A Functional Link for Major TCR Expansions in Healthy Adults Caused by Persistent Epstein-Barr Virus Infection

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Abstract

Dramatic clonal expansions of unknown functional significance have been documented in the T cell receptor (TCR) αβ peripheral blood repertoires of apparently healthy adults. In this study, we provide evidence that persistent infection with the ubiquitous Epstein-Barr virus (EBV) causes major distortions within the memory repertoire of healthy virus carriers. Using complementarity determining region 3 (CDR3) length analysis to measure repertoire diversity, dominant expansions that dramatically skewed the entire TCRBV6 blood repertoire towards oligoclonality were enriched in the CD8+CD45RO+CD45RA− subset of HLA B8+ healthy virus carriers. Evidence of phenotypic heterogeneity between individuals was also observed for these expansions based on their variable coexpression of CD45RO and CD45RA. TCR junctional region sequencing revealed that these expansions were clonal and that they represented commonly selected HLA B8–restricted memory cytotoxic T cells that recognize the immunodominant latent EBV epitope, FLRGRAYGL. Furthermore, the functional identity of these virus-specific CD8+ T cells was confirmed by their FLRGRAYGL–specific cytotoxicity. Therefore, the functional significance of dramatic clonal expansions in healthy adults can be linked in some cases to virus-specific CD8+ T cells that play an essential role in immunosurveillance. This first identified link for expansions in the circulation arises as a normal consequence of repeated exposure of the immune system to environmental antigens and to persistent virus infections. Alternatively, are they autoreactive T cells, similar to B cells in benign monoclonal gammopathies, that are thought to be responding to premalignant conditions and age-related defects?

Diversity within the T cell repertoire can be measured by studying the distribution of T cell receptor (TCR) rearrangements. The majority of T cells express an αβ TCR heterodimer that is generated through somatic recombination of variable (TCRAV and TCRBJ) gene elements during T cell ontogeny (for review see reference 17). Repertoire diversity is further increased by the precise joining of different gene segments and the quasi-random insertion or deletion of nucleotides at the V-(D)-J junctional regions that span the major antigen binding site or complementarity determining region 3 (CDR3) (18–20). Therefore, the CDR3 loop is highly variable in length and in codon usage between functionally distinct TCR clonotypes. Extreme clonotypic expansions do not necessarily elevate the frequencies of TCRBV gene families, as they have been detected within populations with normal TCRBV gene frequencies (9, 12).

Several features of the CD8+ T cell memory response to EBV make it an ideal model system to address a possible link between persistent virus infection and the presence of large clonal expansions within the peripheral blood repertoires of healthy individuals. Firstly, we have shown previously that the class I–restricted memory response to the latent EBV epitope, FLRGRAYGL, is restricted by a single TCRBV6S2/BJ2S7 clonotype that is highly conserved in many HLA B8+ individuals (21). (TCRBV6S2 replaces BV6S3*a under the new designation according to Arden et al. [22].) Secondly, functional assays have estimated that this public clonotype is highly fre-

Dramatic Expansion of Epstein-Barr Virus–specific Clonotypes in Health


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1. Abbreviations used in this paper: CDR, complementarity determining region; CTL, cytotoxic T cell; IM, infectious mononucleosis; TCR, T cell receptor.
quent within the peripheral blood repertoire (23) and that memory EBV-specific cytotoxic T cell (CTL) responses are stably maintained for life (24). The present study has explored the impact that selection of this EBV-specific clonotype has on the TCR β repertoire of healthy virus carriers. By examining the diversity of the TCRBV6 repertoire within different T cell populations of HLA B8* adults, we herein show that expansion of the EBV-specific clonotype in healthy virus-infected individuals dramatically skews the entire CD8* CD45RO* CD45RA* memory BV6 repertoire towards oligoclonality. This study identifies a basis for environmental antigens in the development of extreme T cell expansions in the blood of healthy adults.

Methods

Donors. Peripheral blood samples were taken from two healthy, HLA B8*, long-term EBV-seropositive donors (viral capsid antigen IgG*, EBV nuclear antigen IgG*), D1 and D2, aged 51 and 37 yr, respectively. Peripheral blood was also taken from two HLA B8*, EBV-seronegative donors (viral capsid antigen IgG*, EBV nuclear antigen IgG*), D3 and D4, aged 56 and 55 yr, respectively. PBMCs were isolated from heparinized blood by centrifugation over Ficoll-PAque (Pharmacia Biotechnology, Melbourne, Australia). The HLA B8* status of each donor was initially determined by FACScan analysis of PBMCs using anti–HLA B8 mAb (clone 59HA-1; One Lambda, Los Angeles, CA) and confirmed by serotyping of the donor’s PBMCs.

Isolation and enrichment of human CD8*CD45RA*CD45RO*, CD8*CD45RO*CD45RA*, and CD8*CD45RO*CD45RA* T cells. 1–2 × 10^6 PBMCs were incubated with anti–human CD4 mAb-labeled beads (Dynabeads M-450; DYNAL, Melbourne, Australia) to enrich for CD8* lymphocytes according to the manufacturer’s recommendation. The CD8*–enriched population was centrifuged and the pelleted cells were stained for three-color, immunofluorescent flow cytometry using anti–human CD8 mAb conjugated with tricolor (clone 3B5; CALTAG, Sydney, Australia), anti–human CD45RA mAb conjugated with FITC (clone L48; Becton Dickinson, Sydney, Australia), and anti–human CD45RO mAb labeled with PE (clone UCHL-1; Becton Dickinson). Cells were sorted into three sub-sets, a CD8*CD45RA*CD45RO*, CD8*CD45RO*CD45RA*, and CD8*CD45RO*CD45RA* population, using a Becton Dickinson FACS® Vantage Flow Cytometer. The purity of the recovered cells was > 98%.

RNA isolation and cDNA synthesis. Total RNA was extracted from 1–5 × 10^6 PBMCs or sorted CD8*CD45RA*CD45RO*, CD8*CD45RO*CD45RA*, and CD8*CD45RO*CD45RA* cells using Total RNA Isolation Reagent (Advanced Biotechnologies, London, UK). First strand cDNA was synthesized using an antisense TCRBC primer (Cm) as described previously (21). For all RNA and cDNA reactions, a negative control was included where either cells or RNA were replaced with water.

TCRBV6 PCR amplification. TCRBV6 transcripts were amplified to saturation with a 5’ TCRBV6 family-specific primer (Vβ6) (25) and a nested 3’ TCRBV6-specific primer (Cv) (21). Amplifications were performed in 25-μl reaction volumes using first strand cDNA representing material from 1–5 × 10^6 cells, 10 pmol of each 5’ and 3’ primer, 200 μM dNTPs, 1.5 mM MgCl2, 1.25 U of Taq polymerase (AmpliTaq Gold; Perkin-Elmer Corp., Norwalk, CT), and a GeneAmp PCR 9600 system (Perkin-Elmer Corp.). The PCR conditions consisted of denaturation at 95°C for 15 s, annealing at 55°C for 40 s, and extension at 72°C for 40 s for 35 cycles, followed by a 5-min final extension at 72°C. PCR products were separated on 2% (0.5× Tris-buffered EDTA) NuSieve GTG agarose gels (FMC BioProducts, Rockland, ME), excised, and purified using a QIAEX gel extraction kit (Qiagen, Chatsworth, CA).

Repertoire diversity analysis: CDR3 length determination and quantitation of CDR3 distribution. The technique of CDR3 length determination and quantitation of CDR3 distribution to analyze TCR repertoire diversity is based on the methodology described by Pannetier et al. (26). QIAEX-purified TCRBV6 PCR products were labeled with a nested 3’-FAM fluorophore-labeled primer specific for the TCRBC gene (CβP*: 5’-FAM-TTTCTGATGGCTCAAACAC-3’; Research Genetics Inc., Huntsville, AL) in a PCR run-off reaction. PCR conditions were identical to those described above, except that 2% of QIAEX-purified TCRBV6 PCR product was used as a template for five cycles of elongation (run-off) and a 5-min final extension at 72°C. The fluorescent PCR run-off products were heat-denatured at 95°C for 2 min and were separated on a 6% acrylamide gel together with size standards (GENESCAN-1000 ROX; Applied Biosystems, Brisbane, Australia) on an Applied Biosystems 373A DNA sequencer. Data were processed using the GENESCAN Analysis 2.1 Software (Applied Biosystems) which records the fluorescence intensity in each peak. Percent relative peak intensity is the specific peak area/total area of all peaks.

Repertoire diversity analysis: TCR V-D-J junctional region sequencing. QIAEX-purified TCRBV6 PCR products were ligated into the pGEM-T Vector System (Promega, Madison, WI) and then used to transform E. coli SURE Competent Cells (Stratagene, La Jolla, CA) according to the respective manufacturers’ instructions. Plasmid inserts were amplified by PCR and QIAEX-extracted according to the conditions described above, and then sequenced in both directions using the Vβ6 and Cm primers with a PRISM Ready Reaction DyeDeoxy Terminator Cycle Sequencing Kit and an ABI377 DNA sequencer (Applied Biosystems). Diversity within the BV6 gene family was measured by the frequency at which a particular cloned TCR V-D-J insert occurred. n signifies the number of identical TCR V-D-J junctional region sequences/total number of recombinant clones tested.

Cytotoxicity assay. Unsorted PBMCs and sorted populations of CD8*CD45RA*CD45RO* and CD8*CD45RO*CD45RA* cells from seropositive donor D2 were activated weekly by stimulation with the γ-irradiated (80 Gy) LCL from an HLA A1/B8 homozygous individual, BM, at a stimulator/responder cell ratio of 1:200. After 32 d, these populations were used as effectors against an HLA A1/B8 homozygous PHA T cell blasts, with and without adsorbed FLRGRAYGL peptide (100 μg/ml, 0.5 ml). Peptides were purchased from Chiron Mimotopes (Melbourne, Australia), dissolved in DMso, and diluted in serum-free RPMI 1640 medium for use in cytotoxicity assays. Target cells were incubated with 100 μCi of 3H Cr at 37°C for 90 min, with and without peptide, washed twice by centrifugation, and used in standard 4-h 3H-Cr-release assays. The mean spontaneous lysis for targets in culture medium was < 20%, the mean maximum lysis in 0.5% SDS was > 90% of total uptake, and the variation about the mean specific lysis was < 5%.

Results

EBV-infected healthy adults have dramatically distorted TCRBV6 memory repertoires. Previously we have shown that the class I–restricted memory response to the latent EBV epitope, FLRGRAYGL, is dominated in many HLA B8* individuals by a single TCRBV6S2/BJ2S7 clonotype (21). To determine whether clonal expansions of this public EBV-specific clonotype can be linked to repertoire distortions within healthy individuals, we examined the extent of diversity within the peripheral TCRBV6 repertoire of two normal adult EBV-seropositive, HLA B8* donors, D1 and D2. Both donors have been found previously to have a highly restricted FLRGRAYGL-specific TCR memory response (21), with circulating CTL precursor frequencies of the EBV clonotype as high as 1:2,000 PBMCs reported for donor D1 (23). Repertoire diversity was mea-
Dramatic Expansion of Epstein-Barr Virus–specific Clonotypes in Health

sured by a PCR-based approach that determines the distribution of CDR3 lengths within a given TCRBV family; gaussian-shaped peak profiles represent a diverse array of clonotypes of varying CDR3 lengths, whereas oligoclonal peak profiles have been shown to represent clonally expanded T cells (for review see reference 27). TCRBV6 family repertoire diversity was analyzed ex vivo in unsorted PBMCs and in sorted populations of either CD8<sup>+</sup>CD45RA<sup>−</sup>CD45RO<sup>+</sup> (naive) or CD8<sup>+</sup>CD45RO<sup>−</sup>CD45RA<sup>+</sup> (memory) T cells.

![Figure 1](http://www.jci.org)

Figure 1. Three-color immunofluorescence analysis of PBMCs of adult donor D2. CD8<sup>+</sup>-enriched cells were simultaneously stained with tricolor-conjugated CD8 in combination with FITC-conjugated CD45RA and PE-conjugated CD45RO mAbs. Cells were gated on size and tricolor fluorescence. Three distinct populations could be defined within CD8<sup>+</sup> T cells from adult PBMCs: CD45RO<sup>+</sup>CD45RA<sup>−</sup> (RO<sup>+</sup>RA<sup>−</sup>), CD45RO<sup>−</sup>CD45RA<sup>+</sup> (RO<sup>−</sup>RA<sup>+</sup>), and CD45RA<sup>−</sup> CD45RO<sup>−</sup> (RA<sup>−</sup>RO<sup>−</sup>) cells.

![Figure 2](http://www.jci.org)

Figure 2. CDR3 length distribution in TCRBV6 within different T cell populations of HLA B<sup>8+</sup>, EBV-seropositive (D1, D2), and EBV-seronegative (D3, D4) adults. (A) Profiles are displayed of fluorescence intensity (arbitrary units) as a function of CDR3 size (amino acids) for TCRBV6 of unsorted PBMCs and sorted populations of CD8<sup>+</sup>CD45RA<sup>−</sup>CD45RO<sup>−</sup> (RO<sup>−</sup>RA<sup>−</sup>) and CD8<sup>+</sup>CD45RO<sup>−</sup>CD45RA<sup>−</sup> (RO<sup>−</sup>RA<sup>−</sup>) cells. CDR3 length, defined by Chothia et al. (43), is deduced from the fragment size. Each CDR3 peak is spaced three nucleotides or one amino acid apart. (B) Relative percent peak intensities derived from the CDR3 length profiles of the CD8<sup>+</sup>CD45RO<sup>−</sup>CD45RA<sup>−</sup> (RO<sup>−</sup>RA<sup>−</sup>) subset of each adult are reported. Relative peak intensities are calculated as described in Methods.

EBV-specific TCR clonotypes account for the TCRBV6 expansions in the blood. Repertoire diversity was next examined at the clonotype level by determining the TCR V-D-J junctional region sequences of recombinant clones that contained TCRBV6 inserts from the different T cell populations (Fig. 3, A–C). In the CD8<sup>+</sup>CD45RO<sup>−</sup>CD45RA<sup>−</sup> subset of both seropositive donors, a striking percentage of the total TCRBV6 repertoire was found to be dominated by a BV6S2/BJ2S7 rearrangement that was identical at the amino acid level.
Figure 3. Diversity of TCRBV6 junctional region sequences within different T cell repertoires of HLA B8+ EBV-seropositive, and EBV-seronegative adults. The V-D-J junctional region amino acid sequences of recombinant BV6 clones are shown for unsorted PBMCs and sorted populations of CD8+CD45RA+CD45RO− (RA1 RO2) and CD8+CD45RO+CD45RA− (RO1 RA2) cells of EBV seropositive adults D1 (A) and D2 (B) and the seronegative adult D3 (C). The frequency (n) of each clone was determined as detailed in Methods. For comparison, the V-D-J junctional region of the public FLRGRAYGL-specific clonotype is also shown at the bottom of A and B. Rearrangements corresponding to the public FLRGRAYGL-specific clonotype are highlighted in bold type. In donor D2 (B) a variant of the public clonotype (clone AS27), involving a single amino acid substitution (L to S) in the CDR3 region, was identified that is known to be FLRGRAYGL specific (33). For each clone, the deduced amino acid sequence of the CDR3 loop, defined according to Chothia et al. (43), is shown putatively supported by two framework branches (FW). Out-of-frame rearrangements are designated nonfunctional. Designations for TCRBJ gene elements follow that of Toyonaga et al. (44) and the TCRBV6 subtypes were assigned according to Arden et al. (22). The nucleotide sequences of each of these clones are available from EMBL/GenBank/DDBJ under accession numbers AJ224204–AJ224305.
to the public EBV-specific TCRB chain (Fig. 3, A and B); the impact of this clonotype was 61% dominance (8/13 clones; LC32) in the case of donor D1 and an even higher 83% dominance (15/18 clones; AS26) in donor D2. This expansion did not result from preferential amplification of either the BV6S2 subfamily or of the SLGQAYEIQ CDR3 sequence within the BV6S2 subset since neither of these were found to be overrepresented within the PBMCs and naive populations of either seropositive donor (Fig. 3, A and B) and of the HLA B8* EBV- seronegative donor, D3 (Fig. 3 C). Further confirmation that this TCRB chain’s functional identity was the public EBV-specific clonotype was that for each individual, it displayed a unique codon usage within the V-D-J junctional region that corresponded precisely to the TCRB chain sequence of FLRGAYGL-specific CTLs that previously had been functionally characterized from donors D1 and D2 (data not shown; available from accession numbers AJ224278, AJ224302, and AJ224303) (21) and that it was specific to the two HLA B8* EBV-infected individuals and was not found in any T cell population within the uninfected HLA B8* donor, D3 (Fig. 3 C). Overall, junctional region sequencing showed that the dominant peaks obtained from CDR3 length analysis were clonal and that they corresponded precisely to the public TCRB chain rearrangement that recognizes the EBV-encoded epitope, FLRGAYGL. The PBMCs and naive CD8* CD45RA+CD45RO- repertoires of both virus carriers expressed a polyclonal distribution, showing no signs of dramatic clonal predominance (Fig. 3, A and B). Analysis of data from the seronegative donor, D3, also showed a high degree of clonotype diversity within the PBMCs and CD8* CD45RO+ CD45RA- and CD8* CD45RA+CD45RO- T cell subsets (Fig. 3 C); the only evidence of repertoire perturbation within the memory compartment was a 21% (4/19 clones) expansion of a functionally undefined TCRBV6/V6S2/J2S3 rearrangement (clone JS36). Interestingly, the EBV-specific BV6S2/J2S7 rearrangement was detected, albeit at low levels, within the naive compartment of seropositive donor D2 (Fig. 3 B).

Repeated repertoire analysis on seropositive donor D2 after 7 mo showed that the EBV-specific clonotype’s impressive restriction on TCRBV6 diversity was persistent. Fig. 4 shows an identical CD8* CD45RO+CD45RA- repertoire profile to that obtained 7 mo earlier (Fig. 2 A), with > 70% of clonotypes being dominated by an 8-amino acid CDR3 length expansion (Fig. 4 A) that was identified by sequencing as the BV6S2/J2S7 EBV-specific clonotype (Fig. 4 B).

To fully confirm that the clonal expansions within the memory repertoire represent the public EBV-specific clonotype, the FLRGAYGL-specific cytotoxicity of the memory and naive CD8* populations from seropositive adult D2 was assessed (Fig. 5). After several weeks of in vitro stimulation, unsorted PBMCs and the CD8*CD45RO+CD45RA- subset were found to efficiently lyse target cells sensitized with FLRGAYGL peptide, whereas the CD8* CD45RA+CD45RO- subset showed no detectable cytotoxicity (Fig. 5). These results correlated with the clonotype data that showed a predominance of the EBV-specific BV6S2/J2S7 clonotype within the CD8* CD45RO+CD45RA- subset. In contrast, low lying pools of virus-specific T cells such as those that were detected in the naive subset of this donor (Fig. 3 B) are likely to go undetected since they fall below the sensitivity levels of the cytotoxicity assay. Overall, these studies confirmed a functional link for the monclonally expanded T cells responsible for major repertoire distortions in healthy HLA B8* adults with EBV specificity.

Finally, to measure the full extent of the public EBV-specific clonotype’s impact on TCRBV6 repertoire diversity we analyzed the intermediate stained, triple-positive CD8* CD45RO+ CD45RA+ T cells (Fig. 1) from both HLA B8* seropositive donors for CDR3 length and clonotype distribution (Fig. 6). At present it is unclear whether these T cells represent a transitional phenotype between the naive and memory subsets, or whether they contain memory cells that have reverted to a naive phenotype (28–30). In seropositive donor, D1, a skewed CDR3 profile was obtained (Fig. 6 A), but these expansions did not correspond in length (Fig. 6 A) nor in rearrangement sequence (Fig. 6 B) to the public EBV clonotype. Interestingly, one of these functionally unidentified expansions (clone LC38) was found only within the dual-positive CD45RO* CD45RA- subset (Fig. 6 B) and was not detected in either the naive or memory subsets (Fig. 3 A). The CD8* CD45RO+ CD45RA- repertoire of seropositive donor D2 also displayed evidence of repertoire distortion (Fig. 6 A), but in this donor...
one of the expansions proved to be the EBV-specific clonotype (Fig. 6B). Overall, these results show that not only do EBV-specific memory CTLs dominate the CD45RO+ compartment of CD8+ T cells, they can also impact on repertoire diversity within the intermediate CD45RO+CD45RA− subset of T cells.

Discussion

This study uses a novel approach in monitoring antigen-specific T cells within the peripheral blood that provides evidence of a functional link between persistent EBV infection and T cell expansions in healthy adults. A public BV6S2/BJ2S7 clonotype that recognizes the EBV-encoded class I–restricted epitope, FLRGRAYGL, was found to dominate the TCRBV6 repertoire in the CD8+CD45RO+ memory compartment of normal, EBV-seropositive individuals. So dramatic was the impact of selection of this EBV-specific clonotype that it occupied as much as 80% of the entire TCRBV6 family message. Dominant expansion of a single clonotype within TCRBV6 is significant given that this is one of the most prevalent of the known 25 functional BV families expressed in the normal human repertoire (31, 32), containing a higher than average number of seven functional subfamilies (22). Therefore, selection of the EBV-specific clonotype dramatically distorts a large and diverse BV population. Whether expansion of this clonotype increases the percentage of CD8+ T cells expressing BV6 is at present unknown and is difficult to determine given the lack of antibodies specific for the BV6S2 subfamily that is predominantly rearranged to BJ2S7 within the public EBV-specific clonotype. However, from a previous study that monitored the relative expression of the BV6 family in healthy, HLA B8+ EBV-seronegative and EBV-seropositive adults, no selective increase in TCRBV6 frequency was found to be associated with long-term exposure to EBV (33).

The identification of EBV-specific TCR clonotypes within the CD8+ T cell memory subset is consistent with earlier studies that functionally identified EBV-specific CTLs predominantly within the CD8+CD45RO−CD45RA+ compartment (34). There was also phenotypic heterogeneity between different individuals in detecting the public EBV-specific clonotype within the dual-positive, CD45RO+CD45RA+ cells. The significance of this phenotypic heterogeneity is at present unknown, but it may reflect differential levels of antigen-specific T cell activation in vivo that alter the turnover and/or recycling of antigen-specific cells between the naive and memory pools. Indeed, recent studies by Bunce and Bell (35) suggest that antigen-specific, memory CD4+ T cells are divided between two

Figure 5. EBV-specific cytotoxicity of different T cell populations of HLA B8+. EBV-seropositive adult D2. Specific lysis by unsorted PBMCs and sorted CD8+CD45RO+CD45RA− (RO+RA−) and CD8+CD45RA+CD45RO− (RA+RO−) cells of HLA B8+ PHA blasts, with (filled bars) and without (open bars) adsorbed peptide, FLRGRAYGL. Effectors were tested in standard 4-h 51Cr-release assays. Effector/target ratio: 10:1.

Figure 6. Diversity of the TCRBV6 repertoire within the intermediate stained CD8+CD45RO+CD45RA− (RO+RA−) repertoires of HLA B8+, EBV-seropositive donors D1 and D2. (A) CDR3 length profiles are displayed of fluorescence intensity (arbitrary units) as a function of CDR3 size (amino acids) for TCRBV6. (B) The V-D-J junctional region amino acid sequences of recombinant BV6 clones are shown. TCRBV and J gene segments and CDR3 region loops are presented and assigned as outlined in the legend to Fig. 3. The frequency (n) of each clone was determined as detailed in Methods. The nucleotide sequences of each of these clones are available from EMBL/GenBank/DDBJ under accession numbers AJ009914–AJ009929.

EBV+ ADULT D1

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different compartments, a CD45RA+ and a CD45RO+ subset. In this model antigen restimulation is required for stable maintenance of these memory cells within the CD45RO+ pool. Variable expression of CD45RO and CD45RA may also reflect functional differences among clonotypically identical T cells such as effector and long-term memory functions. A similar observation has been made recently by Callan et al. (36) using soluble tetrameric MHC for detecting virus-specific T cells in primary EBV-infected donors clinically diagnosed with infectious mononucleosis (IM). In these studies they found that in individuals several years after IM, a subset of virus-specific T cells expressing CD45RA could be detected. This was unlike the situation in IM where the majority of antigen-specific cells expressed CD45RO. Whether, as in our study, these cells co-express CD45RA and CD45RO was not determined, but this observation could prove to be important in understanding the maintenance and stability of clonotypic expansions within the circulation.

It has been postulated that life-long exposure to repeated or persistent subclinical virus infection may play a key role in the genesis of dramatically expanded T cell populations within healthy individuals (8, 9, 12, 37). Indeed, several features of CD8+ T cell expansions, including their predominance and persistence within the activated/memory repertoire, are consistent with their development through environmental exposure. We provide evidence in this study that class I-restricted memory CTLs with specificity for EBV contribute to the major expansions that have been documented in the peripheral blood repertoires of healthy individuals. The maintenance of high levels of EBV-specific memory CTLs in healthy individuals throughout life (24) reflects their essential immunosurveillance role in controlling virus infection, a finding that is also characteristic of the long-term persistence of expanded clonotypes in healthy individuals. Indeed, the impressive ability of EBV-specific CTLs to cause complete regression of virus-induced lymphoproliferative lesions in immunosuppressed patients (38, 39) strongly suggests that their prevalence and dramatic impact on repertoire diversity are important for maintaining the life-long asymptomatic virus–host balance in normal health. Overall, EBV immunity is likely to have a major impact on repertoire diversity within a large proportion of the human population given the ubiquitous nature of this herpesvirus infection and the unprecedented level of TCR restriction that appears to be associated with the long-term memory response. We provide evidence in this study that class I–restricted memory CTLs expressing CD45RA and CD45RO were not determined, but this observation could prove to be important in understanding the maintenance and stability of clonotypic expansions within the circulation.

The identified origin of these stably expanded clonotypes and their role in maintaining a balanced host–virus relationship in normal health is extremely important to studies interpreting patterns of clonal dominance in disease. Indeed, distinct patterns of clonal restriction and structural evidence of antigen specificity within the TCR V, J, and CDR3 regions have often been interpreted as evidence for a role of these T cells in disease pathogenesis. However, our findings emphasize the importance of HLA restriction and EBV immunostatus on the outcome of studies comparing peripheral blood repertoire diversity in health and disease. We would also predict that other highly focused, immunodominant memory T cell responses are likely to dramatically skew TCR repertoire distribution in healthy individuals. For example, dominant public TCR responses have also been reported in influenza virus infection (41). Ultimately, knowledge of T cell specificity is needed to address the issue of an immunoregulatory role versus stimulation by unrelated factors of expanded T cells in disease. Interestingly, this study also shows that the CD8+ T cells with an intermediate CD45RO+CD45RA+ phenotype may also harbor major clonotype expansions that are precluded from standard analyses that define strongly positive CD45RA+ and CD45RO+ phenotypes as naive and memory cells, respectively. More recent studies that have used CD45RA and CD27 expression to separate naive, memory, and effector human CD8+ T cells within the circulation (42) might also prove useful in monitoring expansion development and in unraveling their functional significance. Overall, this first identified link for CD8+ T cell expansions provides the basis for future studies monitoring the development of extreme clonal dominance within the normal repertoire and the effects of aging and disease on repertoire progression.

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