Anti-inflammatory effects of zinc and alterations in zinc transporter mRNA in mouse models of allergic inflammation

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There is clinical evidence linking asthma with the trace element, zinc (Zn). Using a mouse model of allergic inflammation, we have previously shown that labile Zn decreases in inflamed airway epithelium (Truong-Tran AQ, Ruffin RE, Foster PS, Koskinen AM, Coyle P, Philcox JC, Rofe AM, Zalewski PD. Am J Respir Cell Mol Biol 27: 286–296, 2002). Moreover, mild nutritional Zn deficiency worsens lung function. Recently, a number of proteins belonging to the Solute Carrier Family 39 (ZIP) and Solute Carrier Family 30 (ZnT) have been identified that bind Zn and regulate Zn homeostasis. Mice were sensitized, and subsequently aerochallenged, with ovalbumin to induce acute and chronic airway inflammation. Mice received 0, 54, or 100 μg of Zn intraperitoneally. Tissues were analyzed for Zn content and histopathology. Inflammatory cells were counted in bronchoalveolar lavage fluid. Cytokine and Zn transporter mRNA levels were determined by cDNA gene array and/or real-time PCR. Zn supplementation decreased bronchoalveolar lavage fluid eosinophils by 40 and 80%, and lymphocytes by 55 and 66%, in the acute and chronic models, respectively. Alterations in Zn transporter expression were observed during acute inflammation, including increases in ZIP1 and ZIP14 and decreases in ZIP4 and ZnT4. Zn supplementation normalized ZIP1 and ZIP14, but it did not affect mRNA levels of cytokines or their receptors. Our results indicate that inflammation-induced alterations in Zn transporter gene expression are directed toward increasing Zn uptake. Increases in Zn uptake may be needed to counteract the local loss of Zn in the airway and to meet an increased demand for Zn-dependent proteins. The reduction of inflammatory cells by Zn in the airways provides support for Zn supplementation trials in human asthmatic individuals.

Zn homeostasis is achieved by the concerted actions of two families of proteins: Solute Carrier Family 39, which com-

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prises the ZRT/IRT-related (ZIP) proteins, are primarily involved in Zn uptake; Solute Carrier Family 30, which comprises the mammalian Zn transporter (ZnT) proteins, mediate intracellular Zn trafficking and Zn efflux (17). In addition, metallothioneins (MTs) participate in intracellular Zn homeostasis by binding Zn and mediating its transfer to cytosolic metalloenzymes (21). With the exception of MTs, studies concerning the characterization and expression of Zn transporters in the lung have been scarce. Here, we describe, for the first time, a study of Zn transporter gene expression in the lungs of mice before and after induction of allergic inflammation. In addition, given our laboratory’s previous findings that Zn deficiency worsens allergic inflammation (37), we investigated whether Zn supplementation had beneficial effects on eosinophilia, airway mucus cells, and other histopathological features of allergic inflammation. Since inflammatory cells are recruited to the lung by specific chemokines and cytokines, including eotaxin, macrophage inflammatory proteins, and monocyte chemotactic proteins, we tested whether Zn supplementation affects the transcript levels of inflammatory mediators, as well as their receptors. The expression of MTs was also studied.

**METHODS**

**Reagents**

Unless otherwise mentioned, all reagents were purchased from Sigma-Aldrich Chemicals (St. Louis, MO), and reagents for RNA manipulation and reverse transcription were purchased from Qiagen (Clifton Hill, Victoria, Australia). Zn-free buffers were prepared as previously described (39).

**Animals**

Female Balb/c mice (aged 4–6 wk; pathogen free) were purchased from the University of Adelaide (Adelaide, Australia). Mice were fed a standard rodent chow (Joint Stock II Feed, Ridley Agricultural Products, Murray Bridge, South Australia, Australia), which contains 95 mg Zn/kg. For tissue collection, mice were anesthetized by an intraperitoneal overdose of pentobarbital sodium (50 mg/kg). For tissue collection, mice were anesthetized with 0.9% saline (Sal-treated mice) or 1% OVA in 0.9% saline (OVA-treated mice) for 20 min, once a day (22). Body weights of the mice were measured every second or third day for the duration of the two protocols. On the day following the last OVA nebulization, mice were anesthetized with an intraperitoneal injection of pentobarbital sodium (50–150 mg/kg body wt) before tissue collection.

**Analysis of Zn Transporter Gene Expression in Mouse Lung**

Lung tissue was stabilized in RNAlater buffer. RNA was isolated using an RNAeasy minikit and digested with DNase, as per kit instructions. Equal amounts of RNA were pooled from the lungs of four to six mice within treatment groups as previously described (3, 24). In some cases, gene expression was also confirmed using RNA from individual mice (e.g., ZnT4, eotaxin, MT-I) (data not shown). cDNA was prepared from 800 ng of total RNA using an Omniscript RT kit with random decamers (1 μM) and oligo(dT) primers (10 μM). A one-eighth volume of the RT reaction was amplified using QuantiTect SYBRgreen PCR Kits. Gene sequences were obtained from GenBank, and primers were designed using the Web-based software Primer3 (30) and purchased from Geneworks (GeneWorks, Hindmarsh, South Australia, Australia). Accession numbers and primer sequences are provided as supplementary information in Table S1 (available online at the American Journal of Physiology Lung Cell Molecular Physiology Web site). The real-time assays were performed using a Bio-Rad MyiQ Single-Color Real-Time PCR Detection System (Bio-Rad, Hercules, CA). Hypoxanthine guanine phosphoribosyl transferase (HPRT) was used as the housekeeping gene because its expression was more consistent than β2-microglobulin and GAPDH between treatment groups. Tissues isolated from mouse brain, liver, and pancreas were used as positive controls. A sample without reverse transcriptase enzyme was included to check for genomic DNA contamination. Reaction for each primer pair was optimized with standard curves. The cycle thresholds (Ct) were obtained for test genes and for HPRT, and their differences were calculated (ΔCt). ΔCt values were transformed into absolute values and expressed relative to HPRT as described by Applied Biosystems (User Bulletin no. 2ABI).

**Zn Supplementation and Induction of Allergic Airway Inflammation**

**Acute model.** Mice were supplemented with 0, 54, or 100 μg actual Zn (in the form of ZnSO₄·7H₂O) in 0.9% saline by intraperitoneal injection, twice a week, from days 0 to 33 or 36. Allergic airway inflammation was induced as previously described (37). Mice were killed over 2 days, on the day following their last nebulization.

**Chronic model.** Chronic allergic inflammation was induced according to McMillan et al. (22). Here, allergic inflammation was induced before Zn supplementation as per the acute model (days 0–34). On day 36, mice were split into four groups (n = 6) for Zn supplementation. From day 34 to day 52, mice were supplemented with either 0 or 54 μg Zn twice a week and nebulized with either 0.9% saline (Sal-treated mice) or 1% OVA in 0.9% saline (OVA-treated mice) for 20 min, once a day (22). Body weights of the mice were measured every second or third day for the duration of the two protocols. On the day following the last OVA nebulization, mice were anesthetized with an intraperitoneal injection of pentobarbital sodium (50–150 mg/kg body wt) before tissue collection.

**Tissue Collection**

Blood for serum Zn measurements was collected by cardiac puncture. The trachea was cannulated, and the lungs were lavaged with 1 ml of ice-cold Zn-free Hanks’ balanced salt solution (HBSS; pH 7.4). Bronchoalveolar lavage fluid (BAL) was centrifuged (800 g, 5 min, 4°C), the cell pellet resuspended in 500 μl of HBSS and retained for differential cell counts. Lung, liver, and spleen tissues were snap-frozen in liquid N₂ for Zn measurements or placed in RNAlater for RNA studies. Some lungs were inflated with 1 ml of 10% phosphate-buffered formalin (Sigma-Aldrich) for histological studies.

**Measurement of Zn in Body Fluids and Tissues**

Labile Zn in serum and cell-free BAL fluid was measured using a Zinquin fluorometric assay as previously described (39). Total Zn in the liver, lung, and spleen were determined by flame atomic absorption spectroscopy (303 atomic absorption spectrophotometer, Perkin-Elmer), as previously described (37).

**Inflammatory Cell Infiltration into BAL Fluid**

Total BAL cell viability was assessed by the exclusion of the vital dye, trypan blue (0.05%). Cell suspensions of 1 × 10⁶ cells/ml were spun onto cytospin slides and stained with May Grunwald (Sigma-Aldrich). A differential cell count of 200 cells was performed in duplicates by two examiners, who were blinded to the treatment groups, using standard morphologic criteria.

**Lung Histology**

Paraffin-embedded sections were processed using standard procedures by staff at the Institute of Medical and Veterinary Science (Queen Elizabeth Hospital, South Australia, Australia). Sections were stained with hematoxylin and eosin for measurement of airway epithelial thickness, alcinan blue/periodic acid-Schiff (PAS) for the identification of mucin-secreting cells, and Martius scarlet blue for identification of collagen. At least 10 images were captured from duplicate slides using a closed-circuit television video color camera mounted on an inverted Nikon TE-300 (×20 objective). Collagen deposition and airway epithelial thickness were measured by image
Eosinophil Peroxidase Activity in BAL Fluid

Eosinophil peroxidase (EPO) content was measured using a colorimetric assay (6) to confirm the cell counts. An aliquot of lavage fluid was taken before centrifugation (i.e., contains cells in suspension), frozen at −80°C, and, on thawing, diluted in Zn-free HBSS. Thirty microliters of each dilution were mixed with 30 μl of OPD substrate solution [12 mM o-phenylenediamine (OPD), 0.11% hexadecyltrimethyl ammonium bromide, 0.005% H2O2, in 0.05 M Tris HCl pH 8.0]. The enzymatic reaction was stopped after 30 min at 22°C by the addition of 30 μl 4 N H2SO4. Absorbance at 490 nm was measured on a plate reader (Titertek multiskan).

Pathway-Specific Gene Array

Only RNA from the acute mouse experiments were used in the cytokine gene experiments because the degree of inflammation, as determined by number of inflammatory cells in the BAL, was much greater than in the chronic model. For SuperArray analysis, 5 μg of RNA (pooled from the same four to six mice used in real-time experiments) were reverse transcribed with Biotin-16-dUTP (Roche Diagnostics Australia, Sydney, Australia) using a SuperArray TrueLabeling RT enzyme kit (SuperArray Bioscience, Frederick, MD) according to manufacturer’s instructions. The cDNA probe mixture was hybridized to the Q Series Mouse Inflammatory Cytokines and Receptors cDNA array (GEArray MM-015, SuperArray Bioscience). The array was analyzed using CDP-Star substrate chemiluminescence and exposure to X-ray film. Data image files were analyzed according to GEArray Expression Analysis Suite provided by Superarray Bio-science (http://GEASuite.superarray.com) and normalized for housekeeping gene signals. Results were confirmed by real-time PCR as described above.

Statistical Analyses

Data are expressed as means ± SE. Data were analyzed by one-way or two-way ANOVAs and Student’s t-tests where appropriate using SPSS statistical software.

RESULTS

Body Weight and Growth Rates

The body weight and growth rates of the mice were unaffected by either Zn supplementation or airway inflammation in both the acute (end point: 18.26 ± 0.17 g; n = 65; overall mean ± SE) and chronic models (end point: 19.44 ± 0.26 g; n = 37, overall mean ± SE).

Inflammatory Cell Infiltration

In the BAL fluid of the OVA-challenged mice, there were significant and substantial increases in eosinophils (Fig. 1, A and B) and lymphocytes (Fig. 1, C and D), in both the acute and chronic models. There was also a significant increase in BAL EPO, confirming the eosinophilia (Fig. 1E). Total BAL macrophages increased significantly in the acute model (Fig. 1E) but not in the chronic model (Fig. 1F). The total number of eosinophils in BAL of OVA-treated mice was higher in the acute model of allergic inflammation (1.63 ± 0.15 × 106 n/kul in acute and 0.85 ± 0.10 × 106 n/kul in chronic, overall mean ± SE).

In the acute model, Zn supplementation 

- Suppresses inflammatory cell infiltration in both acute and chronic models of allergic inflammation.
- Inflammatory cells (solid bars) were identified using standard morphometric criteria from stained cytospins of bronchoalveolar lavage (BAL) fluid collected from n = 8–10 (A, C, and E) and 4–6 mice (B, D, and F). Eosinophil peroxidase activity was measured using an enzymatic reaction with OPD substrate [12 mM o-phenylenediamine (OPD), 0.11% hexadecyltrimethyl ammonium bromide, 0.005% H2O2, in 0.05 M Tris HCl pH 8.0] to confirm the cell counts. Eosinophil peroxidase activity was significantly decreased in BAL EPO, confirming the eosinophilia. Eosinophil peroxidase activity was significantly decreased in BAL EPO, confirming the eosinophilia. Eosinophil peroxidase activity was significantly decreased in BAL EPO, confirming the eosinophilia.

*Significant difference from OVA controls (t-test, P < 0.05).
cells/ml) than in the chronic model (0.39 ± 0.094 × 10^6 cells/ml). Similarly, the numbers of other inflammatory cells were higher in the acute (lymphocytes: 0.55 ± 0.07 × 10^6 cells/ml; macrophages: 0.23 ± 0.03 × 10^6 cells/ml) than in the chronic model (lymphocytes: 0.14 ± 0.028 × 10^6 cells/ml; macrophages: 0.16 ± 0.05 × 10^6 cells/ml).

In both the acute and chronic models, Zn supplementation significantly decreased the number of BAL eosinophils by 40% (Fig. 1, D). Zn supplementation had no significant effect on macrophage numbers in the acute or chronic models.

**Histopathology of the Lung**

Mucous hyperplasia, as determined by increased PAS staining of mucopolysaccharide-containing goblet cells in airway epithelium, was a feature of the airways in OVA-challenged mice [acute (Table 1) and chronic (Table 2) models]. Airway thickness and collagen deposition were also studied in the chronic model, and both increased significantly in OVA-challenged mice (Table 2). In both the acute and chronic models, Zn supplementation had no effect on any of the histopathological features (Tables 1 and 2).

**Table 2. Descriptive data: chronic model of allergic inflammation**

<table>
<thead>
<tr>
<th></th>
<th>Sal</th>
<th>Sal (54 μg Zn)</th>
<th>OVA</th>
<th>OVA (54 μg Zn)</th>
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</thead>
<tbody>
<tr>
<td><strong>Labile Zn in body fluids, μM Zn</strong></td>
<td></td>
<td></td>
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<tr>
<td>Serum (n = 4–6)</td>
<td>13.7±1.2</td>
<td>11.4±3.0</td>
<td>11.9±3.6</td>
<td>10.0±3.7</td>
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<tr>
<td>BAL</td>
<td>0.43±0.02</td>
<td>0.44±0.02</td>
<td>0.44±0.01</td>
<td>0.41±0.03</td>
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<tr>
<td><strong>Total Zn in tissues, nmol/g wet lung</strong></td>
<td></td>
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<tr>
<td>Liver (n = 5–7)</td>
<td>36.9±1.4</td>
<td>32.07±2.6</td>
<td>33.72±5.9</td>
<td>33.9±2.1</td>
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<tr>
<td>Spleen (n = 5–7)</td>
<td>188.5±8.1</td>
<td>185.1±3.0</td>
<td>166.25±6.17</td>
<td>166.0±9.9</td>
</tr>
<tr>
<td>Lung (n = 4–7)</td>
<td>168.0±23.9</td>
<td>151.8±24.8</td>
<td>156.7±14.4</td>
<td>150.6±34.6</td>
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**Histopathology**

Epithelial thickness (n = 4–5) | 20.2±2.4 | 20.8±0.9 | 27.6±1.8* | 27.3±3.2 |
Collagen thickness (n = 4–5) | 6.3±0.9 | 9.0±1.2 | 9.7±0.8* | 11.3±2.3 |
Mucus score (n = 4–5) | 0.02±0.01 | 0.08±0.07 | 1.3±0.4* | 1.1±0.2 |

Values are means ± SE; *Significant difference between Sal and OVA control mice (t-tests, P < 0.05).
expression of ZIP1, ZIP2, ZIP12, and ZIP14; moderate expres-
sion of ZIP3; and relatively high expression of ZIP4, ZIP6, 
ZIP7, and ZIP8 (Fig. 2). Among the ZnTs, there was little 
expression of ZnT7, moderate expression of ZnT1 and ZnT4, 
and relatively high expression of ZnT5 and ZnT6 (Fig. 3). 
ZnT2 expression was only just detectable; ZnT3, ZnT8, and 
ZnT10 were absent (data not shown).

Marked changes in expression of transporters were seen in 
the OVA-challenged mice. Of the ZIP transporters, increases 
were seen in ZIP1 (9.5-fold), ZIP3 (3.4-fold), ZIP6 (2.2-fold), 
ZIP12 (4.7-fold), and ZIP14 (5.3-fold) with allergic inflamma-
tion, whereas there were decreases in the expression of ZIP4 
(4-fold), ZIP7 (2.9-fold), and ZIP8 (3.1-fold) (Fig. 2). Of the 
ZnT family, no changes were seen in expression of ZnT1, 
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fold). ZnT4 mRNA decreased so dramatically in OVA-chal-
lenged samples, that transcript levels were undetectable 
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Zn supplementation was able to restore, at least in part, some 
of the alterations in Zn transporter gene expression induced by 
allergic inflammation (Figs. 2 and 3). For the following ZIP 
proteins that were upregulated by inflammation, there was a 
significant decrease in inflammation-induced expression in 
Zn-supplemented mice. For example, in mice supplemented 
with 100 μg Zn, ZIP1, ZIP3, ZIP6, and ZIP14 expression 
declined by 1.8-, 1.9-, 2.2-, and 1.9-fold, respectively (Fig. 2). 
Conversely, ZIP7 expression, which was downregulated by 
allergic inflammation, significantly increased by 1.9-fold in OVA-
treated mice supplemented with 100 μg Zn. The effects of Zn 
supplementation alone, in the absence of OVA-treatment, were 
varied. The expression of ZIP7 and ZnT7 increased in mice 
supplemented with 54 μg Zn, whereas expression of ZIP6, 
ZIP7, and ZIP8, decreased by 2.9-, 2.4-, and 1.9-fold, respec-
tively, in mice supplemented with 100 μg Zn.

**MT Expression**

MT-I and -II mRNA levels increased in allergic inflamma-
tion by 11- and 34-fold, respectively (Fig. 4). Surprisingly, Zn 
supplementation did not enhance lung MT transcription in 
either the Sal- or OVA-challenged animals (Fig. 4).
Expression of Cytokines and Their Receptors in Acute Allergic Inflammation

The pathway-specific gene array MM-015 (SuperArray Biotechnology, http://www.superarray.com) contains 96 cytokine and receptor cDNAs associated with inflammatory response. Expression analysis identified a group of genes that were induced by airway inflammation that included ccl6 (up 2.2-fold), ccl8 (6.7-fold), ccl9 (6.0-fold), and ccl11 (4.7-fold). Zn supplementation did not modulate the expression of any inflammatory cytokines or receptors represented in the array. Expression of chemokines induced by airway inflammation but not by Zn supplementation was confirmed using real-time PCR (Fig. 5). Complete analysis of gene array is provided as supplementary data (Table S2).

DISCUSSION

In this study, we have demonstrated that multiple Zn transporter proteins are expressed in the mouse lung. We have also shown that Zn homeostasis is perturbed in allergic inflammation. Moreover, marked reductions in the number of inflammatory cells, including eosinophils, in the BAL were observed.
with Zn supplementation. This was accompanied by reversal of the inflammation-induced alterations in the expression of some Zn transporters.

There is clinical evidence linking asthma and Zn deficiency and as such, we hypothesized that proteins involved in maintaining Zn homeostasis might play a role in allergic inflammation (7, 25, 33). The changes we observed in the gene expression of the ZIP family of Zn transporter proteins during inflammation are mainly directed toward maintaining, or increasing intracellular Zn. ZIP1, ZIP3, ZIP6, ZIP12, and ZIP14 have been shown to have specific Zn influx activity [reviewed in Kambe et al. (17)], and the expression of all of these uptake transporter genes increased significantly with inflammation in our model (Fig. 2). Conversely, we observed a marked reduction in the mRNA levels of the epithelial Zn uptake protein, ZIP4, and of the less characterized proteins, ZIP7 and ZIP8. The down-regulation of ZIP4, ZIP7, and ZIP8 during inflammation may be explained by their subcellular localization. ZIP7 is thought to be involved in mobilizing Zn from the Golgi apparatus into the cytoplasm (15), and its downregulation could therefore indicate a need to reduce Zn efflux from the Golgi and to maintain intracompartmental Zn levels during inflammation. ZIP4 is located in the apical surface of intestinal cells (8), and may be lost during inflammation due to shedding of the epithelial airway.

Decreased gene expression of the vesicular transporter, ZnT4 and the Golgi uptake transporter, ZnT6, also occurs in the lung during allergic inflammation. Our laboratory has previously shown that both ZnT4 and Zn ions are localized in intracellular vesicles at the apical surface of airway (38) and kidney cells (29). ZnT4 protein levels also decrease in inflamed airways (Truong-Tran AQ, Murgia C, and Zalewski PD, unpublished observations). Because a ZnT4 mutation resulting in a dramatically reduced expression leads to decreased Zn secretion by mammary and intestinal epithelial cells (1, 19, 26), it is possible that reduced expression of ZnT4 might exert a protective role in inflamed airway epithelium by increasing retention of intracellular Zn ions. Expression of ZnT1, ZnT2, ZnT5, and ZnT7, was unaffected by allergic inflammation. Because ZnT proteins are mostly responsible for intracellular compartmentalization, we suggest that ZnT1, ZnT2, ZnT5, and ZnT7, may play a crucial role in the delivery of Zn to the Zn-dependent proteins that are important for airway function, such as Cu-Zn-SOD, metalloproteinases, and alkaline phosphatase [reviewed in Murgia et al. (25)].

An increase in Zn uptake may be important to the lung during airway inflammation because Zn has antioxidant (13), anti-inflammatory (5), and cell survival-promoting properties (2, 38). In addition, our laboratory has previously shown that the amount of labile Zn decreases in the cells that line the airways during inflammation (37). Moreover, in inflamed airways, there is most likely an increased demand for labile Zn required for Zn-dependent proteins involved in inflammatory processes. Here, we observed a significant increase in MT-I and -II mRNA in inflamed lungs. MTs may deplete Zn in tissue and plasma (23) and thus, contribute to low Zn ion bioavailability in the inflamed airway epithelium. Having said this, it is possible that in inflamed airways the demand for Zn is so high, and Zn turnover so rapid, that a local state of labile Zn deficiency could still persist despite the observed increase in transcript levels of Zn uptake transporters.

Zn supplementation does reverse, at least in part, most of the alterations in Zn transporter gene expression associated with allergic inflammation. This reversal may result from lung cells responding to increased serum Zn. Alternatively, the reversal of the inflammation-induced alterations in Zn transporter expression could be due to the decrease in BAL inflammatory cells. Our gene expression analysis on the whole lung does not discriminate between cell types, and it is therefore possible that inflammatory cell mRNAs contribute to the gene expression patterns reported. Moreover, little is currently known about the regulation of Zn transporters, and it is possible that factors released by inflammatory cells might play a role in mediating Zn transporter expression in the lung. The inflammatory cytokine interleukin-6 has recently been shown to upregulate ZIP14 expression in the liver (20). Future studies now need to define which of the many cell types present in the lung contribute to the expression profiles observed here. In addition, functional protein studies are needed in both the normal and diseased lung.

Increases in eosinophils and their secreted products are known to correlate with disease severity in human asthmatic individuals (9). Here, Zn supplementation significantly decreased the number of eosinophils and other inflammatory cells in the BAL fluid of OVA-treated mice. Eosinophils located in the airway lumen are known to be highly activated (6) in this model, and they release a range of proinflammatory cytokines and cytotoxic proteins that further amplify the inflammatory response. Thus, by decreasing eosinophil number in BAL, Zn supplementation probably results in a less severe inflammatory response. Although evidence that Zn has anti-inflammatory properties is steadily growing [present study; reviewed in Shenkin et al. (32)], the mechanisms involved are not clear. In this study, we tested whether Zn modulated the expression of a range of inflammatory cytokines and their receptors known to be important for recruiting inflammatory cells to the lung. However, the results of our gene array analysis led us to conclude that Zn supplementation does not regulate the gene expression, in our model, of any of the 96 inflammatory mediators or their receptors represented in the array. An alternative hypothesis is that Zn prevents migration of inflammatory cells from the circulation to the sites of inflammation by interfering with the adhesion of inflammatory cells to endothelial cells that line blood vessels; a step that is essential for propagating inflammation (27). Future studies should examine the effects of Zn, and the involvement of Zn transporters, in the migration of inflammatory cells from the airways. In addition to acting as an anti-inflammatory, Zn is thought to play a role in cell growth and repair [reviewed in Murgia et al. (25)]. In our study, Zn supplementation, whether given before the induction of allergic inflammation (acute model), or after (chronic model), had no effect on the histopathology of the airways, as measured by the thickening of the basement membrane, collagen deposition or mucus hyperplasia.

Clinical Prospective

Intervention with Zn supplements may be both preventative and therapeutic because first, maintaining airway Zn levels might lower the risk of developing asthma and second, restoring airway Zn levels in those who already have asthma may lessen the severity of inflammation and airway hyperrespon-
siveness. Zn treatment could be used in conjunction with existing asthma medications. Oral Zn supplements are already commercially available and have been used with variable success in another respiratory disease, cystic fibrosis (18). Other mechanisms that enable the targeting of Zn directly in the asthmatic lung may also be of benefit. As such, understanding the function and regulation of Zn transporters in the lung will be vital.

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