Genetic variants associated with susceptibility to idiopathic pulmonary fibrosis in people of European ancestry: a genome-wide association study


Summary

Background Idiopathic pulmonary fibrosis (IPF) is a chronic progressive lung disease with high mortality, uncertain cause, and few treatment options. Studies have identified a significant genetic risk associated with the development of IPF; however, mechanisms by which genetic risk factors promote IPF remain unclear. We aimed to identify genetic variants associated with IPF susceptibility and provide mechanistic insight using gene and protein expression analyses.

Methods We used a two-stage approach: a genome-wide association study in patients with IPF of European ancestry recruited from nine different centres in the UK and controls selected from UK Biobank (stage 1) matched for age, sex, and smoking status; and a follow-up of associated genetic variants in independent datasets of patients with IPF and controls from two independent US samples from the Chicago consortium and the Colorado consortium (stage 2). We investigated the effect of novel signals on gene expression in large transcriptomic and genomic data resources, and examined expression using lung tissue samples from patients with IPF and controls.

Findings 602 patients with IPF and 3366 controls were selected for stage 1. For stage 2, 2158 patients with IPF and controls were selected. We identified a novel genome-wide significant signal of association with IPF susceptibility near A-kinase anchoring protein 13 (AKAP13; rs62025270, odds ratio [OR] 1.27 [95% CI 1.18–1.37], p=1.12×10⁻⁶⁶) and desmoplakin (DSP; rs2076295, OR 1.44 [1.35–1.54], p=7.81×10⁻²⁸). For rs62025270, the allele A associated with increased susceptibility to IPF was also associated with increased mRNA expression of AKAP13 mRNA in lung tissue from patients who had lung resection procedures (n=1111). We showed that AKAP13 is expressed in the alveolar epithelium and lymphoid follicles from patients with IPF, and AKAP13 mRNA expression was 1.42-times higher in lung tissue from patients with IPF (n=46) than that in lung tissue from controls (n=51).

Interpretation AKAP13 is a Rho guanine nucleotide exchange factor regulating activation of RhoA, which is known to be involved in profibrotic signalling pathways. The identification of AKAP13 as a susceptibility gene for IPF increases the prospect of successfully targeting RhoA pathway inhibitors in patients with IPF.

Funding UK Medical Research Council, National Heart, Lung, and Blood Institute of the US National Institutes of Health, Agencia Canaria de Investigación, Innovación y Sociedad de la Información, Spain, UK National Institute for Health Research, and the British Lung Foundation.

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Introduction

Idiopathic pulmonary fibrosis (IPF) is a chronic, progressive, fibrotic lung disease of unknown cause with a poor prognosis. The incidence of IPF in the UK is about 4.5–7.5 per 100,000 and is increasing, with a median survival of approximately 3 years. Since 2010, two new therapies, pirfenidone and nintedanib, have been approved for the treatment of IPF, but these treatments only slow disease progression and do not halt or reverse pulmonary fibrosis. Furthermore, these drugs are not universally effective and the mechanisms of their antifibrotic effects are unknown. Therefore, a detailed understanding of the genetic risk factors for IPF and their associated molecular pathways is urgently required. The current theory suggests that IPF is characterised by initial damage to the alveolar epithelium, which then signals to various cell types, predominantly fibroblasts and macrophages, promoting tissue damage and

www.thelancet.com/respiratory Published online October 20, 2017 http://dx.doi.org/10.1016/S2213-2600(17)30387-9

Lancet Respir Med 2017  
Published Online  
October 20, 2017  
http://dx.doi.org/10.1016/S2213-2600(17)30387-9  
See Online/Comment  
http://dx.doi.org/10.1016/S2213-2600(17)30393-4  
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Articles

Research in context

Evidence before this study

We searched Web of Science between Aug 21, 2015, and June 7, 2017, with the search terms “pulmonary fibrosis” and “genomic wide” with no restrictions on publication date or language. Numerous genome-wide association studies (GWAS) have reported 16 independent signals associated, at genome-wide significance, with susceptibility to idiopathic pulmonary fibrosis (IPF). Although previous studies have shown that epithelial cell function, lung defence, cell-cell adhesion, and telomere maintenance might play important roles in IPF, the precise mechanisms through which the genes identified in previous GWAS promote IPF are still poorly understood.

Added value of this study

To our knowledge, this study is the largest genetic study of IPF done to date, bringing together 2760 patients with IPF and 8561 controls. We present a novel genome-wide significant genetic association signal and novel gene expression data that implicate A-kinase anchoring protein 13 (AKAP13) as an IPF susceptibility gene. AKAP13 is a Rho guanine nucleotide exchange factor (RhoGEF) that regulates activation of Rho A. RhoA is a molecule with a known role in profibrotic signalling pathways; however, AKAP13 has not previously been implicated in the pathogenesis of IPF. These studies provide genetic veracity for targeting Rho signalling in IPF.

Methods

Study design

This GWAS used a two-stage approach to identify novel genome-wide significant signals associated with susceptibility to IPF. In stage 1, a GWAS was done using patients with IPF from nine different centres in the UK and controls from UK Biobank. Variants showing a significant association (p<5×10⁻⁴) in stage 1 were then further analysed in independent samples of patients with IPF and controls from two US samples, the Colorado consortium and the Chicago consortium (stage 2). We defined statistically significant associations with susceptibility to IPF as variants that met genome-wide significance (p<5×10⁻⁸) after meta-analysis of stages 1 and 2 together. Variants that became less significant in the meta-analysis than in stage 1 alone were not reported as showing an association.

Stage 1 comprised patients with IPF selected from nine different centres across the UK (appendix p 1). All diagnoses were made in accordance with accepted international criteria. Controls were selected from UK Biobank and were matched for age, sex, and smoking distributions, showed no evidence of having any interstitial lung disease, and had genetic data available (appendix p 1). Stringent quality control testing of all samples was done, such as removing individuals with poor call rates, heterozygosity outliers, duplicates, related individuals, ancestry outliers, and sex mismatches (appendix p 1). All individuals were of European ancestry.

Stage 2 comprised two additional independent case-control studies that have been previously described by Noth and colleagues (Chicago consortium) and Fingerlin and colleagues (Colorado consortium). For both these studies, patients with IPF were diagnosed using American Thoracic Society and European Respiratory Society
guidelines. All studies had appropriate institutional review board or ethics approval.

Procedures and statistical analysis
For stage 1, patients with IPF and a third of the UK Biobank controls were genotyped using the Affymetrix Axiom UK BiLEVE array (Affymetrix, Santa Clara, CA, USA). The remainder of the controls were genotyped using the Affymetrix Axiom UK Biobank array (95% identical to the UK BiLEVE array). Genotyping and imputation procedures for studies contributing to stage 1 and 2 are described in the appendix p 1. Because the UK Biobank controls genotyped on the Axiom UK BiLEVE array had originally been selected on the basis of lung function and smoking behaviour, it was reasonable to assume that allele frequency differences between the controls genotyped on the two arrays could feasibly be driven by either technical array artefacts or genuine associations with lung function and smoking. To account for this in our analysis, and to avoid incorrectly reporting associations driven by array as associations with IPF susceptibility, we did additional sensitivity analyses (appendix p 2).

The genome-wide association analysis of IPF susceptibility was done assuming an additive genetic effect and conditioning on age, sex, and the first ten principal components to adjust for ancestry. The analysis was run using a score test because of its computational efficiency, using SNPTEST version 2.5.2. For variants with minor allele count less than 400 and score test p<5×10⁻³, the analysis was rerun using the Firth test using EPACTS version 3.2.4 (appendix p 2).

Independent variants reaching a threshold of p<5×10⁻⁶ in association testing in stage 1 were followed up in stage 2. Conditional analyses were used to identify additional independent signals in the same genomic region (appendix p 2).

In the Chicago consortium, analyses were done using the Firth test, adjusting for age and sex. In the Colorado consortium, analyses were done using the Firth test on a logistic regression model, adjusting for sex and the top three dimensions from a multidimensional scaling model.

For variants that were significantly associated with IPF susceptibility in stage 1 only after conditioning on another variant, the analysis was run in stage 2 conditioning on the same variant. The results from these stage 2 studies were meta-analysed using a fixed-effects model.

For variants that showed a significant (p<5×10⁻⁶) association with IPF risk in stage 1, available association test statistics from stages 1 and 2 were meta-analysed using a fixed-effects model. Signals that had genome-wide significance (p<5×10⁻⁹) when meta-analysing stages 1 and 2 were reported as significantly associated with susceptibility to IPF. A Bayesian approach was used to fine-map those signals to create 95% credible sets (a set of variants that was 95% likely to contain the causal variant; appendix p 3).

To investigate whether the variants showing an association with susceptibility to IPF were also associated with survival time in IPF, a Cox proportional hazards model was fitted in a subset of the stage 1 patients with IPF that had data for survival time. The model made adjustments for age, the first ten principal components, and the recruiting study centre. Analysis was done using the Survival package in R version 2.2.3.

We searched for evidence that genetic variants associated with susceptibility to IPF were independently associated with expression of a particular gene, because an association could implicate a particular gene as the driver of the signal. Variants that were significantly associated with susceptibility to IPF and proxy variants (correlated with linkage disequilibrium r²>0·8) were investigated in three expression quantitative trait locus (eQTL) datasets: a lung eQTL database comprising individuals from three cohorts (University of British Columbia, Laval, and Groningen), a blood eQTL database, and in the Genotype-Tissue Expression project (GTEx) cohort (multiple tissues; appendix p 3).

RT-PCR gene expression analysis was done on RNA extracted from human lung tissues of 46 patients with IPF and 51 controls from the Lung Tissue Research Consortium using standard methods (appendix p 3). Initially, differential gene expression in the lung was compared between the patients with IPF and controls using two-tailed Student’s t test comparing the change in CT values between groups. Linear regression analysis was used to compare A-kinase anchoring protein 13 (AKAP13) expression in controls and patients with IPF while also controlling for age, smoking (ever or never and pack-years), and sex.

Formalin-fixed paraffin-embedded human lung tissue sections were obtained from tissue distant from the tumour that was obtained during lung resection from controls and tissue from patients with IPF at either post-mortem examination or lung transplantation. Immunohistochemistry was done using standard methods (appendix p 3).

We performed in-silico analyses to establish whether known drugs target the proteins identified in the genome-wide and expression analyses or the proteins that interact with them (appendix p 4).

Role of the funding source
The funders had no role in the study design. GlaxoSmithKline Research and Design participated in collection of data and had access to the raw data from a subset of the UK IPF patient data. LVW and RGJ were involved in all stages of study development and delivery, had full access to all data in the study, and had final responsibility for the decision to submit for publication.
**A**

- 677 patients with IPF
  - 65 excluded
    - 8 failed Affymetrix quality control
    - 6 heterozygosity outliers
    - 31 duplicates
    - 1 related
    - 6 ancestry outliers
    - 6 did not have IPF
    - 5 sex mismatches
  - 632 patients with IPF passed quality control
  - 10 excluded for incomplete phenotype
  - 602 patients with IPF selected
  - 3968 individuals included in discovery analysis

**B**

**Chicago consortium**

- 633 patients with IPF recruited
  - 58 excluded
    - 16 self-reported non-European ancestry
    - 28 call rate <97%
    - 10 sex mismatches
    - 4 related
  - 575 patients with IPF passing quality control
  - 33 excluded because they could not be genetically matched to patients
  - 542 patients with IPF selected after genetic ancestry matching
  - 1054 individuals in analysis

**Colorado consortium**

- 1545 controls recruited
  - 118 excluded
    - 26 self-reported non-European ancestry
    - 69 call rate <97%
    - 18 sex mismatches
    - 5 related
  - 1427 controls passing quality control
  - 885 excluded because they could not be genetically matched to patients
  - 542 controls selected after genetic ancestry matching
  - 4683 controls passing quality control

**Summary**

- 7353 individuals in stage 2 meta-analysis
  - 2158 patients with IPF
  - 5195 controls

**Additional notes**

- 502 682 individuals in UK Biobank
  - 349 953 excluded because not genotyped
  - 152 729 individuals with genotyped data
    - 405 390 excluded
      - 480 missingness or heterozygosity
      - 17 308 related
      - 22 603 non-European
      - 148 people with interstitial lung disease
  - 112 190 individuals passed quality control
    - 3366 controls selected
Results

After sample quality control testing and genotype imputation, 602 patients with IPF and 3366 UK Biobank controls (selected on April 18, 2016) were included in the stage 1 analysis of 13076821 variants (figure 1A). The patients were diagnosed between June, 1996, and July, 2013, with the exception of 52 patients who were historical cases with unknown dates of diagnosis. In total, 44 independent signals were associated with susceptibility to IPF (p<5 × 10⁻⁶) and were followed up in stage 2 (figure 2).

A total of 2158 patients with IPF and 5195 controls were included in stage 2 (figure 1B, table 1). Of the 44 variants identified in stage 1, data were available for 27 variants in one or both of the stage 2 studies (appendix pp 8–9). Of these 27 variants, three were significant (p<1.85 × 10⁻³, after Bonferroni correction for 27 tests) in stage 2, and had genome-wide significance (p<5 × 10⁻⁸) in the meta-analysis of stage 1 and 2 together (table 2). A novel association for the single-nucleotide polymorphism (SNP) rs62025270, which was the most strongly associated SNP in a broad signal covering AKAP13 and kelch like family member 25 (KLHL25; figure 3), had genome-wide significance in the meta-analysis of stages 1 and 2 (minor allele A; odds ratio [OR] 1·27 [95% CI 1·18–1·37], p=1·32 × 10⁻⁹). This SNP was also significant in stage 2 alone after Bonferroni adjustment for 27 tests.

![Figure 1: Quality control and sample selection flow chart](image)

(A) Stage 1 genome-wide association study. (B) Stage 2 follow-up analyses. *On identification of a pair of individuals who were second-degree relatives or closer, one individual was excluded. IPF=idiopathic pulmonary fibrosis. †One patient had both call rate <98% and sex mismatch.

![Figure 2: Manhattan plot for the discovery genome-wide association study of IPF susceptibility](image)

The x axis shows chromosomal position and the y axis shows –log₁₀(p value) from the discovery (stage 1) case-control analysis. Green variants are those that reached genome-wide significance in the meta-analysis of stage 1 and 2 results (and any variant in linkage disequilibrium with the lead variant [rö>0·1]). The blue line shows the threshold used for selecting variants for stage 2 (p=5 × 10⁻⁶) and the red line shows genome-wide significance (p=5 × 10⁻⁸). Hollow circles show variants showing an association with genotyping array in the controls, and those that did not show an association with IPF in stage 2 (appendix pp 2 and 6). IPF=idiopathic pulmonary fibrosis.

<table>
<thead>
<tr>
<th>Stage 1</th>
<th>Stage 2: Chicago consortium</th>
<th>Stage 2: Colorado consortium</th>
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</thead>
<tbody>
<tr>
<td>IPF (n=602)</td>
<td>Controls (n=3366)</td>
<td>IPF (n=542) Controls (n=512)</td>
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<table>
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<tr>
<th>Age, years</th>
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<tbody>
<tr>
<td>Mean (SD)</td>
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<tr>
<td>Men</td>
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<tr>
<td>Women</td>
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</table>

Sex

<table>
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<tr>
<th></th>
<th>IPF (n=602)</th>
<th>Controls (n=3366)</th>
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</thead>
<tbody>
<tr>
<td>Men</td>
<td>426 (71%)</td>
<td>2356 (70%)</td>
</tr>
<tr>
<td>Women</td>
<td>176 (29%)</td>
<td>1010 (30%)</td>
</tr>
</tbody>
</table>

Data are n (%) unless otherwise stated. Age was not available for Colorado consortium controls. IPF=idiopathic pulmonary fibrosis. *Age data were only available for 103 individuals.

Table 1: Baseline characteristics of stage 1 and stage 2 samples
Results from case-control analyses for the variants that were significant (after correction for multiple testing) in stage 2 and reached genome-wide significance in the meta-analysis of stages 1 and 2. MAF corresponds to that from the stage 1 study. ORs were calculated using the minor allele as the effect allele. Stage 2 ORs and p values correspond to the meta-analysis of the Chicago and Colorado consortia results.

Table 2: Gene variants with genome-wide significance for idiopathic pulmonary fibrosis

<table>
<thead>
<tr>
<th>Chr Position</th>
<th>Locus</th>
<th>Minor allele</th>
<th>Major allele</th>
<th>MAF</th>
<th>Stage 1</th>
<th>Stage 2</th>
<th>Meta-analysis (stages 1+2)</th>
</tr>
</thead>
<tbody>
<tr>
<td>n2076295</td>
<td>6 756232 DSP</td>
<td>G</td>
<td>T</td>
<td>46.3%</td>
<td>1.67 (1.44–1.92) 4.14×10⁻¹⁰</td>
<td>1.39 (1.29–1.50) 2.47×10⁻⁸</td>
<td>1.44 (1.35–1.54) 7.81×10⁻⁸</td>
</tr>
<tr>
<td>n35705950</td>
<td>11 1241221 MUC5B</td>
<td>T</td>
<td>G</td>
<td>14.3%</td>
<td>4.11 (3.31–5.11) 1.86×10⁻¹⁴</td>
<td>2.46 (2.13–2.85) 3.13×10⁻¹⁴</td>
<td>2.89 (2.56–3.26) 1.12×10⁻¹⁴</td>
</tr>
<tr>
<td>n62025270</td>
<td>15 86300138 AKAP13/KLHL25</td>
<td>A</td>
<td>G</td>
<td>24.7%</td>
<td>1.49 (1.26–1.76) 3.11×10⁻¹⁰</td>
<td>1.22 (1.11–1.33) 9.96×10⁻¹⁰</td>
<td>1.27 (1.18–1.37) 1.32×10⁻⁹</td>
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</table>

<table>
<thead>
<tr>
<th>Chr</th>
<th>Position</th>
<th>Locus</th>
<th>Minor allele</th>
<th>Major allele</th>
<th>MAF</th>
<th>Stage 1</th>
<th>Stage 2</th>
<th>Meta-analysis (stages 1+2)</th>
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<tbody>
<tr>
<td>10</td>
<td>2064</td>
<td>ALPK3</td>
<td>C</td>
<td>T</td>
<td>46.3%</td>
<td>1.67 (1.44–1.92) 4.14×10⁻¹⁰</td>
<td>1.39 (1.29–1.50) 2.47×10⁻⁸</td>
<td>1.44 (1.35–1.54) 7.81×10⁻⁸</td>
</tr>
<tr>
<td>11</td>
<td>6895</td>
<td>SLC28A1</td>
<td>C</td>
<td>T</td>
<td>14.3%</td>
<td>4.11 (3.31–5.11) 1.86×10⁻¹⁴</td>
<td>2.46 (2.13–2.85) 3.13×10⁻¹⁴</td>
<td>2.89 (2.56–3.26) 1.12×10⁻¹⁴</td>
</tr>
<tr>
<td>13</td>
<td>1840488</td>
<td>PDEB</td>
<td>G</td>
<td>T</td>
<td>24.7%</td>
<td>1.49 (1.26–1.76) 3.11×10⁻¹⁰</td>
<td>1.22 (1.11–1.33) 9.96×10⁻¹⁰</td>
<td>1.27 (1.18–1.37) 1.32×10⁻⁹</td>
</tr>
</tbody>
</table>

Results from case-control analyses for the variants that were significant (after correction for multiple testing) in stage 2 and reached genome-wide significance in the meta-analysis of stages 1 and 2. MAF corresponds to that from the stage 1 study. ORs were calculated using the minor allele as the effect allele. Stage 2 ORs and p values correspond to the meta-analysis of the Chicago and Colorado consortia results.

Chr=chromosome. MAF=minor allele frequency. OR=odds ratio.

Table 2: Gene variants with genome-wide significance for idiopathic pulmonary fibrosis

Figure 3: Comparison of case-control association results and lung eQTL results

Region plots for a 2 Mb region on chromosome 15 for the stage 1 case-control GWAS (circles above the x axis) and lung eQTL analysis (squares below the x axis). The x axis shows chromosomal position. The y axis above the x axis shows the –log10(p value) from the case-control analysis and the y axis below the x axis shows the –log10(p value) for AKAP13 expression from the lung eQTL analysis. The blue dotted line shows the significance threshold (p=5×10⁻⁶) used in stage 1 and the red dotted line shows genome-wide significance (p=5×10⁻⁸). Boxes at the bottom show gene locations plotted against the same x axis as the case-control and eQTL results, with AKAP13 highlighted in green. Variants are coloured according to linkage disequilibrium with rs62025270 (shown in blue). eQTL=expression quantitative trait locus. GWAS=genome-wide association study.
consistent direction of effect to previous GWAS; namely variants in MUC5B, DSP, family with sequence similarity 13 member A (FAM13A), TERT, mucin 2 (MUC2), DPP9, and TOLLIP (appendix p 13). Five of the remaining seven signals that were not significant had a consistent direction of effect with previous GWAS.

SNP rs62025270[A] was associated with increased expression of AKAP13 in the lung. To identify the functional consequence of the rs62025270 polymorphism, we assessed associations between rs62025270 and nearby variants and expression of genes (eQTLs). In non-diseased whole-lung tissue from the lung eQTL databases (University of British Columbia n=319, Laval n=409, and Groningen n=363), the minor allele A of rs62025270, associated with increased susceptibility to IPF, was associated with increased expression of AKAP13 (figure 4). SNP rs62025270 is in linkage disequilibrium ($r^2=0.60$) with rs17636666, the variant that was most significantly associated with expression of AKAP13 in lung tissue. This co-localisation of IPF susceptibility association signal and strongest AKAP13 gene expression association signal (eQTL) in lung tissue (figure 3) further suggests that altered expression of AKAP13 has a role in IPF susceptibility. The minor allele A of rs62025270 was also associated with expression of AKAP13 in blood (n=5311; appendix pp 7 and 14), although it was not in linkage disequilibrium ($r^2=0.03$) with the SNP most strongly associated with AKAP13 expression in blood (rs870689). This finding suggests differences in regulation of AKAP13 expression between lung and whole blood, which have different cell-type compositions. Furthermore, the minor allele A of rs62025270 was associated with decreased expression of AKAP13 in blood, rather than increased expression as seen in lung tissue. The SNP rs62025270 was also found to be associated with expression of RNA genes RP11–158M2.3, RP11–158M2.4, RP11–158M2.5, RP11–815J21.3, and RP11–815J21.4 in a range of tissues in GTEx (appendix p 14).

Having identified that the minor allele A of rs62025270 was associated with increased susceptibility to IPF and increased expression of AKAP13 in the lung tissue, we did a further analysis in lung tissue to identify the cellular location of AKAP13 in the lung and compared levels of AKAP13 mRNA from patients with IPF versus controls. Morphological assessment of histological sections from 10 control and 10 patients with IPF showed that AKAP13 protein was expressed primarily in bronchial epithelium (figure 5A) and alveolar type 1 and 2 cells (figure 5B) in control lung samples. High AKAP13 expression was observed in fibrotic regions of lung tissue from patients with IPF, and the cells expressing AKAP13 were primarily epithelial cells, macrophages, and lymphoid aggregates (figure 5C–F). High AKAP13 expression was also seen in epithelial cells from less fibrotic alveolar regions of lungs of patients with IPF, with more AKAP13-expressing cells in alveoli of patients with IPF (figure 5G) than in alveoli of controls (figure 5H). Real-time PCR analysis of samples from 46 patients with IPF and 51 controls established that concentrations of AKAP13 mRNA were 1·42-times higher in whole lung tissue homogenates from patients with IPF.
than in lung tissue from controls (p=0.0011; figure 5I).
Linear regression analysis confirmed that the significant increase in AKAP13 mRNA expression in lung tissue of patients with IPF was maintained after controlling for age, sex, and smoking history (p=2.03×10^{-4}).

We tested the association of rs62025270 with survival time in all patients from stage 1 for whom survival data were available (n=565; 360 with recorded deaths and 205 with censored survival times, with a minimum follow-up time of 1112 days before censoring). The median survival time after diagnosis of IPF was 1621 days (4.4 years; IQR 764–2815 days). rs62025270 showed no association with survival time (hazard ratio 1.01 [95% CI 0.86–1.19], p=0.878).

11 proteins that interact with AKAP13 were identified as known targets for existing drugs or compounds in development, including aspirin, dextromethophan, and GSK-690693 (appendix pp 15–17).

Discussion
We studied 2760 patients with IPF and 8561 controls and identified a novel genome-wide significant association of variant rs62025270 that implicates AKAP13 as a potential driver of IPF pathogenesis. We showed that the minor allele (A) of rs62025270 (minor allele frequency [MAF]=25%), associated with increased susceptibility to IPF, was associated with increased expression of AKAP13 in lung tissue. Morphological analysis of control and diseased lung tissue identified AKAP13 expression primarily in epithelial cells, with some additional expression in lymphoid tissue in patients with IPF. Furthermore, we showed increased expression of AKAP13 in fibrotic lung tissue from patients with IPF compared with samples from healthy controls.

The high AKAP13 expression in epithelial cells further supports the hypothesis that IPF is a disease characterised by epithelial susceptibility to injury, consistent with findings of other genetic risk factors associated with epithelial cell function.13 AKAP13 is a RhoA guanine nucleotide exchange factor (RhoGEF) that is crucial for murine cardiac development. AKAP13-null mice are embryonic lethal because of arrested cardiac development at embryonic day 10.24 Conversely, enhanced AKAP13 signalling has been shown to promote profibrotic signals in cardiac fibroblasts25 and

Figure 5: AKAP13 expression in bronchial mucosa and alveolar cells in patients with IPF and controls
Sections of lung tissue from controls show AKAP13 expression in the bronchial mucosa (A) and alveolar cells (B). Sections of lung tissue from patients with IPF show low AKAP13 expression in fibroblastic foci (C), and high expression in the epithelium lining fibrotic alveoli (D) and distal small airways (green arrow, E). (F) Strong staining in lymphoid follicles associated with fibrotic regions in patients with IPF. (G) Section of lung tissue from a patient with IPF showing that areas of lung less affected by fibrosis have high numbers of alveolar cells expressing AKAP13 (green arrows). (H) In tissue from regions of the lung unaffected by fibrosis in patients with IPF, type 1 (green arrows) and type 2 (blue arrow) alveolar epithelial cells primarily express AKAP13 in the parenchyma. (I) AKAP13 mRNA expression in whole lung tissue homogenates from patients with IPF and controls. Each point shows a sample from one person and the line shows the mean fold change (black bars show ± SE) in AKAP13 mRNA in 46 patients with IPF and 51 controls. Relative expression (relative to housekeeping gene) is plotted on a log₂ scale. AKAP13=A-kinase anchoring protein 13; FF=fibroblastic foci; IPF=idiopathic pulmonary fibrosis; LF=lymphoid follicle.
leads to cardiac hypertrophy in mice. Although AKAP13 has not previously been implicated in the pathogenesis of IPF, it plays a key role in profibrotic signalling pathways. Thrombin and lysophosphatidic acid have been identified as key profibrotic mediators acting via a Gq and RhoA signalling pathway in epithelial cells to promote αvβ6 integrin-mediated transforming growth factor β (TGFβ) activation.28–30 AKAP13 coordinates thrombin and lysophosphatidic acid receptor signalling through Ga12 to RhoA in epithelial cells,29 thereby promoting epithelial injury, thereby promoting IPF. A phase 2 clinical trial assessing the safety and tolerability of a humanised monoclonal antibody (compound BG00011, formerly known as STX-100) in participants with IPF is underway (NCT01371305).

We also identified AKAP13 in lymphoid follicles within fibrotic regions of lung tissue from patients with IPF. Lymphoid follicles without germinal centres are well described in IPF and are thought to be composed primarily of B cells and dendritic cells.34–36 Increased concentrations of plasma B lymphocyte stimulating factor have been reported in patients with IPF compared with either controls or patients with chronic obstructive pulmonary disease, and higher concentrations were associated with severe disease.37 Furthermore, analysis of gene expression profiles from lymphoid follicles identified them as the source of C-X-C motif chemokine ligand 13,38 a biomarker of severe IPF,38,40 suggesting that lymphoid follicles might play an important undefined role in the pathogenesis of IPF. The role of AKAP13 in B-cell function is similarly poorly understood, although it has been shown to be responsible for glucocorticoid responsiveness in lymphocytes stimulated with lysophosphatidic acid,41 and is involved in lymphocyte responses to osmotic stress.42

Because of the known function of AKAP13, it probably has some potential downstream molecular interactions that could be targeted therapeutically, most notably RhoA and Rho kinase.36 II proteins that interact with AKAP13 were identified as known targets for existing drugs or compounds in development (appendix pp 15–17). One of the existing drugs was aspirin, which targets prostanoid-endoperoxide synthase 1 (PTGS1) and PTGS2, and PTGS2 has a well described role in the pathogenesis of IPF.43–46 Another of the drugs was dextromethorphan, a well known cough-suppressant that antagonises N-methyl-D-aspartate receptors.47 Notably, a novel pan AKT inhibitor, GSX-690693, was also identified as a possible asset for targeting AKAP13 binding partners, and the AKT pathway is emerging as an important pathway in fibrogenesis.48

To our knowledge this is the first GWAS implicating AKAP13 at genome-wide significance in IPF susceptibility.49 Additionally, we confirmed seven previously reported associations with IPF susceptibility: the T allele of SNP rs3570950 in the MUC5B promoter (stage 1 p=1·86×10−37) was the strongest genetic risk factor for susceptibility to IPF with an OR of 4·11,50 then DSP (stage 1 p=4·14×10−12), MUC2 (stage 1 p=1·33×10−5), TOLLIP (stage 1 p=1·60×10−5), TERT (stage 1 p=8·25×10−5), DPP9 (stage 1 p=4·17×10−4), and FAM13A (stage 1 p=0·002). 17 variants were identified in stage 1 that have not been previously reported to be associated with IPF (of which 14 were low frequency or rare), but we could not investigate all of these in the stage 2 analyses because not all data were available. These could be additional true positive signals of association with susceptibility to IPF that will reach genome-wide significance in larger and more densely imputed studies.

A strength of our study is that we were able to bring together the largest sample size of patients with IPF and controls available to date and apply a robust and widely used two-stage study design51,52 to identify a novel genetic signal of association with IPF susceptibility. Furthermore, our stage 1 study samples were genotyped using the Affymetrix Axiom UK BiLEVE and UK Biobank arrays, which are optimised for imputation of individuals with European ancestry, and were genome-wide imputed using the most comprehensive imputation panel resource available at the time. This enabled analysis of 13076821 variants genome-wide with MAF of more than 0·1%.

This study also has some limitations. Although clinical investigators were careful to exclude other fibrotic lung diseases, a small number of non-IPF cases of pulmonary fibrosis might have been included. However, the advantage of collating a large dataset is that the effects of misclassification on the analysis are reduced. Furthermore, we expect that misclassification would lead to attenuation of signals rather than produce false-positive findings, which was supported by our replication of nine previously reported signals of association with IPF in our previously unreported stage 1 data. This included five signals that reached a Bonferroni-adjusted significance threshold for 16 tests (p<3·13×10−4), and two additional signals that reached genome-wide significance (MUC5B p=1·86×10−37 and DSP p=4·14×10−12). In addition, the diagnostic practices between the UK and USA might be different but the concordant results from the three case-control studies reassures us that these observations are robust.

A previous study of 119 patients with IPF and 50 donor lung controls from the Lung Tissue Resource Consortium reported a small decrease of AKAP13 expression in patients with IPF compared with controls using gene expression data from the Affymetrix Gene ST1·0 array, whereas our data using RT-PCR showed a moderate increase of AKAP13 expression in patients with IPF compared with controls. The discordance
between these results could be due to a number of factors, including the difference in normalisation strategies between the two techniques and sample heterogeneity. The eQTL data that we present from control lung tissue shows that the minor allele A of rs62025270, associated with susceptibility to IPF, is also expressed in alveolar cells. Therefore, these data provide strong independent evidence that increased AKAP13 expression in alveolar cells has a role in IPF, and the cellular heterogeneity within the fibrotic lung samples used for RNA analysis is likely to explain this discordance.

In summary, we report a novel genome-wide significant association for IPF susceptibility with SNP rs62025270 and present evidence that this SNP might exert its effect via expression of the nearby gene AKAP13. AKAP13 is a RhoGEF that is known to interact with a central fibrogenic pathway—G protein-coupled receptor activation of RhoA—and expression is increased in fibrotic regions of lungs from patients with IPF. Expression of AKAP13 occurs primarily in the epithelium thereby reinforcing the idea that epithelial processes are central to IPF pathogenesis. The identification of a RhoGEF that regulates a pathway known to be involved in the pathogenesis of IPF, a pathway for which drugs are in development, could potentially provide a novel target for antifibrotic therapy for IPF.

Contributors
RGJ, LVW, and MDT designed and supervised the study. RB, AH, RBH, VN, GS, NT, HLB, SPH, MRH, NH, TM, RJM, ABM, PLM, HP, DMR, MKBW, WAF, RPM, EO, IS, and IPH recruited and genotyped patients. RJA, JP, CF, TEF, JMO, BG-G, S-FM, TO, AEJ, MO, IVY, YB, DCN, DDS, WT, NS, IN, and DAS did analyses and experiments. RJA, LVW, and RGJ wrote the manuscript with input from all authors.

Declaration of interests
JMO reports grants from the National Heart, Lung, and Blood Institute (NHLBI), American Lung Association, American Thoracic Society; personal fees from Genentech and Boehringer Ingelheim. IVY reports grants from the National Institutes of Health (NIH). GS reports a travel grant for ERS 2017 from Boehringer Ingelheim. SPH reports grants, personal fees, and non-financial support from Boehringer Ingelheim, Chiesi, AstraZeneca, and Roche. TM has received industry-academic funding from GlaxoSmithKline (GSK) R&D and UCB; and has received consultancy or speakers fees from Aepalis, AstraZeneca, Bayer, Biogen Idec, Boehringer Ingelheim, Cipla, GSK R&D, InterMune, ProMetic, Roche, Sanofi-Aventis, Sunamed, and UCB. HP reports personal fees and non-financial support from Boehringer Ingelheim and Roche. MKBW reports travel support for the American Thoracic Society and British Thoracic Society meetings from Boehringer Ingelheim. WAF is an employee and shareholder of GSK. DCN is a full time employee of Merck & Co (Merck Research Labs). DDS reports grants and personal fees from AstraZeneca, Boehringer Ingelheim, Merck Frost Centre for Therapeutic Research, Novartis, Regeneron, and Sanofi Aventis. WT reports grants from Merck and the Dutch Asthma Fund; personal fees from Pfizer, GSK, Chiesi, Roche Diagnostics/Ventana, Biotest, Merck Sharp & Dohme, Novartis, Lilly Oncology, Boehringer Ingelheim, and AstraZeneca. IPH reports grants from UK Medical Research Council (MRC), Pfizer, Boehringer Ingelheim, and Biotest. IN reports personal fees and consultancy, advisory board, speaker, and study contracts for Boehringer Ingelheim and Genentech from Boehringer Ingelheim and Genentech; personal fees from ImmuneWorks, Sanofi Aventis, Global blood therapeutics; and has a patent for Toll-interacting protein (TOLLIP) and pharmacogenetics pending. DAS reports grants from National Institute of Health/NHLBI, Veterans Administration, Department of Defense Focused Program Grant; is an employee of a company with an aim of early detection and early intervention of IPF from Eleven P15; and has patents pending on Compositions and Methods of Treating or Preventing Fibrotic Diseases and Biomarkers for the diagnosis and treatment of fibrotic lung disease and patents issued for Methods and Compositions for Risk Prediction, Diagnosis, Prognosis, and Treatment of Pulmonary Disorders. MDT and LVW report grants from GSK and Pfizer. RGJ reports grants from GSK, UK MRC, Biogen, MedImmune, and Galecta; personal fees from Boehringer Ingelheim, GSK, Intermune, MedImmune, PharmAkea, Roche, Pulmatix, Plant Therapeutics, and NuMedii; and is a Trustee for the charities Action for Pulmonary Fibrosis and the British Thoracic Society. LVW has performed unpaid consultancy for GlaxoSmithKline. All other authors declare no competing interests.

Acknowledgments
This research has been done using the UK Biobank Resource under application 8899 (led by IS). This Article presents independent research funded partially by the UK National Institute for Health Research (NIHR). The views expressed are our own and not necessarily those of the NHS, the NIHR, or the UK Department of Health. This research used the ALICE High Performance Computing Facility at the University of Leicester. We would like to thank the staff at the Respiratory Health Network Tissue Bank of the Fonds de recherche du Québec focused on cancer for their valuable assistance with the lung eQTL database at Laval University. Genotyping of the stage 1 samples was funded by an MRC Strategic Award to IPH, MDT, LVW, and David Strachan (MC_PC_12030). RGJ has an MRC grant (G0901226). IPH has an MRC grant (G0900861). DAS has grants from the National Heart, (B0101H1097163 and P01 HL092870). BG-G was supported by a fellowship from ACICIS (TESIS201500057), TMW is supported by an NIHR Clinician Scientist Fellowship (NIHR reference CS-2013–13–017). LVW holds a GlaxoSmithKline/British Lung Foundation Chair in Respiratory Research. MO is a fellow of the Parker B Francis Foundation. MDT and LVW report grants from GSK, UK MRC and the Dutch Asthma Fund, personal fees from Pulmatrix, Pliant Therapeutics, and NuMedii; and is a Trustee for the charities Action for Pulmonary Fibrosis and the British Thoracic Society. LG holds a GlaxoSmithKline/British Lung Foundation Chair in Respiratory Research. MO is a fellow of the Parker B Francis Foundation.

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