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Molecular Signatures Distinguish Human Central Memory from Effector Memory CD8 T Cell Subsets

Tim Willinger,† Tom Freeman,‡ Hitoshi Hasegawa,‡ Andrew J. McMichael,* and Margaret F. C. Callan*§

Memory T cells are heterogeneous in terms of their phenotype and functional properties. We investigated the molecular profiles of human CD8 naive central memory (T_{CM}), effector memory (T_{EM}), and effector memory RA (T_{EMRA}) T cells using gene expression microarrays and phospho-protein-specific intracellular flow cytometry. We demonstrate that T_{CM} have a gene expression and cytokine signaling signature that lies between that of naive and T_{EM} or T_{EMRA} cells, whereas T_{EM} and T_{EMRA} are closely related. Our data define the molecular basis for the different functional properties of central and effector memory subsets. We show that T_{EM} and T_{EMRA} cells strongly express genes with known importance in CD8 T cell effector function. In contrast, T_{CM} are characterized by high basal and cytokine-induced STAT5 phosphorylation, reflecting their capacity for self-renewal. Altogether, our results distinguish T_{CM} and T_{EM}/T_{EMRA} at the molecular level and are consistent with the concept that T_{CM} represent memory stem cells. The Journal of Immunology, 2005, 175: 5895–5903.

Immunological memory is a fundamental feature of the adaptive immune system. It enables the immune system to respond more rapidly and vigorously to infectious pathogens that have been encountered previously. In particular, memory CD8 T cells play a major role in host defense by rapid recognition and lysis of virus-infected cells. A memory response differs both quantitatively and qualitatively from a primary response (1–3). Thus, compared with a naive population, the precursor frequency of Ag-specific memory cells is increased and, furthermore, these cells have an enhanced capacity to respond to Ag. Despite recent progress, a clear understanding of the molecular and cellular basis of T cell memory is still lacking.

Within human CD8 T cells, van Lier and colleagues (4) first demonstrated the presence of phenotypically and functionally distinct subsets of primed T cells by analyzing expression of CD27 and CD45RA. Although naive CD8 T cells express both of these cell surface glycoproteins, cells expressing CD27 but not CD45RA were reported to have functional properties suggestive of “memory” cells and those that expressed CD45RA but not CD27 had functional properties suggestive of “effector” cells (4).

Subsequently, Lanzavecchia and coworkers (5, 6) expressed CCR7 and CD45RA to define subsets of CD8 T cells. According to this scheme, naïve T cells (T_{N}) (3) express both CCR7 and CD45RA whereas primed CD8 T cells can be considered as belonging to one of three different subsets. Two of these lack expression of CD45RA and thus lie broadly within the van Lier memory subset. Of these, central memory cells (T_{CM}) express CCR7 while effector memory (T_{EM}) cells lack expression of CCR7. In humans, but not in mice, there is a third T cell memory subset, T_{EMRA}, that includes cells that express CD45RA but lack expression of CCR7. T_{CM} and T_{EM} can be distinguished by their different homing and effector capacities (6). Like naive cells, T_{CM} express CD62 ligand (CD62L) and CCR7 and home to secondary lymphoid organs. In contrast, expression of a different set of chemokine receptors (e.g., CXCR3) allows T_{EM} and T_{EMRA} to gain access to inflamed peripheral tissues. Human T_{EM} and T_{EMRA} in particular, are more differentiated in terms of effector function than T_{CM} (4, 7–11). They display potent ex vivo cytotoxicity and produce Th1 cytokines upon stimulation, whereas T_{EM} mainly produce IL-2 and Th2 cytokines. Further studies have shown that T_{CM} have a higher proliferative potential and greater resistance to apoptosis, whereas T_{EM}/T_{EMRA} have a skewed TCR repertoire and are characterized by a “senescent” replicative history (9, 10, 12–14).

The importance of both T_{CM} and T_{EM} subsets for the control of infectious diseases and the effectiveness of vaccines has been shown in several murine studies (15–17). In mice, Ahmed and colleagues (18) have demonstrated a linear differentiation pathway T_{N}→effector→T_{EM}→T_{CM} following acute lymphocytic choriomeningitis virus (LCMV) infection. Two other models of CD8 memory T cell differentiation have been proposed: the signal strength/progressive differentiation model by Lanzavecchia and coworkers (6) and the “independent” differentiation model by Pannetier and colleagues (19). However, in humans the developmental relationship among T_{CM}, T_{EM}, and T_{EMRA} is still controversial.

In this study, we have conducted gene expression and kinase phospho-protein profiling of CD8 memory subsets to investigate their molecular programs and their cytokine responsiveness and to

*Medical Research Council Human Immunology Unit, Weatherall Institute of Molecular Medicine, Oxford, United Kingdom; ‡Medical Research Council Rosalind Franklin Centre for Genomics Research, Wellcome Trust Genome Campus, Hinxton, Cambridge, United Kingdom; §University School of Medicine, Shigenobu, Ehime, Japan; and †Division of Medicine, Imperial College London, and Department of Rheumatology, Chelsea and Westminster Hospital, London, United Kingdom

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2 Address correspondence and reprint requests to Dr. Tim Willinger, MRC Human Immunology Unit, Weatherall Institute of Molecular Medicine, The John Radcliffe, Oxford OX3 9DS, U.K. E-mail address: TimW@hammer.imm.ox.ac.uk

3 Abbreviations used in this paper: T_{N}, naïve T cell; FDR, false discovery rate; GMFI, geometric mean fluorescence intensity; GO, gene ontology; MDS, multidimensional scaling; T_{CM}, central memory T cell; T_{EM}, effector memory T cell; T_{EMRA}, effector memory RA T cell; CD62L, CD62 ligand; LCMV, lymphocytic choriomeningitis virus; ID, identifier.
gain insight into their relationship at the molecular level. We elected to define memory subsets according to the Lanzavecchia model in view of the capacity of the model to distinguish between two apparently functionally distinct subpopulations of CD45RA−primed T cells (TCM and TEM) and the extensive debate in the literature concerning the lineage relationship between TCM and TEM or TEMRA cells. Our results define a molecular basis for the different functional properties of human CD8 T cell memory subsets and place TCM and TEM cells between TEMRA and TCM/TEMRA cells in terms of their molecular signatures.

Materials and Methods
Isolation of CD8 T cell subsets
PBMC were obtained from buffy coat preparations from four healthy donors by density gradient centrifugation using lymphoprep (Nycomed) in accordance with institutional ethics approval. We isolated CD8 T cells by positive immunomagnetic selection using dynabeads (Dynal) with detachment of the anti-CD8 mAb. Purity of the selected CD8+ cells was >98% as assessed by flow cytometry. The CD8− T cells were then stained with phycoerythrin (PE)-labeled CD45RA (BD Biosciences, San Diego, CA) and CD45RA (BD Biosciences) and sorted into TCM (CCR7+CD45RA−), TEM (CCR7−CD45RA+), TEMRA (CCR7−CD45RA−), and TCMRA (CCR7−CD45RA+) populations on a MoFlow Cytometer (DakoCytomation). Purity of isolated subpopulations was 95–98%. Cell purification procedures were conducted at 4°C to minimize in vitro-induced changes in gene expression.

Preparation of cRNA and array processing
Total RNA was extracted from purified CD8 T cell populations using TRI reagent (Sigma-Aldrich) followed by RNA cleanup with the RNeasy kit (Qiagen). We confirmed integrity of the total RNA by Lab-on-a-Chip 2100 Bioanalyzer (Agilent) quality control. Double-stranded cDNA was synthesized using a modification of the SMART-PCR protocol described by Pepe-lidis et al. (20). This protocol has been validated regarding the fidelity of amplification and compares favorably with the direct labeling approach in terms of sensitivity, speed and cost-effectiveness. Briefly, 300–600 ng of total RNA was reverse transcribed using a modified SMART CDS Primer IIA containing a 5′ T7 promoter sequence. After double-stranded DNA synthesis, the cDNA was subjected to 15 rounds of PCR according to the manufacturer’s recommendations. Biotin-labeled cRNA was generated from 2 μg of double-stranded cDNA by one round of in vitro transcription with the BioArray High Yield RNA Transcript Labeling kit (Enzo). cRNA yields were >50 μg. The cRNA was fragmented by incubation with the fragmentation enzyme (Promega) and sorted into TCM (CCR7+CD45RA−), TEM (CCR7−CD45RA+), TEMRA (CCR7−CD45RA−), and TCMRA (CCR7−CD45RA+) populations on a MoFlow Cytometer (DakoCytomation). Purity of isolated subpopulations was 95–98%. Cell purification procedures were conducted at 4°C to minimize in vitro-induced changes in gene expression.

Microarray data analysis
We used the comprehensive software package BRB-ArrayTools (21, 22) for data analysis. First, the robust multiarray average algorithm was applied for normalization, background correction, and to calculate fold expression changes (23). Then, to minimize the negative effects of random noise, we performed the following filtering steps: First, transcripts showing minimal variation across the set of arrays (log intensity variation, p > 0.01 with the test hypothesis that gene i has the same variance as the median variance) were removed. Second, transcripts with mostly unreliable expression (GCOS present call ≤4 in 16 samples) were also excluded. This resulted in 10,854 probe IDs that were used for further unsupervised analysis to examine the relationship among samples. First, we used standard average-linkage hierarchical clustering to cluster the samples using the Pearson correlation as the distance metric. Gene sets were centered before clustering. The so-called R (reproducibility) measure described in Ref. 24 was used to evaluate the robustness of the clusters. The R measure is based on the average pairwise expression data between Gaussian noise and measuring the similarity of the new clusters to the original clusters. R measure = 1 indicates perfect cluster reproducibility. Second, multidimensional scaling (MDS) analysis was conducted using the Pearson correlation to measure between sample distances. MDS is related to principal components analysis and allows the representation of high-dimensional data in three-dimensional space. The Pearson correlation subtracted from unity was used to measure the distance between two CD8 T cell subsets by calculating the average linkage distance (distance range, 0–2) (25). The average linkage distance represents the mean of all pairwise distances (linkages) between samples from the two CD8 subsets concerned. We identified genes that were differentially expressed among the four CD8 subsets using a random variation F test. The random variation F test permits sharing information among genes about within-class variation without assuming that all genes have the same variance. It is therefore well suited to the analysis of microarray data with a relatively small number of replicates. Genes were considered statistically significant if their p < 0.001. We used a multivariate permutation test (21) to provide 95% confidence intervals that the false discovery rate (FDR) was <1% (1000 random permutations). The multivariate permutation test is nonparametric and does not require the assumption of Gaussian distributions. Using the significance of microarray analysis algorithm (27) produced similar results. We also performed a global test of whether the expression profiles differed between the different CD8 populations by permuting the labels of which arrays corresponded to which population. For each permutation, the p values were recomputed and the number of genes significant at the level of 0.05 with the test hypothesis that gene i has the same variance as the median variance were calculated for both unstimulated and stimulated CD8 T cell populations. All data have been deposited in the European Bioinformatics Institute ArrayExpress public database. Accession number: E-TABM-40.

Gene ontology (GO) overrepresentation analysis
On-eto was used to translate gene lists into functional profiles and to identify overrepresented GO annotation categories (28). Multiples (probes corresponding to the same gene) were removed before analysis. Enrichment of GO categories and associated p values were calculated based on hypergeometric distribution statistics. We obtained similar results when applying a χ2 test. Multiple testing correction was conducted with the Bonferroni step-down (Holm) procedure (α = 0.05). The Holm procedure is based on the family-wise error rate and a conservative global measure of type I error.

Analysis of cytokine signaling by phospho-specific intracellular FACS
PBMC were stimulated in serum-free RPMI 1640 (Invitrogen Life Technologies) for 15 min at 37°C in 5% CO2 with or without cytokines, at the following concentrations: IL-2 (200 U/ml), IL-4, IL-6, IL-7, IL-10, IL-12, IL-15, IL-18, TNF-α, IFN-γ, and IFN-γ (50 ng/ml). All cytokines were purchased from R&D Systems apart from IL-2 (Biotest), IL-7/TNF-α (PeproTech), and IL-18 (Leinco Technology). We conducted simultaneous staining of PBMC for surface markers and for intracellular phosphorylated STAT and NF-κB proteins according to the protocol developed by Nolan and colleagues (29). Briefly, PBMC were fixed in 1.5% formaldehyde for 10 min at room temperature and permeabilized in methanol for 15 min on ice. Membrane was followed by a rehydration step before permeabilization at room temperature. We used CD262-FITC/PE, CD45RA-allophycocyanin, and CD8-PerCP Abs for surface staining and phospho-specific Abs against STAT (Y701)-PE, STAT3 (Y705)-PE, STAT5 (Y694)-PE, STAT6 (Y641)-Alexa Fluor 488 (all BD Biosciences), and CD8-PerCP Abs for surface staining and phospho-specific Abs against STAT1 (Y705)-PE, STAT3 (Y705)-PE, STAT4 (Y693)-Alexa Fluor 488, STAT5 (Y694)-PE, STAT6 (Y641)-Alexa Fluor 488 (all BD Biosciences), NF-κB-p65 (5536)-Alexa Fluor 488 (Cell Signaling Technology) for intracellular staining. Isotype-matched irrelevant Abs were used as controls. Specificity of intracellular phospho-staining was verified by using blocking phospho-peptides (1 μg/sample; Santa Cruz Biotechnology). Geometric mean fluorescence intensities (GMFI) of phospho-STAT/NF-κB proteins were calculated for the protocol developed by Nolan and colleagues (29). Briefly, PBMC were fixed in 1.5% formaldehyde for 10 min at room temperature and permeabilized in methanol for 15 min on ice. Membrane was followed by a rehydration step before permeabilization at room temperature. We used CD262-FITC/PE, CD45RA-allophycocyanin, and CD8-PerCP Abs for surface staining and phospho-specific Abs against STAT1 (Y705)-PE, STAT3 (Y705)-PE, STAT4 (Y693)-Alexa Fluor 488, STAT5 (Y694)-PE, STAT6 (Y641)-Alexa Fluor 488 (all BD Biosciences), NF-κB-p65 (5536)-Alexa Fluor 488 (Cell Signaling Technology) for intracellular staining. Isotype-matched irrelevant Abs were used as controls. Specificity of intracellular phospho-staining was verified by using blocking phospho-peptides (1 μg/sample; Santa Cruz Biotechnology). Geometric mean fluorescence intensities (GMFI) of phospho-STAT/NF-κB proteins were calculated for the protocol developed by Nolan and colleagues (29). We determined differences in phosphorylation by obtaining the log ratios of GMFI of stimulated vs unstimulated cell populations. Differences in basal phosphorylation were compared by calculating each sample’s GMFI log, ratio divided by the minimum among all samples. We then performed phosphorylated kinase clustering analysis using Cluster and Treeview programs (Michael Eisen, University of California, Berkeley, CA). One-way ANOVA was used to determine the significance of differences in phosphorylation between CD8 T cell subsets. Post hoc testing was conducted using Tukey’s significant difference test (α = 0.05).

Results
Relationships between CD8 memory T cell expression signatures
We isolated highly purified CD8+ T cells (CCR7+CD45RA−), TCM (CCR7+CD45RA+), TEM (CCR7−CD45RA+), and TEMRA (CCR7−CD45RA−) populations from four healthy donors for
gene expression profiling using Affymetrix oligonucleotide microarrays. Unsupervised data analysis methods were used to explore the relationship between CD8 T cell subsets. First, we subjected the 16 samples (four replicates per subset) to hierarchical clustering using a filtered set of 10,854 probe IDs. We found that for both TN and TCM all four replicates clustered together (Fig. 1A). In contrast, TEM and TEMRA samples from the same donors formed individual clusters. Thus, two main clusters could be distinguished: TN/TCM and TEM/TEMRA. We confirmed the robustness of these two main clusters by obtaining a high overall cluster reproducibility measure (R index = 0.949, dendrogram cut at level of four clusters). Second, we performed MDS analysis to assess the distances between the expression signatures of the CD8 T cell subsets. MDS could separate TEM and TEMRA, but these two populations were still in close proximity (Fig. 1B). In contrast, their transcriptional profiles placed TCM replicates between TN and TEM/TEMRA. We also calculated average linkage distances between TN and the different memory subsets as a measure for their relatedness. This showed that the gene expression profile of TCM was closer to TN than were the profiles of TEM or TEMRA (Fig. 1C). Furthermore, we determined the number of differentially expressed genes between the CD8 T cell subsets by individual pairwise comparisons: It was highest for TN vs TEMRA and TCM vs TEMRA and lowest for TEM vs TEMRA (data not shown), again confirming the dichotomy TN/TCM vs TEM/TEMRA. Finally, we conducted a global permutation test to assess whether gene expression profiles between the CD8 subsets differed. The significance values (TEM vs TEMRA P = 0.05714; all other pairwise comparisons P = 0.02857) again suggest that TEM and TEMRA have the most similar gene expression profiles among all CD8 T cell subsets. In summary, analysis of our results, using several different approaches, indicate that the TEM and TEMRA subsets are closely related, whereas TCM have an expression signature that is distinct from that of the other primed T cells and is more closely related to the TN population.

**Genes differentially expressed between CD8 T cell memory subsets**

Next, we identified genes that showed significant differential expression among the four CD8 T cell subsets. We used stringent statistical criteria, including a permutation test to minimize the FDR (see Materials and Methods). A total of 2092 probe IDs corresponding to 940 named genes met our criteria for differential expression: p < 0.001, FDR <1% with 95% confidence. Hierarchical clustering of the differentially expressed genes revealed six main clusters (Fig. 2). Number of probe IDs in each cluster was as follows: 103 (cluster 1), 1369 (cluster 2), 92 (cluster 3), 16 (cluster 4), 129 (cluster 5), and 383 (cluster 6). Two major patterns could be identified among the clusters: First, genes with low expression in TN with increasing expression from TCM → TEM → TEMRA (clusters 2 and 3), termed “effector memory signature.” Second, genes with high expression in naive cells with decreasing expression from TCM → TEM → TEMRA (clusters 5 and 6), termed “naive signature.” Cluster 1 consisted of genes with higher expression in TCM and TEMRA. Cluster 4 comprised genes with a “TCM-specific” expression pattern. Surprisingly, very few genes fell within this category and probe IDs for CD28 accounted for 3 of the 16 included in this cluster (Fig. 2). Overall, >70% of all differentially expressed genes had expression levels in TCM that were intermediate between their expression levels in the TN population and the TEM and TEMRA subsets. These analyses again suggest that, at the

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4 The online version of this article contains supplemental material.
level of gene expression, T<sub>CM</sub> represent a differentiation state that is intermediate between T<sub>N</sub> cells and the T<sub>EM</sub> and T<sub>EMRA</sub> subsets.

The effector memory signature of human CD8 T cells

Genes in clusters 2 and 3 (effector memory signature) appear to represent genes that underpin the known high effector capacity of T<sub>EM</sub> and T<sub>EMRA</sub>. We identified GO categories that displayed statistical overrepresentation among cluster 2 and 3 genes (hypergeometric statistics, Holm multiple testing correction, α = 0.05): GO Biological Processes such as “immune response,” “cytolysis,” and “protein transport” were overrepresented among the effector memory signature genes (Table I). Thus, T<sub>EM</sub> and T<sub>EMRA</sub> highly expressed genes encoding lytic granule proteins like granzyme A (GZMA), granzyme B (GZMB), granzyme H (GZMH), and perforin (PRF1) as well as TNFSF10 (TRAIL) and TNFSF6 (FASL) that mediate perforin-independent apoptosis of target cells.4 Also T<sub>EM</sub> and T<sub>EMRA</sub> showed strong expression of genes involved in protein sorting to granules and granule transport/exocytosis such as HPS3, MYO5A, RAB27A, and RABGGTA. Humans with genetic defects of any of these genes have impaired T cell cytotoxicity (30). Finally, genes encoding inflammatory cytokines (e.g., IFNG (IFNγ)) and chemokines (e.g., CCL5 (RANTES)) were also present in clusters 2 and 3. Consistent with this, in T<sub>EM</sub> and T<sub>EMRA</sub> subsets, we found higher expression of transcription factors that control effector function in CD8 T cells (31), i.e., EOMES, TBX21 (T-BET), REL, NFATC2, and NFATC3.4

In the case of some proteins, particularly those expressed at the cell surface, Abs capable of detecting expression are available. Using these we have confirmed higher expression of CCR7, CD62L, CD27, and CD28 in T<sub>N</sub> and T<sub>CM</sub> subsets at the protein level (data not shown). Apart from effector molecules, differential expression of other genes from clusters 2 and 3<sup>4</sup> between different CD8 T cell subsets has previously been described at the protein level: ITGAL (CD11a), ITGB2 (CD18), ITGAM (CD11b), ITGA4 (CD49d), KLRB1 (CD161), KLRD1 (CD94), killer Ig-like receptor family members, and TNFRSF6 (CD95). Therefore, the results of the protein expression studies are consistent with the results of our gene expression study. Overall, this further strengthens the validity of our gene expression data.

Cytokine signaling signatures of CD8 T cell memory subsets

We observed differential expression of cytokine receptor mRNA in our microarray analysis (Table II). For example, naive CD8 T cells were characterized by higher expression of receptors for IL-6 (IL-6ST) and IL-7 (IL-7R). In contrast, T<sub>EM</sub> and T<sub>EMRA</sub> showed preferential expression of receptors for IL-2 family cytokines (IL-2RB,
IL-2RG) and for inflammatory Th1-type cytokines (TNFR2, IL-12RB1, IL-18R1, IL-18RAP, IFNGR1). This prompted us to investigate cytokine signaling in CD8 T cell subsets at the single-cell level using multiparameter flow cytometry (32, 33). In doing so, we aimed to generate a functional data set that could be subject to clustering and scaling analysis and give further insight into the relationship between the TCM and TEM/TEMRA subsets.

Activated STAT and NF-κB proteins that transduce cytokine signals were detected with phospho-specific Abs by intracellular FACS staining. Methanol permeabilization can compromise detection of some surface Ags (29), and we observed loss of discrimination for CCR7 surface staining (data not shown). Therefore, we substituted CCR7 with CD62L as a surface marker to identify CD8 T cell subsets in conjunction with CD45RA. CCR7 and CD62L expression largely overlap in CD8 T cells (Ref. 10, and own data not shown). In all, for each of the four T cell subsets, we analyzed basal expression levels of intracellular phosphorylated STAT1, STAT3, STAT4, STAT5, STAT6, and NF-κB. We also analyzed expression levels of phosphorylated STAT1 in cells stimulated with IFN-γ or IFN-α, phosphorylated STAT3 in cells stimulated with IL-6 or IL-10, phosphorylated STAT4 in cells stimulated with IL-12 or IFN-γ, phosphorylated STAT5 in cells stimulated with IL-2, IL-7, or IL-15, phosphorylated STAT6 in cells stimulated with IL-4, and phosphorylated NF-κB in cells stimulated with IL-18 or TNF-α. Examples of phospho-specific intracellular staining are shown in Fig. 3. Interestingly, ex vivo CD8 T cells had elevated levels of P-STAT1 and P-STAT5, which could be increased further by cytokine stimulation (Fig. 3A). We confirmed specificity of intracellular phospho-staining by using blocking phospho-peptides (data shown). In addition, we found

### Table I. GO categories overrepresented in effector memory signature (clusters 2 and 3)∧

<table>
<thead>
<tr>
<th>GO Biological Process</th>
<th>No. of Genes</th>
<th>p</th>
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</thead>
<tbody>
<tr>
<td>Immune response</td>
<td>47</td>
<td>0</td>
</tr>
<tr>
<td>Cellular defense response</td>
<td>15</td>
<td>0.000000002</td>
</tr>
<tr>
<td>Intracellular signaling cascade</td>
<td>35</td>
<td>0.00000304</td>
</tr>
<tr>
<td>Signal transduction</td>
<td>66</td>
<td>0.00000563</td>
</tr>
<tr>
<td>Cell growth and/or maintenance</td>
<td>29</td>
<td>0.00028800</td>
</tr>
<tr>
<td>Cell motility</td>
<td>13</td>
<td>0.000432000</td>
</tr>
<tr>
<td>Response to stress</td>
<td>10</td>
<td>0.001663760</td>
</tr>
<tr>
<td>Cytolysis</td>
<td>3</td>
<td>0.002187597</td>
</tr>
<tr>
<td>Nucleobase, nucleoside, nucleotide,</td>
<td>6</td>
<td>0.010724858</td>
</tr>
<tr>
<td>and nucleic acid metabolism</td>
<td>12</td>
<td>0.011990255</td>
</tr>
<tr>
<td>Cell surface receptor-linked signal</td>
<td>15</td>
<td>0.012280396</td>
</tr>
<tr>
<td>transport</td>
<td>8</td>
<td>0.015343897</td>
</tr>
<tr>
<td>Cell matrix adhesion</td>
<td>6</td>
<td>0.015350114</td>
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<tr>
<td>Lipid transport</td>
<td>5</td>
<td>0.020518426</td>
</tr>
<tr>
<td>Response to oxidative stress</td>
<td>16</td>
<td>0.034058535</td>
</tr>
<tr>
<td>Cell proliferation</td>
<td>3</td>
<td>0.040130732</td>
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</table>

∧The association of genes from clusters 2 and 3 (Fig. 2) with biological processes was analysed using Onto-Express. Biological processes (GO tree levels 4 and 5) with a total number of three or more genes and p < 0.05 are displayed.

### Table II. Expression of cytokine receptor mRNA in CD8 T cell subsets∧

<table>
<thead>
<tr>
<th>Gene Symbol</th>
<th>p</th>
<th>TNL</th>
<th>TN</th>
<th>TCM</th>
<th>TEM</th>
<th>TEMRA</th>
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<tbody>
<tr>
<td>IL6ST</td>
<td>&lt;0.000000</td>
<td>596.9</td>
<td>235.2</td>
<td>164.9</td>
<td>171.3</td>
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<tr>
<td>TGFBR1</td>
<td>&lt;0.000000</td>
<td>349</td>
<td>197.5</td>
<td>465.1</td>
<td>853.6</td>
<td></td>
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<tr>
<td>TGFBR3</td>
<td>0.0000003</td>
<td>302.1</td>
<td>1065.7</td>
<td>1541.1</td>
<td>2021.2</td>
<td></td>
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<tr>
<td>IL10RA</td>
<td>0.0000016</td>
<td>571.6</td>
<td>1034.8</td>
<td>1393.5</td>
<td>1299.4</td>
<td></td>
</tr>
<tr>
<td>TGFBR2</td>
<td>0.0000022</td>
<td>233.6</td>
<td>141.5</td>
<td>123.5</td>
<td>126.8</td>
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<tr>
<td>IL28</td>
<td>0.0000024</td>
<td>933.5</td>
<td>2021.4</td>
<td>2767.1</td>
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<tr>
<td>TNFRSF1B</td>
<td>0.0000034</td>
<td>181.6</td>
<td>480.3</td>
<td>763.9</td>
<td>775.6</td>
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<tr>
<td>IL18RAP</td>
<td>0.0000074</td>
<td>136.3</td>
<td>366.3</td>
<td>966.5</td>
<td>902.4</td>
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<tr>
<td>ACVR1C</td>
<td>0.0000168</td>
<td>201.5</td>
<td>124.9</td>
<td>97.1</td>
<td>84.5</td>
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<td>CRLF3</td>
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<td>851.4</td>
<td>1077.4</td>
<td>1299.3</td>
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<td>73.9</td>
<td>108.4</td>
<td>110.7</td>
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<td>IL12RB1</td>
<td>0.0001641</td>
<td>496.3</td>
<td>577.6</td>
<td>900.6</td>
<td>982.4</td>
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<td>IL27RA</td>
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<td>220.8</td>
<td>115</td>
<td>151.3</td>
<td>215.5</td>
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<td>IL2RG</td>
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<td>1978.9</td>
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∧This table lists differentially expressed genes encoding cytokine receptors. Gene expression values (RMA expression measures), fold change values relative to TNL (in bold), and associated p are shown.
that, as known from the literature, some cytokines did not induce phosphorylation of certain STAT proteins, e.g., STAT1 and STAT3 in response to IL-6 and in T N,T CM, and T EM, we observed high STAT5 phosphorylation in response to IL-7 (Fig. 3B). In contrast, TNF-α induced higher NF-κB phosphorylation in T EM/T EMRA. These results are in line with the differential mRNA expression of receptors for IL-6, IL-7, and TNF-α derived from the microarray data.

In all we performed experiments on samples of blood taken from 10 different donors and found differences in levels of basal STAT/NF-κB phosphorylation between the four different T cell subsets. Interestingly, T CM were characterized by significantly higher cumulative basal STAT/NF-κB phosphorylation compared with T EM and T EMRA subsets (T CM vs T EM, p = 0.006, T CM vs T EMRA, p = 0.001, one-way ANOVA/Tukey’s post hoc test). We also found higher basal P-STAT1 (p = 0.037) and P-STAT5 levels (p = 0.013) in T CM compared with T EMRA.

Furthermore, the four different T cell subsets responded differently, in terms of changes in STAT/NF-κB phosphorylation, to stimulation with cytokines (Fig. 4). Despite their already elevated P-STAT5 levels, overall T CM had higher induction of STAT5 phosphorylation in response to IL-2 family cytokines (IL-2: T CM vs T N, p < 0.001, T CM vs T EM, p = 0.044, T CM vs T EMRA, p < 0.001; IL-7: T CM vs T EMRA, p < 0.001, IL-15: T CM vs T N, p = 0.002, T CM vs T EMRA, p = 0.011). In T N we detected strong phosphorylation of STAT1 in response to IFN, STAT3 in response to IL-6, STAT5 in response to IL-7, and STAT6 in response to IL-4. Overall, T N and T CM displayed the highest cumulative cytokine-stimulated phospho-response (T N vs T EMRA, p = 0.01, T CM vs T EMRA, p = 0.02). Finally, we found preferential phosphorylation of NF-κB in response to IL-18 and TNF-α in the T EM and T EMRA subsets (IL-18: T EM vs T N, p < 0.001, T EM vs T CM, p < 0.001, T EM vs T EMRA, p = 0.008; TNF-α: T EM vs T N, T EM vs T CM, T EM vs T EMRA vs T N, and T EMRA vs T CM, all p < 0.001). Thus, human CD8 T cell subsets are characterized by the differential activation of cytokine signaling pathways.

We clustered CD8 T cell subsets based on their cytokine signaling profiles. The 18-parameter phospho-signature, based on the 6 basal and 12 stimulated levels of phosphorylated STAT and NF-κB molecules, again placed T CM between T N and T EM and T EMRA subsets (Fig. 5A). Interestingly, the responses to the proinflammatory cytokines IL-12, IL-18, and TNF-α clustered together and formed a bigger cluster with IL-10 and IL-15. In contrast, IFNs were found in a cluster with IL-4, IL-6, and IL-7. We also performed MDS analysis based on our FACS phospho-proteome data. Similar to the gene expression data, T CM took up an intermediate place between T N and T EM/T EMRA (Fig. 5B). Consistent with this, the average linkage distance between T CM and T N was smaller than that between T EM or T EMRA and T N (Fig. 5C). Thus, the cytokine signaling signatures support the observations from transcriptional profiling in terms of the molecular relationship of CD8 memory cells.

Discussion

In this study, we identified both the gene expression and cytokine signaling profiles of CD8 T N, T CM, T EM, and T EMRA cells. Our results provide a molecular basis for the different functional properties of different memory subsets, especially in terms of their self-renewal and effector capacity. They also shed light on the relationship between the primed T cell subsets.

In contrast with a recent study (34) that used the van Lier classification of CD8 T cells, we used the Lanzavecchia model as a basis for our experiments. This allowed us to compare the properties of the T CM subset with those of other T cell populations. Interestingly, we found a clear dichotomy between T CM and the two effector memory (T EM and T EMRA) CD8 T cell subsets at the molecular level. Analysis of both gene expression and cytokine signaling showed that T CM cells were significantly more closely related to T N cells than T EM or T EMRA cells were. Furthermore, the results of the gene expression analysis imply that T CM cells form a population that is broadly intermediate between T N and T EM or T EMRA cells. The observation that there are very few truly “T CM-specific” genes is most consistent with the idea that these cells form part of a continuum of differentiation or functional states (35–37). However, it is possible that some of the defining features of T CM are epigenetically imprinted, but not yet actively transcribed, and are therefore not identified by transcriptional profiling.

In many respects, the genetic profile of CD8 T CM cells suggests they are equipped with features of both naive and effector memory cells. Thus, T CM possess some stem cell-like qualities, such as a high proliferative capacity, that are also found in the T N cell population. In this regard, T CM displayed high basal and IL-2 family-induced STAT5 phosphorylation. Cytokines of the IL-2 family, which mainly signal through STAT5, are known to play an important role in the differentiation and homeostasis of CD8 T cells (38, 39). Thus, IL-15 can induce the homeostatic proliferation of CD8 memory T cells, whereas IL-7 has recently been implicated in the survival of murine CD8 memory precursors, which can be
identified by selective expression of the IL-7Rα (40). Furthermore, a recent study found that STAT5 regulates the self-renewal and differentiation of human memory B cells (41). Therefore our results might explain why TCM have a greater expansion potential and self-renewal capacity than effector memory cells, TEMRA in particular. In contrast, we found that both effector memory subsets strongly express genes involved in CD8 T cell effector function. However, our data also show that the gene expression profile of TCM is biased to some extent toward effector differentiation, characteristic of effector memory cells. Thus, mRNAs encoding effector molecules like perforin, granzyme A, IFN-γ, and RANTES were up-regulated in TCM compared with T N.

The lineage relationship between CD8 T cell subsets remains controversial. Our study is cross-sectional in design and therefore does not directly address questions relating to T cell lineage. It is however interesting to consider the results of our study in the light of recently proposed models. Lanzavecchia and colleagues (6) have suggested a signal strength model of T cell memory differentiation. According to this model, TCR signal strength determines the memory cell fate a naïve T cells acquires: A low Ag dose leads to the differentiation T N → noneffector → TCM, whereas a high Ag dose to T N → effector → TEM differentiation. Their work also suggests that human TCM further differentiate into TEM following Ag stimulation and into TEMRA in response to homeostatic cytokines (9). The results of our microarray analysis showing that the gene expression profile of TCM cells is largely intermediate between T N and TEM or TEMRA subsets would be consistent with this type of model. In contrast, another model based on the idea that TCM and TEM are independent populations has been proposed by Pannetier and coworkers (19), who found that the TCR repertoires of influenza-specific TCM and TEM are largely distinct. We did not find many truly TCM- and TEM-specific genes and this argues against an independent TCM/TEM differentiation pathway. Finally, Ahmed and coworkers (18) have defined a linear differentiation pathway T N → effector → TEM → TCM in a murine model of acute LCMV infection. Interestingly, this TEM → TCM conversion does not occur in chronic LCMV infection (42). A second study by Pannetier and colleagues (43) using murine H-Y-specific CD8 T cells confirmed this linear differentiation pathway although there was also evidence for an independent TCM/TEM differentiation pathway. The observation that TCM cells are intermediate between T N and TEM cells does not obviously support this type of linear differentiation model. However, the present study is cross-sectional in nature and therefore we do not exclude the possibility that TEM convert to TCM. Interesting questions about the plasticity of the genetic program of the CD8 memory T cell remain and further work will be needed to address these issues. Finally, it is noteworthy that the studies by Ahmed and Pannetier have not examined the TEMRA subset in relation to TCM and TEM as we did in the present work. Effector memory cells re-expressing CD45RA form a sizeable population in human peripheral blood and are likely to have an important role in human CD8 T cell memory.
In conclusion, our genomic and phospho-proteomic study demonstrates a dichotomy between CD8 T<sub>CM</sub> and T<sub>EM/TEMRA</sub> cells at the molecular level and suggests that human T<sub>CM</sub> cells represent an intermediate state between the T<sub>N</sub> and the T<sub>EM/TEMRA</sub> populations in terms of CD8 memory differentiation and function. By defining molecular signatures for CD8 memory subsets, we provide a framework for the further molecular characterization of human CD8 T cell memory.

**Acknowledgments**

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**Disclosures**

The authors have no financial conflict of interest.

**References**


**FIGURE 5.** Cytokine signaling signatures of CD8 memory subsets. *A.* Hierarchical clustering of cytokine phospho-responses in CD8<sup>+</sup> T cell subsets. Complete linkage clustering using the Pearson correlation was conducted to define a 18-parameter biosignature for CD8 subsets. The color bar indicates the mean log<sub>2</sub> ratios of cytokine-stimulated vs unstimulated phospho-specific fluorescent intensities from 10 donors. Basal responses are relative to the minimum among samples. *B,* MDS analysis of CD8<sup>+</sup> T cell subsets. The three-dimensional plot shows the between sample distances for 10 replicate CD8<sup>+</sup> T cell subset samples based on the 18-parameter biosignature from *A.* Pearson correlation was used as the distance metric. Each dot represents a single replicate sample. Color coding: T<sub>N</sub> (red), T<sub>CM</sub> (green), T<sub>EM</sub> (dark blue), and T<sub>EMRA</sub> (light blue). *C* Average linkage distances between CD8<sup>+</sup> T<sub>N</sub> and memory subsets. Average linkage distances between each CD8 memory T cell subset and T<sub>N</sub> were calculated as described in Materials and Methods based on the 18-parameter biosignature from *A.* Error bars represent SEs (SD of pairwise linkages divided by the square root of the number of linkages).


