Idiopathic Pulmonary Fibrosis Genetics in Different Populations
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Abstract

Rationale: A genome-wide association study was conducted that identified multiple susceptibility loci for pulmonary fibrosis in non-Hispanic white (NHW) individuals. We wanted to determine whether these findings could be extended to other populations.

Methods: DNA was received from collaborators and plated. This was followed by TaqMan® genotyping on the V7a 7 real-time PCR instrument. The genotyped populations included a Korean cohort, 239 of which had IPF and 102 controls, and a Mexican cohort, composed of 100 IPF patients and 120 controls. SNPs identified as significant in the genome-wide association study among non-Hispanic, white individuals were chosen to be looked at in the Mexican and Korean populations.

Results: We ran logistic regression under the additive model, adjusting for age and sex. Our significance level was *P < 0.05.

Conclusions: Results of the GWAS were replicated in five SNPs in the Mexican population and four SNPs in the Korean population. The FAM13A SNP (rs2609255) was significantly associated with IPF in both the Mexican and Korean populations. FAM13A has been found to be associated with a number of lung conditions in previous studies, such as asthma and chronic obstructive pulmonary disease (COPD). Our results are consistent with the suggestion of the gene’s role in lung function. SNP rs2034650, located on Chromosome 15 but not associated with a gene, is significant in both the Korean and Mexican populations and may be studied in future projects.

Idiopathic Pulmonary Fibrosis

Idiopathic pulmonary fibrosis (IPF) is a progressive interstitial lung disease of unknown etiology, with an appearance of usual interstitial pneumonia on lung biopsy. (Ref. 1) IPF causes the lungs to become scarred and stiffened, which makes breathing increasingly difficult. No known cure exists, and no medication has been shown to improve the outcome of patients with this condition. (Ref. 2)

Genome-Wide Association Study

Table: Final SNPs identified as significant.

Genotyped Populations

Mexican: 100 IPF and 120 controls collected by Moises Selman MD. DNA extracted from whole blood samples.

Korean: 239 IPF and 102 control subjects collected by Dong Soon Kim PhD. DNA source (blood or lung tissue) unknown.

References and Acknowledgements

References:

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\* John Rappaport, MD, Director, Wald-Waid Center.
\* Regina Richard, MSW, PhD, Director, Office of Diversity and Inclusion, School of Pharmacy, University of Colorado, Denver Health Sciences.
\* Moisés Selman, MD, Department of Research, Instituto Nacional de Medicina Respiratoria, Mexico City, DF, Mexico.
\* Dong Soon Kim, PhD.
\* Colorado Leaders, Interns, and Mentors in Business.

Results

Logistic regression run under the additive model with adjusting for age and sex.

TaqMan® SNP Genotyping Assay

DNA was received from collaborators and plated for genotyping on the Tecan Freedom EVO robot at normalized concentrations (10 ng/µL). This was followed by TaqMan® genotyping on the V7a 7 real-time PCR instrument.

Conclusions

• Results of the GWAS were replicated in five SNPs in the Mexican population and four SNPs in the Korean population.

• The FAM13A SNP (rs2609255) was significantly associated with IPF in both the Mexican and Korean populations. FAM13A has been found to be associated with a number of lung conditions in previous studies, such as asthma and chronic obstructive pulmonary disease (COPD). Our results are consistent with the suggestion of the gene’s role in lung function.

• SNP rs2034650, located on Chromosome 15 but not associated with a gene, is significant in both the Korean and Mexican populations and may be studied in future projects.

Comparison to the original study in non-Hispanic white individuals. Significant SNPs in the Mexican population are marked with green stars and significant SNPs in the Korean population are marked with red stars. Not all significant SNPs were labeled on the original Manhattan plot, so not all of our data points could be shown in comparison.

DNA → Plating and Normalization → Genotyping