



Editorial

Genetic predisposition to COPD

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Chronic obstructive pulmonary disease (COPD) is a major cause of global morbidity and mortality and categorized by irreversible airflow obstruction. COPD is presently the fourth leading cause of death and by 2030 COPD will be third leading cause of death according to the World Health Organization (WHO) reports. It was observed that minority of cigarette smokers have chance to develop COPD. But investigation suggests that subsequent to smoking other factors seem to be of play significant role for the development of the COPD. Epidemiological data demonstrated that genetics to be one of those factors, as COPD is known to aggregate in families and this provides evidence that genetic predisposition plays an important role in COPD. Related traits and genome wide association investigation of COPD have exposed multiple genetic loci association and risk of COPD. The heritability of COPD cannot be completely elucidated by identifying the genetic risk factors as achieving genome-wide significance. The mutual influence of genetic variation to COPD risk has not been completely understood.

The most significant genetic factor in the development of COPD is the Z allele of α 1-antitrypsin, which results in plasma levels of this protein that are 10–15% of that produced by the normal M allele. Several investigations have revealed that genetic factors other than α 1-antitrypsin deficiency may be participating in the susceptibility of cigarette smokers to chronic airflow obstruction. The consequence of various documented risk alleles on risk of COPD, mainly in cohorts of severely affected subjects, has not been clearly demonstrated. Different meta-analysis of genetic associations with COPD in multiple cohorts has the benefit of edu-

ating influence to perceive the further susceptibility risk variants by merging information across investigation, which may add to our understanding of disease mechanisms. Busch et al¹ studied meta-analyses and found two single-nucleotide polymorphisms (SNPs; rs112458284 and rs6860095) in genome-wide studies that were associated stage III–IV COPD at genome-wide significance levels. Busch et al¹ also describe two genetic risk scores based on COPD and lung function-associated SNPs and shown their applications in explaining COPD severity and COPD affection status risk. Our previous studies demonstrated that SNPs in DNA repair genes (X-ray repair cross-complementing group 1 and apurinic/apyrimidinic endonuclease-1) have impact on the COPD².

Large numbers of genetic studies published to date have used the various genes, whereby a limited number of variants genotype of different genes felt to be conceivable contributors to COPD susceptibility are examined. Unfortunately, the result of all those studies is often inconsistent. This is likely due to different geographical location, limited power from less sample sizes and inadequate statistical rigor.

As stated above genetic factors as dangerous liaisons to trigger the onset of a cascade of events resulting in disequilibrium which are essential in the initial stages of COPD development. Future studies in identifying these mechanisms is important in preventing the progress of the disease as this will open up several windows for identifying early treatment strategies before the 'point of no return' is reached. Understanding the pathways in which genetic factors influence COPD will uncover pathogenesis of the disease.

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