CCR8 Expression Identifies CD4 Memory T Cells Enriched for FOXP3^+ Regulatory and Th2 Effector Lymphocytes

Dulce Soler, Tobias R. Chapman, Louis R. Poisson, Lin Wang, Javier Cote-Sierra, Mark Ryan, Alice McDonald, Sunita Badola, Eric Fedyk, Anthony J. Coyle, Martin R. Hodge and Roland Kolbeck

*J Immunol* 2006; 177:6940-6951; doi: 10.4049/jimmunol.177.10.6940
http://www.jimmunol.org/content/177/10/6940

---

**References**
This article cites 68 articles, 29 of which you can access for free at:
http://www.jimmunol.org/content/177/10/6940.full#ref-list-1

**Subscription**
Information about subscribing to *The Journal of Immunology* is online at:
http://jimmunol.org/subscription

**Permissions**
Submit copyright permission requests at:
http://www.aai.org/About/Publications/JI/copyright.html

**Email Alerts**
Receive free email-alerts when new articles cite this article. Sign up at:
http://jimmunol.org/alerts
CCR8 Expression Identifies CD4 Memory T Cells Enriched for FOXP3+ Regulatory and Th2 Effector Lymphocytes

Dulce Soler,1 Tobias R. Chapman, Louis R. Poisson, Lin Wang, Javier Cote-Sierra, Mark Ryan, Alice McDonald, Sunita Badola, Eric Fedyk, Anthony J. Coyle,2 Martin R. Hodge, and Roland Kolbeck3

CD4+ Th2 cells are important regulators of allergic inflammation. CCR8 is thought to play a role in Th2-mediated responses, however, expression of CCR8 in peripheral blood has not been fully characterized. Using a fluorescent form of the ligand selective for CCR8 (F-CCL1), we identified the leukocytes expressing CCR8 in human, monkey, and mouse peripheral blood. CCR8 expression is primarily restricted to a subset of human CD4 memory T lymphocytes (15%). Approximately 40% of CCR8+CD4+ T cells express Th1 cytokines IL-4 or IL-13 while 13% express the Th1 cytokine IFN-γ. In fact, 50% of all Th2, but only 5% of Th1, cells express CCR8. Upon anti-CD3/anti-CD28 mAb-mediated activation, CCR8+CD4+ T cells secrete 3- to 7-fold higher levels of IL-4, IL-5, IL-9, and IL-13 and 10- to 20-fold lower levels of IFN-γ or IL-17, compared with CCR8−CD4+ memory T cells. Two-thirds of CCR8+CD4+ T cells express cutaneous lymphocyte-associated Ag while the majority lack gut-homing receptors. CCR8+CD4+ cells express CCR7 and CCL17 and are present in spleen and lymph nodes of mice. Approximately 25% of CCR8+CD4+ T cells express CD25high while 20% of CCR8+CD4+ express the T regulatory cell transcription factor FOXP3 accounting for 60% of all FOXP3-expressing CD4+ T cells. In conclusion, CCR8 marks a diverse subset of CD4 memory T cells enriched for T regulatory and Th2 cells which have the potential for recruitment into sites of allergic inflammation where they could participate in the induction and regulation of the allergic response. The Journal of Immunology, 2006, 177: 6940–6951.

The Journal of Immunology, Millennium Pharmaceuticals, Cambridge, MA 02139

Received for publication February 10, 2006. Accepted for publication August 28, 2006.

The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked advertisement in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

1 Address correspondence and reprint requests to Dr. Dulce Soler, Millennium Pharmaceuticals, 35 Landsdowne Street, Cambridge, MA 02139. E-mail address: dsoler@mphi.com
2 Current address: MedImmune, One MedImmune Way, Gaithersburg, MD 20878.
3 Current address: Peptimmune, 64 Sidney Street, Cambridge, MA 02139.

4 Abbreviations used in this paper: TNPM, nonpolarized memory T cell; TCM, central memory (TCM), and effector memory (TEM) T cells. TCM expand and acquire T-effector functions in response to Ag re-encounter while TEM represent a circulating pool of polarized T cells capable of producing immediate effector functions upon restimulation. CD4+ TEM cells include Th1 and Th2 cells which migrate to inflamed peripheral tissues where they secrete effector cytokines (IFN-γ by Th1 and IL-4, IL-5, IL-9, and IL-13 by Th2 cells, respectively) involved in amplifying the immune response (1, 2). In recent years, other populations of memory T cells that have the capacity to down-regulate immune responses through either cell-to-cell contact or the release of soluble mediators such as IL-10 and TGF-β, so-called regulatory T (TREG) cells, have gained increased attention (3). A subpopulation of TREG cells, known as naturally occurring TREG, are generated in the thymus during T lymphocyte development and are best characterized by high expression levels of the IL-2R α-chain (CD25) and by the expression of the forhead family transcription factor FOXP3 which is necessary for their development and function (4, 5).

Migration of diverse T cell subsets during homeostasis and inflammation is controlled by the concerted expression of adhesion molecules, such as integrins and selectins, and chemokine receptors. For example, coexpression of L-selectin (CD62L) and the chemokine receptor CCR7 by T cells is a prerequisite for homing to lymphoid tissues (6–8) while expression of the integrin α4β7 or cutaneous lymphocyte-associated Ag (CLA) are required for lymphocyte migration to the gastrointestinal tract or the skin, respectively (9–11).

Chemokine receptors belong to the class of seven transmembrane G protein-coupled receptors and have been shown to mediate a variety of biological processes upon chemokine binding, including angiogenesis, leukocyte activation, and chemokine-induced transendothelial migration through integrin activation and subsequent transmigration (12). Chemokines are small secreted proteins (~8 kDa) which can be divided into four subfamilies based on the spacing of two conserved cysteine residues (12). They can also be distinguished by their pattern of regulation: 1) lymphoid chemokines such as CCL19, CCL21, and CXCL13 are constitutively expressed in lymphoid tissues and mediate the migration of leukocytes into and within lymphoid tissues by engagement of their respective receptors CCR7 and CXCR5 (6, 13, 14), 2Q) chemokines constitutively expressed in nonlymphoid tissues, for example, CCL1 in the skin which attracts CCR8+ T cells (15), and 3) inducible chemokines such as CCL11 (16), CCL17 (17, 18), and CXCL10 (19) attract effector cells into inflamed tissues through engagement of CCR3, CCR4, and CXCR3, respectively.

We and others have recently reported the expression of the chemokine CCL1 by IgE-activated mast cells in vitro and in vivo, implicating CCL1 in the recruitment of inflammatory cell types involved in allergic inflammation (Refs. 20–22 and J. A. Gonzalez, Y. Qiu, J. M. Lora, A. Al-Garawi, J. L. Villeval, J. Boyle, C.
Martinez, G. Marquez, I. Goya, Q. Hamid, et al., submitted for publication). Indeed, CCR8, the only identified receptor for CCL1, belongs to a small group of chemokine receptors, including CCR3 and CCR4 that have been shown to be preferentially associated with Th2 effector cells (23–25). Th2 cells are recruited to sites of allergic mucosal inflammation such as IgE class switching, mast cell and eosinophil activation, mucus hypersecretion, and airway hyperresponsiveness. The functional involvement of the CCR8/CCR11 axis in the recruitment of Th2 effector cells in vivo is supported by an increase in CCR8+ CD4 T cell numbers in allergic asthma (Ref. 26 and J. A. Gonzalo, Y. Qiu, J. M. Lora, A. Al-Garawi, J. L. Villeval, J. Boyce, C. Martinez, G. Marquez, I. Goya, Q. Hamid, et al., submitted for publication) and by a recent study demonstrating CCL1 and CCR8 up-regulation in atopic dermatitis (21).

There are also reports suggesting CCR8 expression by CD4+CD25+ TREG cells, skin-homing CLA+ T cells, monocytes, NK cells, and dendritic cells (21, 27–32). Recently, the majority of CD4+CD8+ T cells were reported to express CCR8 as well as both, CD45RA (2D7), CCR7 (7H12), CCR9 (3C3), CCR10 (1B5), CXCR3 (1C6), CXCR6 (7F3), and CD62L (Dreg56), CD94 (HP-3D9), CD16 (3G8), CD29 (MAR4), and CD19 (HIB19), CD27 (M-T271), CD45R0 (UCHL1), CD56 (B159), CD16 (3G8), CD20 (2H7), CD25 (M-A251), and CD45RA (5H9) from Dictagene. Fluorochrome-conjugated Abs to human proteins were obtained from R&D Systems and recombinant human CCL1 was obtained from R&D Systems and recombinant human CCL1 was obtained from Biomerieux.

Isolation of CCR8+ and CCR8− CD4+ populations Complete medium consisted of RPMI 1640, 2 mM l-glutamine, 100 μM nonessential amino acids, 1 mM sodium pyruvate, 10 μg/ml penicillin/streptomycin (all obtained from Invitrogen Life Technologies), and 10% United States-defined FBS (HyClone). The isolation of CCR8+ and CCR8− CD4+ memory T cells from human blood was performed as follows. Human PBMCs were isolated from fresh buffy coats (Oklahoma Blood Institute) by centrifugation on Ficoll-Paque PLUS (Amersham Biosciences). Pure (>98%) CD4+ memory T cells were obtained by negative selection using a CD4 memory T cell isolation kit (Miltenyi Biotec) according to the manufacturer’s instructions. These cells were then frequently stained with mM F-CCL1 and used for chemotaxis experiments. CCR8− CD4+ memory T cells were sorted at 37°C and the following day by FACS into CCR8− and CCR8+ populations were typically of >97% purity. To examine the coexpression of CD25, CCR8, and FOXP3, CCR8− CD4+ memory T cells were also sorted into CD25− and CD25+ subpopulations before CCR8 sorting. Briefly, PBMCs were isolated as above and CD4+ T cells isolated using a CD4+ T cell isolation kit II (Miltenyi Biotec). These cells, CD25− T cells were isolated using a CD4+CD25+ regulatory T cell isolation kit (Miltenyi Biotec) and put to one side. Naïve CD4+ cells and CD45RO+ memory T cells were separated from the remaining CD25− CD4+ cells using CD45RO+ microbeads (Miltenyi Biotec). Both CD4 memory− populations were stained with F-CCR11 (1 μM overnight) and anti-CD45RO-FITC and sorted based on CCR8/CD45RO expression by FACS as above.

Chemotaxis assays After CD4+ memory T cells had been sorted into CCR8+ and CCR8− subsets by FACS, they were incubated for 24 h at 37°C in complete medium to allow for washout of F-CCR11 labeling and receptor recyling to the cell surface. Cell migration was subsequently assessed using 5-μm pore polycarbonate membranes in a 96-well microtiter-MIC plate format (Millipore). Before performing the experiment, the upper surface of the chemotaxis membrane was precoated with a confluent monolayer of ECV-304 cells. CCL1 was diluted in chemotaxis buffer (CTXB: HBSS with 10 mM HEPES and 0.1% fatty acid-free BSA) to the indicated concentrations and added to the lower well of the chemotaxis plate. A total of 100 μl of cell suspension (2 × 106 cells) was added to the upper wells and the plate was incubated at 37°C for 4 h in a humidified 5% CO2 incubator. After incubation, the chemotaxis monolayers were removed and the migrated cells in the lower chamber were loaded with Calcein AM dye (Invitrogen Life Technologies) before reading with the Discovery-1 cellular imaging platform. The resulting data were analyzed using MetaMorph software (both...
Molecular Devices) and expressed as the mean chemotactic index (average number of migrating cells exposed to chemokine divided by the number of cells exposed to CTX alone) from triplicate samples ± SD.

**Intracellular cytokine staining**

For intracellular staining, immediately after sorting, cells were stimulated with 10 ng/ml PMA and 1 μg/ml ionomycin (both Sigma-Aldrich) for 6 h, the last 5 h in the presence of 10 μg/ml brefeldin A (BD FastImmune; BD Biosciences) in complete medium at 37°C. Cells were washed with PBS and fixed with 4% paraformaldehyde, before being permeabilized with 0.5% saponin in PBS (no Ca2+/Mg2+). Cells were stained with combinations of the following Abs for 30 min at room temperature: mouse Abs to IL-4 PE (3007) and IL-13-PE (3020) (both BD Systems), a rat Ab to IL-10-PE (JES3-9D7) and a mouse Ab to IFN-γ FITC (25723.11) (both BD Biosciences) and a rat Ab to IL-4-allophycocyanin (MP4-25D2) (eBioscience). Samples were subsequently washed one time with saponin buffer, one time with PBS, and analyzed by flow cytometry.

**Analysis of cytokine mRNA expression and protein secretion**

To examine cytokine expression and secretion, sorted cells were resuspended in complete medium containing 50 ng/ml IL-2 (R&D Systems) and 10 ng/ml anti-CD3 (BD Pharmingen) and plated at 2 × 10^4/well in a 96-well EIA high protein-binding plates (Costar) that had been precoated with anti-CD3 (10 μg/ml BD Pharmingen). Cells were incubated for 6 and 24 h and supernatants were removed and stored at −80°C. Supernatants were sent to Pierce Endogen for Multiplexed Searchlight ELISA (Pierce) analysis of the following cytokines: IL-4, IL-8, IL-9, IL-10, IL-13, IFN-γ, TNF-α, TGF-β and TSP-1. The cell pellets after supernatant removal were also stored at −80°C in preparation for RNA extraction to examine cytokine gene expression, described as follows.

**Quantitative RT-qPCR**

Total RNA was isolated using RNAeasy technology on a Biorobot 8000 workstation and DNase treated according to the manufacturer’s protocol (Qiagen). The purity and yield of the RNA were assessed using the NanoDrop ND-1000. Integrity of the RNA was measured with RNA 6000 Nano LabChip on an Agilent 2100 Bioanalyzer (Agilent Technologies) and calculated using the RNA Integrity Number algorithm. First-strand cDNA synthesis was performed with a reverse transcription system (Applied Biosystems) according to the manufacturer’s protocol, except that both oligo-dT and random hexamers were used for priming. The integrity of cDNA samples was assessed via qTAM analysis of 18S and β2-microglobulin transcripts by real-time PCR in an ABI PRISM 7700 (Applied Biosystems). Primers and MGB Eclipse probes (NanoGen) for real-time PCR were designed using Primer Express (Applied Biosystems) and were run in initial high-density microarray analysis. Transcripts of interest were assayed in a multiplexed format, using human β2-microglobulin RNA, as an endogenous control; analysis of MAS 5.0 data from corresponding U133A/B GeneChip probe sets (Affymetrix) used in initial high-density microarray analysis. Quantitative RT-qPCR was thoroughly verified by 1 competition with excess unlabeled CCL1 (Fig. 1, A and B) or TCA-3 for mouse samples, 2 absence of staining in lymphocytes of CCR8-deficient mice (Fig. 1C), and importantly, by 3 competition with several small molecule antagonists shown to be selective for CCR8 vs all other chemokine receptors and a large panel of other G protein-coupled receptors. In addition, MC148-huFc, an engineered fusion protein containing at the N terminus MC148, a selective CCR8 viral chemokine antagonist (33), also gave the same pattern of staining as F-CCL1, and both chemokines were competitive with each other (data not shown).

All non-CD4 expression of CCR8 is confined to small subsets of CD8 T lymphocytes (2 ± 1.6%; n = 12) and CD56+ NK cells (0.7 ± 0.46%; n = 12) (Table I). The Th2/T cytotoxic cell-associated PGD2 receptor, CRTH2 (34), is expressed in a subset of CCR8+ CD8+ T cells (Fig. 1A). Within the CD56+ NK cell compartment, CCR8 expression is associated preferentially (16 ± 3.8%) with a small subset that expresses high CD56 levels (CD56<sup>hi</sup>CD4<sup>+</sup>CD56<sup>hi</sup>CD16<sup>−</sup>) (Fig. 1A) (35, 36). All other subsets of NK cells investigated including NKT cells, CD8<sup>+</sup>CD56<sup>−</sup> and CD8<sup>+</sup>CD56<sup>−</sup> NK cells, had levels of expression similar to the total CD56<sup>+</sup> population. CCR8 expression was not observed in CD4<sup>+</sup>CD45RO<sup>−</sup> or CD4<sup>+</sup>CD45RA<sup>−</sup> naive T cells (Fig. 1A), or CD4<sup>+</sup>CD45RA<sup>+</sup>CD45RO<sup>−</sup> T cells, CD19<sup>+</sup> B lymphocytes, plasma myeloid (CD11<sup>+</sup>CD123<sup>−</sup>B2CDA<sup>−</sup>) or myeloid (CD123<sup>−</sup>B2CDA<sup>−</sup>) dendritic cells, CD123<sup>+</sup> basophils, CD14<sup>+</sup> monocytes, CD16<sup>+</sup> neutrophils, or
of NK (NK1.1; 0.4%) cells and NKT cells (2%) (data not shown). Leukocyte types and numbers expressing CCR8 in peripheral blood of human, monkey, and mouse are summarized in Table I. In addition, we identified CCR8+CD4 memory T cells, NK and NKT cell populations in naive mouse spleens (14, 1, and 3%, respectively) and lymph nodes (24, 3, and 4%, respectively) but not in the corresponding tissues derived from CCR8-deficient mice (data not shown).

In summary, our data clearly indicate that CD4+ memory T cells are the predominant cell type expressing CCR8 in peripheral blood across species (human, monkey, mouse) and that these cells either have the potential to migrate into secondary lymphoid organs and/or acquire a CCR8+ phenotype during activation in these lymphoid tissues as indicated by the presence of CCR8+CD4+ memory T cells in naive mouse spleens and lymph nodes.

Activated CCR8+CD4 memory T cells preferentially produce Th2 cytokines in vitro

Th effector cells are best characterized by the types of cytokines expressed upon activation: Th1 effector cells produce IFN-γ whereas Th2 effector cells produce IL-4, IL-5, IL-9, and IL-13. To investigate the potential of CCR8+CD4 memory T cells to express either Th1 or Th2 cytokines, we sorted CD4 memory T cells isolated from human peripheral blood into CCR8+ and CCR8− populations (purity >97%) (Fig. 2A) and determined the relative cell numbers expressing IL-4, IL-10, IL-13, and IFN-γ by intracellular staining following activation in vitro. To ensure that the sorted populations were representative of their respective counterparts in blood, we compared their relative phenotypic frequencies with respect to expression of CLA, CD25, CCR5, CR7, CD62L, CD27, and CRTH2 and found no significant differences. As shown in Fig. 2, B and C, the percentage of activated cells expressing IL-4 was 6-fold higher in the CCR8+ than in the CCR8− population (CCR8+ 26 ± 3%; CCR8− 4 ± 1%) and cells expressing IL-13 were 10-fold more frequent in the CCR8+ than in the CCR8− population (CCR8+ 20 ± 2%; CCR8− 2 ± 0.6%). Conversely, cells expressing IFN-γ were 3-fold more frequent in the CCR8+ population (CCR8+ 13 ± 4%; CCR8− 42 ± 8%). Approximately one-third of all CCR8+ IL-4− and IL-13-expressing cells coexpressed both cytokines most likely reflecting a probabilistic distribution of expression of each cytokine as recently demonstrated for in vitro-cultured Th2 cells (37). Within the CCR8+ population, there was very little coexpression of IL-4 or IL-13 with IFN-γ, whereas ~50% of IL-4− and IL-13-expressing CCR8− cells coexpressed IFN-γ likely representing still uncommitted Th0 cells. Both cell populations exhibited a similar frequency of IL-10-expressing cells (2%). In summary, ~40% of all CCR8+ memory T cells express either IL-4 or IL-13 after activation, consistent with Th2 effector function. When compared with the total number of CD4 memory T cells the CCR8+ population contains ~40% of all IL-4, 60% of all IL-13, 15% of all IL-10, but only 5% of all IFN-γ-expressing cells (Fig. 2D). Of particular significance is the almost complete inclusion of all IFN-γ-producing Th1 effector cells in the CCR8+ population (95%).

The enrichment of Th2 effector cells within the CCR8+CD4 memory T cell population was further supported by the higher levels of IL-4 (3 ± 0.9-fold), IL-5 (5 ± 1-fold), IL-9 (2 ± 0.5-fold), and IL-13 (3 ± 0.8-fold) secreted by CCR8+ than by CCR8−CD4 memory T cells 24 h after anti-CD3/anti-CD28 activation (Fig. 2E). Levels of the Th1 cytokine IFN-γ (12 ± 6-fold) and IL-17 (8 ± 0.1-fold) were greater in the CCR8+ population. The differences in IL-9 (6-fold), IL-13 (7-fold), and IL-17 (20-fold) levels were even more pronounced 48 h after activation (data not shown).

### CCR3+CD49d+ eosinophils (data not shown).

Similarly, CD4 memory T cells were the predominant cell type expressing CCR8 in peripheral blood from cynomolgus monkeys (~10%; Fig. 1B; Table I) and naive mice (~10%; Fig. 1C, Table I), respectively. We also identified low numbers of CCR8+CD8+ T cells and NK cells in peripheral blood from cynomolgus monkeys (Table I) and as in humans, the CD56brightCD16− NK population was enriched for CCR8+ cells (data not shown). In mice, CCR8 was not expressed on CD8+ T cells but it was expressed by a small number of NK (NK1.1; 0.4%) cells and NKT cells (2%) (data not shown). Leukocyte types and numbers expressing CCR8 in peripheral blood of human, monkey, and mouse are summarized in Table I. In addition, we identified CCR8+CD4 memory T cells, NK and NKT cell populations in naive mouse spleens (14, 1, and 3%, respectively) and lymph nodes (24, 3, and 4%, respectively) but not in the corresponding tissues derived from CCR8-deficient mice (data not shown).

In summary, our data clearly indicate that CD4+ memory T cells are the predominant cell type expressing CCR8 in peripheral blood across species (human, monkey, mouse) and that these cells either have the potential to migrate into secondary lymphoid organs and/or acquire a CCR8+ phenotype during activation in these lymphoid tissues as indicated by the presence of CCR8+CD4+ memory T cells in naive mouse spleens and lymph nodes.

**FIGURE 1.** CCR8 expression is mainly restricted to a subset of memory CD4+ T cells in human, monkey, and mouse peripheral blood. A, Flow cytometric analysis of human blood stained with 5 nM F-CCL1 alone (PBS) or with 40 nM unlabeled CCL1 and markers for CD4 cytometric analysis of human blood stained with 5 nM F-CCL1. The percentage of CCR8-expressing cells is indicted in the top right quadrant of each plot. For CCR8 vs CRTH2 expression in the CD8 gate, the frequency of all four possible subsets is indicated. B, Flow cytometric analysis of cynomolgus monkey whole blood stained with CCL1, CD4, and CD45RA. CCR8 expression was examined in the naive CD4+ T cell (CD4+CD45RO−), memory CD4+ T cell (CD4+CD45RO+), CD8+ T cell, lymphocyte, and CD56bright cell gates, and specificity of staining was demonstrated in all cases by competition with unlabeled CCL1. The percentage of CCR8-expressing cells is indicated in the top right quadrant of each plot. For CCR8 vs CRTH2 expression in the CD8 gate, the frequency of all four possible subsets is indicated. C, Flow cytometric analysis of mouse whole blood, as well as spleen and lymph node cell suspensions from wild-type and CCR8-deficient mice stained with CCL1, CD4, and CD44mab. CCR8 expression was examined in the gated memory CD4+ cell population (CD4+CD44mab). These plots are representative and complete data set are summarized in Table I.
not shown). Protein levels correlated with mRNA levels as determined by quantitative real-time PCR 6 or 24 h after anti-CD3/anti-CD28 activation (Fig. 2F). The cytokine expression data clearly indicate that CCR8 expression selects for a subset of peripheral blood CD4 memory T cells enriched in Th2 effector cells.

Phenotypic characterization of CCR8+ CD4 memory T cells

CCR8+CD4+ T cells have been proposed to express skin-homing receptors and T<sub>H<sub>REC markers but a complete phenotypic characterization in whole blood has not been reported. To further characterize blood-derived CCR8+CD4+ T cells and their homing potential, we investigated their phenotype in detail.

CCR4 and CCR10, as well as CCR8 and CLA, have been proposed to be critically involved in skin-specific T cell homing during homeostasis and inflammation (15, 38–40). Approximately two-thirds of CCR8+CD4 memory T cells express the skin homing receptor CLA (66 ± 12%; n = 20) the majority of which (86 ± 12%; n = 10) also express the chemokine receptor CCR10 (Fig. 3B, Table II). The CCR8+CD4 memory T cell subset contains ~36 ± 5% of all CLA<sup>+</sup> and 65 ± 7% of all CCR10+CD4 memory T cells. In addition, while CCR8+CD4 memory T cells contain ~22 ± 6% of all CCR4+CD4 memory T cells (Table II), CCR4 is expressed by nearly the entire CCR8+ population (97 ± 3%) (Fig. 3B; Table II). It is therefore possible that homing of the CCR8+CLA<sup>+</sup> cells is restricted to the skin under conditions where one or a combination of appropriate chemokines are expressed in the skin.

Interestingly, we observed that within the CCR8+ population, IL-4- and IL-13-producing cells were enriched 2-fold in the non-skinn homing (CLA<sup>-</sup>CCR8<sup>-</sup>) as compared with the skin-homing (CLA<sup>+</sup>CCR8<sup>+</sup>) subset (30 vs 15% and 21 vs 16% for IL-4 and IL-13, respectively). Conversely, IFN-γ-producing cells were 2-fold enriched in the CLA<sup>+</sup>CCR8<sup>+</sup> population when compared with the CLA<sup>-</sup>CCR8<sup>-</sup> subset (12 vs 6%). However, in the CCR8<sup>-</sup> subsets, the frequency of IL-4, IL-13, or IFN-γ-producing cells appeared to be independent of CLA expression. Therefore, Th2 cytokine-producing effector cells are enriched in the CCR8+CLA<sup>+</sup> population, presumably a subset capable of homing to the lung.

The integrin α<sub>4</sub>β<sub>2</sub> (CD49d/CD29) has been implicated in lung homing by virtue of its interaction with VCAM-1 (41). All CCR8+CD4<sup>+</sup> T cells express the β<sub>2</sub> subunit CD29, however, we found that only half of CCR8<sup>+</sup>CD4<sup>+</sup> T cells express α<sub>4</sub> although the vast majority of CCR8<sup>+</sup>CD4<sup>+</sup> T cells express this α subunit. Interestingly, the majority of CLA<sup>+</sup>CCR8<sup>+</sup> cells express high levels of α<sub>4</sub> while the skin-homing cells were mostly negative or intermediate/low for α<sub>4</sub> (Fig. 3D) and expressed α<sub>5</sub> (data not shown). It is thus possible that the CLA<sup>-</sup>CCR8<sup>-</sup>α<sub>4</sub><sup>high</sup>β<sub>2</sub><sup>+</sup> subset, enriched in Th2 cells (see above), might preferentially migrate to the lung and participate in allergic inflammation of the airway.

### Table I. CCR8 expression in human, monkey, and mouse peripheral blood<sup>a</sup>

<table>
<thead>
<tr>
<th>Species</th>
<th>% CCR8&lt;sup&gt;+&lt;/sup&gt; Mean ± SD</th>
<th>% of total CCR8&lt;sup&gt;+&lt;/sup&gt; leukocytes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Human</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CD4 memory T cells</td>
<td>15 ± 4</td>
<td>50 ± 91</td>
</tr>
<tr>
<td>CD8&lt;sup&gt;T&lt;/sup&gt; cells</td>
<td>2.1 ± 1.6</td>
<td>12 ± 8</td>
</tr>
<tr>
<td>NK cells</td>
<td>0.7 ± 0.4</td>
<td>12 ± 3</td>
</tr>
<tr>
<td>Monkey</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CD4 memory T cells</td>
<td>11 ± 4</td>
<td>10 ± 77</td>
</tr>
<tr>
<td>CD8&lt;sup&gt;T&lt;/sup&gt; cells</td>
<td>0.8 ± 0.4</td>
<td>10 ± 22</td>
</tr>
<tr>
<td>NK cells</td>
<td>1.2 ± 0.7</td>
<td>5 ± 4</td>
</tr>
<tr>
<td>Mouse</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CD4 memory T cells</td>
<td>9 ± 1.4</td>
<td>5 ± 76</td>
</tr>
<tr>
<td>CD8&lt;sup&gt;T&lt;/sup&gt; cells</td>
<td>0.4 ± 0.09</td>
<td>5 ± 23</td>
</tr>
</tbody>
</table>

<sup>a</sup> The frequencies of CCR8<sup>+</sup> cells in the indicated cell populations is the average ± SD of multiple donors (n). The percentage of total CCR8<sup>+</sup> cells contained within each population is shown in the rightmost column for each species.
FOXP3 expression by CCR8+ CD4 memory T cells

The forkhead transcription factor family member FOXP3 is the most specific marker for thymic-derived T\textsubscript{REG} cells and is required for T\textsubscript{REG} cell development and function (4). CCR8 has recently been shown to be expressed by CD4\textsuperscript{+}CD25\textsuperscript{+} T\textsubscript{REG} cells and to mediate CCL1-dependent migration of those cells in vitro (27–29). It is however unclear to what degree CCR8 expression is confined to T\textsubscript{REG} cells. To address this issue, we used a FOXP3-specific Ab
and enumerated CCR8+ and CCR8− CD4 memory T cells whose nuclei were positive for FOXP3, as determined by costaining with the nuclear dye DAPI. FOXP3 protein localized to the nuclei of ~21% of all CCR8+ cells and only 3% of CCR8− cells (Fig. 4, A and B), accounting for ~60 and 40% of all FOXP3+ CD4 memory T cells, respectively (Fig. 4C). All CCR8−FOXP3+ cells express CD25 and represent 50–70% of the CCR8−CD25+ population (Fig. 4D). No FOXP3+ nuclei could be identified in CD4 naive T cells or in the absence of the FOXP3 Ab indicating staining specificity (data not shown). Interestingly, cells with high-intensity FOXP3 staining exclusively localized to the CCR8+ population. The distribution of FOXP3+ cells across the different cell populations investigated was supported by FOXP3 mRNA expression data, showing the highest FOXP3 mRNA levels in CD25+CCR8+ and CD25+CCR8− memory T cells (Fig. 4E). In addition, activation with anti-CD3/anti-CD28 for 6 h resulted in increased FOXP3 mRNA levels (3- to 5-fold) in the CD25+CCR8+ and CD25+CCR8− subsets with no effect on the CD25− subsets (data

FIGURE 3. Phenotypic analysis of human peripheral blood memory CD4 T cells expressing CCR8. A, Flow cytometry plots indicating the gates used in B–G. The frequencies of all four possible subsets in each plot are indicated in the top right quadrant. B, CCR8 coexpression with the skin-homing cell surface markers CLA, CCR10, and CCR4. C, CCR8 expression analysis in CD4 memory T cells stained with the gut-homing receptor αβ (left plot); analysis of CCR9 vs αβ expression in CCR8+CD4+ T cells (middle plot) and in CCR8−CD4− T cells (right plot). The quadrants were established to distinguish the αβbright and αβdim populations rather than according to the isotype control. D, Analysis of CLA vs CD49d (αβ) expression in CCR8+CD4+ T cells (left plot); CCR8 expression in CD4 memory T cells stained with CD62L (middle plot) and coexpression of lymphoid-homing receptors CCR7 and CD62L in CCR8+CD4+ T cells (right plot). E, CCR8 and CD25 coexpression in CD4 memory T cells (left plot); expression of CLA vs CD25 in CCR8+CD4+ T cells (middle plot) (quadrants were established to distinguish the CD25high (from CD25int) and coexpression of CCR8 with CD27 in CD4 memory T cells (right). F, Coexpression of CCR8 with CRTTH2, CCR3, and ICOS in memory CD4 T cells. G, Coexpression of CCR8 with CCR5, CCR3, and CXCX6. Shown are representative examples from multiple donors.
not shown). The high overlap of FOXP3, CD25\textsuperscript{high}, CLA, and CCR10 expression (see above and Table II) indicates the existence of a minority of the entire CCR8\textsuperscript{+} T cell population (\textasciitilde20\%) (Fig. 4B).

### CCR8\textsuperscript{+}CD4 memory T cells migrate in response to CCL1

The main proposed biological function mediated by CCR8 is ligand-induced cell migration. We compared the responsiveness of sorted CCR8\textsuperscript{+} and CCR8\textsuperscript{-} memory T cells to CCL1 in transwell chemotaxis assays to address functional expression of CCR8 on CD4 memory T cells. The CCR8\textsuperscript{+} cells specifically migrated to CCL1, which induced a maximum response at 0.3 nM (Fig. 5) whereas the CCR8\textsuperscript{-} cells were unresponsive. Both populations responded similarly well to the CCR7 ligand CCL21 (data not shown).

### Discussion

CCR8 has been proposed to play a role in Th2-mediated responses, in T\textsubscript{REG} function, and in skin immunosurveillance but the precise phenotype of CCR8-expressing cells in the periphery is poorly characterized. We describe the phenotype and functional properties of CCR8\textsuperscript{+} cells in peripheral whole blood.

The selectivity, specificity, and high affinity of CCL1 for CCR8 presented the possibility of preparing a fluorescently labeled variant of CCL1 that could be used as a probe for the identification of leukocytes expressing CCR8. A subpopulation of CD4\textsuperscript{+}CD45RO\textsuperscript{+} memory T cells (15\%) is the most abundant leukocyte type expressing CCR8 in human (>90\%), monkey (77\%), and mouse (76\%) peripheral blood. CCR8 is also expressed by small populations of CD8\textsuperscript{+} T cells and CD56\textsuperscript{+} NK cells. Most intriguingly, we identified preferred association of CCR8 with CD56\textsuperscript{high}/CD94\textsuperscript{high}/CD16\textsuperscript{+} NK cells in some of the donors investigated. These cells might represent a unique population of activated NK cells in vivo (35, 36), as supported by a study reporting CCR8 expression by adherent and IL-2-activated, but not nonactivated, NK cells in vitro (31).

Very limited expression of CCR8 on T cells in peripheral blood has been reported recently by Schaeftli et al. (15) using a newly developed anti-CCR8 polyclonal Ab raised against the N-terminal peptide. However, in contrast to their report, we found that all CCR8\textsuperscript{+}CD4 T cells did not coexpress CD45RO and CD45RA but exclusively express high levels of CD45RO, indicative of memory T cells. The reasons for this discrepancy are unclear although post-translational modifications in the N-terminal peptide of chemokine receptors are known to occur and could affect cross-reactivity of the Ab to primary cells. In addition, specificity of the polyclonal anti-CCR8 Ab to primary cells was not demonstrated as conclusively as we demonstrated specificity and selectivity of F-CCL1 binding. The same report suggests that 30–40\% of peripheral blood-derived CCR8\textsuperscript{+} T cell clones cultured in vitro express IFN-\gamma, and only 10\% express IL-4. This is in contrast to our results indicating that \textasciitilde40\% of all CD4\textsuperscript{+}CCR8\textsuperscript{+} T cells are Th2 cells while 13\% are Th1 cells. This difference could be due to the use of T cell clones as compared to freshly isolated peripheral blood T cells. Although \textasciitilde13\% of CCR8\textsuperscript{+} memory T cells expressed IFN-\gamma, this population only represents \textasciitilde5\% of all IFN-\gamma-producing CD4 memory T cells, whereas CCR8\textsuperscript{-} Th2 cells represent \textasciitilde50\% of all Th2 cells. These results are in agreement with reports indicating expression of CCR8 on in vitro differentiated and activated Th2 cells (23, 24, 48). We also found that levels of secreted IL-17 are far greater in the CCR8\textsuperscript{-} population. IL-17 has recently been suggested to be a crucial mediator of autoimmune responses thought to be Th1 in nature (49). Most recently, IL-17-producing CD4\textsuperscript{+} memory Th cells (Th17) have been proposed to represent a separate differentiation lineage than Th1 or Th2 cells (50).

The presence of a small population of CCR8\textsuperscript{+} Th1 effector cells was also supported by CCR8 coexpression with the Th1-associated chemokine receptors CXCR3 (30\%), CCR2 (27\%), CCR5 (24\%), and CXCR6 (11\%). However, while CD4 memory T cell subsets expressing these receptors are enriched in Th1 effectors, they also contain a significant frequency of nonpolarized cells and Th2 effectors and thus their expression is not restricted to Th1 cells (25). More interestingly, although \textasciitilde40\% of CCR8\textsuperscript{+}CD4 cells are Th2 effectors, only 9\% expressed CRTH2 which is considered the most
reliable marker for peripheral Th2 effector cells (34, 51, 52). Although CRTH2 expression in CD4 T cells is restricted to Th2 effectors, our data clearly indicate that CRTH2 is expressed only on a fraction of all peripheral blood Th2 cells in agreement with the findings of Iwasaki et al. (52) who found CRTH2 expression in about half of Th2 cells in a broad panel of subjects. Other chemotactic receptors associated with Th2 cells, including CCR8 (Refs. 23 and 24 and data presented herein), CCR3 (53), and CCR4 (23, 54), might be involved in mediating migration of these cells into inflamed tissues. CCR8 is the chemokine receptor most highly enriched in Th2 cells. In fact, we and others have reported increased numbers of CCR8+ T cells in asthmatic lung biopsies (Ref. 26 and J. A. Gonzalo, Y. Qiu, J. M. Lora, A. Al-Garawi, J. L. Villeval, J. Boyce, C. Martinez, G. Marquez, I. Goya, Q. Hamid, et al., submitted for publication) and atopic skin lesions (21). In addition, we observed a correlation between mRNA levels of CCR8 with those of IL-13, IL13-Rα2, IL-5, eosinophil cationic protein, and mast cell tryptase in human asthmatic lung biopsies. CCR8 mRNA was also detected in cells isolated by laser capture microscopy from bronchial alveolar-associated lymphoid tissue from normal (nonasthmatic) subjects (E. Fedyk, unpublished observation). The presence of CCR8+ Th2 effector cells in peripheral blood (data herein), their accumulation at sites of allergic inflammation, and the concomitant identification of activated mast cells as a major source producing CCL1 in vivo indicates an important role for the CCL1-CCR8 axis in the orchestration of allergic mucosal inflammation. In support of this notion is the phenotype of CCR8-deficient mice in a mast cell-dependent model of allergic airway inflammation, including reduced lung inflammation, Th2 cytokine levels, airway hyperresponsiveness, and mucus hypersecretion.

FIGURE 4. FOXP3 expression by 20% of CCR8+ CD4 memory T cells. A, Freshly isolated CCR8+ and CCR8− CD4 memory T cells were stained with an Ab specific for FOXP3 and the nuclear dye DAPI. The merged images are shown. B, Percentage of CCR8+ (■) and CCR8− (□) cells expressing nuclear FOXP3 (average ± SD of three independent experiments). C, Percentage of total FOXP3+ CD4 memory T cells which are CCR8+ (■) or CCR8− (□) (average ± SD of three independent experiments). D, Representative flow cytometry analysis of sorted CD4 memory T cells based on CCR8 and CD25 expression (upper panel). Representative images of nuclear FOXP3 staining of the sorted populations (lower panel). E, Real-time PCR analysis of FOXP3 mRNA expression in the four subsets shown in D and in naive CD4 T cells.
mal skin as well as functional expression of CCR8 on CD4+ and CD8+ T cells isolated from normal skin have been reported (15), suggesting a functional role of the CCL1-CCR8 axis in skin-specific immunosurveillance. In another study, increased levels of CCL1 in atopic dermatitis lesions correlated with increased numbers of CCR8+ T cells suggesting an involvement of CCR8 in mediating T cell migration to inflamed skin (21). Nevertheless, functional involvement of CCR8 in skin-specific T cell homing during homeostasis and/or acute inflammation remains to be demonstrated. We report here coexpression of the chemokine receptors CCR10 and CCR4 on CCR8+ CLA+ CD4 memory T cells. Both receptors have been shown to mediate T cell recruitment to inflamed skin (39, 57). The relative contribution of CCR4, CCR8, and CCR10 or their synergistic cooperation in mediating skin-specific T cell migration, as demonstrated for CCR4 and CCR10 (39), still requires more detailed investigation using gene-deficient mice or function blocking Abs. Tissue microlocalization of functionally distinct T cell subsets may involve the sequential action of several chemokine receptors with one receptor mediating migration from blood while others may mediate migration within the tissue.

The expression of CCR8 by thymus-derived TREG cells is supported by several studies showing functional CCR8 expression (cell migration) on human thymic CD4+ CD25+ (29) and peripheral blood-derived CD4+ CD25+ TREG (28). High expression of the IL-2Rα subunit CD25 is considered the most reliable cell surface marker for naturally occurring TREG cells, although CD25 is also up-regulated on activated T cells (5). TREG cells have been shown to play an important role in controlling autoimmunity and in the regulation of pathological and physiological immune responses (58). Our data indicate that ~25% of the CCR8+ CD4+ memory T cells express high CD25 levels and that 50% of total CD4+ CD25high cells are contained within the CCR8 compartment. These results are in good agreement with the fact that ~20% of the CCR8+ T cells and 3% of the CCR8− T cells express FOXP3 (with all FOXP3 staining confined to the CD25+ sorted subsets). The CCR8+ cells expressing FOXP3 represent ~60% of all FOXP3+ CD4+ memory T cells. Of note is the observation that FOXP3 staining intensity was highest in CCR8+ T cells, which might correlate with a stronger suppressor phenotype. Virtually all CD4+ CD25+ T cells in the thymus express CCR8 (29) suggesting that CCR8 expression might be lost in the periphery by a subset of originally CCR8+ FOXP3+ cells, although we cannot completely exclude the possibility of contamination of the CCR8− subset with a small fraction of CCR8+ cells. However, the concordance of CD25high staining in whole blood among the CCR8+ and CCR8− subsets with the FOXP3 data in the sorted populations, makes this possibility unlikely. CCL1 is expressed in the thymus and CCR8/ CCL1 interactions may play a role in TREG cell development by either directing the localization of these cells to specific thymic structures or by rescuing them from negative selection upon TCR/MHC activation given that CCR8 signaling has been shown to have antiapoptotic effects (59–62). However, it should be noted that CCR8-deficient mice do not exhibit any of the characteristics of the severe autoimmune and lymphoproliferative disorder resulting from FOXP3 deficiency (63, 64). Therefore, either the role of CCR8 in TREG development and function is not essential or chemokine receptor redundancy (e.g., CCR4) compensates for the absence of CCR8 function. This is supported by a recent study that demonstrates involvement of CCR4 in TREG migration into cardiac allografts (65). We conclude that CCR8 expression is not restricted to CD4+ TREG cells, but that the CCR8+ CD4+ T cell population is enriched in FOXP3+ TREG cells.
In summary, we provide data indicating that the chemokine receptor CCR8 is expressed by a small and heterogeneous population of peripheral blood CD4 memory T cells enriched in Th2 effector and T<sub>REG</sub> cells. CCR8<sup>+</sup> CD4<sup>+</sup> memory T cells comprise two major subsets according to their tissue-homing specificity: skin-homing cells, which account for approximately two-thirds of CCR8<sup>+</sup> CD4<sup>+</sup> cells and nonskin, nongut homing cells which account for about one-third of CCR8<sup>+</sup> CD4<sup>+</sup> cells. Within each homing subset, the relative frequencies of T<sub>SPM</sub>, T<sub>EM</sub>, and CD25<sup>high</sup> cells are very similar as in the total CCR8 population. The major difference between these two homing subsets is the relative frequencies of Th1 and Th2 cells. In the skin-homing subset, the frequencies of Th1 and Th2 effectors are similar while in the systemic homing subset, the frequency of Th2 effectors is three to five times higher. Altogether, CCR8 may participate in the induction and amplification phase of inflammatory responses to pathogen or allergen by recruiting T<sub>EM</sub> cells. At the same time it may also participate in the recruitment of T<sub>REG</sub> cells contributing to the establishment of the appropriate balance of effector/regulatory cells which will influence the final outcome of the inflammatory response. T<sub>REG</sub> cells would provide the regulatory function required to contain collateral damage that may be caused by an exaggerated immune response and/or also participate in the resolution of inflammatory responses. CCL1/CCR8 interactions may also be important for intratissue migration of T<sub>REG</sub> to target cells producing CCL1, including dendritic or T cells. In this regard, APCs and Th1 cells have been reported to produce CCL1 (66, 67). CCR8<sup>+</sup> T<sub>REG</sub> attraction by Th1 cells might further shift the balance toward a Th2 response. Whereas the functional involvement of CCR8 in skin-specific T cell recruitment still needs to be validated, data in mouse models of allergic airway inflammation (Ref. 68 and J. A. Gonzalo, Y. Qiu, J. M. Lora, A. Al-Garawi, J. L. Villeval, J. Boyce, C. Martinez, G. Marquez, I. Goya, Q. Hamid, et al., submitted for publication) indicate the functional importance of the CCL1-CCR8 axis in Th2 responses. Thus, functional inhibition of the chemokine receptor CCR8 or its ligand CCL1 might prove a valuable strategy for the treatment of allergic diseases such as asthma or atopic dermatitis.

**Disclosures**

The authors have no financial conflict of interest.

**References**


