# Bioinformatics analysis of immune cell infiltration, immune-related genes, and signaling pathways in the blood of allergic rhinitis patients

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## Abstract

Background: Allergic rhinitis (AR) is a chronic inflammatory disease of the upper respiratory tract, which has an increasing prevalence worldwide. The aim of this study was to explore the associated immune cell infiltration and molecular mechanisms of AR based on a bioinformatics analysis. Methods: GSE43497 and GSE50223 datasets for whole blood and CD4+ T cells, respectively were downloaded from the Gene Expression Omnibus (GEO) database. Differences in AR-associated immune cell infiltration were analyzed using CIBERSORT. A gene set enrichment analysis (GSEA) was performed using clusterProfiler software. Results: There was an upregulation in the proportion of CD8+ T cells, whereas there was a significant down-regulation of neutrophils in the whole blood of allergen-treated AR patients compared to diluent-treated patients. A correlation was identified between immune cells and immune-related genes. NF-kappa B and Toll-like receptor signaling pathways were also positively regulated in AR patients following allergen treatment. CD4+ T cell genes and associated cytokines significantly differed in allergen-treated AR patients compared to healthy and diluent-treated AR patients. Conclusion: Our analysis revealed that T cell receptor signaling pathways and Th1/Th2 cell differentiation may be involved in the mechanism of AR development. This study is the first bioinformatic analysis identifying immune cell infiltration and its underlying mechanism in AR from combined microarray data and provides novel insight for further research into the molecular mechanisms of AR.

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