A Functional Polymorphism in the CHRNA3 Gene and Risk of Chronic Obstructive Pulmonary Disease in a Korean Population

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Purpose: A genome-wide association study has identified the 15q25 region as being associated with the risk of chronic obstructive pulmonary disease (COPD) in Caucasians. This study intended as a confirmatory assessment of this association in a Korean population.

Methods: The rs6495309C>T polymorphism in the promoter of nicotinic acetylcholine receptor alpha subunit 3 (CHRNA3) gene was investigated in a case-control study that consisted of 406 patients with COPD and 394 healthy control subjects.

Results: The rs6495309 CT or TT genotype was associated with a significantly decreased risk of COPD when compared to the rs6495309 CC genotype (adjusted odds ratio=0.69, 95% confidence interval=0.50-0.95, P=0.02). The effect of the rs6495309 C>T on the risk of COPD was more evident in moderate to very severe COPD than in mild COPD under a dominant model for the variant T allele (P-value of test for homogeneity=0.02).

Conclusions: We confirmed the association between the 15q25 region and the risk of COPD in a Korean population.

Polymorphisms in microRNA Target Sites and Susceptibility to Chronic Obstructive Pulmonary Disease

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Background: The stringent recognition requirement between microRNA (miRNA) and its target site suggests that naturally occurring polymorphisms in miRNA target sites might have significant functional implications for miRNA binding and post-transcriptional regulation and consequently affect susceptibility of chronic obstructive pulmonary disease (COPD).

Methods: To investigate the influence of putative polymorphisms in miRNAs target sites on COPD, we searched out polymorphisms in miRNA target sites through bioinformatics analysis and conducted a case-control study including 286 patients and 287 healthy controls.

Results: Among the 392 polymorphisms of miRNA target sites examined, we found that 5 polymorphisms (GTF3C5 rs7324G>A, NUCB1 rs1058491G>A, C16orf55 rs17177787C>G, ARHGEF15 rs3744649G>T, and PTST1 rs3757417 T>G) had a significant effect on the risk of COPD. In silico analysis revealed that the rs7324 on GTF3C5, rs1058491 on NUCB1, rs3757417 on TPST1, rs17177787 on C16orf55 and rs3744649 on ARHGEF15 were targeted by miR-1469, miR-492, let-7i, has-miR-7-1 and miR-197, respectively.

Conclusion: Our findings provide the first evidence that polymorphisms in miRNA target sites could affect susceptibility to COPD.