**CXCR6 within T-helper (Th) and T-cytotoxic (Tc) type 1 lymphocytes in Graves’ disease (GD)**

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Abstract

**Objective**: In Graves’ disease (GD), stimulating anti-TSH receptor antibodies are responsible for hyperthyroidism. T-helper 2 (Th2) cells were expected to be involved in the underlying immune mechanism, although this is still controversial. The aim of this study was to examine the expression of CXCR6, a chemokine receptor that marks functionally specialized T-cells within the Th1 and T-cytotoxic 1 (Tc1) cell pool, to gain new insights into the running immune processes.

**Methods**: CXCR6 expression was examined on peripheral blood lymphocytes (PBLs) and thyroid-derived lymphocytes (TLs) of GD patients in flow cytometry. CXCR6 cDNA was quantified in thyroid tissues affected by GD (n = 16), Hashimoto’s thyroiditis (HT; n = 2) and thyroid autonomy (TA; n = 11) using real-time reverse transcriptase PCR.

**Results**: The percentages of peripheral CXCR6⁺ PBLs did not differ between GD and normal subjects. CXCR6 was expressed by small subsets of circulating T-cells and natural killer (NK) cells. CXCR6⁺ cells were enriched in thyroid-derived T-cells compared with peripheral CD4⁺ and CD8⁺ T-cells in GD. The increase was evident within the Th1 (CD4⁺ interferon-γ⁺ (IFN-γ⁺)) and Tc1 (CD8⁺IFN-γ⁺) subpopulation and CD8⁺ granzyme A⁺ T-cells (cytotoxic effector type). Thyroid-derived fibroblasts and thyrocytes were CXCR6⁻. There was no significant difference between the CXCR6 mRNA levels in GD compared with HT and normal TA tissues. The lowest CXCR6 mRNA levels were obtained from thyroid nodules from TA patients and GD patients with low thyroid peroxidase autoantibody levels.

**Conclusions**: CXCR6 was overexpressed in Th1 and Tc1 TLs compared with PBLs in GD. CXCR6 could be a marker for lymphocytes that have migrated into the thyroid and assist in the thyroid, independently of the bias of the underlying disease.

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Introduction

Graves’ disease (GD) and Hashimoto’s thyroiditis (HT) are organ-specific autoimmune diseases characterized by diffuse or focal lymphocytic infiltration. In GD, stimulating anti-thyroid-stimulating hormone (TSH) receptor (TSHR) autoantibodies overstimulating the TSHR are responsible for hyperthyroidism. In HT, normal thyroid tissue is replaced mainly by lymphocytes organized in ectopic follicles. The destruction of thyrocytes causes hypothyroidism.

The expected underlying immune mechanisms of both diseases led to the application of the common CD4⁺ T-helper 1 (Th1)/Th2 paradigm of immunology. Th2 cells producing interleukin 4 (IL-4), IL-5, IL-10 and IL-13 are involved in humoral immunity, as was first expected for GD. In HT, Th1 cells are thought to produce interferon-γ (IFN-γ) and act on cell-mediated immune responses leading to thyrocyte destruction. Similarly to CD4⁺ T-cells, the CD8⁺ type 1 cytotoxic (Tc1) and Tc2 cells differentially secrete type 1 and type 2 cytokines, respectively. In addition to cytokine secretion, Tc1 and Tc2 populations mediate cytolytic effects, with Tc1 cells utilizing both perforin- and Fas-based killing pathways, whereas Tc2 cells primarily utilize perforin-mediated cytolysis (1).

However, recent results from clinical studies and newly established mouse models (2–7) have clearly shown that the assumption that GD and HT are immune responses dominated by Th2 or Th1/Tc1, respectively, is an oversimplification. The role of the Th1/Th2 balance is especially controversial in murine models of Graves’ hyperthyroidism. Suppression of TSHR-specific Th1 immune responses by exogenous IL-4 was associated with inhibition of hyperthyroidism in BALB/c mice injected with adenovirus-expressing TSHR (TSHR-adeno model), indicating the critical role of Th1 cytokines (4). In contrast, BALB/c IL-4-knockout but not IFN-γ-knockout mice failed to develop Graves’ hyperthyroidism when injected with TSHR-expressing M12 B lymphoma cells, suggesting the importance of endogenous IL-4. In the IL-4- and IFN-γ-knockout
TSHR-adenovirus model, both IL-4 and IFN-γ are implicated in the development of hyperthyroidism (7).

Besides determining the ratio of type 1 and type 2 specific cytokine responses – in most cases IFN-γ/IL-4 – or the immunoglobulin subclass of TSHR antibodies (IgG2a/IgG1), analysis of chemokine receptors and their ligands allows insights into the running autoimmune process (2, 3). Among the over 50 chemokines and 20 chemokine receptors, only a few are thought to mark functionally specialized T-cells within the total Th1 and Tc1 T-cell pool (8, 9).

CXCR6 (Bonzo, STRL33, TYMSTR) (10–12) and its ligand CXCL16 (SR-PSOX) belong to the few unique chemokine/receptor pairs that suggest special immune functions, whereas most other pairs show promiscuity and overlap in cell and tissue expression. CXCR6 seems to mark functionally specialized T-cells within the total Th1 and Tc1 cell pool (13). In contrast, the chemokine receptor is displayed by very few (1–2%) Th2 or Tc2 cells. CXCL16 (13–15) is structurally different from most other chemokines. It is a type I transmembrane protein with four distinct domains: one chemokine domain tethered to the cell surface via a mucin-like stack, which in turn is attached to transmembrane and cytoplasmic domains. CXCL16 acts as an adhesion molecule when expressed on the cell surface (16). Upon cleavage from the cell surface, the soluble chemokine shows chemoattractive activity (17).

Recently published studies indicate a unique role for CXCR6 and its ligand in attracting activated lymphocyte subsets during inflammation, while also facilitating immune responses via cell contact (16, 18, 19).

There are no data on the distribution of CXCR6 in thyroid autoimmunity and few on autoimmune diseases at all (20). The aim of our study was to investigate CXCR6 and CXCL16 mRNA expression in thyroids affected by GD compared with thyroid tissue from patients with HT and non-autoimmune thyroid autonomy (TA) to gain new insights into the running immune processes within the thyroid and to characterize the lymphocytic subpopulations involved. In GD, we isolated thyroid-derived lymphocytes (TLs) and compared the expression of CXCR6 with that of peripheral blood lymphocytes (PBLs) from the same patients. The potential thyroid-cell sources of the receptor and its ligand were defined.

Materials and methods

Patients

Thyroid diseases were diagnosed on the basis of clinical, biochemical and immunological features as well as from scintiscans. Antibodies against the TSHR (TSH-binding-inhibiting immunoglobulin; TBII) and thyroid peroxidase (TPO) were measured in serum obtained up to 2 weeks before operation with commercial RIA kits (TRAKhuman DYNOSTEST®, anti-TPO, DYNOTEST®; Brahms Diagnostica GmbH, Berlin, Germany). The numbers of focal lymphocytic infiltrates and ectopic germinal centers were counted on hematoxilin/eosin-stained sections of thyroid samples within an area of 226 mm² as described in (21).

For mRNA quantitation, we used thyroid tissues from GD (n = 16, all females; mean age ± S.E.M. 35.6 ± 3.7 years), HT (n = 2, both females; 18 and 34 years) and TA (n = 11, five females; 55.7 ± 5.2 years) patients (same collective as described in detail in (22)). Four out of these 16 GD patients used for mRNA analysis were further included for flow-cytometric analysis (Table 1).

All GD patients were treated with anti-thyroid drugs but not corticosteroids at the time of surgery. The duration of GD until enrolment was longer than 15 months in most cases. Peripheral blood samples from 10 normal adults (two male, eight female; mean age 33.7 ± 2.7 years) without any history of autoimmune disease were used as controls. The study was approved by the local Committee of Medical Ethics.

Isolation of cells and cell lines used in this study

Thyroid samples were obtained during operation. TLs were isolated after mechanical tissue disaggregation via free access

Table 1 Age, sex, duration of disease until enrolment, signs of Graves' ophthalmopathy (GO), treatment with anti-thyroid drugs and corticosteroids of patients with GD analyzed for CXCR6 expression on PBLs and TLs in flow cytometry.

<table>
<thead>
<tr>
<th>Patient no.</th>
<th>Patient no. in reference (22)</th>
<th>Age</th>
<th>Sex</th>
<th>Duration of disease (months)</th>
<th>Anti-thyroid drug treatment</th>
<th>Corticosteroid treatment</th>
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and Ficoll density-gradient centrifugation. Thyrocytes were enriched after enzymatic digestion of the tissue as described in (23). Outgrowing fibroblasts were obtained by culturing small pieces of thyroid samples. PBLs were isolated by Ficoll density-gradient centrifugation. Anaplastic thyroid carcinoma cell lines SW-1736, Hth-74, C-634 (kindly provided by N.-E. Heldin, University of Uppsala, Uppsala, Sweden) and 8505 C, follicular lines FTC-133 and FTC-238 and papillary line B-CPAP (DSMZ, Braunschweig, Germany), as well as Chinese hamster ovary (CHO) cells (ATCC) were cultured in Dulbecco’s modified Eagle’s medium/10% fetal calf serum.

**Examination of the CXCR6 antibody**

Since we always measured a lower number of T-cells expressing CXCR6 than described in (10), the specificity and sensitivity of the monoclonal antibody (mAb) used was examined. First, PBLs were cultured with 100 ng/ml IL-15 (Immunotools, Friesoythe, Germany) over 6 days, and the number of CXCR6$^+$ cells was determined by flow cytometry. Secondly, the CXCR6-encoding cDNA was cloned in the vector pcDNA3.1 Zeo(+) (Invitrogen GmbH, Karlsruhe, Germany) using the primer pair 5'-CCG GAA GCT TAC CAT GGC AGA GCA TGA TTA CC-3' (sense) and 5'-GGA ATT CGA TTA ACC CTG TGC TCT AT-3' (antisense). CHO cells were transiently transfected with the construct using Lipofectamine (Invitrogen). mAb binding was measured after 48 h by flow cytometry.

**Analysis by flow cytometry**

Directly fluorochrome-labeled mAbs were supplied by R & D Systems GmbH (Wiesbaden, Germany; CXCR6-PE, IFN-$\gamma$-FITC), DakoCytomation Denmark A/S (Glostrup, Denmark; CD3-RPE-Cy5, CD8-RPE-Cy5, CD62L-FITC, CD4-FITC), ImmunoTech (Marseille, France; CD45R0-FITC) or BD Biosciences Europe (Heidelberg, Germany; CD4-Cy5, CD19-PerCP, granzyme A-FITC).

To enrich intracellular cytokines, cells were treated with PMA (10 ng/ml), ionomycin (1 $\mu$mol) and Golgi-Plug (1 $\mu$mol/ml; BD Biosciences) in RPMI 1640/10% fetal calf serum for 4 h. Since ionomycin markedly diminishes CXCR6 expression, cells must be pre-stained with the anti-CXCR6 antibody before treatment (24).

Cytometers were fixed and permeabilized using Cytofix/Cytoperm solutions (BD Biosciences) before staining to analyze intracellular cytokines and granzyme A. This procedure is not necessary if only cell-surface antigens are analyzed. Unfixed or fixed PBLs or TLs (3 x 10$^5$) were incubated with mAbs at the desired concentration for 30 min at 4°C. The following mAb combinations were used: (1) CXCR6-PE; CD3-RPE-Cy5; CD8-FITC, CD4-FITC. CD45R0-FITC. CD62L-FITC or CD56-FITC; (2) CXCR6-PE; CD8-RPE-Cy5 or CD4-Cy5; IFN-$\gamma$-FITC and (3) CXCR6-PE; CD8-RPE-Cy5; granzyme A-FITC. The cells were analyzed by flow cytometry (FACScan$^\text{R}$, Becton Dickinson, Mountain View, CA, USA) using electronic gating on lymphocyte subpopulations. The Mann–Whitney test was used to determine statistical significance.

**Real-time reverse transcriptase (RT)-PCR**

Total cellular RNA was isolated with the Qiagen total RNA isolation kit (Qiagen GmbH, Hilden, Germany). cDNA was synthesized from 1 $\mu$g RNA in a 20-ml standard reaction mixture containing 200 U RNaseH reverse transcriptase (Invitrogen). Quantitative PCR was performed on a Rotorgene (Corbett Research, Mortlake, Australia) real-time machine by using SYBR$^\text{R}$ Green I as a double-strand DNA-specific binding dye and continuous fluorescence monitoring. Amplification was carried out in a total volume of 20 ml containing 0.5 $\mu$M of each primer, 1–3 mM MgCl$_2$, 1 U Taq polymerase (Roche), 10 x Taq buffer (500 mM KCl/100 mM Tris/HCl, pH 8.3; Roche), 2 mM of each dNTP and 1 $\mu$l SYBR$^\text{R}$ Green (1:2000; Molecular Probes Europe, Leiden, The Netherlands) dissolved in DMSO and 1 $\mu$l cDNA diluted 1:5.

The PCR primers were CXCR6 sense (5'-CCT GCC TTA ACC CTG TGC TCT AT-3') and antisense (5'-ATG TCA TCC CCC TTG GTT TCA-3'), CXCL16 sense (5'-GGG GGC AGT CAC CGC AGT CCT-3') and antisense (5'-ATT AGC CGG GTG TGG TGG TGA GTA GCA-3') or CD18 sense (5'-GGC GCA CAA GCT GGC TGA AAA CCA AA-3') and antisense (5'-AGC GCC CAG ATG ATC AAC GAC TG-3'), respectively. CD18 mRNA was measured in order to quantify leukocytic infiltration (25). Sizes of PCR products were: CXCR6 459 bp; CXCL16 518 bp, and CD18 372 bp. Glyceraldehyde 3-phosphatase dehydrogenase (GAPDH) transcripts were measured with a ready-to-use quantitative PCR test kit (Roboscreen, Leipzig, Germany) (26). External cDNA standards were constructed by blunt-end cloning of PCR fragments into pGEM-T vector (Promega, Mannheim, Germany). Plasmid DNA was prepared (Plasmid Mini Kit; Qiagen), quantified and stabilized in the PCR tubes (27). Amounts were calculated from a reference curve obtained from the simultaneously processed standard curve. Data were expressed as zeptomoles (amol; 10$^{-21}$ mol) of cDNA per attomole (amol; 10$^{-18}$ mol) of GAPDH cDNA.

**Results**

**Flow cytometry**

We first examined whether the available CXCR6 mAb was suitable for flow cytometry. IL-15 increased the number of CXCR6$^+$ PBLs by about 5-fold as shown in a typical case in Fig. 1A. Moreover, transiently transfected CHO cells expressing human CXCR6 were...
CXCR6. The number of positive cells varied non-significantly whether we used a direct or indirect CXCR6 labeling system (Fig. 1B).

Secondly, PBLs of normal subjects and GD patients as well as TLs of GD patients were analyzed for CXCR6 expression. All results are summarized in Table 2. Table 2A contains a general overview on the cellular composition of PBLs and TLs. The percentage of memory T-cells (CD3⁺CD45RO⁺) increased in the thyroid compared with periphery. TLs differed from their PBLs counterparts in terms of lymph-node-homing capabilities since CD62L was expressed at only 27% of TLs but 79% of PBLs. The percentage of T-cells capable to produce IFN-γ was higher in the thyroid compared the periphery. IFN-γ⁺ cells were more present in CD8⁺ than CD4⁺ PBLs and TLs.

The expression pattern of CXCR6 within these lymphocytic subpopulations was also characterized (Table 2B, Fig. 2). The percentage of CD3⁺ and, further subdivided, CD4⁺ and CD8⁺ T-lymphocytes expressing CXCR6 in PBLs did not vary between normal subjects and patients with GD. However, these CD4⁺CXCR6⁺ and CD8⁺CXCR6⁺ T-cells were enriched 3–5-fold in the thyroid compared with the periphery. The increase in CXCR6⁺ cells was evident within the Th1 (CD4⁺IFN-γ⁺) and Th1 (CD8⁺IFN-γ⁺) T-cell subpopulations (Fig. 2A and B). A higher percentage of peripheral as well as thyroid-derived CD8⁺ T-cells, compared with CD4⁺ T-cells, expressed CXCR6. Since the percentage of CXCR6⁺ T-cells producing IL-4 was very low in PBLs and TLs (<1%; not shown), we do not suggest a function for CXCR6⁺ Th2 or Th2 cells in the thyroid.

Table 2. CXCR6 expression of TLs and PBLs from patients with GD and normal controls (n=10) analyzed by flow cytometry using multicolor analysis and lymphocyte gating.

<table>
<thead>
<tr>
<th>Characterization of lymphocytes</th>
<th>Relative number of cells expressing the marker (%) in each lymphocyte subpopulation</th>
</tr>
</thead>
<tbody>
<tr>
<td>100% CD3⁺</td>
<td>TLs (GD)</td>
</tr>
<tr>
<td>CD62L⁺</td>
<td>8.3±0.4</td>
</tr>
<tr>
<td>CD45RO⁺</td>
<td>1.0±0.3</td>
</tr>
<tr>
<td>CD4⁺</td>
<td>9.1±1.5</td>
</tr>
<tr>
<td>CD8⁺</td>
<td>10.5±1.0</td>
</tr>
<tr>
<td>100% CD8⁺</td>
<td>TLs (GD)</td>
</tr>
<tr>
<td>Granzyme A⁺</td>
<td>2.5±0.4</td>
</tr>
<tr>
<td>IFN-γ⁺</td>
<td>50.5±6.4</td>
</tr>
<tr>
<td>100% CD4⁺</td>
<td>TLs (GD)</td>
</tr>
<tr>
<td>CXCR6⁺</td>
<td>20.1±3.7</td>
</tr>
</tbody>
</table>

*Significant differences between TLs and PBLs in GD patients; **significant differences between PBLs from GD patients and controls; percentage of labeled cells (means±S.E.M.).
Granzymes are important effector molecules for cytotoxic lymphocytes and induce granule-mediated apoptosis in target cells. Some 40–50% of CD8+ cells expressed intracellular granzyme A in both PBLs and TLs from GD patients. Within these peripheral CD8+ granzyme A+ cells, only a few (<4%) expressed CXCR6, whereas nearly 20% carried the receptor in the thyroid (Fig. 2C). The majority of CD8+ CXCR6+ peripheral and thyroid-derived cells were positive for granzyme A.

CD3+CD56+ T-cells are effector cells with strong cytotoxic activity against target cells. In this regard, CXCR6 was expressed on higher percentages of CD3+CD56+ than on less cytotoxic CD3−CD56− cells.

Most peripheral CD3+CXCR6+ cells have extralymphoid tissue-homing potential since 60% failed to express CD62L. Approximately 90% of thyroid-derived CXCR6+CD3+ T-cells lack CD62L (Table 2, Fig. 2D). Peripheral and thyroid-derived B-cells did not express CXCR6 (not shown).

**CXCR6 and CXCL16 mRNA in thyroid tissues and thyroid-derived cells**

Real-time PCR revealed that thyroid tissues from all GD patients with high TPO levels and both HT patients...
were positive for CXCR6 mRNA, whereas no signal was present within some tissues from GD patients with low or no TPO levels and TA tissues (Fig. 3A). We found a slight correlation between CXCR6 and (1) CD18 mRNA levels ($r = 0.51$; $P = 0.044$) and (2) TPO antibody levels ($r = 0.66$; $P = 0.05$) in GD patients. There was no correlation between CXCR6 mRNA levels and TBII ($P = 0.60$) or the number of lymphocytic infiltrates ($P = 0.60$) in these patients. We found no difference in CXCR6 mRNA levels in GD compared with normal TA tissue. Lowest levels were present in TA nodules. Here, three out of nine samples were negative for CXCR6 mRNA.

Using simple RT-PCR, PBls and TLs were CXCR6 mRNA-positive, whereas no signal was obtained from thyroid-derived fibroblasts (Fig. 3C). Thyrocytes showed only a very faint signal. Thyroid carcinoma cell lines were positive for CXCR6 mRNA. The expression level varied considerably.

Quantifying CXCL16 cDNA in thyroid tissues (Fig. 3B), the levels were somewhat high compared with other chemokines quantified (21, 25, 28). Surprisingly, CXCL16 cDNA levels within the two HT tissues were within the same range as those of many GD and normal TA tissues. This suggests that cells other than the known CXCL16 producers such as dendritic cells and macrophages may express CXCL16 mRNA. Indeed, besides TL, thyrocytes were strongly positive for this chemokine mRNA (Fig. 3C). Thus, the CXCL16 mRNA levels tend to represent the presence of this chemokine within several cell types of the thyroid than a specific expression by immunocompetent cells.

**Discussion**

We have demonstrated here that CXCR6, a chemokine receptor present on a small subset of specialized circulating Th1 and Tc1 cells, is expressed on a higher percentage of TLs than PBls from GD patients.

The data raise the question of the CXCR6’s function in the thyroid. The result agrees with our own previous study on CXCR3 and CCR5 (29), chemokine receptors that are thought to be predominantly, but not exclusively, found on Th1 cells. Both receptors were expressed on a higher percentage of TLs compared with PBls, and may be involved in the recruitment of lymphocytes to the thyroid in GD (30, 31). We suggest that, in addition to CXCR3 and CCR5, CXCR6 may be a marker for cells that have migrated into thyroid tissue and assist there, independently of the bias of the underlying disease. This is confirmed by the fact that most of the CXCR6$^+$ T-cells in the thyroid lost their lymph-node-homing capabilities since they were CD62L$^-$.

The antigen is downregulated in response to migration and activation by proteolytically cleaving from the cell surface (32). Moreover, our assumption is supported by recent studies demonstrating that CXCR6$^+$ T-cells were enriched in tissue sites of inflammation, such as rheumatoid joints and inflamed livers (13, 18).

Although a higher percentage of TLs compared with PBls were CXCR6$^+$ in GD, we did not find a difference between CXCR6 mRNA levels in the thyroid tissues from different patients groups. Mistakes in CXCR6 mRNA determination were unlikely since quantitation of the chemokine receptor/ligand pair CXCR5/CXCL13 in the same cDNAs samples resulted in significantly higher levels in GD compared with TA samples and the highest levels in HT tissues (21). Our results suggest that the number of CXCR6$^+$ and thus Th1 and Tc1 cells in HT may not be higher than in other thyroids, including non-autoimmune TA. There are several possible explanations for this result. As in GD tissues, the chronic lymphocytic infiltrate does not reflect the initiation, but rather the maintenance or perturbation, of the immune process in HT tissues.
since a substantial number of thyrocytes are always destroyed at the time of surgery (33, 34). The time of action of specialized Th1 and Tc1 cells may be over during HT. This assumption is confirmed by reports showing a significant increase in IFN-γ-inducible chemokines CXCL10 (IP-10) and CXCL9 (Mig) strongly associated with Th1-mediated immune responses in thyroid tissue specimens obtained from subjects affected by recent-onset GD (2, 35, 36). An increase in serum CXCL10 levels has only been found in newly diagnosed GD patients, compared with healthy subjects and patients with long-standing disease. An inverse correlation between circulating CXCL10 levels and disease duration has been demonstrated (37). This means that changes in the composition of regulating T-cell subsets involved, and thus chemokines and their receptors, occur within the thyroid but also at the periphery, depending on the duration of GD.

Data on CXCR6 in autoimmunity are very limited (20). An increase of CXCR6+ cells was shown in arthritic synovial fluid, which was discussed as playing a role of the receptor in the traffic of effector T-cells that mediate type 1 inflammation. The paucity of data published on CXCR6 may be due to the discrepant results obtained with the available antibodies and the first data published (10). The percentages of CXCR6+ T-cells in normal subjects in our study were lower, although we used the same mAb and staining technique as in (10) (15 versus 4.1% CXCR6+ cells within CD3+). Thus, we first showed that the mAb used indeed detects CXCR6 and that the percentage of CXCR6+ T-cells does not depend on direct or indirect labeling methods. Moreover, IL-15 increased the number of CXCR6+ PBLs by about 5-fold, which was in accordance to data obtained by Unutmaz et al. (10).

CXCR6+ T-cells are thought to represent type 1 cells, which mainly regulate cellular but not humoral immune responses. This might explain the missing correlation of CXCR6 mRNA with TBI1 and the slight correlation of CXCR6 mRNA with TPO antibodies. TPO antibodies better reflect the immune responses in long-standing disease compared with TBI1 (38). Additionally, thyroid autoantibodies might not be produced exclusively by the thyroid itself (39–41).

The correlation between CXCR6 mRNA and CD18 mRNA is weak. CD18 mRNA also includes the mRNA of those lymphocytes that were not located within infiltrates or germinal centers, but scattered throughout the tissue and, additionally, the mRNA of non-lymphoid leukocytes, the macrophages. We do not know where CXCR6+ lymphocytes are located within Graves’ thyroids or whether or not they accumulate on certain structures. This may explain why we missed a correlation between CXCR6 and defined lymphocytic infiltrates and germinal centers.

Does the ligand of CXCR6, CXCL16, yield any additional information on the function of this chemokine/receptor pair in the thyroid? CXCL16 not only attracts CXCR6 expressing T-cells, natural killer (NK) cells and NK/T-cells to the site of inflammation and injury, but also mediates firm adhesion of CXCR6-expressing cells in its transmembrane form (16, 19). The chemokine is induced by pro-inflammatory stimuli such as tumour necrosis factor-α and IFN-γ (17). Surprisingly, we did not find any differences between CXCL16 mRNA levels in the thyroid tissues analyzed. Normally, CXCL16 is only expressed by macrophages, dendritic cells and CD19+ B-cells (14, 42). In our study, a strong CXCL16 mRNA signal was obtained from thyrocytes and thyroid carcinoma cell lines. Thus, CXCL16 also seems to be produced by epithelial cells, which confirms older studies showing that thyrocytes were potential cytokine producers (43). Untreated thyrocytes secrete CXCL8 (IL-8) and the other chemokine that binds to the CXCR2, CXCL1 (GRO-α) (28). CCL2 (monocyte chemoattractant protein-1; MCP-1) is a chemokine that attracts T-lymphocytes as well as monocytes, and can be also produced by thyrocytes (44). Thyrocytes from autoimmune thyroid disorders produce the chemokines CXCL9 and CXCL10 after stimulation (36). All these studies suggest a possible role for thyrocytes on accumulation of leukocytes in the tissue from the blood. Unfortunately, useful CXCL16 antibodies for immunohistology or establishment of protein screening assays were not available.

In summary, our study demonstrates that the percentages of Tc1 (CD8+IFN-γ+) and Th1 (CD4+IFN-γ+) cells as well as cytotoxic effector cells (CD8+granzymeA+) expressing CXCR6 were increased in TLs compared with PBLs in GD patients. However, we did not find any difference between CXCR6 mRNA levels in thyroid tissues from different patient groups. CXCR6 could be a marker for cells that have migrated into the thyroid and assist there, independently of the bias of the underlying disease.

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