Clonal Vα12.1+ T Cell Expansions in the Peripheral Blood of Rheumatoid Arthritis Patients

By Harout DerSimonian,* Masahiko Sugita,* David N. Glass,‡ Agnes L. Maier,* Michael E. Weinblatt,* Thierry Rème,§ and Michael B. Brenner*

From the *Department of Rheumatology and Immunology, Brigham and Women’s Hospital, Harvard Medical School, Boston, Massachusetts, 02115; the ‡Division of Rheumatology, Children’s Hospital Medical Center, Cincinnati, Ohio 45229; and §INSERM U 291, 34197 Montpellier Cedex 5, France

Summary

Rheumatoid arthritis (RA) represents a heterogenous disease characterized by chronic polyarthritis. Most patients with adult RA inherit HLA-DR4 or -DR1 major histocompatibility complex (MHC) genes. While the molecular basis for this genetic predisposition is unknown, the major function of these MHC-encoded molecules is to present peptides to T lymphocytes. It is hypothesized that an endogenous or environmental antigen initiates a MHC-restricted immune response mediated by T lymphocytes, which is followed by a chronic inflammatory reaction involving many cell types. In chronic RA, previous or ongoing antigenic activation might result in detectable skewing of the peripheral α/β T cell receptor (TCR) repertoire. Here we demonstrate a marked expansion of Vα12.1-bearing CD8+ T cells in the peripheral blood (mean, 22%; range, 10-43%) of >15% of RA patients. A major proportion of these patients shared HLA-DQ2 in addition to the expected high frequency DR1 and DR4 alleles. Detailed molecular analysis in three of the RA patients with elevated Vα12.1+ T cells identified repeated TCR α chain sequences consistent with clonal Vα12.1+,CD8+ T cell expansion. In addition to shared TCR Vα12.1 germline gene usage among unrelated subjects, a conserved Jα motif was also detected. Together, these results suggest an antigen-driven mechanism of T cell expansion in these patients and may offer a new approach in examining specific antigens that stimulate T cells in RA.

1 Rheumatoid arthritis (RA) is an autoimmune disease that manifests itself in patients with chronic inflammation, synovial proliferation, and progressive joint damage (1). Several lines of evidence point to a role for T cells in the pathogenesis of RA. These include a genetic predisposition associated with MHC class II genes, whose products function to present antigens to T cells (2-4), the presence of activated T cells in inflamed synovial tissues and peripheral blood (5), and the therapeutic utility of treatments that at least partially inhibit T cell function (6, 7).

The major population of T lymphocytes that recognize antigen in the context of self-MHC molecules bear the TCR α/β heterodimer in association with the CD3 complex (8). Each chain is divided into a V region that recognizes the Ag/MHC complex and a C region that anchors the molecule to the cell surface. The TCR α/β chains are assembled by somatic recombination of discontinuous germline gene segments during T cell development. Polymerization of template-independent N region and template-dependent P nucleotide insertions at the junctions, Dβ usage, the imprecise joining of the germline gene segments (selected from a large pool), and the combinatorial association of TCR α/β polypeptides help to generate an extensive diversity in the TCR α/β repertoire (9).

During T cell development, only a small fraction of the thymocytes are able to emigrate into the periphery as mature CD4+ or CD8+ T cells. Negative selection events delete self-reactive TCR α/β-bearing T cells (10, 11), while positive selection events rescue single-positive CD4+ or CD8+ T cells (12-14). Positive selection yields mature CD4+ T cells that are predominantly self-MHC class II restricted or CD8+ T cells that are predominantly self-MHC class I restricted (15). The binding of antigen peptides to MHC molecules has provided a molecular explanation for the corecognition of Ag/MHC by the TCR α/β (16). TCR gene sequences and hypothetical modeling based on Ig molecules suggest that the TCR V regions (especially those regions cor-
responding to CDR1 and CDR2) contact the MHC molecule, while the highly diverse V-(D)-J junctional region (corresponding to CDR3) contacts antigenic peptides bound to the MHC molecule (9, 17).

There are strong correlations between TCR V gene usage and T cell antigen recognition specificity in animal studies (18). Striking T cell repertoire correlations also have been obtained for experimental allergic encephalomyelitis (EAE), an experimental model of autoimmune disease in mice and rats (19). It has been shown, for instance, that induction and maintenance of the disease is dependent on myelin basic protein–specific T cell clones that utilize a restricted pool of Vα, Jα, and Vβ gene segments. Since, antigenic specificity in RA is not known, it has been difficult to establish T cell clones from RA patients to study antigen recognition and TCR V gene usage. The identification of a restricted T cell population based on TCR gene usage in RA might be useful in identifying the relevant autoantigens and offer new therapeutic approaches for this disease.

Here, we used a Vα12.1-specific 6D6 mAb (20) in cell surface staining to identify a subset (17%) of RA patients that showed a striking elevation in the number of Vα12.1+,CD8+ T cells in PBL. Analysis of the Vα12.1+,CD8+ T cells in three unrelated individuals by nucleotide sequencing revealed evidence for clonal T cell expansion. Most of the patients with TCR Vα12.1–elevated CD8+ T cells also shared the HLA-DQ2 phenotype. These results provide evidence suggesting that antigen-driven expansion of T cells may be a component of chronic RA.

Materials and Methods

**Immunofluorescence and Flow Cytometry.** Flow cytometric analyses were performed using directly conjugated antibodies. Two-color analyses on PBL were carried out as described previously using FITC-coupled anti-CD4 or anti-CD8 mAb (Immunotech, Marseille, France). Tricolor is a two-stage PE-Texas red fluorescence and a photograph was taken with a black-and-white camera. After merging both slides in a 256 optimized color bitmap, a photograph was taken with a color screen photographic device. CD8+ cells are seen in green and Vα12.1+ cells are seen in red. The double-stained Vα12.1+CD8+ T cells are seen in yellow.

**Polymerase Chain Reaction.** Subsets of T cells were enriched using anti-CD4, anti-CD8, or anti-Vα12.1 mAbs with magnetic beads (Dynal, Inc., Great Neck, NY). For example, CD8-enriched T cells were isolated by depletion of CD4+ T cells using anti-CD4 mAb and magnetic beads, while CD4-enriched T cells were isolated by depletion of CD8+ T cell using anti-CD8 mAb and magnetic beads. Each of these depleted populations was further subjected to enrichment using anti-Vα12.1 mAb and magnetic beads. Purification of RNA from these cells was carried out according to Chomczynski and Sacchi (22). cDNA for the direct PCR method of amplification was synthesized in a reverse transcription reaction using AMV reverse transcriptase, 5 μg of total RNA, and 500 ng of oligo(dT)12-18 primer before amplification with Vα12.1- and Cα-specific primer combination. For inverse (i)PCR, double-stranded cDNA was synthesized from total RNA (2 μg) and circularized using T4 DNA ligase (23). Using a pair of Cα or Cβ primers oriented in an outward direction from one another, ∼700-bp PCR products were generated corresponding to the full-length TCR α or β chain transcripts (24). PCR primers were Vα12.1-specific, 5′GGGATCGAGCTGACCCATGGAGGCGACG; Cα-specific, 5′GGGAACTTTGACCCATGGAGGCGACG; Cβ-specific, 5′GGGTCAGACCTCAGTGCAGACAGA; Cα-inverse, 5′CATCTGGGCGCGCTGTAGTGGTCTC; Cβ-inverse, 5′GGTGGCGACACAGGCACTCCGGGTTGG; Cα-inverse, 5′GGATCGCCTCCGCATGGTCAAGGAGAGGAGG.

**Cloning and Sequencing.** PCR products were cloned into M13 plasmids and sequenced by the dideoxynucleotide chain termination method using the modified T7 polymerase (Sequenase; United States Biochem. Corp., Cleveland, OH). The sequencing products were resolved on polyacrylamide gels, and autoradiography was carried out according to standard methods.

**Serologic HLA Typing.** HLA class I and class II antigens were typed serologically by the Brigham and Women’s Hospital Tissue Typing Laboratory (Boston, MA). Serotyping of HLA-A, -B, -C, -DR, and -DQ was performed using standard microcytotoxicity techniques.

**Results**

*Vα12.1-bearing CD8+ T Cells Are Elevated in Patients with RA.* The relative percentage of TCR Vα12.1 on CD4+ or CD8+ T cell subsets in the peripheral blood of RA patients was assessed by two-color fluorescence staining and flow cytometry using the Vα12.1-specific mAb 6D6 (20). Analysis of both RA patient (n = 46) and healthy control (n = 68) PBL showed similar frequencies of Vα12.1 expression by CD4+ T cells (mean, 2.6%; range, 1–4%). Likewise, one group of 38 patients contained percentages of TCR Vα12.1+ T cells in the CD8+ subset (mean, 3.6%; range, 1–7%) that were similar to those found in healthy controls. However, a second group of RA patients had elevated percentages of Vα12.1+ T cells in the CD8+ subset that ex-
Vα12.1+ T Cells Are Represented as Clonal or Oligoclonal Expansions. The precise molecular structure of the Vα12.1+ TCR α chain was determined by cDNA cloning and sequencing from the CD8+ cells purified from three Vα12.1-elevated patients. PCR products containing Vα12.1 rearrangements were generated by direct amplification using Vα12.1- and Co-specific oligonucleotide primers. For each patient a distinct Vα12.1-containing sequence corresponding to a functional TCR α chain transcript was repeated extensively (Fig. 2A). For example, in patient 1, in whom 43% of the CD8+ T cells were Vα12.1+, all 15 cDNA TCR α sequences obtained were identical. Similarly, 9 of 16 identical sequences were obtained in patient 2, in whom 29% of the CD8+ T cells were Vα12.1+. Analysis of patient 3, in whom 22% of CD8+ T cells were Vα12.1+, exceeded 7.4%, 2 SD above the mean of healthy individuals. (Fig. 1). Vα12.1+ T cell expansions in the CD8+ population were found in 8 of 46 (17%) RA patients and were absent in all 68 healthy controls (Fisher’s exact test, p = 0.00047). Among these eight patients Vα12.1 was expressed on 43, 29, 27, 26, 22, 20, 12, and 10% (mean, 22%) of the CD8+ T cells, respectively (Fig. 1, Vα12.1 elevated). The elevations of Vα12.1+ T cells was a stable phenomenon since similar values were obtained over a 24-mo period in several of the subjects (data not shown).

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identified two distinct repeated sequences; of these, one sequence accounted for 16 of 24 clones, and the second repeated sequence was identified in 4 of 24 clones. Although the junctional sequences were different in the two repeated Vα12.1 sequences in patient 3, both used the same Jα gene segment, JαA6 (Fig. 2 A).

These results were confirmed using the iPCR methodology, which utilizes circularized DNA and a pair of α chain C region oligonucleotide primers oriented away from one another (23, 24). TCR Vα-containing transcripts were cloned and sequenced from Vα12.1+, CD8+ T cells purified from PBL. This analysis of patients 1 and 3 revealed the same repeated TCR α chain sequences that were found with the direct PCR amplifications (Fig. 2 A). A similar analysis of healthy subjects revealed diverse TCR α chain sequences with no occurrence of repeated sequences (data not shown). Among the repeated sequences found in the three patients examined, the Vα12.1 was rearranged to distinct Jα gene segments: JαA1, JαA12, and JαA6 in patients 1, 2, and 3, respectively. Interestingly, all of these Jα gene segments encode the same amino acid dipeptide sequence (pro-tyr) at their 3' ends (Fig. 2 A). Notably, only 6 of the 80 known Jα genes encode this dipeptide sequence, and may constitute a family of functionally related Jα gene segments (25–28; DerSimonian, H., and M. B. Brenner, manuscript in preparation).

We also analyzed the TCR β chain transcripts in the purified Vα12.1+, CD8+ T cells using the iPCR methodology. Hence, all potential Vβ transcripts in Vα12.1+, CD8+ T cells from patients 1 and 3 were cloned and sequenced (Fig. 2 B). All 18 Vβ cDNA clones in the purified Vα12.1+, CD8+ T cells were identical in patient 1. Moreover, 12 of 20 cDNA clones from patient 3 were identical but differed from the repeated Vβ sequence identified in patient 1. Since the repeated sequence in patient 3 predicted a Vβ8-encoded TCR, cell surface coexpression of Vα12.1 and Vβ8 gene products on CD8+ T cells was demonstrated by flow cytometry using the Vα12.1-specific mAb (6D6) and the Vβ8-specific mAb (16G8; 29), confirming the molecular cloning results (Fig. 2 C).

**Expanded Vα12.1+ T Cells Carry the “Memory” Phenotype.** Staining of Vα12.1+ T cells with mAb specific to various activation antigens was carried out in two-color flow cytometry analysis as shown for Vα12.1-elevated patient 1 (Fig. 3 A). Such analyses for patients 1–3 are summarized in histo-

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**Figure 3.** Vα12.1+ T cells activation phenotype. Two-color staining of Vα12.1+ T cells from fresh PBMC of one Vα12.1-elevated patient is displayed by dot plot analysis. (A) PBL from patient 1 shows costaining with FITC-coupled anti-Vα12.1 mAb on the x-axis vs. PE-coupled anti-CD45RO (UCHL1; 3%), anti-IL-2Ra (B1.49.9; 31), anti-IL-2Rβ (TU27; 32), anti-VLA-1 (TS2/7; 33), or anti-HLA-DR (LB3.1; 34) mAb staining on the y-axis. (B) Bar graph representation of percent positive for the two-color staining using the anti-IL-2Ra, anti-IL-2Rβ, anti-HLA-DR, anti-VLA-1, and anti-CD45RO mAbs for CD8+ T cells in healthy donors 1–3 (left) and for Vα12.1+, CD8+ T cells in patients 1–3 (right).

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gram format (Fig. 3 B). A majority (>85%) of the expanded peripheral \( \text{Vot}12.1^+, \text{CD}8^+ \) T cells expressed the memory marker CD45RO+* In addition, 10–30% of these cells expressed detectable levels of VLA-1, an antigen expressed on long-term or chronically activated T cells (35, 36), HLA-DR antigens, and IL-2R \( \alpha \) chain. These results are consistent with previous antigen activation and reveal ongoing activation by a fraction of the \( \text{Vot}12.1^+, \text{CD}8^+ \) peripheral T cells in the \( \text{Vot}12.1 \)-elevated RA patients. They stand in contrast to the lower percentages of CD8+ T cells from healthy subjects expressing these activation markers (Fig. 3 B). Only percentages of IL-2R \( \alpha \) chain–bearing cells are similar in normal CD8+ T cells from healthy donors and \( \text{Vot}12.1^+, \text{CD}8^+ \) T cells from the RA patients.

**Distribution of \( \text{Vot}12.1^+, \text{CD}8^+ \) T Cells in the Synovium.**

The primary finding in this study is the expansion of \( \text{Vot}12.1^- \) bearing CD8+ T cell population in the peripheral blood of a subset of RA patients. Two of these \( \text{Vot}12.1^- \)-elevated patients received a medically indicated joint operation during the course of study allowing analysis of their synovial tissues. Frozen sections were stained for two-color confocal fluorescence microscopy with anti-\( \text{Vot}12.1 \) mAb 6D6 (red) and anti-CD8 or anti-CD4 mAb (green). Each two-color fluorescent slide was screened for at least 50 cells containing at least five lymphocyte-rich areas (at 240x). The black-and-white fluorescent pictures from each photomultiplier were simultaneously recorded and merged after recoloring. An example of such an evaluation of double-positive (\( \text{Vot}12.1^+, \text{CD}8^+ \)) cell staining is shown as the merged product of the CD8+ (top left) and \( \text{Vot}12.1^+ \) (top right) by scanning of the same field (Fig. 4). Each double-stained cell is seen in yellow (\( \text{Vot}12.1^+, \text{CD}8^+ \)), composed of green (CD8+) and red (\( \text{Vot}12.1^+ \)) color overlap. Synovial membrane staining of the two \( \text{Vot}12.1^- \)-elevated patients (nos. 2 and 4) revealed that 8.5 and 10% of CD8+ T cells in their synovial tissue expressed \( \text{Vot}12.1^+ \), compared with 29 and 27% of their peripheral blood CD8+ T cells, respectively (Table 1). Thus, the \( \text{Vot}12.1^+, \text{CD}8^+ \) T cells appear to represent a substantial number of the synovial tissue CD8+ T cells, but not as large a fraction as of the peripheral CD8+ T cells. Two \( \text{Vot}12.1^- \)-normal patients (nos. 25 and 46) were also examined and they expressed 3.6 and 6.2% \( \text{Vot}12.1^+, \text{CD}8^+ \) cells in their synovial tissues compared with 4.9 and 5.3% in their peripheral blood samples, respectively. Too few synovial tissue analyses from (peripheral) \( \text{Vot}12.1^- \)-evaluated donors were made to allow a statistical assessment.

**Patients with Expanded \( \text{Vot}12.1^+ \) T Cells Share HLA-DQ2.**

The MHC alleles present among the RA patients were analyzed and compared in both the \( \text{Vot}12.1^- \)-elevated and \( \text{Vot}12.1^- \)-normal groups. As expected, DR1 and DR4 alleles were prominently represented in both groups. Interestingly, the proportion of HLA-DQ2 (which is in strong linkage disequilibrium with DR3 and DR7) was substantially higher among the \( \text{Vot}12.1^- \)-elevated versus the \( \text{Vot}12.1^- \)-normal group (Fisher's exact test, \( p = 0.002 \)), as it was found in 7 of 8 (88%) (Table 2) compared with 10 of 38 (26%) patients, respectively. This difference was similar to that of \( \text{Vot}12.1^- \)-elevated patients when compared to the expected positivity of 33% in an outbred North American population (\( \chi^2 5.05, p < 0.025 \)) (37). While the significance of increased DQ2 frequency for the risk of developing RA is unknown, the clonal (or oligoclonal) expansions of \( \text{Vot}12.1^+, \text{CD}8^+ \) T cells appear to be more likely in DQ2-positive individuals. Patients in the \( \text{Vot}12.1^- \)-elevated group did not differ clinically, however, from the \( \text{Vot}12.1^- \)-normal group with respect to age, sex, duration of disease, rheumatoid factor positivity, erythrocyte sedimentation rates, or arthritis activity measured by number of painful joints and global assessments.
Table 1. Relative Frequency of \( \text{V}_{\alpha}12.1^+ \) T Cells in the CD4 and CD8 Subsets

<table>
<thead>
<tr>
<th>Patients</th>
<th>2</th>
<th>4</th>
<th>25</th>
<th>46</th>
</tr>
</thead>
<tbody>
<tr>
<td>Peripheral blood</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>( \text{V}_{\alpha}12.1/\text{CD4} )</td>
<td>2.8%*</td>
<td>2.6%</td>
<td>1.5%</td>
<td>1.8%</td>
</tr>
<tr>
<td>( \text{V}_{\alpha}12.1/\text{CD8} )</td>
<td>29%</td>
<td>27%</td>
<td>4.9%</td>
<td>5.3%</td>
</tr>
<tr>
<td>Synovial tissue</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>( \text{V}_{\alpha}12.1/\text{CD4} )</td>
<td>3.7%</td>
<td>6.7%</td>
<td>0.0%</td>
<td>0.3%</td>
</tr>
<tr>
<td>( \text{V}_{\alpha}12.1/\text{CD8} )</td>
<td>8.5%</td>
<td>10.0%</td>
<td>3.6%</td>
<td>6.2%</td>
</tr>
<tr>
<td>CD4/CD8</td>
<td>55:45</td>
<td>58:42</td>
<td>44:56</td>
<td>61:39</td>
</tr>
</tbody>
</table>

* Percentage of \( \text{V}_{\alpha}12.1^+ \) T cells in the CD4+ or CD8+ T cell subset was calculated according to the formula in Materials and Methods: percent of \( \text{V}_{\alpha}12.1^+,\text{CD4}^- \) (or \( \text{V}_{\alpha}12.1^+,\text{CD8}^- \)) / percent of total CD4+ (or CD8+) T cells.

Table 2. Patients with Expanded \( \text{V}_{\alpha}12.1^+ \) T Cells in the CD8 Subset

<table>
<thead>
<tr>
<th>RA patient</th>
<th>CD8+ T cells expressing ( \text{V}_{\alpha}12.1^+ )</th>
<th>HLA class I</th>
<th>HLA class I</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>%</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>43*</td>
<td>A__ , B44,</td>
<td>DR7 , DQ2</td>
</tr>
<tr>
<td></td>
<td></td>
<td>A32, B60, Cw3</td>
<td>DR4, DQ3</td>
</tr>
<tr>
<td>2</td>
<td>29</td>
<td>A1, B8</td>
<td>DR3, DQ2</td>
</tr>
<tr>
<td></td>
<td></td>
<td>A2, B__,</td>
<td>DR4, DQ3</td>
</tr>
<tr>
<td>3</td>
<td>22</td>
<td>A2, B52</td>
<td>DR3, DQ2</td>
</tr>
<tr>
<td></td>
<td></td>
<td>A11, B48</td>
<td>DR10, DQ__</td>
</tr>
<tr>
<td>4</td>
<td>27</td>
<td>A2, B35, Cw4</td>
<td>DR1 , DQ1</td>
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<td></td>
<td></td>
<td>A11, B57, Cw3</td>
<td>DR2,</td>
</tr>
<tr>
<td>5</td>
<td>26</td>
<td>A30, B14,</td>
<td>DR7 , DQ2</td>
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<tr>
<td></td>
<td></td>
<td>A23, B13</td>
<td>DR1 , DQ1</td>
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<tr>
<td>6</td>
<td>20</td>
<td>A23, B27, Cw2</td>
<td>DR4 , DQ1</td>
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<td></td>
<td></td>
<td>A24, B42,</td>
<td>DR5 , DQ__</td>
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<tr>
<td>7</td>
<td>12</td>
<td>A2, B7,</td>
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<tr>
<td></td>
<td></td>
<td>A29, B44,</td>
<td>DR7, DQ4</td>
</tr>
<tr>
<td>8</td>
<td>9</td>
<td>A30, B7,</td>
<td>DR3, DQ2</td>
</tr>
<tr>
<td></td>
<td></td>
<td>A11, B40,</td>
<td>DR10, DQ1</td>
</tr>
</tbody>
</table>

Typing for HLA class I and II was carried out serologically using standard microcytotoxicity techniques.

* mAb 6D6 surface staining.

† Confirmed by PCR sequence-specific probe analysis.

Discussion

In this study, staining with \( \text{V}_{\alpha}12.1^+ \)-specific mAb and flow cytometry identified a subset of RA patients with elevated numbers of \( \text{V}_{\alpha}12.1^+,\text{CD8}^- \) T cells in the peripheral blood. The molecular analysis revealed that these T cells were clonally (patients 1 and 2) or oligoclonally (patient 3) expanded, evidenced by TCRs encoded by repeated \( \text{V}_{\alpha}12.1 \) gene sequences. The marked expansion in \( \text{V}_{\alpha}12.1^+,\text{CD8}^- \) T cells reported here was detected because fluorescence staining with the \( \text{V}_{\alpha}12.1 \)-specific mAb could be readily performed on a large number of subjects with CD4+ and CD8+ T cells analyzed separately. Such screening approaches may be necessary to detect a particular TCR usage phenomenon when it occurs in only a subset of patients. The \( \text{V}_{\alpha}12.1 \)-elevated patients described here may correspond to an immunologically defined subset even though clinically these patients were similar to the \( \text{V}_{\alpha}12.1 \)-normal group. This study, examining the TCR repertoire in RA, differs from other analyses in several aspects (38). Other studies have predominantly focused on the VB repertoire (39-41), performed analyses on the synovial fluid or tissue and on mixtures of both CD4+ and CD8+ T cells (24, 39-44), and generally have examined only a few donors (24, 41-43). Nevertheless, previous examples of repeated TCRs \( \text{V}_{\beta}14 \) and \( \text{V}_{\beta}17 \) (as well as \( \text{V}_{\beta}2 \), \( \text{V}_{\beta}3 \), and \( \text{V}_{\beta}13.2 \) sequences) in synovial fluid or tissue have suggested that clonal T cell expansion maybe an important aspect of this disease (40, 41).

Several examples of restricted \( \text{V}_{\alpha} \), \( \text{J}_{\alpha} \), and \( \text{V}_{\beta} \) usage in murine T cells have been reported that characterize a particular T cell response to known foreign antigens, for example, \( \text{V}_{\alpha}11 \) and \( \text{V}_{\beta}3 \) in response to cytochrome \( c \) (45-47), \( \text{V}_{\alpha}2 \) and \( \text{V}_{\beta}1 \) in response to \( \lambda \) repressor cl protein (48), \( \text{V}_{\alpha}4 \) and \( \text{V}_{\beta}10 \) in response to lymphocytic choriomeningitis virus glycoprotein (49, 50), and \( \text{V}_{\alpha}2.3 \) or \( \text{V}_{\alpha}4 \) rearranged to the same \( \text{J}_{\alpha} \) gene segment, together with \( \text{V}_{\beta}8.2 \) in the myelin basic protein–induced EAE animal model of autoimmune disease (51-53). Thus, a strong antigen-driven activation may cause proliferation of T cell clones that utilize specific \( \text{V}_{\alpha} \), \( \text{J}_{\alpha} \), and \( \text{V}_{\beta} \) sequences that ultimately dominate as clonal (or oligoclonal) populations of circulating T cells in patients with chronic RA. While the mechanism responsible for the clonal \( \text{V}_{\alpha}12.1^+ \) T cell expansion in this subset of RA patients is not known, the restricted \( \text{V}_{\alpha}/\text{J}_{\alpha} \) usage in unrelated patients and the CD45RO expression by the elevated \( \text{V}_{\alpha}12.1^+ \) T cells provide support for an antigen-driven activation mechanism.

The additional occurrence of the P-Y residues in the \( \text{J}_{\alpha} \)-encoded sequences of these TCRs is another interesting feature of their structure. Preliminary TCR modeling suggests this segment of the \( \text{J}_{\alpha} \) is near the switch or hinge region that joins the V and C domains. Residues at this site would be unlikely to participate in antigen–MHC recognition, but are predicted to be solvent exposed and might interact with an accessory cellular ligand or impose an effect on TCR $\alpha$ chain conformation if this region of the TCR is analogous to the counterpart region in Ig (A. R. Rees, personal communication, University of Bath, UK). A relationship between HLA-DQ2 and the TCR \( \text{V}_{\alpha}12.1^+ \) clonal expansion can only be inferred at present. One hy-
hypothesis would indicate that within the thymus HLA-DQ2 or a closely linked gene might act to select for the individual clone, or alternatively HLA-DQ2 might act as the restriction element in presenting antigen to Vdo12.1+ T cells in the periphery. It is surprising that the expansion of a CD8+ T cell subset would be associated with the expression of a MHC class II allele since CD8+ T cells generally recognize peptide antigens presented by MHC class I molecules (15). However, a role for MHC class II and HLA-DQ-encoded molecules in particular in the activation and expansion of CD8+ T cells has been suggested in a number of experimental and clinical conditions where these cells function as regulatory or cytolytic lymphocytes (54–57). It is notable that the human antigen–specific T cell clones so far characterized show a bias for HLA-DQ restriction. For example, CD8+ T cell clones derived from blood or lesions of patients with lepromatous leprosy were restricted to HLA-DQ (54). Alternatively, peptides derived from HLA-DQ molecules may be relevant antigens presented by other HLA molecules. For instance, it has been shown that HLA-B7-derived peptides can be presented by DR11.1 (58), that HLA-DR3-derived peptides can be presented by HLA-DPw3 (59), and in a cross-species system HLA-Cw3-derived peptides were presented on murine H-2Kd (60). Further, recent peptide elution experiments from human and mouse MHC molecules have identified numerous peptide sequences encoded by other MHC alleles (61, 62).

Whether the Vdo12.1+ T cell population or the antigen to which it responds are critical to the pathology of the rheumatoid disease process itself remains to be determined. Nevertheless, clonal expansions that account for a mean of 22% of the CD8+ T cells in the peripheral blood are such large populations numerically that it seems likely that they may have an important functional impact. Since the expansion is in the CD8+ pool of peripheral blood T cells, these may be a regulatory T cell subset, rather than the predominant proinflammatory T cell in the synovium. Defining this aberration in a subset of patients may have relevance to the diagnosis and treatment of this disease. These clonal T cell populations together with associated MHC molecules offer newly identified tools to examine specific T cell antigens in this autoimmune disorder of unknown etiology.

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Address correspondence to Michael Brenner, Seeley Mudd Building, Room 504, 250 Longwood Avenue, Boston, MA 02115.

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