Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis

Allergic rhinitis is the most common clinical presentation of allergy, affecting 400 million people worldwide, with increasing incidence in westernized countries. To elucidate the genetic architecture and understand the underlying disease mechanisms, we carried out a meta-analysis of allergic rhinitis in 59,762 cases and 152,358 controls of European ancestry and identified a total of 41 risk loci for allergic rhinitis, including 20 loci not previously associated with allergic rhinitis, which were confirmed in a replication phase of 60,720 cases and 618,527 controls. Functional annotation implicated genes involved in various immune pathways, and fine mapping of the HLA region suggested amino acid variants important for antigen binding. We further performed genome-wide association study (GWAS) analyses of allergic sensitization against inhalant allergens and nonallergic rhinitis, which suggested shared genetic mechanisms across rhinitis-related traits. Future studies of the identified loci and genes might identify novel targets for treatment and prevention of allergic rhinitis.