++</td>
</tr>
<tr>
<td>–––</td>
<td>–––</td>
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<tr>
<td>–––</td>
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</table>

+++ strong T cell response; (+), weak T cell response at the highest Ag concentration only; –––, no T cell response; and WT, wild-type.

Although peptide binding to DQ2 increased after deamidation, it alone could not account for the dramatic improvement in T cell recognition. In standard T cell assays as that shown in Fig. 5D, the peptide Ag was present during the entire assay time such that in theory, an apparent 10-fold lower binding affinity to HLA-DQ2 of the native gliadin α-II peptide (9) could be compensated by a 10-fold higher peptide concentration in T cell assay. However, as shown in Fig. 5D, a 2-log higher concentration of the native peptide was necessary to elicit T cell responses comparable to that observed with the deamidated peptide. This difference in recognition was confirmed when the native and deamidated gliadin epitopes were offered as part of Ab molecules (Troybodies) (25) that targeted cell surface receptors of the APC (Fig. 5E). The efficient presentation of the Troybody reagents allowed more accurate assessment of Ag recognition, and importantly the conversion of Gln to Glu that to some extent occurred in the workup of synthetic peptides could be excluded as a confounding factor. Finally, to remove HLA-DQ2 binding affinity differences in the assay, we engineered soluble recombinant HLA-DQ2 molecules in which the native and the deamidated DQ2-α-II epitope peptides were tethered covalently to the peptide binding groove via a 6-aa peptide linker. Biotinylated DQ2-αII.Q molecules, either containing a peptide with a native sequence (QPQLPYQPQE) or equivalent amounts of biotinylated DQ2-αILE molecules containing the deamidated epitope (QPPELPYQPQE), were immobilized on streptavidin plates and presented to hybridoma cells expressing the DQ2-α-II-reactive TCR. In this assay, where T cell recognition of titrated amounts of stable DQ2-αII complexes were tested, a near 2-log difference in T cell recognition elicited by the deamidated and native Ag was observed (Fig. 5F). This showed...
clearly that the DQ2-α-II-reactive TCR was able to differentiate between the native Gln residue and the deamidated Glu residue despite that these residues were positioned in the P4 pocket and should not be solvent exposed.

Given the conspicuous presence of a positively charged Arg residue at the tip of the CDR3β loop, one can envision that this may be the TCR residue that “reads” the Glu residue of the DQ2-α-II complex through a charge-to-charge interaction. This notion was supported by a vigorous proliferative response elicited by the DQ2-α-II E4D peptide where the Glu residue in P4 was replaced by another negatively charged residue, Asp (Table II). To note, we never observed Lys, another positively charged residue, in position 5 of the CDR3β loops of DQ2-α-II-reactive, Vβ6.7-positive TCRs. Similarly, a TCR displaying Lys that was introduced into this position by in vitro mutagenesis was not reactive to the DQ2-α-II ligand (Fig. 5A). This demonstrates the presence of additional structural constraints that may modify the charge-to-charge interaction between Arg in the CDR3β and Glu in the DQ2-α-II peptide.

In addition to the highly conserved Arg residue in position 5, the neighboring residues, which were often non-germline encoded, also exhibited certain degrees of conservation. The residue in position 4 of the canonical 11-aa CDR3β loop was most often Ile or Leu, whereas the position 6 C-terminally to the conserved Arg residue was most often occupied by Ser, His, Tyr, or Ala residues. Collectively, the canonical CDR3β loop sequence ASS(I/L)R/S/H/Y/A/TDTQY was present in 67% of the Vβ6.7-positive TCRs (96 of total 143 single cells) reactive to DQ2-α-II and represent more than 86% (96 of 111) of the CDR3β loops with a length of 11 aa. Thus, the positively charged Arg residue in the TCR is probably the primary residue interacting with the negatively charged Glu residue of the peptide, demonstrated by its highly conserved occurrence, with additional contributions from neighboring residues that showed clear nonrandom distribution, but nevertheless less conservation.

Discussion

Gluten-reactive CD4+ T cells from celiac disease patients represent a unique source of disease-relevant human T cells. The TCR repertoire of these cells is the result of natural Ag-driven selection and expansion in a human HLA-associated inflammatory disease. By use of highly specific MHC tetramers and sequencing of TCRs from a large number of single T cells, either derived from in vitro-generated TCCs or directly isolated from peripheral blood of celiac disease patients, we provide a comprehensive characterization of the TCR repertoire of T cells specific for immunodominant gluten epitopes. Our results provide novel insights into how CD4+ T cells that are centrally involved in the development of celiac disease recognize posttranslationally modified gluten Ags and reveal that a non-germline-encoded part of TCR is central in recognition of a posttranslationally modified residue.

Analysis of TRBV7-2 sequences obtained from single-cell sequencing of DQ2-α-II tetramer-positive T cells revealed in vivo clonal expansion, convergent recombination, semipublic response, and the notable conservation of an Arg residue at position 5 of CDR3β. Importantly, the observations were made from direct sequencing of Ag-specific cells that have not been subjected to culture and thus any bias introduced by in vitro expansion. Moreover, similar results were found in all four celiac disease patients studied, and identical Vβ-chain amino acid sequences were found in direct sequencing of tetramer-sorted peripheral blood T cells and TCR sequencing of in vitro-generated TCCs derived from intestinal biopsies of a different set of celiac disease patients.

The fact that most of the Arg residues in our data set are non-germline encoded indicates that this trait has been subjected to selection, presumably driven by the cognate Ag, the DQ2-α-II epitope. This epitope has undergone a posttranslational modification (i.e., a deamidation from Gln to Glu). Our data suggest that the in vivo-selected TCRs specifically sense this posttranslationally modified epitope. This epitope has undergone a posttranslational modification at the P4 position of the epitope. The amino acid residue positioned in the P4 pocket should not be much solvent exposed so it is not obvious how this sensing takes place. The exact determination will require a crystal structure, but obtaining this is unfortunately not trivial. We, as well as others (31), have previously tried to solve the crystal structure of the DQ2: DQ2-α-II complex without success. Our functional data demonstrate that the Glu residue of the DQ2-α-II peptide can be replaced by Asp suggesting that the negative charge is important for TCR recognition. Further, our mutational analysis of a prototype TCR indicates that the Arg residue in the CDR3β loop is critical for TCR recognition. It is hence conceivable that there is direct interaction between the negatively charged P4 Glu residue of the peptide and the positively charged Arg residue of the CDR3β loop in the TCRs.

In our data set, we observed semipublic TCR response (i.e., similar Vβ sequences were found to be dominant in different

FIGURE 6. SPR analyses of scTCRs s.β109R and s.β109A with soluble DQ2-αII and DQ2-CLIP2. Representative sensograms are shown. A–D, In all experiments, Neutravidin was immobilized to ~4500 RU, followed by capture of ~3500 RU biotinylated DQ2-αII (A, B) or DQ2-CLIP2 (C, D) molecules. Soluble scTCR s.β109R (A, C) and mutant s.β109A (B, D) were then injected at various concentrations ranging from 0.32 to 5 μM at 25°C.
individuals). Altogether, the CDR3β sequence ASS(L/R)(S/H/Y/ A)TDTQY was observed in roughly two thirds of all sorted VP6.7 and DQ2-α-II double-positive cells from four different patients. Public TCR response arises from either highly recurrent TCRs that are exported from the thymus to the periphery in relatively high frequency or as a result of high-affinity interaction with the peptide–MHC complex formed by in vivo expansion. Our data cannot differentiate the relative contribution of these two not mutually exclusive mechanisms. Affinity studies of a larger panel of prototypical versus non-prototypical DQ-α-Ⅱ-reactive TCRs or analysis of the TCR repertoire of naïve DQ-α-Ⅱ-reactive T cells will give answers to this question.

In several human autoimmune diseases, increasing evidence suggests that T cells bypass tolerance by recognizing autoantigens that have been posttranslationally modified. This is observed in anticitrulline response (2) or glycosylation-dependent T cell response (3) in rheumatoid arthritis, disulfide bond formation in the gluten response (4) or glycosylation-dependent T cell response (5) in celiac disease. In vivo TCR selection exerted by a posttranslational modification can represent an example of in vivo TCR selection exerted by a posttranslational Glu residue in P4, interacts with the TCR and contributes to disease (16). Identification of a gliadin T-cell epitope in coeliac disease: general importance of gliadin degradation for intestinal T-cell recognition. J. Immunol. 169: 2114–2115.


Supplementary material

Supplementary Figure 1

The monoclonal antibody OT145 binds Vβ chains encoded by both TRBV7-2*01 and TRBV7-2*02 alleles. Healthy volunteers were genotyped for TRBV7-2*01 / *02 alleles using a custom Taqman SNP genotyping kit targeting the g251→a (*01 vs. *02) polymorphic site assayed on a StepOnePlus qPCR machine (ABI). Genomic DNA from non-T-cell sources was isolated from PBMC, frozen cryo-sections or EBV transformed B cell lines with DNeasy blood and tissue kit (QiaGen). Peripheral blood cells were subsequently stained with FITC conjugated OT145 and APC conjugated anti-human CD4 (Diatec). There is a clear CD4+ T cell population that stain OT145 in all three *02/*02 homozygous individuals tested.
Supplementary Figure 2

Over-usage of V\(\beta\)6.7 in DQ2-\(\alpha\)II tetramer positive cells in in vitro expanded T cell lines. Polyclonal T cell lines TCL496.1.2 (A), TCL.KT.CD.E3 (B&D) and TCL465.1.4 (C) were stained with V\(\beta\)6.7 and DQ2-\(\gamma\)II (A), DQ2-\(\alpha\)I (B) or DQ2-\(\alpha\)II (C&D) tetramer. The percentage of V\(\beta\)6.7 positive cells among tetramer-positive cells is shown.
Supplementary Figure 3

Complete amino acid and nucleotide sequence alignment of all DQ2-α-II reactive TRBV7-2-CDR3β loops that contain conserved Arg in position 5. All sequences derived from blood were obtained with TRBV7-2 specific single cell PCR of Vβ6.7 and DQ2-αII tetramer double positive cells, and all sequences derived from duodenum were sequenced from in vitro generated DQ2-α-II reactive T cell clones. The conserved Arg residue and the corresponding encoding nucleotides are in red, TRBV7-2*01 sequences are in black and TRBV7-2*02 sequences are in blue. Non-germline encoded amino acid residues are underlined.
Supplementary Figure 4

WT and mutant 364.14 TCR transfected hybridoma cells express similar levels of CD3ε and Vβ6.7. (A) BW58α-β-.hCD4 cells not transfected with TCR (black) and cells retrovirally transduced with WT 364.14 TCR (red), β109A (green), β109K (blue) or β109E (yellow) mutant TCRs were stained with PE conjugated hamster-anti-mouse-CD3ε. (B) BW58α-β-.hCD4 cells transfected with human non-TRBV7-2 TCR (TCR489: TRBV9, black line) and cells retrovirally transduced with WT 364.14 TCR, β109A, β109K or β109E mutant TCRs were stained with Vβ6.7 antibody (clone OT145) followed by secondary PE conjugated goat-anti-mouse-IgG.