The Cytotoxic T-Cell Response to Herpes Simplex Virus Type 1 Infection of C57BL/6 Mice Is Almost Entirely Directed against a Single Immunodominant Determinant

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Many virus infections give rise to surprisingly limited T-cell responses directed to very few immunodominant determinants. We have been examining the cytotoxic T-lymphocyte (CTL) response to herpes simplex virus type 1 (HSV-1) infection. Previous studies have identified the glycoprotein B-derived peptide from residues 498 to 505 (gB498-505) as one of at least three determinants recognized by HSV-1-specific CTLs isolated from C57BL/6 mice. We had previously found that in vitro-derived CTLs directed to gB498-505 show a characteristic pattern of T-cell receptor (TCR) usage, with 60% of gB498-505-specific CD8+ T cells expressing BV10+ TCR β chains and a further 20% expressing BV8S1. In this report, we confirm that this TCR V-region bias is also reflected in the ex vivo response to HSV-1 infection. A high proportion of activated CD8+ draining lymph node cells were found to express these dominant V regions, suggesting that a substantial number of in vivo responding T cells were directed to this one viral determinant. The use of an HSV-1 deletion mutant lacking the gB498-505 determinant in combination with accurate intracellular gamma interferon staining allowed us to quantify the extent of gB-specific T-cell dominance. Together, these results suggested that between 70 and 90% of all CD8+ HSV-1-specific T cells target gB498-505. While deletion of this determinant resulted in an attenuated CD8+ T-cell response, it also permitted the emergence of one or more previously unidentified cryptic specificities. Overall, HSV-1 infection of C57BL/6 mice results in an extremely focused pattern of CD8+ T-cell selection in terms of target specificity and TCR expression.

While some virus-specific cytotoxic T lymphocyte (CTL) responses show considerable diversity at the level of determinant recognition, many are confined to an extremely restricted number of antigenic targets. Both the helper T-cell and CTL populations activated by even the most complex of pathogenic agents are frequently directed to less than a handful of major or immunodominant determinants (49, 58). Such focusing on just a few key determinants provides a simple means for viruses to escape immune surveillance. Even the most complex virus can potentially evade T-cell recognition by limited mutations within these few dominant determinants (2, 18, 42). These types of CTL escape variants are found within human immunodeficiency virus-infected patients, where they are thought to contribute to progressive immune evasion with a corresponding gradual worsening of disease (6, 35, 43). Alternatively, this immunodominance can potentially provide advantages to the infected individual, such as the ability to mount a rapid and high-affinity response while minimizing the possibility of cross-reactivity with self components (20).

Immunodominance is likely to arise as a consequence of a combination of factors which span the complete class I-restricted presentation and T-cell recognition process. Firstly, the strength of peptide-class I interaction has been shown to be a key parameter in determining immunodominance (13, 50, 54, 55), while antigen processing can also play an important role in controlling the hierarchy of presented peptides (41). In addition, there is emerging evidence that competition at the level of T-cell–antigen-presenting cell interaction could potentially influence the composition of the responding CTL populations (11). Finally, T-cell receptor (TCR) expression and selection appear to make critical contributions toward the extent of determinant dominance in what would otherwise be a complex immune response (58).

Of all these parameters, it has proven most difficult to assess the TCR contribution to immunodominant T-cell responsiveness. Firstly, the extensive and detailed characterization of a T-cell repertoire specific for any given peptide represents a major undertaking, especially at the clonal level. Combined with this, antiviral CTLs of a single specificity can be quite diverse in terms of their TCR expression (8, 14, 26, 31). Most importantly, it is often difficult to determine the relationship between antigen-specific TCR selection and the preexisting repertoire found within the naive T-cell pool, especially when the specificity is associated with a highly diverse TCR expression.

Given this, antigens that select restricted patterns of TCR expression are providing important insights into how the TCR repertoire can potentially influence immune responsiveness to complex pathogens (8, 9, 51). We have characterized CTLs selected by a murine H-2d-restricted determinant from the herpes simplex virus (HSV) glycoprotein B (gB) encompassing residues 498 to 505 (gB498-505) (15, 16). These CTLs are known to protect mice against lethal infection with this virus (4, 5, 25, 34). Extensive analysis of TCR expression at both the population and the clonal level has revealed an unusually consistent pattern of TCR V-region utilization combined with a high degree of diversity in terms of clonally distributed TCR se-
quence expression (15, 16, 27, 53). These repeating patterns of TCR element usage within the gB response provide an opportunity to examine how the naive T-cell repertoire composition can affect the CTL response directed to this virus. An important element in this analysis is an accurate assessment of the gB determinant’s contribution to the overall HSV type 1 (HSV-1)-specific immune response. Limiting dilution analyses have previously suggested that gB_{498–505} peptide-specific cells comprise less than a quarter of the HSV-specific CTL population (45, 57). In this report, we have reexamined this issue by quantifying the relative contribution of gB_{498–505} with preferential TCR V-region usage and gamma interferon (IFN-γ) expression within the lymph nodes draining the site of primary cutaneous HSV-1 infection. In contrast to previous reports, we have found that the gB_{498–505} determinant is truly immunodominant, with up to 90% of all HSV-1-specific CD8+ T cells isolated from infected C57BL/6 mice being specific for this single viral determinant.

MATERIALS AND METHODS

**Mice.** Female C57BL/6 mice at 6 to 8 weeks of age were purchased from the Monash University Central Animal Facility. Mice were immunized intradermally in the hind feet with 4 μl phosphate-buffered saline (PBS) per mouse on September 21, 2017 by guest http://jvi.asm.org/ Downloaded from

**Peptide and cells.** Primary mouse embryonic fibroblasts (PMEF) from day 13 C57BL/6 embryos were generated in the laboratory by Claerwen Jones and propagated in Dulbecco’s modified Eagle medium supplemented with 10% fetal bovine serum (FBS) (Swinburne University, Melbourne, Australia).

**Viruses.** The KOS strain of HSV-1 was propagated and titrated in Vero cells. The KOS-derived gB-deletion mutant strains KΔ318 and KΔ5C (21) were grown and titrated by using the gB-producing D6 cell line, which complements the gene inactivation. Both mutant viruses were also checked for the absence of plaque formation on Vero cells to exclude any possibility of reversion to wild type.

**Ex vivo analysis of BV element expression.** Draining popliteal lymph nodes were removed from mice immunized 5 days previously with either the KOS, KΔ318, or KΔ5C virus or gB_{498–505} peptide emulsified in CFA. Lymph node cells were triple labelled with anti-CD3-phycoerythrin (PE) (Pharmingen, San Diego, Calif.), anti-CD8-allophycocyanin (Pharmingen); and a panel of biotinylated antibodies specific for TCR BV elements, BV2, BV4, BV7, BV10, BV11, BV12 from Pharmingen and BV7 from Caltag, followed by streptavidin-fluorescein isothiocyanate (FITC) (Molecular Probes, Eugene, Oreg.). The BV8 and BV5 subfamily member staining was carried out with hybridoma supernatants from antibodies MR9-4 (BV5S1 specific) (3), MR9-4 (BV5S1 and BV5S2 specific) (3), MR5-2 (BV5S1 and BV5S2 specific) (28), F23.2 (BV5S2 specific) (29), and F23.3 (BV8S1, BV8S2, and BV8S3 specific) (52) followed by the FITC-labelled isootype-specific secondary antibodies (Pharmingen). After staining, cells were analyzed by flow cytometry with a FACScalibur (Becton Dickinson) cell sorter, and data analysis was performed with CELLQuest software (Becton Dickinson). Viable cell counts were determined for all samples on the basis of trypan blue exclusion prior to stimulation. The number of CD8+ cells producing IFN-γ was calculated by multiplying the percentage of IFN-γ+ cells by the total cell number per mouse determined by the cell counts.

**RESULTS**

The accumulation of CD8+ T cells expressing TCR BV10 and BV8S1 in the lymph nodes draining the site of HSV-1 infection is a direct consequence of gB specificity. We have previously shown that cultured CTL lines specific for the gB_{498–505} determinant consistently show a biased expression of two major TCR β-chain elements (16). Nearly 60% of CD8+ gB-specific T cells derived from mice infected with HSV-1 were found to express TCR BV10+ β chains while a further 20% contained the BV8S1 element. This in vitro-derived V-element bias was also evident in T cells isolated directly ex vivo after footpad infection with HSV-1. Figure 1 shows the relative expression of each of 12 TCR BV elements on activated CD8+ T cells isolated from the popliteal lymph nodes from mice immunized in the hind feet with the KOS strain of HSV-1. In this case, interleukin-2 receptor (CD25) expression was used as a marker of T-cell activation. These results reveal a preferential accumulation of BV10 and, to a lesser extent, of BV8S1 cells within the CD25+ CTL subset. This is largely consistent with an earlier finding of a BV10+ TCR accumulation in the CD8+ T-cell blast subset (15) and emphasizes that this bias represents a preferential activation of the gB-specific T cells within the lymph nodes draining the site of HSV-1 footpad infection.

To further examine the association between gB specificity and BV10 accumulation, we examined the CTL response to KOS-derived gB-deletion mutant strains of HSV-1, KΔ5C and KΔ318 (Fig. 2). The KΔ5C deletion encompasses residues 43 to 595, which include the immunodominant epitope gB_{498–505} peptide, while gB residues 616 to 711 are deleted in the KΔ318 mutant, so that the truncated gene product still

![FIG. 1. TCR BV expression by CD25+ CD8+ T cells following HSV-1 infection. Draining popliteal lymph nodes were harvested at the peak of infection from mice immunized in the hind feet 5 days previously with the KOS strain of HSV-1. Lymph node cells were stained for CD8 and CD25 expression in combination with BV-element-specific antibodies and then subjected to flow cytometric analysis. BV-element expression in the CD25+ subset, shown by the white bars, corresponds to the expression level seen in unimmunized controls (data not shown).](http://jvi.asm.org/Downloadedfrom)
contains the $K^b$-restricted CTL determinant. It should be noted that neither the $K\Delta 318$ nor the $K\Delta 5C$ strain expresses a functional gB, and consequently, both can undergo only a single round of replication following infection. Mice were immunized with either the wild-type KOS strain of HSV-1 or the gB-deletion mutant strains $K\Delta 318$ and $K\Delta 5C$. Figure 3 shows that mice immunized with the $K\Delta 5C$ virus generate no gB-specific cytotoxicity, whereas the $K\Delta 318$ virus gives a strong gB-specific CTL response equivalent to that of immunization with wild-type KOS virus. The level of cytotoxicity directed against a subdominant determinant from the viral ribonucleotide reductase RR822–829 (48) remains the same across all three virus strains and serves as a control to demonstrate effective infection and some CTL activation by the $K\Delta 5C$ mutant. Analysis of BV-element expression on cells isolated from mice immunized with $K\Delta 5C$ showed no evidence for any other V-element bias occurring in the absence of a gB-specific response (data not shown). In contrast, lymph node cells isolated from $K\Delta 318$-infected animals showed preferential TCR BV10 accumulation approaching the level seen after KOS immunization (Fig. 4). It is also interesting to note that the level of BV10 accumulation following immunization with the gB<sub>498–505</sub> peptide is equivalent to that achieved following immunization with the whole virus, arguing that CD8<sup>+</sup> T cells directed to the gB<sub>498–505</sub> determinant must represent a considerable proportion of all C57BL/6-derived CTLs directed to the whole HSV-1.

The gB-derived determinant (gB<sub>498–505</sub>) is the major target recognized by HSV-1-specific CD8<sup>+</sup> T cells. The preceding data suggesting a significant gB dominance was in conflict with previous estimates of its contribution to the overall HSV-1-specific CTL response. Early limiting dilution analyses showed that only 5 to 25% of virus-specific CTLs derived from HSV-1-infected C57BL/6 mice were specific for the gB<sub>498–505</sub> determinant (45, 57). However, we have consistently found that, on average, more than 40% of activated CD8<sup>+</sup> T cells from the draining lymph nodes preferentially express BV10<sup>+</sup> β chains (Fig. 4 and data not shown) with highly conserved junctional sequences indicative of gB-specific CTLs (15). Given that approximately 60% of in vitro-derived CTL lines directed to gB<sub>498–505</sub> express these same TCR β-chains (16), our results

![Figure 2: Schematic diagram of the gB-deletion mutant strains $K\Delta 5C$ and $K\Delta 318$. The $K\Delta 5C$ mutant lacks amino acids 43 to 595, which encompass the gB<sub>498–505</sub> determinant, while the truncated polypeptide produced by the $K\Delta 318$ mutant lacks only amino acids 616 to 711 and thus retains the determinant.](image)

![Figure 3: CTL target specificities following cutaneous infection with KOS, $K\Delta 318$, or $K\Delta 5C$ virus. Mice were immunized in the hind feet with wild-type KOS or gB-deletion mutant viruses, and the draining popliteal lymph nodes were removed 5 days postinfection. Lymph node cells were cultured for 3 days in the absence of exogenous antigen and then assayed in a 4-h $^{51}$Cr-release assay for reactivity against EL4 cells pulsed with 1 μg of either the gB<sub>498–505</sub> or RR<sub>822–829</sub> peptide per ml.](image)
suggest that CTLs targeting this one peptide must represent at least two-thirds of the total HSV-specific response. This is an underestimate since it excludes nonspecific lymph node T-cell activation. Even at its lowest, this value is a significantly higher proportion of the overall HSV-1 response than that estimated from the earlier limiting dilution analyses.

To clarify this issue, we quantified the relative contribution of gB-specific T cells to the overall virus-specific CD8+ T-cell response following immunization with each of the mutant virus strains by measuring IFN-γ production within lymph node cells draining the site of infection. Popliteal lymph node cells taken at day 5 postinfection, which is the peak of the CTL response (26a), were stimulated for 6 h with PMEF loaded with the gB498–505 or RR 822–829 peptide or PMEF infected with the KOS virus to induce IFN-γ production. Intracellular IFN-γ staining in CD8+ T cells could be detected only following stimulation with appropriately presented PMEF, for example, those infected with HSV-1 (compare Fig. 5A with 5B). Moreover, all IFN-γ-expressing CD8+ T cells were found to coexpress CD25 (Fig. 5C), consistent with our previous report that the gB-specific cells are found within the activated T-cell subset (15).

The results presented in Fig. 6 show that the viruses containing the gB determinant, KOS and KΔ318, induce nearly equal proportions of IFN-γ-producing CD8+ T cells when stimulated with either the isolated gB498–505 peptide or cells infected with the complete HSV-1 virus. From the results presented in Fig. 6, we estimate that about 92 and 95% of HSV-1-specific CD8+ T cells induced by KOS and KΔ318 infection, respectively, are directed to the gB498–505 determinant. T cells specific for the RR822–829 determinant make up a relatively minor proportion of responding lymph node cells, with less than 0.5% of all lymph node CD8+ T cells being specific for this determinant. A third H-2b-restricted determinant derived from HSV-1 ICP27 (ICP27 445–452) has also been identified (44), although we could find no IFN-γ+ T cells directed to this determinant (data not shown). Immunization with the gB498–505 deletion mutant KΔ5C induced a lower, but still respectable, level of intracellular IFN-γ staining when the CD8+ lymph node cells were stimulated with HSV-1-infected PMEF, but gB activity was absent from this response (Fig. 6). Surprisingly, while the KΔ5C mutation virtually abolished the response to the dominant gB498–505 determinant, the emerging specificities did not appear to be directed to the previously identified sub-
dominant determinant RR822–829 (Fig. 6) or ICP27445–452 (data not shown). Consequently, deletion of the immunodominant gB determinant from the HSV-1 genome reveals the existence of one or more hidden or cryptic class I-restricted determinants expressed by this virus.

Finally, the gB dominance of the HSV-1 CD8^+ T-cell response was confirmed by determining the proportion of lymph node cells expressing IFN-γ after in vitro stimulations with either the gB 498–505-containing viruses (KOS and K\textsubscript{D}318) or the K\textsubscript{D}5C variant, which lacks this determinant (Fig. 7). Lymph node cells from mice infected with the replication-defective mutant strains were used for this experiment. The results clearly showed that stimulation with K\textsubscript{D}5C-infected PMEF caused a significant reduction in the K\textsubscript{D}318-specific IFN-γ response, confirming that gB\textsubscript{498–505} dominates the CD8^+ T-cell response when it is present within the immunizing virus. It should also be noted that, while gB accounts for the bulk of the response, 20 to 30% of K\textsubscript{D}318-specific CTLs appear to be responding to non-gB determinants, although this may be due in part to an increased representation of non-gB determinants on K\textsubscript{D}5C-infected stimulator cells.

Deletion of the immunodominant gB\textsubscript{498–505} determinant attenuates the CD8^+ T-cell response to HSV-1 in C57BL/6 mice and results in expansion of T cells specific for one or more cryptic determinants. The data presented in Fig. 6 suggests that removal of the immunodominant gB\textsubscript{498–505} determinant results in expansion of CTLs directed to a cryptic determinant within HSV-1. However, the actual level of expansion cannot be assessed from the proportion of cells expressing IFN-γ since the deletion viruses induce a lower level of T-cell activation and lymph node cell recruitment compared with the wild-type KOS virus (data not shown). Therefore, rather than presenting the results as proportions, we examined the total number of HSV-1-specific, IFN-γ-producing CD8^+ T cells within lymph nodes draining tissues infected with the KOS virus and two mutant strains of virus (Fig. 8). While Fig. 6 shows that the majority of HSV-1-specific CD8^+ T cells from K\textsubscript{D}5C-immunized animals were now specific for an otherwise cryptic determinant, Fig. 8 shows that, in terms of actual IFN-γ^+ CD8^+ T-cell numbers recovered from responding lymph nodes, this response was less than half that of K\textsubscript{D}318 virus-immunized mice. Comparison of results for KOS and K\textsubscript{D}318 shows the attenuation associated with differences in virus replication, since both give responses that are largely gB\textsubscript{498–505} specific (Fig. 6) while only KOS is able to undergo multiple rounds of replication. In contrast, the decrease in IFN-γ^+ CD8^+ T-cell numbers shown by comparing K\textsubscript{D}318 and K\textsubscript{D}5C comes about from the deletion of gB residues 43 to 495, which include the gB\textsubscript{498–505} CTL determinant. Regardless of the attenuation, these results still represent an overall increase in otherwise silent T cells specific for determinants other than the usually dominant gB\textsubscript{498–505}.

**DISCUSSION**

Our results show that the primary HSV-1-specific CD8^+ T-cell response to cutaneous HSV-1 infection is largely directed against a single immunodominant gB-derived determi-
null. Even our lowest estimation, based on preferential V-region usage, necessitates that more than two-thirds of HSV-1-specific T cells are specific for the gB498–505 determinant, while the IFN-γ results suggest that this peptide is likely to be targeted by 70–90% of all virus-specific CD8+ T cells. This range is at odds with previous limiting dilution analyses which predicted that 5 to 25% of HSV-1-specific CTLs isolated from lymph nodes draining the site of infection were directed to this determinant (45, 57). One possible explanation for the differences between our results and those published previously is that only a small proportion of gB-specific responders detected by TCR or IFN-γ analyses are actually cytotoxic, which was the parameter used in the limiting dilution assays. Alternatively, it is now recognized that the limiting dilution analyses, as distinct from direct determination with TCR expression or IFN-γ production, grossly underestimate the actual proportion of specific precursors within a responding cell population (10, 11, 22, 39).

There are two other H-2b-restricted HSV-1-derived determinants that have so far been identified, RRA228-829 and ICP27,445-452 (44, 48), and these were expected to make some contribution to the T-cell response to virus infection. Here we show that the RRA228-829-specific T cells are found at relatively low, but detectable, frequencies. In contrast, we could not detect any ICP27,445-452-specific T cells, either by IFN-γ production or by cytotoxicity assays (data not shown). Differences in virus substrate usage or subtle host variations may explain the observed lack of ICP27 response in our hands. Regardless, our results provide direct quantitation of the frequency of T cells responding to the dominant gB498–505 determinant and suggest that they make up the bulk of HSV-1-specific T cells as well as a major proportion of the total activated CD8+ T-cell subset found within lymph nodes draining the site of primary infection. While the estimates of absolute responding cell numbers are greater than those calculated from previous limiting dilution analyses (45, 57), they are largely in line with our earlier predictions based solely on direct TCR sequence analysis of the cutaneous HSV-1 response (15). This study suggested that specific T cells make up a larger proportion of responding cell populations than previously appreciated, subsequently documented in more detail for CTL responses involving systemic infections (10, 11, 39).

Given the complexity of HSV-1, which encodes over 100 viral products (47), it may appear unexpected that virtually the entire HSV-1-specific CTL response is directed against a single class I-restricted determinant. However, dominance by one or a very few key determinants is often observed in T-cell responses to even the most complex antigen (49, 58). Even so, the gB498–505-specific immunodominance highlights a number of interesting features. For example, antiviral responses tend to be directed to proteins synthesized during the earliest phases of the viral replication cycle (17), and yet the gB protein is produced relatively late in infection (47). There was a formal possibility that the immunogenic components might have come from the virion itself rather than from de novo protein synthesis, as noted in the CTL response to the betaherpesvirus human cytomegalovirus (33). This would have explained why gB could so efficiently generate a CTL response. However, immunization experiments involving the mutant viruses KΔ318 and KΔ5C clearly showed that at least for these variants the gB-specific response is reliant on de novo protein synthesis. Both these replication-deficient gB-deletion mutants acquire the functional gB molecules necessary for infection from the D6 virus-packaging cell line (21), but only the determinant-expressing KΔ318 was able to prime gB498–505-specific T cells (Fig. 3). Significantly, not only was the anti-gB response maintained with the replication-defective KΔ318 virus but it was surprisingly potent compared to that of a fully competent par-
ent virus. Efficient CTL induction has been reported previously for another replication-defective HSV-1 strain (36). In that case, it was suggested that prolonged infection by the input variant was the major contributor to the efficiency of this immune response (37).

While the results clearly emphasize the importance of the gB498–505 determinant, its elimination in the KΔ5C mutant revealed the existence of an otherwise silent CTL determinant. Interestingly, there was little increase in the response to the already-defined subdominant determinant R532–539. Lewicki et al. (30) showed that mutation of all three codominant determinants from lymphocytic choriomeningitis virus (LCMV) resulted in the emergence of an otherwise hidden response to “cryptic” epitopes already present in the virus. A similar emergence of undefined cryptic determinants is also noted here, although the deletion of the dominant gB498–505 nonetheless results in some level of immune response attenuation. For example, the total IFN-γ response by CD8+ T cells from animals immunized with the gB498–505-deletion virus KΔ5C was about half that found for the similarly defective mutant, KΔ318, that contains the immunodominant determinant. While this decrease is modest, it nonetheless provides evidence that elimination of a dominant determinant does make the resultant variant “less fit” at generating an effective immune response. This type of response attenuation has been noted in other systems involving mutations of immunodominant, but not subdominant, target peptides (38, 40).

Probably the most striking feature of the dominant gB498–505-specific response is the highly restricted pattern of TCR usage within the responding population. CTL responses to immunodominant determinants are characterized by both restricted (1, 19, 32, 46, 51) and unconstrained (8, 12, 14, 26) patterns of TCR usage. We previously found that nearly 80% of all gB-specific CTLs use the two preferred BV elements, BV81 and BV10 (16). Combined with the data presented here showing up to 90% of all HSV-specific CTLs being directed to this one determinant, these two V regions define over 80% of all CD8+ T cells that respond to this virus in C57Bl/6 mice. A similar level of V-region bias is also found in one of the few other antiviral CTL responses showing similar levels of overwhelming single-determinant dominance. Over 90% of all LCMV-specific CTLs derived from BALB/c mice are directed to a single nucleoprotein-derived peptide (39, 56), and three BV elements encompass 70% of the overall antiviral response (51). Moreover, both the LCMV (51) and HSV (16) TCR BV biases are associated with highly restricted junctional sequences encoding the TCR β chain CDR3, which is involved in direct contact with the presented peptide (23, 24, 53). Despite this, there is considerable diversity within the remainder of the β-chain sequence and little conservation in TCR-α chain pairing within the gB498–505-specific T cells (16, 53). We found that different individuals responded with a highly diverse and unique set of TCR sequences (16), although all had the consistent pattern of TCR BV usage shown here.

The extent of the determinant immunodominance described in this report, coupled with the highly consistent pattern of TCR gene expression, argues that the gB498–505-specific T cells, and therefore their specific TCRs, are relatively abundant within the naive lymphocyte population. Indeed, while peptide affinity can control immunodominance (13), there is increasing evidence that T-cell frequencies and TCR availability also play important roles in this selection (20, 54, 55). The conserved pattern of TCR BV usage and the restricted junctional sequence in the gB498–505-specific response permit comparison between these antigen-selected T-cell populations and the naive receptor repertoire, as recently reported for a simple tumor model which also expanded a CTL population with a very restricted TCR BV10-junctional sequence combination (7). However, in our case, the responding cell population represents nearly all the CD8+ T cells specific for a much more complex antigenic system, in the form of HSV-1, providing a unique opportunity to examine how the naive receptor repertoire can control the overall immune response to an infectious agent.

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