

## ORIGINAL ARTICLE

# Crucial role for lung iron level and regulation in the pathogenesis and severity of asthma

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## **Online Repository**

## Supplementary Methods

### Study approvals

All experiments were conducted with approval of the Human/Animal Research Ethics Committees of the University of Newcastle, Australia and the Unbiased Biomarkers in Prediction of respiratory disease outcomes (U-BIOPRED) centre.

### Human subjects

Airway biopsy tissues and bronchoalveolar lavage (BAL) were collected from 11 severe, 12 mild-moderate asthmatics and 13 healthy subjects. To measure non-haem iron content in BAL supernatant, BAL samples were also collected from a second set of severe or mild-moderate asthma patients and healthy subjects (10 subjects in each group). Subjects with severe or mild-moderate asthma had mean FEV1% predicted at  $86.92 \pm 2.726$  ( $p < 0.01$ ) and  $76 \pm 5.389$  ( $p < 0.001$ ), respectively, compared to healthy controls ( $102.7 \pm 4.494$ , **Table 1**). BAL was collected from another set of 10 subjects in each group: severe (mean FEV1% predicted,  $66.33 \pm 7.427$ ,  $p < 0.01$ ) or mild-moderate asthma (mean FEV1%,  $89.6 \pm 4.759$ ) or healthy controls (mean FEV1%,  $97.5 \pm 5.861$ ) (**Table 2**). Human bronchial airway epithelial cells (pBECs), airway smooth muscle (ASM) cells and lung fibroblasts donor characteristics are shown in **Tables E5 and 6**. Patient exclusion criteria included current smokers, recent exacerbation, respiratory tract infection in the last 4 weeks and age younger than 18yrs.

### Human BAL

For each donor, BAL was collected by instilling sterile warm saline (2x 60mL) into the airways using elective fiberoptic bronchoscopy, as described previously (1). Collected BAL was

filtered through a nylon filter apparatus, centrifuged (400x g, 10 mins) and then supernatant was stored at  $-80^{\circ}\text{C}$  for future analysis. BAL cell pellets were resuspended in PBS and cytopspins were prepared, stained with Diff-quick solutions for 30 sec, solution II (fixative) for 30 sec, solution I for 30 sec, dehydrated and air-dried overnight for cover slipping. Differential cells were analysed based on morphology as previously described (1).

### **Quantification of iron-laden BAL cells**

Total iron positive cells and iron score index levels were calculated by enumerating the different grade of iron scored cells (Grade 0, 1, 2 and 3) using Perls'-DAB stained (*see below*) BAL cytopspins.

### **Mouse models of iron overload**

We utilised two models of iron overload to assess the effects of iron on asthma. We first used female *Hfe*<sup>-/-</sup> and WT mice (36 weeks old) (2) on an AKR background strain that were fed a normal diet. Disruption of this gene results in deficiency in hepcidin production, leading to increased systemic iron levels (2-4). In addition, female BALB/c mice (6-8 weeks of age) were fed a diet of mouse chow that contains 2% carbonyl iron (19410mg Fe/Kg diet, Specialty Feeds, Western Australia) *ad libitum* for 8 weeks. This results in a similar level of iron load in the liver as *Hfe*<sup>-/-</sup> mice. WT BALB/c mice were also maintained on control iron diet (~49 mg Fe/Kg diet) or low iron diet (~2.5mg Fe/Kg diet, Speciality Feeds, Western Australia) for 8 weeks as a comparison. All mice were housed at  $22 \pm 2^{\circ}$  temperature with humidity range of 30-70 under 12 hours dark/light cycling conditions.

### **HDM-induced chronic experimental asthma**

WT AKR and *Hfe*<sup>-/-</sup> female mice (~36 weeks old), and WT BALB/c female mice (8 weeks old) fed low iron, control and high iron diets were intranasally administered HDM extract (25µg, 50 µl PBS, Greer Laboratories, Lenoir, NC) or vehicle (PBS) 5 days per week for 6 weeks. After 6 weeks, liver and lung tissues were collected for further analysis, and AHR was measured.

### **Perls' and DAB-enhanced Perls' stain**

The single lobed lungs from mice were perfused with saline, inflated and fixed with formalin, paraffin-embedded, and sectioned (4-6µm). Sections were deparaffinised with xylene and a graded series of ethanol. Deparaffinised mouse lung sections or BAL cell cytopins prepared from clinical and experimental samples were submerged in fresh 1% Potassium Ferrocyanide (AnalaR), pH 1 (Perls' solution), for 30 min on a shaker. Each slide was washed briefly in distilled water, incubated in methanol containing 0.01M NaN<sub>3</sub> (MERCK) and 0.3% H<sub>2</sub>O<sub>2</sub> for 1 h on a shaker. Slides were rinsed in 0.1M PBS (pH7.4) and iron staining was enhanced by 1 h of incubation with 0.025% 3, 3'-Diaminobenzidine-4HCl (DAB, MP Biomedical) and 0.005% H<sub>2</sub>O<sub>2</sub> in 0.1M PBS (pH 7.4) on a shaker. Slides were then washed in distilled water, dehydrated with a series of graded ethanol, cleared with xylene, and cover slipped using DEPEX mounting medium (BDH Chemical).

### **Non-haem iron assay for the assessment of iron levels in BAL supernatants and tissue**

Non-haem iron content in BAL supernatants from severe or mild-moderate asthma patients or healthy controls, and in murine liver and lung tissues were measured as previously described (5). For the latter, briefly, ~50mg of wet tissues of liver or lung were homogenised in 1 ml of 0.9% NaCl solution on ice. Iron standard solutions ranging in concentration from 0 to 8µg/ml

were prepared from a stock solution of 5mM FeSO<sub>4</sub> (BDH Chemical). Then 100µl of iron standards or BAL supernatant or tissue homogenates were mixed with 50µL of 3.8M (12%) HCl and incubated at 85°C for 30 min. Then, 25µL of 50% trichloroacetic acid (Sigma-Aldrich, Australia) was added into each tube followed by incubated on ice for 10 min. After centrifugation (235 xg, room temperature, 20 min), 100 µl of supernatant was removed from each tube and added in triplicate to clear 96-well plates. Finally, 100µl of colour reagent (816µM bathophenanthroline disulfonic acid, 1.9M sodium acetate, 0.2% (v/v) thioglycolic acid; Sigma) was added to each well to develop colour and absorbance was measured at 560nm using a microplate reader (Synergy2, Millennium Science). After subtracting absorbance of blank samples, iron concentrations were calculated from the standard curve.

## Gene expression analysis by RT-qPCR

Total RNA was extracted from frozen mouse lung tissues using Trizol reagent (Invitrogen, Life Technologies, Australia) as described previously (6). Mouse total RNA (1µg) was reverse transcribed into cDNA using Bioscript (Bioline, Australia) and random hexamer primers (Invitrogen, Life Technologies, Australia). For human airway biopsy tissues, total RNA was isolated using QIAGEN RNeasy Mini kit for human airway biopsy tissue homogenates (Qiagen, Venlo, Netherlands, Cat# 990394) according to the manufacturer's instructions. Human cDNA was collected using a reverse transcription kit (Applied Biosystems, USA). The level of mRNA transcripts for iron regulatory molecules and cytokines were measured by SYBR-green qPCR using Eppendorf RealPlex (Eppendorf, Germany) and relative expression was normalised to transcripts of *HPRT* (mouse gene expression) or beta actin (human gene expression) (7-9). The formula used for calculating relative expression of each gene of interest was  $2^{-(Ct \text{ gene of interest} - Ct \text{ HPRT})}$  (10). Primer sequences are shown in **Tables E1 and 2**. Total mRNA from primary human ASM cells and lung fibroblast culture experiments was isolated using the

ISOLATE II RNA Mini Kit and transcribed into cDNA using the SensiFAST™ cDNA Synthesis Kit (Bioline, Alexandria, Australia), according to the manufacturer's instructions. Assays were carried out in triplicate using a reaction mixture containing the Bioline SensiFAST Probe Hi-ROX Master Mix and TaqMan primer sets for *TNC* (Hs01115665\_m1) and the ubiquitously expressed ribosomal RNA (18S rRNA) as a housekeeping gene. qPCR was performed using the StepOnePlus detection system and data were collected and analysed by StepOne software (Applied Biosystems, Melbourne, Australia).

## **Mouse BAL**

BAL collection, processing and cytopsin preparations were performed as described previously (11). BAL cells cytopsin slides were stained with May-Grunwald-Giemsa, differential immune cells were counted ( $\approx 175$ ) using light microscopy at 40x magnification based on key morphological characteristics (12, 13).

## **Lung tissue eosinophil and airway mucus-secreting cell numbers**

Lung sections were deparaffinised and stained with chrome salt fixation (for eosinophils) or periodic acid–Schiff (for mucus-secreting cells). Numbers of eosinophils and PAS positive cells (i.e. mucus secreting cells) were counted per 100 $\mu$ m around the airways at 100x magnification as previously described (12, 13).

## **Small airway remodelling**

Airway remodelling in terms of collagen thickness around the small airways was evaluated in at least 6 small airway images (40x magnification) from Sirius Red and Fast Green-stained (Sigma Aldrich, USA) mouse lung sections using ImageJ (version 1.47, Media Cybernetics, Rockville, MD, USA) as previously described (11).

## **AHR**

AHR in terms of central airway resistance ( $R_n$ ) in response to nebulised methacholine (MCh) was measured using FlexiVent apparatus (FX1 System; SCIREQ, Montreal, Canada). Briefly, mice were anaesthetised with a mixture of ketamine (100mg/kg, Parnell) and xylazine (10mg/kg, Troy Laboratories, Smithfield, Australia). Following tracheostomy, cannulae were inserted into their tracheas and ligated (7, 12-14).  $R_n$  (tidal volume of 8mL/kg at a respiratory rate of 450 breaths/min) was measured in response to increasing doses of nebulised MCh (up to 30mg/kg; Sigma-Aldrich, Sydney, Australia) (14).

**IL6, IL8 and transferrin detection.** Levels of IL-6 and IL-8 in cell-free supernatants were measured by sandwich ELISA, using commercial antibody kits according to the manufacturer's instructions (R&D Systems, MN). The detection limit of both assays was 15.6 pg/ml. Levels of transferrin in BAL supernatants were measured using commercial ELISA kit according to the manufacturer's instructions (Abcam: ab157724).

## **Flow cytometric analysis of macrophage populations in murine lung tissue.**

Flow cytometry was performed on murine whole lung single cell suspensions to determine the number and activation of macrophage subsets (15). Lung tissue was processed into single cell suspensions *via* enzymatic digestion with collagenase D (2mg/mL, Roche, Sydney, Australia), DNase I (400U/mL, Roche) and a gentleMACS™ Dissociator (Miltenyi Biotec). Total lungs cells were collected, and red blood cells lysed (155mM  $\text{NH}_4\text{Cl}$ , 12mM  $\text{NaHCO}_3$ , 0.1mM ethylenediaminetetraacetic acid [EDTA], pH 7.35, 5mins, 4°C). Total cell counts were performed using a haemocytometer under a light microscope (20x magnification) and trypan blue (Sigma-Aldrich) exclusion. Total cells stained with fluorescently conjugated antibodies



specific for CD45, F4/80, CD11c, CD11b, Ly6C, SiglecF and TFR1 (**Table E3**) (BD Biosciences, San Diego, USA; Biolegend, San Diego, USA). Live cell discrimination was assessed with Zombie yellow fixable viability dye (Biolegend). Cells were then analysed using a LSR Fortessa X-20 (BD Biosciences) and FACSDiva software (BD Biosciences). After exclusion of cell debris, doublets and dead cells, macrophage subsets were determined based on antigen expression (**Table E4**).

**Isolation of macrophages from whole lung tissue.** Lungs were processed into single cell suspensions and stained with fluorochrome-conjugated antibodies as above. Tfr1<sup>+</sup> macrophages were isolated by fluorescence-activated cell sorting using an ARIA III (BD Biosciences) into PBS with 5% FCS.

### **RNA extraction from isolated macrophages and reverse transcription (RT).**

Total RNA was extracted from sorted Tfr1<sup>+</sup> macrophages using miRNeasy mini kit (Qiagen, Chadstone, Australia) as per manufacturer's instructions. Sorted cells were collected into Qiazol® (750µL) and stored at -80°C until RNA extraction. Upon thawing of cells, chloroform (140 µL) was added and vortexed prior to phase separation by centrifugation (15min, 4°C, 12,000xg). The aqueous phase was collected before automated RNA extraction using Qiacube apparatus (Qiagen). This automated protocol supplemented samples with 100% molecular grade ethanol prior to centrifugation. Samples were transferred to spin columns and washed with RWT buffer. RPE buffer was added to columns prior to further centrifugation. Purified RNA was eluted using RNase-free water. RNA purity and concentration were determined using a NanoDrop™ 1000 Spectrophotometer (Thermo Fisher Scientific, North Ryde, Australia). The 260/230nm and 260/280nm absorption ratios accepted as pure RNA was >1.90, and >2.00, respectively. RNA from isolated macrophages was reverse transcribed to cDNA

using the miScript II RT kit (Qiagen) as per manufacturer's instructions. Samples were supplemented with miScript HiFlex buffer (4µl), 10x miScript Nucleics mix (2µl) and miScript reverse transcriptase mix (2µl). Reverse transcription was achieved using a Bio-Rad T100 Thermal Cycler (60min, 37°C; 5min, 95°C). Samples were then stored at -20°C until quantification by qPCR.

**ASM cell and lung fibroblasts culture.** Primary human ASM cells and lung fibroblasts were isolated from the parenchyma of lungs from patients undergoing lung transplantation as previously described (16). Patient demographics are described in **Table E6**. Cells were seeded in 12 or 96 well plates at  $4.5 \times 10^4$  cells/mL in DMEM with 5% fetal bovine serum and 1% antibiotic-antimycotic, and cultured to near confluence (72h, 37°C, 5% CO<sub>2</sub>). Cells were serum starved in DMEM with 0.1% bovine serum albumin for 24h prior to stimulation. Cells were stimulated with a range of ferric ammonium citrate (FAC) concentrations for 48h, with additions replenished at 24h. Cell free supernatants or total RNA lysates were collected at 48h and stored at -20°C for analysis. All experiments were carried out using fibroblasts between passage 2 and 4.

**Primary bronchial airway epithelial cells (pBECs) cultured at the air-liquid interface (ALI) (17).** Human pBECs were obtained from healthy controls, and patients with severe asthma. pBECs were raised and maintained in placental collagen-coated T75 tissue culture flasks (Interpath, Australia) with Bronchial Epithelial Cell Growth Medium (BEGM™, Lonza, USA), supplemented with BEGM™ SingleQuots™ supplements and Growth Factors (BEGM™ BulletKit™, Lonza), penicillin/streptomycin (Life Technologies, USA) and amphotericin B (Sigma, USA). Cell monolayers at 70%-80% confluency were detached with 1:10 trypsin-ethylenediaminetetraacetic acid/Dulbecco's phosphate buffered saline (1:10

trypsin-EDTA/D-PBS, 4mL). Trypsin enzyme activity was neutralised with foetal bovine serum (FBS) and cells were resuspended in ALI initial medium. Detached cells were then enumerated and seeded at  $2 \times 10^5$  cells/500 $\mu$ L initial media onto the apical compartment of a 12-well plate (Corning, USA) containing a 12mm polyester membrane transwell (0.4 $\mu$ m pore size, Sigma). ALI initial media was also added to the basal compartment (1.5mL/well) and refreshed (1.5mL/well) 24h after seeding. At 72h post-seeding, all apical media was removed and basal media replaced with ALI final medium (1.5mL/well). This timepoint was demarcated as “day 0” of ALI culture and the beginning of the experimental period. Basolateral media was replaced every two days with 1.5mL fresh ALI final medium. Apical surfaces of the ALI cultures were washed with sterile 1xD-PBS (500uL/well) weekly, and trans-epithelial electrical resistance measured (Epithelial Volt/ohmmeter 2 [EVOM<sub>2</sub>], Coherent Scientific) to track monolayer formation. This weekly apical wash also served to remove any mucus build-up from the cultures. Patient cells were grown at ALI in culture conditions (37°C, 5% CO<sub>2</sub>) for 28 days to ensure maximal differentiation. Following sufficient differentiation of the cells basal media was replaced with ALI minimal media (1.5 mL/well) and incubated overnight (37°C, 5% CO<sub>2</sub>). Apical compartments of each well were then supplemented with minimal media and 1xD-PBS (500uL) and basal minimal media was replaced (1.5mL) prior to the second overnight incubation (37°C, 5% CO<sub>2</sub>). At the end of the protocol, apical and basal media was removed and stored at -80°C for further analysis. Cells from the apical ALI membrane insert were also harvested and stored in Qiazol<sup>®</sup> lysis reagent (700uL, Qiagen, -80°C) for further processing.

## Statistics

Comparisons between two groups were performed using a non-parametric Mann-Whitney test. Comparisons between multiple groups were performed using Kruskal-Wallis one-way analysis of variance (ANOVA) with uncorrected Dunn’s post-hoc test. AHR data were analysed using

two-way repeated measures ANOVA with Bonferroni post-hoc test. Correlation analyses were performed using Spearman rank correlation. All statistical analysis was performed using GraphPad Prism V.7 Software (San Diego, California, USA).

## **Supplementary results**

### **HDM-induced experimental asthma**

Intranasal HDM-treatment increases the number of immune cells (macrophages, neutrophils, eosinophils) in BAL, airway tissue eosinophil numbers, mucus secreting cell numbers, and collagen deposition in airway tissue and this is associated with increased airway hyper-responsiveness (AHR) (**Figure E2 A-F**).

## **Supplementary discussion**

We show a significant increase in iron positive BAL cells in subjects with severe and mild-moderate asthma compared to healthy controls. Increased numbers of iron-laden cells have been reported in patients with COPD (18), IPF (19) and cigarette smokers (20). The increased iron in the lung of cigarette smokers may not be dyshomeostasis, but actual loading of lungs with additional iron on inhalation. However, these findings do suggest that increased numbers of iron laden cells in the airways is a key feature of several lung diseases. Our data is also consistent, with a recent case report where haemosiderin-laden macrophages were identified in BAL from an 8-year old child with recurrent iron-deficiency anaemia (IDA) and allergic asthma and later diagnosed with idiopathic pulmonary haemosiderosis (IPH) (21). However,

since this study is based on a single patient it is unclear whether IDA and/or macrophage haemosiderin are associated with allergic asthma or IPH.

To protect from the potentially harmful effects of excess free iron, iron regulatory systems must be tightly regulated in the body. Although little is known about the iron metabolism in the lung, as with other organs, iron homeostasis in the lung is maintained by a range of iron regulatory molecules, including iron uptake (transferrin receptors, TFR1, TFR2); divalent metal transporter 1 (DMT1); zinc transporter protein 14 (ZIP14); natural resistance-associated macrophage protein 1 (NRAMP1) and lactoferrin receptor (LFR); transport (Transferrin, TF), storage (ferritin heavy and light chain, FTH, FTL) and export (ferroportin, FPN) from cells. Iron-responsive proteins (IRPs) control the expression of these genes through binding with the 5' or 3' untranslated regions of these genes mRNA (22).

We show that *NRAMP1* expression is higher in the airways of mild-moderate asthma patients and tends to further increase in severe asthma compared to healthy controls (**Figure 3C**). NRAMP1 has been reported to affect IgE responses, the development of Th2 cell responses and mast cell degranulation in ovalbumin-induced allergic asthma in mice (23). We also show increased *TFR2* in the airways of severe asthma patients (**Figure 3A**). TFR2 acts as an iron sensor of transferrin-bound iron (Fe-TF) that stimulates hepcidin production (24). In addition, ZIP14 levels have been shown to increase in airway cells in iron overload and decrease in iron deficiency in mice (25). We show increased *FTH* and *IRP1* expression in airways of mild-moderate but not severe asthma patients (**Figure 3D, F**). Furthermore, *FTL* expression reduced ( $p=0.06$ ) in the airways of severe compared to mild-moderate asthma patients (**Figure 3E**). Another study suggested that *FTL* has anti-inflammatory effects, which agree with our findings (26). In addition, we find that the only known iron exporter, *FPN* expression is not altered in asthma (**Figure 3H**). All these data provide strong evidence that

there is an environment of increased iron sequestration into cells in asthmatic airways that leads to increased cellular but reduced extracellular iron levels in BAL in asthma.

To explore the relationship between iron and asthma, we performed a series of studies to determine the effects of LID on key disease features. Decreasing systemic iron levels using a LID had no effect on lung iron levels but increased AHR in the absence of HDM-induced experimental asthma. However, we also show that a LID reduces iron accumulation in HDM-induced experimental asthma and protects against some of the key features of disease. These findings highlight the complexity and importance of systemic:local iron regulatory interactions in the pathogenesis of asthma, and also demonstrates that both low and high systemic iron may promote/increase the severity of key disease features in different contexts, which is consistent with the controversy in the literature (27-32).

Whilst our findings demonstrate that increased iron accumulation in cells and tissues in the airways and lung is linked to key features of asthma and plays a role in the worsening of lung function and disease severity, they do not elucidate the underlying mechanisms involved in iron-mediated effects. A large body of evidence suggests that iron-induced oxidative stress may play a key role (24). Iron accumulation has been suggested to induce oxidative stress and contribute to the pathogenesis of Alzheimer's disease, atherosclerosis and Parkinson's disease (33), and there is a clear involvement of oxidative stress in asthma (34, 35). Increased production of ROS and reactive nitrogen species (RNS) and reduced or inactivated antioxidant responses occur in patients with bronchial asthma (36-40). Lipid peroxidation in plasma and exhaled breath condensate (EBC) is inversely correlated with airflow obstruction in asthma (41). In addition, total antioxidant capacity in plasma and sputum, and SOD levels in plasma and airway epithelial cells (AEC) have been reported to be positively associated with airflow obstruction in asthmatics (41). Chronic inflammation can generate ROS (42), and overproduction of ROS/RNS reportedly leads to airway inflammation and remodelling, mucus

overproduction, tissue injury and lung function decline in clinical and experimental asthma studies (43, 44). Notably, a significant increase in iron and MDA levels in plasma have been shown in asthmatics, and there is a positive correlation between MDA and iron levels (32), suggesting that increased systemic iron may promote asthma. Furthermore, increased levels of oxidative stress (increased MDA, catalase, SOD, GPX and nitrotyrosine levels) and inflammatory responses (increased HIF1 $\alpha$ , NF- $\kappa$ B and TNF $\alpha$  levels) with increased iron accumulation in the lung have been shown in rats treated with low molecular weight iron dextran (45). Based on this evidence, increased iron may drive disease through increased oxidative stress in tissues that drives many of the key features of disease.

Ferroptosis, a process of iron-dependent programmed cell death, has recently been suggested to be a key molecular mechanisms implicated in kidney, brain, liver, heart and lung pathology (46-51). Recently, Wenzel *et al.*, uncovered evidence for phosphatidylethanolamine-binding protein 1 (PEBP1)-dependent regulatory mechanisms of ferroptotic death in AEC in asthma (52). Since we show that experimental asthma results in increased iron accumulation in lung cells and tissues as well as evidence for increased iron sequestration in clinical airway samples, it is possible that increased iron accumulation-mediated ferroptotic cell death may contribute to disease pathogenesis. However, further studies are required to explore mechanisms of the association between iron and ferroptosis in asthma pathogenesis and to determine the Fe<sup>2+/3+</sup> status and localisation within airway cells.

In the lung, iron can also be derived from non-dietary sources e.g smoking, pollution or geogenic iron. Increased iron accumulation in the lung as a result of these exogenous exposures may also contribute to lung pathology. Indeed, Indeed, a recent study has shown that increased concentrations of iron in particulate matter result in lung impairment 7 days-post intranasal exposure in mice (53). It is also important to note that infections are associated with the development of asthma phenotypes and that humans and mice with asthma or allergic

airway disease have altered microbiomes and predispose to respiratory infections that increase the severity or exacerbate their disease (24) . Excess iron can also increase susceptibility to respiratory infections (24), which may modify the immune system and promote disease pathogenesis.

Due to the limited availability of appropriate airway tissue samples, and the prospective nature of our analyses, we needed to draw bronchoscopy samples from two different cohorts. We note that there was no significant difference in asthma control questionnaire (ACQ) and BAL cellular profiles in the cohorts that we used for BAL non-haem iron studies. Our findings from these two different cohorts highlight that iron levels and regulation are altered in asthma.

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## Supplementary figure legends

**Figure E1.** Iron diets and HDM-induced experimental asthma protocol.

**Figure E2.** House dust mite (HDM)-induced experimental asthma. Six-8-week-old wild-type (WT) BALB/c mice were intranasally administered HDM antigen for 5 days per week for 6 weeks and then major features of experimental asthma were assessed. Total and differential immune cells were enumerated in bronchoalveolar lavage and cytopsin slides stained with May-Grunwald-Giemsa (A). Tissue eosinophil numbers were assessed in chrome salt fixation-stained lung sections (B). Mucus secreting cells (MSCs) were enumerated around inflamed airways in PAS-stained lung sections (C, D). Area of collagen deposition surrounding the basement membrane of small airways was quantified in Sirius red-stained lung tissue sections, in 6-8 airways/mouse, using *ImageJ* (E). Airway hyper-responsiveness (AHR) was measured in terms of central airway resistance (Rn) to inhaled increasing concentrations of nebulised methacholine (Mch) using Flexivent apparatus (F). Scale bar: 50  $\mu$ m. Data are presented as mean  $\pm$  SEM ( $n=6-8$ ), pooled from two repeat experiments. \*\* $p<0.01$ ; \*\*\* $p<0.001$ ; \*\*\*\* $p<0.0001$  compared to PBS controls.

**Figure E3. Bronchoalveolar lavage (BAL) cell profiles in house dust mite (HDM)-induced experimental asthma in WT and *Hfe*<sup>-/-</sup> AKR mice.** HDM was administered to ~36 week-old wild-type (WT) and *Hfe*<sup>-/-</sup> AKR mice for 5 days per week for 6 weeks and then differential immune cells were enumerated in BAL and cytopsin slides stained with May-Grunwald-Giemsa. Data are presented as mean  $\pm$  SEM ( $n=6-10$ ), pooled from 2 repeat experiments. \* $p<0.05$ ; \*\* $p<0.01$ ; \*\*\* $p<0.001$ .

## Supplementary tables



**Table E1.** Custom-designed primers for human mRNA used in qPCR analyses.

**Table E2.** Custom-designed primers for mouse mRNA used in qPCR analyses.

**Table E3.** Antibodies used for flow cytometry

**Table E4.** Antigenic definitions for macrophage analyses conducted by flow cytometry

**Table E5.** Human bronchial airway epithelial cells (pBECs) donor characteristics

**Table E6.** Human airway smooth muscle cell and lung fibroblast donor characteristics

**Figure E1.**

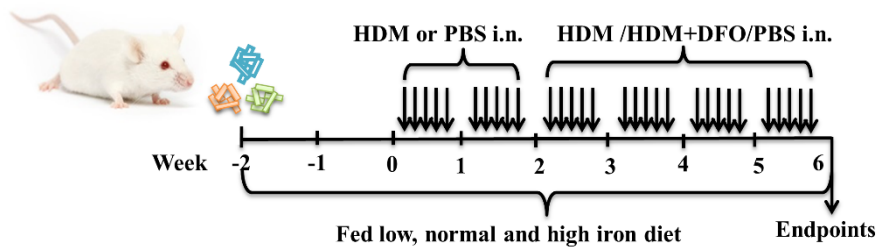


Figure E2.

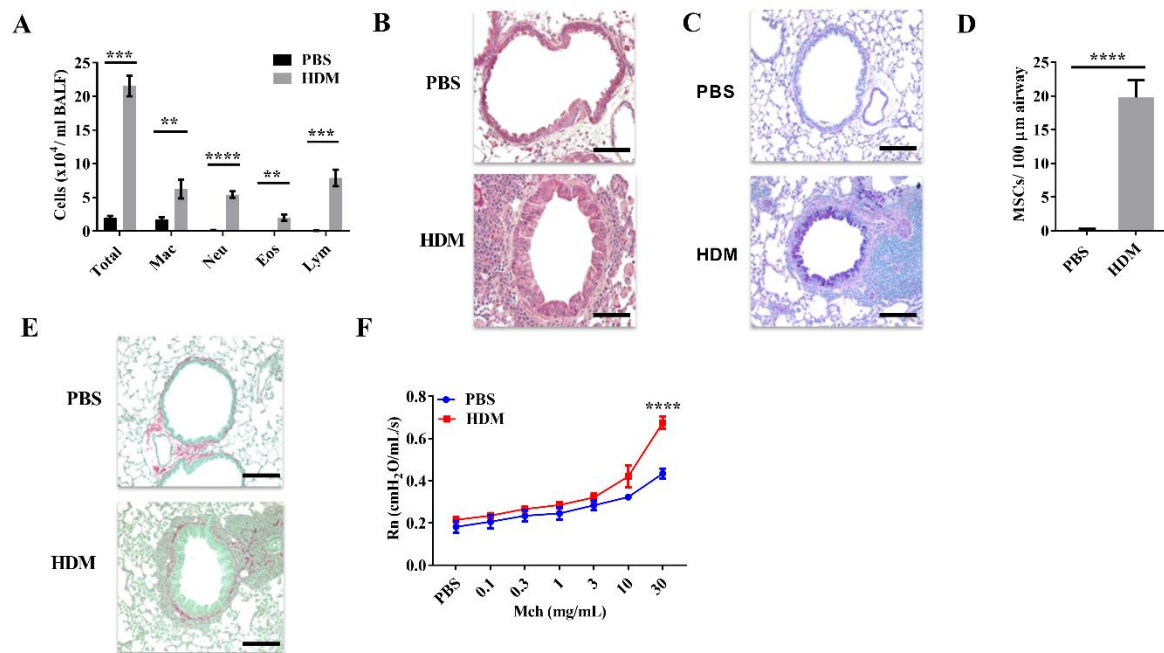
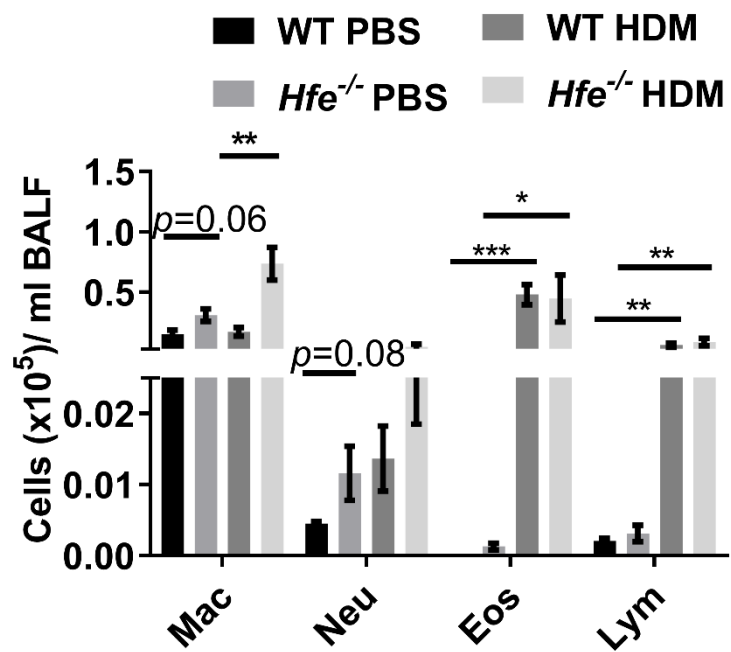


Figure E3.



**Table E1.**

<b>Primer</b>	<b>Primer sequence (5' → 3')</b>	<b>Target gene</b>
<i>Beta Actin Forward</i>	CTGGCACCACACCTTCTA	<i>Beta Actin</i>
<i>Beta Actin Reverse</i>	GGTGGTGAAGCTGTAGCC	<i>Beta Actin</i>
<i>DMT1 Forward</i>	GGT GTT GTG CTG GGA TGT TA	<i>DMT1</i>
<i>DMT1 Reverse</i>	AGTACATATTGATGGAACAG	<i>DMT1</i>
<i>FPN Forward</i>	CTGTGCCCATAAATCTCTGTC	<i>FPN</i>
<i>FPN Reverse</i>	CCATTTATAATGCCTCTTTTCA	<i>FPN</i>
<i>HAMP Forward</i>	CTGTTTTCCCACAACAGACG	<i>HEPC1</i>
<i>HAMP Reverse</i>	CAGCACATCCCACACTTTGA	<i>HEPC1</i>
<i>TFR1 Forward</i>	AGGAACCGAGTCTCCAGTGA	<i>TFR1</i>
<i>TFR1 Reverse</i>	ATCAACTATGATCACCAGAGT	<i>TFR1</i>
<i>TFR2 Forward</i>	GGAGTGGCTAGAAGGCTACCTCA	<i>TFR2</i>
<i>TFR2 Reverse</i>	GGTCTTGGCATGAACTTGTC	<i>TFR2</i>
<i>FTL Forward</i>	CCATGAGCTCCCAGATTCTG	<i>Ft L</i>
<i>FTL Reverse</i>	TTCCAGAGCCACATCATCGC	<i>Ft L</i>
<i>FTH Forward</i>	CCAGAACTACCACCAGGACT	<i>Ft H</i>
<i>FTH Reverse</i>	CACATCATCGCGGTCAAAGT	<i>Ft H</i>
<i>ZIP14 Forward</i>	GCTTATGGAGAACCACCCCT	<i>ZIP14</i>
<i>ZIP14 Reverse</i>	AGGTTCTGTGTCCTTGAC	<i>ZIP14</i>
<i>NRAMP1 Forward</i>	TTCTCGTCCAAAGGAGCAGG	<i>NRAMP1</i>
<i>NRAMP1 Reverse</i>	GTTGCAGGCGGAACAGAAAG	<i>NRAMP1</i>
<i>IRP1 Forward</i>	CGTGCAGTCGGAGGAACAC	<i>IRP1</i>
<i>IRP1 Reverse</i>	TCGAAAATGGTAAGCGCCCA	<i>IRP1</i>

**Table E2.**

<b>Primer</b>	<b>Primer sequence (5' → 3')</b>	<b>Target gene</b>
<i>Hprt Forward</i>	AGGCCAGACTTTGTTGGATTGAA	<i>Hprt</i>
<i>Hprt Reverse</i>	CAACTTGCGCTCATCTTAGGCTTT	<i>Hprt</i>
<i>Il13 Forward</i>	TGCTTGCCTTGGTGGTCT	<i>Il13</i>
<i>Il13 Reverse</i>	GGGGAGTCTGGTCTTGTGTG	<i>Il13</i>
<i>Tfr1 Forward</i>	CCCATGACGTTGAATTGAACCT	<i>Tfr1</i>
<i>Tfr1 Reverse</i>	GTAGTCTCCACGAGCGGAATA	<i>Tfr1</i>
<b><i>Il10 Forward</i></b>	AGGCGCTGTCATCGATTCT	<i>Il10</i>
<b><i>Il10 Reverse</i></b>	ATGGCCTTGTAGACACCTTGG	<i>Il10</i>
<b><i>Ifng Forward</i></b>	CTGGAGGAACTGGCAAAAGG	<i>Ifng</i>
<b><i>Ifng Reverse</i></b>	TTGCTGATGGCCTGATTGTC	<i>Ifng</i>
<b><i>Tgfb1 Forward</i></b>	CCCGAAGCGGACTACTATGCTA	<i>Tgfb1</i>
<b><i>Tgfb1 Reverse</i></b>	GGTAACGCCAGGAATTGTTGCTAT	<i>Tgfb1</i>

**Table E3.** Antibodies used for flow cytometric staining

<b>Antigen</b>	<b>Fluorophore</b>	<b>Clone</b>	<b>Manufacturer</b>
CD45	PerCP	30F-11	Biolegend
CD11c	Brilliant violet (BV)421	N418	Biolegend
CD11b	Alexa Fluor (AF)700	M1/70	BD Biosciences
SiglecF	Phycoerythrin (PE)	E50-2440	BD Biosciences
F4/80	BV711	T45-2342	Biolegend
Ly6C	PE-Cy7	A1-21	BD Biosciences
TFR1	APC	R17217	Biolegend

**Table E4.** Antigen definitions for macrophage flow cytometric staining

Granulocyte type	Antigen definition
Total macrophages	CD45 <sup>+</sup> , F480 <sup>+</sup> , CD11c <sup>hi/+/-</sup> , SiglecF <sup>-/hi</sup>
Alveolar Macrophage	CD45 <sup>+</sup> , F4/80 <sup>+</sup> , CD11b <sup>-</sup> , CD11c <sup>hi</sup> SiglecF <sup>hi</sup>
Interstitial Macrophage	CD45 <sup>+</sup> , F4/80 <sup>+</sup> , CD11b <sup>+</sup> , CD11c <sup>+</sup> , SiglecF <sup>-</sup> , Ly6C <sup>-</sup>
Monocytes	CD45 <sup>+</sup> , F4/80 <sup>+</sup> , CD11b <sup>+</sup> , CD11c <sup>-</sup> , SiglecF <sup>-</sup> , Ly6C <sup>+</sup>

**Table E5.**

Characteristic	Healthy	Asthmatics
Number of subjects, n	8	7
Age, yr	62.63 ± 5.873	56.86 ± 5.595
Sex, M/F	2/6	2/5
FEV1% predicted	84.25 ± 5.230	78.43 ± 6.931
FEV1/FVC	0.747 ± 0.030	0.723 ± 0.021
ACQ	-	2.400 ± 0.623
Total cells (x10 <sup>6</sup> /mL BAL)	0.667 ± 0.391	3.717 ± 3.345
Macrophages (%)	47.75 ± 13.93	41.67 ± 13.48
Neutrophils (%)	22.75 ± 11.00	44.29 ± 14.64
Eosinophils (%)	0.850 ± 0.217	1.833 ± 0.363
ICS, yes/no	NA	7/0
ICS dose <sup>s</sup>	NA	717.10 ± 114.7
LABA, yes/no	NA	6/1
LAMA, yes/no	NA	2/5
SABA, yes/no	NA	3/4
OCS, yes/no	NA	0/7

M/F, male/female; FEV1, forced expiratory volume in one second; FVC, forced vital capacity; ACQ, asthma control questionnaire; BAL, bronchoalveolar lavage; NA, not applicable; ICS, inhaled corticosteroids; LABA, long-acting  $\beta$ 2-agonist; LAMA, long-acting muscarinic antagonist; SABA, short-acting  $\beta$ -agonist; OCS, oral corticosteroids; yr, year. <sup>s</sup>Equivalent to Fluticasone  $\mu$ g/day. Data are shown as mean  $\pm$  SEM.

**Table E6.**

Patient No.	Disease	Gender	Age
1	Pulmonary fibrosis	F	54
2	Pulmonary fibrosis	M	64
3	Bronchiectasis	M	60
4	IPF	M	65
5	Telomere-associated pulmonary fibrosis	F	45
6	COPD	M	61
7	NSCC	F	60
8	Pulmonary fibrosis	M	68
9	Emphysema	F	57
10	Emphysema	M	65
11	bronchiectasis	F	38
12	BOS (re-do)	F	28

13	Emphysema	M	60
14	Pulmonary fibrosis	M	53

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M, male; F, female.