Eosinophil Chemotactic Chemokines (Eotaxin, Eotaxin-2, RANTES, Monocyte Chemoattractant Protein-3 (MCP-3), and MCP-4), and C-C Chemokine Receptor 3 Expression in Bronchial Biopsies from Atopic and Nonatopic (Intrinsic) Asthmatics

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Atopic (AA) and nonatopic (NAA) asthma are characterized by chronic inflammation and local tissue eosinophilia. Many C-C chemokines are potent eosinophil chemoattractants and act predominantly via the CCR3. We examined the expression of eotaxin, eotaxin-2, RANTES, monocyte chemoattractant protein-3 (MCP-3), MCP-4, and CCR3 in the bronchial mucosa from atopic (AA) and nonatopic (intrinsic; NAA) asthmatics and compared our findings with atopic (AC) and nonatopic nonasthmatic controls (NC). Cryostat sections were processed for immunohistochemistry (IHC), in situ hybridization (ISH), and double IHC/ISH. Compared with AC and NC, the numbers of EG2⁺ cells and the cells expressing mRNA for eotaxin, eotaxin-2, RANTES, MCP-3, MCP-4, and CCR3 were significantly increased in AA and NAA (p < 0.01). Nonsignificant differences in these variants were observed between AA and NAA and between AC and NC. Significant correlations between the cells expressing eotaxin or CCR3 and EG2⁺ eosinophils in the bronchial tissue were also observed for both AA (p < 0.01) and NAA (p = 0.01). Moreover, in the total asthmatic group (AA + NAA) there was a significant inverse correlation between the expression of eotaxin and that of the histamine PC20 (p < 0.05). Sequential IHC/ISH showed that cytokeratin⁺ epithelial cells, CD31⁺ endothelial cells, and CD68⁺ macrophages were the major sources of eotaxin, eotaxin-2, RANTES, MCP-3, and MCP-4. There was no significantly different distribution of cells expressing mRNA for these chemokines between atopic and nonatopic asthma. These findings suggest that multiple C-C chemokines, acting at least in part via CCR3, contribute to bronchial eosinophilia in both atopic and nonatopic asthma.


I t is widely accepted that a subgroup of asthmatic patients are not demonstrably atopic (the so-called intrinsic variant of the disease) (1). Intrinsic asthmatics are skin test negative to extracts of common allergens, and there is no evidence of allergen-specific serum IgE Abs. Serum total IgE concentrations are within the normal range. There is also no clinical or family history of allergy. There has been debate about the relationship of this variant of the disease to atopy (2). Although the onset of the disease may be triggered by viral infection, such as a respiratory influenza-like illness, some authors have suggested a role for IgE and atopy in so-called intrinsic asthma (3). These data indicate that intrinsic asthmatics may be allergic to an as yet undetected allergen and that these patients might benefit from allergen-free environments, as previously demonstrated in atopic asthma (4). Our previous work indicated that although intrinsic asthma has some clinical characteristics similar to those of extrinsic asthma, it does not appear to be a distinct immunopathologic entity (5–8). Thus, in a series of bronchial biopsy studies using in situ hybridization (ISH) and immunohistochemistry (IHC), alone or in combination, both variants of the disease were characterized by an allergic-like bronchial mucosal inflammation, including eosinophils, IL-4⁺ and IL-5⁺ Th2-type cells, RANTES, MCP-3, and FcεRI⁺ cells (5–8). The only difference seemed to be a strong macrophage signal, i.e., there were increased numbers of CD68⁺ cells and cells mRNA⁺ for GM-CSF receptor α-chain in intrinsic asthma compared with extrinsic asthma (9).

In the present study we have extended these observations by measuring the expression of eotaxin, eotaxin-2, MCP-4, and CCR3 in bronchial biopsies from intrinsic and extrinsic asthma. Unlike RANTES, MCP-3, and MCP-4, which ligate several C-C chemokine receptors, eotaxin and eotaxin-2 bind exclusively to CCR3. The two C-C chemokines are also selective in their biological activity on eosinophils and basophils, although CCR3 may also be transiently expressed on Th2 cell lines. For these reasons we have tested the hypothesis that the range of C-C chemokines, including eotaxin and eotaxin-2, as well as the eotaxin receptor, CCR3, is

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Abbreviations used in this paper: ISH, in situ hybridization; FEV₁, forced expiratory volume in 1 s; BAL, bronchoalveolar lavage; IHC, immunohistochemistry; MCP, monocyte chemoattractant protein; AA, atopic asthmatics; NAA, nonatopic asthmatics; AC, nonasthmatic controls; NC, nonatopic nonasthmatic controls; RAST, radioallergosorbent; APAAP, alkaline phosphatase-antialkine phosphatase.

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similar in both atopic and nonatopic asthma, indicating a common mechanism of local eosinophilia in both subgroups.

Materials and Methods

Study patients

The study was approved by the ethics committees of the Royal Brompton Hospital (London, U.K.) and the Hochgebirgsklinik (Davos Wolfgang, Switzerland). Each participant gave informed consent before entering the study. Bronchial biopsy specimens were obtained from 10 atopic asthmatics (AA), 10 nonatopic asthmatics (NAA), and 10 nonatopic nonasthmatic controls (NC) as previously characterized (5). The patients studied were recruited from the Royal Brompton Hospital (London, U.K.) and the Hochgebirgsklinik. Asthmatic subjects had a clear history of asthma, requiring intermittent inhaled β₂-agonist therapy, and documented reversible airway obstruction (20% improvement in forced expiratory volume in 1 s (FEV₁) either spontaneously or after administration of inhaled β₂-agonist), and a histamine PC₂₀ provocation test result ≥6 mg/ml in the previous 2 wk.

Fiberoptic bronchoscopy

The bronchoscopy procedure was performed using an Olympus model IT30 bronchoscope (Olympus, Tokyo, Japan) at the same time of day (9 a.m.) in all the subjects. Bronchoscopy was performed in all subjects following premedication with 2.5 mg of salbutamol by nebulizer, 0.6 mg of atropine, and 5–10 mg of midazolam administered i.v. Biopsies were taken from the right middle and lower bronchi using Olympus alligator forceps following premedication with 2.5 mg of salbutamol by nebulizer, 0.6 mg of atropine, and 5–10 mg of midazolam administered i.v. Biopsies were taken from the right middle and lower bronchi using Olympus alligator forceps (model FB15C). All asthmatics were given an additional 2.5 mg of nebulized salbutamol, and the safety of our protocol was prospectively monitored in all subjects. Bronchial biopsy specimens were obtained from 10 atopic asthmatics (AA), 10 nonatopic asthmatics (NAA), 10 nonasthmatic atopic controls (AC), and 10 nonatopic nonasthmatic controls (NC) as previously characterized (5). The patients studied were recruited from the Royal Brompton Hospital (London, U.K.) and the Hochgebirgsklinik. Asthmatic subjects had a clear history of asthma, requiring intermittent inhaled β₂-agonist therapy, and documented reversible airway obstruction (20% improvement in forced expiratory volume in 1 s (FEV₁) either spontaneously or after administration of inhaled β₂-agonist), and a histamine PC₂₀ provocation test result ≥6 mg/ml in the previous 2 wk.

Immunohistology

Sections (6 μm) were freshly cut from frozen bronchial biopsies. For identification of eosinophils, basophils, eotaxin, and CCR3 protein product, IHC of bronchial biopsies was performed using alkaline phosphatase-antialkaline phosphatase (APAAP) method as described previously (6, 7, 12). Rabbit anti-mouse Ig, APAAP, and control IgG were purchased from Dako (High Wycombe, U.K.). EG2, a mAb against human activated eosinophils, was purchased from Pharmacia (Uppsala, Sweden). A mouse anti-human eotaxin mAb (2G6) and anti-human CCR3 mAb (7B11) were provided by Drs. C. Mackay, P. Ponath, and W. Newman (LeukoSite, Palo Alto, CA) and Dr. B. J. Rottman (Southampton, U.K.). BB1, a mAb recognizing a human basophil granular protein, was a gift from Dr. A. F. Walls (Southampton General Hospital, Southampton, U.K.). This mAb did not react with lymphocytes, monocytes, platelets, neutrophils, eosinophils, mast cells, or any other cell type or tissue structure (17).

The optimal concentrations of all Abs used were determined in pilot experiments. Briefly, the sections were incubated with 20% human serum in PBS for 20 min, then incubated with monoclonal anti-human eotaxin (2G6, 1/50), or monoclonal mouse anti-CCR3 (7B11, 1/50) in 20% human serum/ PBS overnight at room temperature. Slides then were treated with rabbit anti-mouse IgG (1/30, 30 min) and APAAP (1/30, 30 min), respectively. For immunostaining of BB1+ basophils, the slides were pretreated with 0.1% saponin (Sigma)/PBS for 30 min, incubated with BB1 Ab (1/10) overnight at room temperature, then processed as described above. Positive cells stained red after development with Fast Red (Sigma). Omission or substitution of the primary Ab with an irrelevant Ab of the same species

Table I. Clinical characteristics of AA, NAA, AC, and NC and normal controls

<table>
<thead>
<tr>
<th>Subject</th>
<th>Age</th>
<th>Sex</th>
<th>Blood Eosinophils (%)</th>
<th>FEV₁ (% predicted)</th>
<th>Histamine PC₂₀ (mg/ml)</th>
<th>Serum (total IgE) (IU/ml)</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA (n = 10)</td>
<td>28.5 (22–55)</td>
<td>2/8</td>
<td>2.9 (0.8–5.7)</td>
<td>77.5 (55.0–104.0)**</td>
<td>1.1 (0.02–3.0)</td>
<td>230.5 (73.0–570.0)*</td>
</tr>
<tr>
<td>NAA (n = 10)</td>
<td>53.5 (42–62)***</td>
<td>4/0</td>
<td>9.0 (1.9–14.2)</td>
<td>75.5 (58.0–112.0)****</td>
<td>1.05 (0.12–6.8)</td>
<td>56.0 (17.0–124.0)*</td>
</tr>
<tr>
<td>AC (n = 10)</td>
<td>25.5 (21–33)</td>
<td>2/8</td>
<td>3.7 (1.1–8.2)</td>
<td>103.5 (91.0–112.3) &gt;16</td>
<td>&gt;16</td>
<td>162.0 (77.0–808.0)*</td>
</tr>
<tr>
<td>NC (n = 10)</td>
<td>20.5 (18–28)</td>
<td>4/6</td>
<td>1.5 (0.1–5.0)</td>
<td>98.5 (82.0–119.0) &gt;16</td>
<td>&gt;16</td>
<td>21.0 (4–47.0)</td>
</tr>
</tbody>
</table>

* Results are expressed as median, and range is given in parentheses.

References

1. J. Van Damme and G. Opdenakker (Rega Institute for Medical Research, University of Leuven, Leuven, Belgium) (7, 15). Riboprobes were prepared from cDNA for these chemokines and CCR3 as previously described (6, 7, 12). Briefly, riboprobes (antisense or sense) were synthesized in the presence of ATP, GTP, CTP, and [15S]UTP and appropriate RNA polymerases (T7, SP6, or T3), respectively.

Permeabilization, prehybridization, and hybridization protocols were described previously (6, 7, 12). Incubation in N-ethylmaleimide, iodoacetamide, and triethanolamine reduced nonspecific binding of the [15S]UTP-labeled probes. Furthermore, the experiments were performed under very high stringency condition (hybridization at 50°C and posthybridization washing at 60°C, 0.1% SSC) to minimize nonspecific hybridization. Negative controls employed hybridized with the sense probe and pretreatment of slides with RNAse A (Promega, Southampton, U.K.) before hybridization with the antisense probe. For autoradiography, slides were dipped into K-5 emulsion (Ilford, Basildon, U.K.) and exposed at 4°C for 2 wk in absolute darkness in a desiccated environment. The slides were developed (D-19 developing solution, Eastman Kodak, Rochester, NY), rinsed, and counterstained with Harris hematoxylin. Dense deposits of silver grains on autoradiographs were present over cells expressing chemokine mRNA. Slides were counted in duplicate, blind to the patients’ clinical status, using an eyepiece graticule, as previously described (6, 7, 12). The results were expressed as the total number of positive cells per field (per 0.202 mm²) of submucosa. The coefficient of variability of the duplicate counts obtained from all slides was <5%.
was used as a negative control. All the slides were counted in duplicate under blind conditions to the patients’ clinical status. Results were expressed as the total number of positive cells per field (0.202 mm²) of submucosa. The coefficient of variability of the duplicate counts obtained from all slides was <5%. No immunoreactivity was observed in sections stained with omission of the primary Ab or substitution of this Ab with an irrelevant Ab of the same species.

Sequential IHC and ISH
To identify the cell sources of eotaxin, eotaxin-2, RANTES, MCP-3, and MCP-4 mRNA, sequential IHC/ISH was employed as previously described (6, 12). Briefly, cell phenotypes were first identified by IHC using the APAAP technique and phenotype-specific murine mAb. The mAb used were directed against human epithelial cells (cytokeratin, clone MNF 116), endothelial cells (CD31, clone JC70A), macrophages (CD68, clone EBM11), mast cell tryptase (clone AA1), neutrophil elastase (clone NP57; Dako), T cells (CD3; Becton Dickinson, Oxford, U.K.), and eosinophil cationic protein (EG2). Sections from five atopic asthmatics and five nonatopic asthmatics with high expression of eotaxin, eotaxin-2, RANTES, MCP-3, and MCP-4 RNA were chosen. After developing with Fast Red for cell phenotypes, ISH was performed using digoxygenin-labeled riboprobes (6, 12) specific for these C-C chemokines. The mRNA-positive signals were visualized using nitro blue tetrazolium/bicinchoninic acid (Sigma) as the chromogen (6, 12). The numbers of positive cells expressing phenotypic markers, chemokine mRNA, or both were counted in the epithelial area and submucosa in whole sections. The results were expressed as the percent distribution of cells expressing eotaxin, eotaxin-2, RANTES, MCP-3, and MCP-4 mRNA and the percentage coexpressed by each cell type within the epithelium and submucosa of biopsies.

Statistical analysis
Data were analyzed with the aid of a commercially available statistical package (Minitab for Windows, Minitab release 9.2, Minitab, State College, PA). The Mann-Whitney U test was then used for intergroup comparison (with Bonferroni’s correction). Correlation coefficients were obtained by Spearman’s rank-order method. A p value <0.05 was accepted as statistically significant.

Results

Patient population
Details of the study population are shown in Table I. As expected, atopic asthmatics had significantly elevated total serum IgE compared with NAA and NC (p < 0.01). Both AA and NAA had significantly lower FEV₁ and histamine PC₂₀ than those of AC and NC. Unlike NC, AA, NAA, and AC had relatively high blood eosinophil accounts (Table I). Compared with AA, AC, and NC, the nonatopic asthmatics were significantly older. The total serum IgE in NAA was slightly higher than in NC, although it was significantly lower than in AA and AC. These observations are consistent with previous findings (5–7).

EG2⁺ eosinophils and BB1⁺ basophils
The numbers of EG2⁺ eosinophils in the bronchial mucosa from both atopic and nonatopic asthmatic patients were significantly elevated compared with those in both nonasthmatic control groups.
Although the number of BB1^+ basophils was ~10-fold less than that of EG2^+ eosinophils, the numbers of BB1^+ basophils in bronchial biopsies from asthmatics (AA and NAA) were significantly elevated compared with control values (AC+ NC; p < 0.05; Fig. 1). There were no statistically significant differences between AA and NAA, although the mean numbers of BB1^+ basophils in AA were slightly higher than those in NAA.

Eotaxin and eotaxin-2

Bronchial biopsies from asthmatic patients had elevated numbers of cells encoding mRNA for eotaxin, which significantly increased compared with those from both the atopic and nonatopic control subjects without asthma (p < 0.001; Fig. 2). No significant differences between either AA and NAA or AC and NC were observed. Immunohistochemistry revealed increases in the numbers of eotaxin-immunoreactive cells in the bronchial mucosa of asthmatics compared with nonasthmatic controls (p < 0.05; Fig. 2). There was no significant difference in the numbers of eotaxin-immunoreactive cells in the epithelium and throughout the submucosa, either as isolated cells or as aggregates. Cells encoding mRNA for eotaxin-2 were also significantly increased in the bronchial mucosa of asthmatic patients regardless of their atopic status compared with those in nonasthmatic controls (Fig. 2). Taking the atopic and nonatopic subjects with asthma as a group, significant inverse correlations were detected between the bronchial mucosal expression of eotaxin (mRNA and protein) and the histamine PC_{20} (r = 0.5; p < 0.05; Fig. 3). The numbers of eotaxin^+ (mRNA and protein) cells in asthmatics (AA+NAA) were also significantly correlated to the numbers of EG2^+ cells (r = 0.75; p < 0.001). Eotaxin-2 mRNA^+ cells were also significantly correlated with numbers of EG2^+ eosinophils (r = 0.5; p < 0.05), but not with FEV_1 or PC_{20}.

MCP-3, MCP-4, and RANTES

Bronchial biopsy sections from the atopic and nonatopic asthmatics had significantly elevated numbers of MCP-4 mRNA^+ cells per unit area of bronchial biopsies compared with both atopic and nonatopic control subjects without asthma (Fig. 4). A significant increase in the numbers of cells expressing mRNA for both RANTES and MCP-3 was also detected in the biopsies from asthmatics compared with nonasthmatic controls (Fig. 4). None of these C-C chemokines significantly correlated with eosinophils or markers of asthma severity. MCP-4 and RANTES mRNA were located throughout of epithelial area and submucosa. MCP-3 mRNA were generally located in submucosa, and low numbers were detected within the epithelial layer.

CCR3

The numbers of CCR3-expressing cells (mRNA and protein) were significantly elevated in asthmatics compared with AC and NC (Fig. 5). However, nonsignificant differences between either AA and NAA or AC and NC were observed. In the asthmatic group (AA+NAA), numbers of CCR3 (mRNA and protein)-positive cells were directly correlated with EG2^+ eosinophil numbers (r = 0.8; p < 0.001) and inversely with histamine PC_{20} (r = 0.51; p < 0.05).

Cell sources of eotaxin, eotaxin-2, RANTES, MCP-3, and MCP-4

Cells expressing mRNA for C-C chemokines were determined by double IHC/ISH. In the epithelium, up to 70% of mRNA-positive cells were colocalized to cytokeratin^+ epithelial cells. The remains of the mRNA^+ cells were CD68^+ macrophages, CD3^+ T cells, or tryptase^+ mast cells (Fig. 6). In the submucosa, CD31^+ endothelial cells, CD68^+ macrophages, and CD3^+ T lymphocytes were the major cell sources expressing these C-C chemokines (Fig. 7). No significant differences in the various cell types expressing mRNA for these chemokines in either epithelium or submucosa were observed between AA and NAA (r = 5 for each group). The percentages of each cell type coexpressing mRNA for eotaxin, eotaxin-2, RANTES, MCP-3, and MCP-4 in the epithelium and the submucosa are summarized in Tables II and III.
Discussion

In this study we compared the expression of C-C chemokines and CCR3 between atopic and nonatopic asthmatics and control subjects. We confirmed our previous findings on MCP-3 and RANTES (7) and extended the observations to include other eosinophil chemotactic chemokines. Thus, to our knowledge, this is the first systematic comparison of expression of eotaxin, eotaxin-2, and MCP-4 in the pathogenesis of intrinsic asthma, although elevated expression of eotaxin and MCP-4 has been shown to be a feature of allergic asthmatics (12, 18–20). We have also studied the cell source of eosinophil chemotactic chemokines in both intrinsic and extrinsic asthma. Our findings suggest that multiple C-C chemokines may contribute to eosinophil, and possibly basophil, recruitment to the asthmatic airway.

Whether these mediators are elaborated by the same mechanisms and through the same pathways in atopic and nonatopic asthma is presently unclear. Walker and colleagues have suggested that intrinsic and extrinsic asthma might be regarded as distinct immunopathological entities, since they found evidence that atopic asthma was characterized by a cytokine profile typical of Th2-type response in bronchoalveolar lavage (BAL) fluid, while intrinsic asthma was associated with isolated, elevated expression of IL-5 (21). They postulated that the absence of production of IL-4 explained the lack of IgE elevation in these patients. On the other hand, studies that have examined C-C chemokine as well as cytokine expression in atopic and nonatopic asthma have provided evidence for similarities, rather than differences, in the immunopathogenesis of these clinically distinct forms of the disease.

For example, elevated numbers, compared with controls, of activated T cells, eosinophils (22), high affinity IgE receptor-bearing cells (8), IL-5 and IL-4 mRNA, and protein product-positive cells have been shown to be features of the bronchial mucosa of both atopic and nonatopic asthma (5, 6). Furthermore, no differences in the number of mRNA-positive cells for IL-13 (23), RANTES, and MCP-3 were detected (7).

Using mAb EG2 and BB1, the numbers of eosinophils and basophils were evaluated in the bronchial biopsies from asthmatics at baseline and from controls. Immunohistochemistry showed that the numbers of EG2⁺ eosinophils were significantly higher in asthmatics (AA and NAA) than controls (AC and NC; Fig. 1). Although the number of EG2⁺ eosinophils was slightly higher in NAA than in AA, there were no significant differences between...
AA and NAA. This is consistent with previous findings (5–7).
Unlike eosinophils, BB1+ basophils were undetectable in the
biopsies from either AC or NC, suggesting that BB1+ basophils are
not infiltrated into tissue in the normal situation. Compared with
controls (AC + NC), small, but statistically significant, numbers of
BB1+ basophils were detected in bronchial mucosa from asthmatics
(AA + NAA: p < 0.05; Fig. 1). The number of BB1+ basophils in AA
was higher than that in NAA, but the difference was not
statistically significant. Interestingly, the number of BB1+ baso-
phils was much less than that of EG2+ eosinophils in bronchial
mucosa. The reason is unclear. BB1 is an mAb directed against a
basophil granule constituent with a molecular mass of 124 kDa
(17). Thus, completely degranulated basophils, if present, may be
undetected.
In general, chemokine expression was elevated in both asth-
matic groups compared with nonasthmatic controls. There was a
trend for more pronounced expression in nonatopic patients com-
pared with atopic asthmatics of similar severity. This could be the
result of elevated numbers of macrophages and other inflammatory
cells detected in the bronchial mucosa of intrinsic asthmatics and
could be responsible, in turn, for the relatively increased numbers
of blood and airway eosinophils in intrinsic asthma. We and others
had previously shown that eotaxin expression in bronchial biopsies
from atopic asthmatics correlated with eosinophil infiltration and
clinical features (12, 18, 19). In this study, eotaxin mRNA and
protein product-positive cells significantly correlated with EG2+
eosinophils and histamine PC 20 in asthmatics (AA + NAA). There
was also a significant correlation between eotaxin-2 mRNA− cells
and EG2+ eosinophils (see Results). Both eotaxin and eotaxin-2
activate and attract eosinophils, basophils, and Th-2 cells (24),
but not other leukocytes, and appear to act exclusively via CCR3 re-
ceptor (25). In terms of structure, however, eotaxin and eotaxin-2
are distant, sharing only 39% identical amino acids, while there is
a 43% homology for MCP-4, 39% for MCP-3 and eotaxin, and
32% for RANTES (25). In addition, MCP-3, MCP-4, and RAN-
TES have chemotactic activity for eosinophils and basophils (26,
27). Thus, it is likely that several chemokines contribute to eosin-
ophil recruitment in allergic inflammation. Eotaxin-deficient mice
had reduced eosinophils in BAL fluid early, but not late, after
allergen challenge (28). Using the allergen-induced human skin
late-phase reaction as a model, we found that that expression of
eotaxin and MCP-3 was associated with the early 6-h recruitment
of eosinophils, while eotaxin-2, RANTES, and MCP-4 appear to be
involved in later 24-h infiltration of eosinophils (29). These
observations suggest that different mechanisms may guide the
early vs late eosinophilia in allergic inflammation. Taha et al. (20)
showed that eotaxin and MCP-4 mRNA increased in bronchial

Table II. Percentages of each cell type coexpressing chemokine mRNA for eotaxin, eotaxin-2, RANTES, MCP-3, and MCP-4 within the epithelium of bronchial biopsies from AA (n = 5) and NAA (n = 5)*

<table>
<thead>
<tr>
<th>Cell Markers</th>
<th>Eotaxin mRNA+ Cells (% of each cell type)</th>
<th>Eotaxin-2 mRNA+ Cells (% of each cell type)</th>
<th>RANTES mRNA+ Cells (% of each cell type)</th>
<th>MCP-3 mRNA+ Cells (% of each cell type)</th>
<th>MCP-4 mRNA+ Cells (% of each cell type)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cytokeratin+ epithelial cells</td>
<td>49 ± 5</td>
<td>49 ± 7</td>
<td>45 ± 11</td>
<td>43 ± 3</td>
<td>52 ± 12</td>
</tr>
<tr>
<td>CD68+ macrophages</td>
<td>25 ± 6</td>
<td>31 ± 8</td>
<td>21 ± 4</td>
<td>22 ± 4</td>
<td>32 ± 6</td>
</tr>
<tr>
<td>CD3+ T cells</td>
<td>35 ± 8</td>
<td>28 ± 9</td>
<td>25 ± 6</td>
<td>19 ± 9</td>
<td>31 ± 4</td>
</tr>
<tr>
<td>Tryptase+ mast cells</td>
<td>27 ± 7</td>
<td>28 ± 3</td>
<td>7 ± 7</td>
<td>16 ± 11</td>
<td>6 ± 4</td>
</tr>
<tr>
<td>EG2+ eosinophils</td>
<td>3 ± 2</td>
<td>7 ± 4</td>
<td>6 ± 6</td>
<td>14 ± 9</td>
<td>19 ± 5</td>
</tr>
<tr>
<td>Elastase+ neutrophils</td>
<td>0 ± 0</td>
<td>11 ± 9</td>
<td>0 ± 0</td>
<td>0 ± 0</td>
<td>2 ± 2</td>
</tr>
<tr>
<td>CD31+ endothelial cells</td>
<td>5 ± 5</td>
<td>5 ± 5</td>
<td>4 ± 4</td>
<td>4 ± 4</td>
<td>7 ± 4</td>
</tr>
</tbody>
</table>

* A combination of ISH (using digoxigenin-labeled riboprobes for each chemokine) and IHC (employing mAb against several phenotype markers as indicated) was used. The results were expressed as mean ± SEM.
mucosa of atopic asthmatics and that eotaxin mRNA+ cells significantly correlated with eosinophils. BAL fluid from asthmatic patients contained chemotactic activity for eosinophils that was attributable in part to both eotaxin and MCP-4 (18). However, a combination of eotaxin, MCP-4, and RANTES accounted for only about 50% of the eosinophil chemotactic activity in the BAL, suggesting the existence of other eosinophil chemotactic factors (18). In view of this multiplicity of potential influences on eosinophils, it is perhaps surprising that we found a direct correlation between human endothelial cells in vitro (49), indicating that these mediators may contribute to the eosinophil influx by up-regulating eotaxin and other C-C chemokines. CCR3 mRNA is mainly associated with eosinophils, with limited expression by macrophages and mast cells (12), although a recent report identified CCR3 on blood basophils (50). Heath et al. (16) have shown that >95% of the response of eosinophils to eotaxin, RANTES, MCP-3, and MCP-4 is mediated through CCR3 receptor and could be blocked completely with an anti-CCR3 mAb. On the other hand, basophils express CCR1-CCR4 (24). In addition, it is known that RANTES interacts with two more receptors, CCR1 and CCR4 (24, 51), and that MCP-3 binds to CCR1 and CCR2 (24, 52), while MCP-4 binds to CCR2 and CCR3 (24, 31, 53). Thus, these C-C chemokines may contribute to the infiltration of other inflammatory cells, including macrophages in the bronchial mucosa of asthmatics.

It is worth noting that the elevated airway expression of all the chemokines studied was demonstrably not a feature of atopy per se, but instead a feature specific to asthma. In addition, it is noteworthy that C-C chemokine mRNA expression was detectable in a proportion of the control subjects. Similar observations were found in animal model. For instance, eotaxin expression and eosinophil infiltrates were detectable in lamina propria of the jejunum from normal wild-type mice, while eosinophils were reduced in the jejunum in eotaxin-deficient mice (54). Thus, a basal physiological degree of chemokine expression in the airway may be required for the trafficking of patrolling leukocytes involved in host defense.

Thus, we present evidence that combined production of various eosinophil-active chemokines within the bronchial mucosa is a characteristic feature of bronchial asthma regardless of its atopic status. The mechanisms controlling the transcriptional regulation of C-C chemokines are still poorly understood. CCR3 seems to be the principal receptor for eosinophil responses to C-C chemokines, and blocking this receptor could be a promising therapeutic tool in the management of asthma.

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