ORIGINAL ARTICLE

Distinct and replicable genetic risk factors for acute respiratory distress syndrome of pulmonary or extrapulmonary origin

Paula Tejera,¹ Nuala J Meyer,² Feng Chen,³ Rui Feng,⁴ Yang Zhao,¹ D Shane O’Mahony,⁵ Lin Li,¹ Chau-Chyuan Sheu,⁶ Rihong Zhai,¹ Zhaoxi Wang,¹ Li Su,¹ Ed Bajwa,⁷ Amy M Ahasic,⁸ Peter F Clardy,⁹ Michelle N Gong,¹⁰ Angela J Frank,⁷ Paul N Lanken,² B Taylor Thompson,⁷ Jason D Christie,²,⁴ Mark M Wurfel,⁵ Grant E O’Keefe,⁵ David C Christiani¹,⁷

ABSTRACT

Background The role of genetics in the development of acute lung injury (ALI)/acute respiratory distress syndrome (ARDS) from direct or indirect lung injury has not been specifically investigated. The aim of this study was to identify genetic variants contributing to ALI/ARDS from pulmonary or extrapulmonary causes.

Methods We conducted a multistage genetic association study. We first performed a large-scale genotyping (50K ITMAT-Broad CARE Chip) in 1717 critically ill Caucasian patients with either pulmonary or extrapulmonary injury, to identify single nucleotide polymorphisms (SNPs) associated with the development of ARDS from direct or indirect insults to the lung. Identified SNPs (p≤0.0005) were validated in two separated populations (Stage II), with trauma (Population I; n=765) and pneumonia/pulmonary sepsis (Population II; n=838), as causes for ALI/ARDS. Genetic variants replicating their association with trauma related-ALI in Stage II were validated in a second trauma-associated ALI population (n=224, Stage III).

Results In Stage I, non-overlapping SNPs were significantly associated with ARDS from direct/indirect lung injury, respectively. The association between rs1190286 (POPDC3) and reduced risk of ARDS from pulmonary injury was validated in Stage II (p<0.003). SNP rs324420 (FAAH) was consistently associated with increased risk of ARDS from extrapulmonary causes in two independent ALI-trauma populations (p<0.006, Stage II; p<0.05, Stage III). Meta-analysis confirmed these associations.

Conclusions Different genetic variants may influence ARDS susceptibility depending on direct versus indirect insults. Functional SNPs in POPDC3 and FAAH genes may be driving the association with direct and indirect ALI/ARDS, respectively.

INTRODUCTION

Two different pathogenic pathways can lead to the development of acute lung injury (ALI) and its more severe manifestation, acute respiratory distress syndrome (ARDS): a direct or pulmonary insult that directly affects lung parenchyma, and/or an indirect or extrapulmonary insult that results from an acute systemic inflammatory response and yields pulmonary endothelial damage.¹ Since this distinction was posed by the American European Consensus Conference (AECC) in 1994, the question of whether ARDS of different origins represents two different syndromes, and the possible clinical implications of this differentiation, have been widely debated. Conflicting results have been reported among different clinical studies, largely due to the fact that the classification of the type of injury that leads to ARDS is not always straightforward. Furthermore, it is possible that direct and indirect insults coexist simultaneously in the same patient, and patients in each category can also present different degrees of severity of lung injury.²–⁵ In spite of these contradictory results, there is a growing body of evidence suggesting that pathophysiological characteristics differ between the two types of primary insults. Clinical data and experimental models support differences in pathophysiology, lung morphology, respiratory mechanics and response to different ventilator strategies and pharmacological agents between ARDS from pulmonary and extrapulmonary origin.¹–⁹ Genetic factors are known to play an important role in ARDS development.¹⁰–²² While several studies have indicated an effect modification by the type of injury in the genetic associations with the risk of ARDS,²³–²⁶ the potential role of genetics underlying the differences between ARDS resulting from pulmonary and extrapulmonary injury has not been investigated in detail. In this study, we explore the hypothesis that different genetic susceptibility profiles could underlie the development of ARDS from different insults. To identify common genetic variants contributing to the development of ARDS from different origins, we conducted a large-scale genomic association study involving ~2100 genes on a critically ill patient population of 1717 subjects with either direct or indirect lung injury as predisposing conditions for ARDS. Three critically ill populations with severe trauma or pneumonia/pulmonary sepsis as the risk factor for ALI/ARDS were used to validate our primary results.

METHODS

Study populations

The initial phase of the study included subjects admitted to an adult intensive care units (ICU) at the Massachusetts General Hospital (MGH) and
the Beth Israel Deaconess Medical Center (Boston) with pulmonary or extrapulmonary injury as predisposing condition for ARDS. Details of the study design have been described previously.\textsuperscript{27, 28} Stage II consisted of two independent replication populations. Population I included patients admitted to the Harborview Medical Center (HMC, Seattle, Washington, USA) ICU for 48 h or longer following major trauma.\textsuperscript{29} Population II consisted of ARDS cases with pneumonia/sepsis from pulmonary sources as a risk factor for ARDS, collected as part of the Fluid and Catheter Treatment Trial (FACTT), Albuterol for the treatment of ALI (ALTA) and EDEN-Omega trials conducted by the NHLBI ARDS Network (http://wwwARDSnet.org/clinicians/studies). Controls for this population were non-ARDS patients with pulmonary injury from the discovery set (MGH). Stage III consisted of subjects admitted to the surgical ICU of the University of Pennsylvania (HUP) after a major trauma and with an injury severity score (ISS) ≥16, corresponding to severe trauma.\textsuperscript{30–32}

At each stage, eligible patients were followed for the development of ARDS as defined by AECC criteria.\textsuperscript{1} At each site, the institutional review board and/or human subjects committee reviewed and approved the study. Full description of the cohorts is provided in the online supplementary material (see also online supplementary figure S1).

Genotyping strategy and quality control

Genotyping of the discovery population was carried out using the 50K single nucleotide polymorphism (SNP) ITMAT-Broad_CARe (IBC) array (Illumina, San Diego, California, USA).\textsuperscript{33} As a candidate gene chip designed to capture variation in loci important to inflammatory, metabolic and vascular phenotypes, the IBC chip also includes many genes with plausible role in ALI development (http://bmic.upenn.edu/cvdsnip) (further justification for the use of this platform is provided in the online supplementary material). Patients in Stage II were genotyped using the Infinium II HumanHap610K-quad BeadChip (Illumina).\textsuperscript{34–36} Genotyping data were filtered for only those SNPs passing the threshold for significant association at Stage I (p<0.0005).\textsuperscript{36, 37} Patients in Stage III were also genotyped using the IBC chip (Illumina),\textsuperscript{38} and genotyping data were filtered for SNPs passing Stages I and II (see online supplementary figure S2, study overview). For those IBC SNPs not typed on the genome-wide array, genotype imputation was carried out using MACH V3.0\textsuperscript{39} and 1000 Genomes European ancestry samples as reference panel. Genotype data were subjected to rigorous quality control measures in order to remove poor quality SNPs as well as individuals of non-European ancestry. Further details about genotyping strategy and quality control are provided in the online supplementary material.

Statistical analysis

We used logistic regression to perform SNP-based association analyses with ALI/ARDS risk as implemented in PLINK.\textsuperscript{39} The genotype-specific OR for ALI/ARDS susceptibility were estimated using the χ\textsuperscript{2} test. An additive model of genetic risk was assumed, adjusting for clinical covariates available at each stage. Analyses were restricted to subjects of European ancestry. The impact of population stratification was evaluated by calculating the genomic control inflation factor\textsuperscript{40} in Stage I, and by using principal components analysis\textsuperscript{41} and multidimensional scaling analysis\textsuperscript{42–45} in Stages II and III, respectively. A three-stage association study was performed.\textsuperscript{36, 37, 41–43} We used a p value ≤5×10\textsuperscript{−4} to pass Stage I (instead of 10\textsuperscript{−6} (0.05/50 000 SNPs in the IBC Chip)) in order to reach satisfactory power for our cohort. The significance of the associations observed in Stage I was then established by independent replication of our findings in Stages II and III of the study. The statistical power at each stage was determined using Quanto software (http://hydra.usc.edu/gxe/). Further details of power calculation and selection of significance thresholds at each stage are provided in the online supplementary material. Aggregate effects of common SNPs were assessed by calculating polygenic risk score, using a ‘count method’ as previously described.\textsuperscript{46} Meta-analysis of the discovery and replication cohorts was performed using an inverse variance-weighted method under fixed and random-effects models as implemented in PLINK.\textsuperscript{39} A p value <0.0005 in the meta-analysis was considered as suggestive evidence of significance. Heterogeneity among study populations was assessed with the Cochran’s Q-statistic.\textsuperscript{48} Correlation between SNP associated with ARDS and gene expression levels was examined in silico using the Gene Expression Variation (GENEVAR) project database at the Wellcome Trust Sanger Institute (http://www.sanger.ac.uk/resources/software/genevar/) and expression data from three cell types (fibroblast, lymphoblastoid cell line and T-cell) derived from umbilical cords of 75 Geneva GenCord individuals.\textsuperscript{49} The correlation between the number of risk alleles, and normalised mRNA levels was examined by linear regression using the Genevar V5.1.1 Java tool.\textsuperscript{50} Further details of our analyses are presented in the online supplementary material.

RESULTS

Stage I

After quality control, 1717 critically ill Caucasian patients at risk for ARDS, and with only one type of lung injury, were included in the first stage of the study (see online supplementary figure S2). Among them, 417 were ARDS cases and 1300 were non-ARDS. The demographics and baseline clinical characteristics for these subjects are shown in table 1. A total of 29 483 autosomal SNPs passed quality control in Stage I (see online supplementary table S1). SNP-level quality control metrics were: genotyping call rate >95%, minor allele frequency (MAF) ≥0.05 and Hardy–Weinberg equilibrium (HWE) p≥0.001. The chromosomal distribution of all p values is shown in online supplementary figure S3. The calculated genomic control for the association with pulmonary and extrapulmonary injury-related ARDS (λ=1.000 and λ=1.018, respectively, see online supplementary figure S4) did not indicate stratification in the discovery population.\textsuperscript{47}

Assuming an additive model, and after adjustment by age, gender and Acute Physiology And Chronic Health Evaluation (APACHE) III score, we identified a total of 17 SNPs (annotated to 12 genes) and 8 SNPs (in 7 genes) significantly associated with pulmonary and extrapulmonary injury-related ARDS (p value ≤0.0005), respectively (table 2).

Of note, no SNPs associated with pulmonary injury-related ARDS were associated with extrapulmonary injury-related ARDS. The converse was likewise true. No variant exhibited even a marginal association in both types of lung injury (see online supplementary table S2). The same result was observed when the effect of SNPs significantly associated with ARDS (p≤0.0005) in the pulmonary and extrapulmonary subgroups was evaluated jointly, by the use of a multi-SNP genotypic risk score. Additional details of this analysis are provided in the online supplementary material.

Stages II and III

SNPs demonstrating an association with the development of ARDS in the discovery set (table 2) were tested for validation in Stage II, using two different populations. SNPs associated
with ARDS resulting from extrapulmonary injury were validated in Population I (trauma patients) consisting of 597 cases and 168 non-ALI. SNPs associated with ARDS from direct lung injury were validated in Population II consisting of 592 ARDS cases from NHBLI ARDS Network (180 FATT samples, 84 ALTA samples, 112 Omega samples, and 16 ALTA/Omega coenrolled samples) with pneumonia and pulmonary sepsis as causes of ARDS. Controls for this population were those from discovery population with direct injury (n=446). SNPs replicating the association with the development of extrapulmonary injury-related in Population I were tested in Stage III using the ALI-associated trauma cohort (HUF) (n=224). About 33% of these subjects developed ALI during the first 5 days post-trauma. Characteristics of the replication populations in Stages II and III and available clinical data are shown in table 1.

In Stage II, over 600 000 (Linkage Disequilibrium (LD))-bin-tagging SNPs were assayed using the Human 610-Quad platform, of which 530 459 passed all quality control measures (genotyping call rate ≥95%; HWE p value ≥10-4; and MAF ≥0.01) were included in the analyses (see online supplementary table S1). The genomic inflation factor for this set was 1.027. The results of all genotyped SNPs were filtered for the SNPs significantly associated with ARDS from direct or indirect injury in Stage I (p ≤0.0005). Association results for the SNPs selected for validation in Stage II are summarised in table 3.

Seven of the eight SNPs associated with extrapulmonary injury-related ARDS and tested in Stage II Population I (trauma-related ALI) failed to replicate the association with ALI (p≥0.006). Only SNP rs324420 in FAAH showed significant association with an increased risk of ALI from extrapulmonary sources in Population I with an OR=1.58 (95% CI 1.14 to 2.18), and a p=0.0007. The association was robust after adjustment for additional information (age, ISS and APACHE II, OR=1.59, p=0.0131).

SNP rs324420 has been associated with obesity.50 Because obesity may influence ALI outcome,52 53 we tested whether the rs324420-ARDS association was modified by body mass index (BMI), using logistic regression and BMI data from discovery population. After adjustment, rs324420 remained independently associated with increased risk of ARDS development (OR=1.77; p=0.0002).

SNPs associated with extrapulmonary injury-related ARDS in Stage I were replicated using an ALI (as opposed to ARDS) trauma-specific cohort (Population I). ALI and ARDS represent different manifestations of the same syndrome, only the severity of the hypoxaemia differentiates ALI from ARDS.1 We performed a sensitivity analysis of the results in Stage II to test if differences in the clinical phenotype ALI versus ARDS might influence our findings (see online supplementary material for additional information). Approximately 70% of our ALI cases in the replication population also met the criteria for ARDS. To assess the robustness of the replication results, the association analyses were repeated after recategorising ALI cases (defined as PaO2:FIO2 <300 mm Hg) in Population I (Stage II) into ARDS cases (PaO2:FIO2 <200 mm Hg).1 The association of SNP rs324420 with ARDS in Stage I was replicated in Stage II, without any differences in the magnitude and direction of the association (see online supplementary table S3).

After demonstrating a reproducible association with increased risk of ALI/ARDS from extrapulmonary sources in Stages I and II (Population I) of our study, SNP rs324420 was tested for validation in a third critically ill population (HUP) with severe trauma (ISS >16) as risk factor for ALI.30 32 In Stage III, SNP rs324420 also showed a reproducible association with increased ALI risk: OR=1.85 (95% CI 1.08 to 3.19), p=0.026 (adjusted for age, ISS, modified APACHE III score, blunt trauma and total amount of packed red blood cells transfused in the first 24 h post-trauma). Sensitivity analyses looking at ARDS versus ALI as the phenotype were not carried out in Stage III, since approximately 97% of the subjects in this population also met the criteria for ARDS.32

The association results of the discovery (Stage I) and replication cohorts (Stages I and III) were then combined by meta-analysis. In the combined analysis, rs324420 showed the only significant SNP associated with the development of extrapulmonary injury-related ALI/ARDS, and showed increased statistical significance with a p=2×10E-06 and
SNPs associated with pulmonary injury-related ARDS

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SNPs associated with extrapulmonary injury-related ARDS

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*p Values were adjusted for age, gender and APACHE III score in Stage I population.

ARDS, acute respiratory distress syndrome; Chr, chromosome; HWE, Hardy–Weinberg equilibrium; MAF, minor allele frequency; SNP, single nucleotide polymorphism.

DISCUSSION

Evidence indicates that ALI/ARDS derived from a pulmonary insult has different pathophysiological, biochemical, radiological and mechanical patterns from ALI/ARDS caused by an extrapulmonary injury. The current study was aimed at gaining understanding of the genetic contribution to the development of ALI/ARDS from extrapulmonary and pulmonary sources. Using a large-scale genotyping approach (50,000 SNPs in ~2000 genes) and a multistage study design, we identified different genetic profiles underlying ALI/ARDS development from different insults to the lung. There was no overlap between SNPs associated with ARDS from direct or indirect insults in our study. No variant exhibited even a marginal association in both types of lung injury either in the individual analysis, or when their effects were combined in a multi-SNP genotypic risk score. Our analyses suggest nonexistence of shared risk factors contributing to the development of ARDS from direct or indirect insults. However, it is possible that variants with smaller effects, not detected in our study, may be contributing to the development of ARDS from both pulmonary and extrapulmonary sources. Therefore, negative findings from Stage I should be interpreted with caution.
Among the top SNPs associated with extrapulmonary injury-related ARDS in the discovery phase, SNP rs324420 successfully replicated its association with ALI in the second and third stages of our study (trauma-related ALI, with the same third stages of our study (trauma-related ALI), with the same association as observed in Stage I and tested for validation in Stage II using a trauma-related ALI population (Population I, Harborview trauma cohort). 57 SNP rs324420 leads to a non-synonymous change (pneumonia/pulmonary sepsis), respectively, and those associations were robust after adjusting for clinical variables (p=0.0131 and p=0.0094, respectively). 2012; 49 680. doi:10.1136/jmedgenet-2012-100972

### Table 3 SNPs associated with ALL/ARDS in Stage II

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<td>A</td>
<td>Imputed</td>
<td>0.07/0.09</td>
<td>1.05 (0.60 to 1.86)</td>
<td>0.8509</td>
</tr>
<tr>
<td>rs2070887</td>
<td>VWF</td>
<td>G</td>
<td>Typed</td>
<td>0.08/0.08</td>
<td>1.14 (0.69 to 1.88)</td>
<td>0.5928</td>
</tr>
<tr>
<td>rs10490072</td>
<td>BCL11A</td>
<td>C</td>
<td>Imputed</td>
<td>0.24/0.23</td>
<td>1.09 (0.78 to 1.52)</td>
<td>0.6125</td>
</tr>
</tbody>
</table>

SNPs associated with pulmonary injury-related ARDS in Stage I (p<0.0005) were tested for validation in Stage II using two different populations with indirect (Population I) and direct (Population II) lung injury as risk factor for ALI/ARDS. Both populations were genotyped with the Human 610-quad platform.

In Stage II, SNPs rs324420 and rs1190286 demonstrated a reproducible association with increased risk of ALI from indirect insult (trauma) and decreased risk of ARDS from pulmonary injury (p<0.0005). These results suggest that the defective FAAH protein may affect lipid homeostasis by modifying ECs levels, however, the mechanistic expression and activity. A recent study confirmed direct effect of SNP rs324420 in ECs system activation suggesting that this SNP may be a risk factor for obesity caused by elevated plasma levels of endocannabinoids. Because obesity may influence ALI outcome, we tested whether BMI represented a confounding bias in the association rs324420-ARDS. After adjustment for BMI, rs324420 remained independently associated with increased risk of ALI from indirect lung injury.

Although previous reports conflict with regard to the effects of genetic variation in FAAH and body composition, recent evidence suggests that it has a more direct influence on lipid homeostasis. SNP rs324420 has been recently associated with increased serum triglycerides and reduced high-density lipoprotein cholesterol (HDLc) level among subjects in one of the largest family-based obesity study cohorts. These results suggest that the defective FAAH protein may affect lipid homeostasis by modifying ECs levels, however, the mechanistic link between genetic variations in FAAH, ECs/CB1 signalling...
and lipoprotein biology is still poorly understood. Plasma lipoproteins, especially HDL, have been reported to exert immunomodulatory effects in vivo.\textsuperscript{60} HDLs have been suggested to play a crucial role in innate immunity by regulating the inflammatory response as well as reducing the severity of organ injury.\textsuperscript{61} HDLc has also been shown to be protective in inflammatory disease models in which local or systemic inflammation are important determinants.\textsuperscript{62} Based on these observations, the association between SNP rs324420 in \textit{FAAH} gene and the development of ALI/ARDS could be explained by the adverse effect of rs324420 on HDLc levels which may lead to a reduction of the protective effect that HDLc exerts against conditions associated with systemic inflammation. Further studies will be needed to investigate the relation between \textit{FAAH} variation, HDLc levels and ALI/ARDS development.

In the discovery and replication cohorts, as well as in the combined meta-analysis, rs324420 showed the strongest association with ALI/ARDS development compared with any other \textit{FAAH} SNP. Based on our association data and the functional nature of the variant rs324420 (C/A, P129T),\textsuperscript{48, 49} this polymorphism is a strong candidate to be considered as the causative allele underpinning the association with extrapulmonary injury-related ALI/ARDS. However, it is also possible that this SNP serves only as a marker in linkage disequilibrium with the causal variant. Further functional studies would be necessary to confirm the causality of rs324420 in the development of ALI/ARDS.

Besides rs324420, no other SNP associated with extrapulmonary injury-related ARDS in Stage I replicated its association in the second stage of our study. Since our replication population in Stage II (Population I) is a homogenous trauma population, lack of replication for the remaining SNPs associated with extrapulmonary injury-related ARDS could be indicative of inherent differences between trauma and other causes of extrapulmonary injury. In line with this, several studies have reported improved outcomes for patients with trauma-related ALI than those with non-trauma-related ALI.\textsuperscript{63, 64} Less severe lung epithelial and endothelial injury may explain the better outcomes of the trauma population, suggesting a different pathophysiology underlying ALI development in trauma patients than other lung injury patients.\textsuperscript{65}

Our study also identified several SNPs associated with pulmonary injury-related ARDS in the discovery set. Among them, rs1190286 in \textit{POPDC3} gene showed a replicated association with decreased risk of ARDS from pulmonary sources in Stage II Population I (pneumonia/pulmonary sepsis). Additional significant associated SNPs were identified in \textit{PDE4B}, \textit{ABCC1} and \textit{TNFRS11} genes (table 4 and see online supplementary table S5) by meta-analysis. Meta-analysis also confirmed rs1190286 as the most significant SNP associated with decreased risk of ARDS from pulmonary sources. By using imputation, we identified a block of intronic SNPs (containing rs1192806) in tight linkage disequilibrium, and also significantly associated with a decreased risk of pulmonary injury-related ARDS. We found a significant correlation between minor allele of rs1190298 and rs599904 (in that block) and decreased \textit{POPDC3} mRNA levels. \textit{POPDC3} is one of the three members of the Popeye domain-containing (POPCD) gene family (POPCD1-3). Popdc1-null mice show an impaired ability to regenerate skeletal muscle. Null mutants for Popdc2 and Popdc5 proteins have not been developed yet; however, the fact that Popdc1 phenotype is not lethal suggests a potential redundant role of Popdc2 and Popdc5 in skeletal muscle regeneration.\textsuperscript{66} Our results provide evidence that variants in \textit{POPDC3} gene associated with a decreased \textit{POPDC3} mRNA expression level are protective from
Figure 1 Association of rs1190298 and, rs9399904 with mRNA POPDC3 levels. Linear regression analyses were performed based on the mRNA expression profiling and genotypic data from fibroblast cell line obtained from the Gene Expression Variation database. The correlation between single nucleotide polymorphisms rs1190298 and rs9399904 and POPDC3 expression levels was significant (r=0.276; p=0.0164 and r=0.304; p=0.0079, respectively).

ARDS development. Due to the LD among SNPs in POPDC3, future research will be needed to determine the causal SNPs that is driving the association with ARDS, and to elucidate the role for Popdc3 in the lung.

Our study includes several strengths. First, we used a large and well-defined discovery ARDS cohort, where patients were carefully assigned into pulmonary and extrapulmonary groups, excluding ambiguous cases, and reducing possible bias from misclassification. Second, we performed a large-scale deep coverage genotyping strategy (IBC Chip) ensuring the coverage of most of the targeted genes with a density greater than the standard genome-wide genotyping platforms.33 Third, we implemented a multistage study design,36 37 and used three separate populations and multiple genotyping platforms to test the validity of our associations. The replication of our findings with the same direction and magnitude as observed in Stage I, and the association with genetic variants affecting protein expression and activity,58 reduces the chance of false positive associations and strengthens the chance that the observed genotypes are likely to play a role in development of ALI/ARDS secondary to direct or indirect insults to the lung.

Our study also has several limitations. By contrast to hypothesis-free genome-wide-based platform, the candidate gene approach used in our study limits our findings to those genes in the chip, excluding the discovery of novel loci relevant to ALI/ARDS development.

The statistical threshold to declare significance when using a dense, hypothesis-driven candidate gene SNP array is uncertain.65 None of our stage I results would be declared if a conservative Bonferroni method to account for 50 000 SNPs was applied. However, there are limitations to reliance on extreme p values to prioritise candidate gene associations. The Bayesian design of the IBC chip, combined with replication of our association in three different populations, and the functional nature of the ARDS-associated SNP, lend support to FAAH and POPDC3 as novel susceptibility genes for the development of ALI/ARDS from extrapulmonary and pulmonary sources, respectively.

SNPs associated with extrapulmonary injury-related ARDS in Stage I were replicated using trauma-related ALI populations. A total of 90% of subjects in Population I had blunt trauma, and they were classified as having ALI from extrapulmonary origin. However, it is possible that at least some of these patients had a concurrent injury to the thorax. We could not adjust our results for pulmonary contusion because this level of phenotypic data was unavailable. While our a priori hypothesis was that the trauma population would serve as a replication population for indirect-cause ARDS associations, we did test whether any direct-cause ARDS Stage I variants replicated in Population I. No replications were observed lending support for the classification of blunt trauma as an extrapulmonary insult (see online supplementary table S6). None of the direct-cause ARDS variants were validated in Stage III population either (data not shown).

Population II (pneumonia/pulmonary sepsis) was used in the validation of the SNPs associated with pulmonary injury-related ARDS. None of the indirect-cause ARDS Stage I variants were validated in this population (see online supplementary table S7).

As we mentioned in the Methods section, controls in Population II were non-ARDS patients with pulmonary injury from the discovery set. We selected the same control group as in Stage I since no other population was available at the time of the study. The MAF of rs1190286 in Population II was 0.20/0.14 (controls/cases). The MAF in the control group (0.20) was slightly higher than the MAF reported at HapMap (http://hapmap.ncbi.nlm.nih.gov/) and 1000 genomes (http://www.1000genomes.org/) datasets (0.14 and 0.15, respectively). These differences may suggest that the observed association between rs1190286 and decreased risk of ARDS from direct lung injury might be spurious, and could be driven by the systematic differences in allele frequencies between our selected control group and cases in Population II. Our analyses did not indicate stratification in the discovery population (either in the pulmonary or extrapulmonary groups: λ=1.000 and λ=1.018, respectively). We believe that the differences in MAF of rs1190286 between our control group and HapMap/1000 genomes datasets are due to the very nature of our control population, and might indicate a protective element from the development of ARDS. Unlike the subjects recruited at HapMap/1000 genomes studies, subjects in our control group were not healthy subjects but critically ill patients at risk of ARDS. These subjects were ascertained according to the proposed criteria for the correct design of association studies for complex diseases.66 69 Selecting healthy subjects as controls would bias the results by blending the real differences in allelic frequencies between the affected and control populations, reducing the statistical power of our study or yielding false associations.70

Finally, our study was also limited to Caucasians. Replication across different populations would be necessary to determine if the observed associations are also present in non-European populations.

To our knowledge, our study represents the first attempt to comprehensively estimate the genetic contribution underlying the differences in the development of ALI/ARDS from pulmonary and extrapulmonary sources. Our data and its replication in three critically ill populations suggest that different injury-related genetic variants may contribute to susceptibility to ALI/ARDS from direct versus indirect insults, lending...
support to the concept that ALL/ARDS is not a stereotyped response of the lung to injury. The identification of injury-specific genetic profiles may lead to a better understanding of the range of different pathways that lead to pulmonary dysfunction, and may help to improve the present definitions of the pulmonary and extrapulmonary injury categories. The pathophysiology of ALL/ARDS caused by different original insults is a necessary first step toward the development of therapeutic interventions that target specific aspects of these disease processes. The inclusion of patients into these two genetically defined injury categories should be considered in the design of future trials in the study of ALL/ARDS.

Author affiliations
1Department of Environmental Health, Harvard School of Public Health, Boston, Massachusetts, USA
2Division of Pulmonary, Allergy and Critical Care, Perelman School of Medicine at the University of Pennsylvania, Philadelphia, Pennsylvania, USA
3Department of Epidemiology and Biostatistics, School of Public Health, Nanjing Medical University, Nanjing, Jiangsu, China
4Center for Clinical Epidemiology and Biostatistics, Perelman School of Medicine at the University of Pennsylvania, Philadelphia, Pennsylvania, USA
5Division of Pulmonary and Critical Care Medicine, Department of Medicine, Harborview Medical Center, University of Washington, Seattle, Washington, USA
6Division of Pulmonary and Critical Care Medicine, Kaohsiung Medical University Hospital, Kaohsiung Medical University, Kaohsiung, Taiwan
7Pulmonary and Critical Care Unit, Department of Medicine, Massachusetts General Hospital, Harvard Medical School, Boston, Massachusetts, USA
8Section of Pulmonary and Critical Care Medicine, Department of Medicine, The Anlyan Center, Yale University School of Medicine, New Haven, Connecticut, USA
9Division of Pulmonary, Critical Care, and Sleep Medicine, Beth Israel Deaconess Medical Center (BIDMC), Harvard Medical School, Boston, Massachusetts, USA
10Division of Critical Care Medicine, Department of Medicine, Montefiore Medical Center, Department of Epidemiology and Population Health, Albert Einstein College of Medicine, Bronx, New York, USA

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Competing interest None.

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Distinct and replicable genetic risk factors for acute respiratory distress syndrome of pulmonary or extrapulmonary origin

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