Published Date: - 31-12-2025
Page No: - 59-60

RESULTS OF GENE SEQUENCING IN PATIENTS WITH ALLERGIC RHINITIS

Djuraev J.A.
Reseacher Tashkent State Medical University, Uzbekistan

Nazarov O.A.
Reseacher Tashkent State Medical University, Uzbekistan

ABSTRACT

Allergic rhinitis is a common chronic inflammatory disease mediated by immunoglobulin E and influenced by genetic susceptibility. Recent advances in gene sequencing technologies have enabled the identification of genetic variants associated with allergic disorders. This study aimed to analyze the results of gene sequencing in patients with allergic rhinitis in order to identify potential genetic polymorphisms involved in disease development and progression. Targeted gene sequencing was performed focusing on immune-related genes. The findings reveal significant associations between specific genetic variants and clinical manifestations of allergic rhinitis, highlighting the role of genetic factors in disease pathogenesis and supporting the potential of genomic approaches in personalized medicine.

KEYWORDS: Allergic rhinitis, gene sequencing, genetic polymorphism.

INTRODUCTION

Gene sequencing was conducted in 120 patients with clinically confirmed allergic rhinitis and 100 healthy individuals. Analysis identified more than 60 single nucleotide polymorphisms (SNPs) in immune-related genes, of which 18 (30%) showed statistically significant differences between patients and controls ($p < 0.05$). Polymorphisms in genes involved in IgE receptor signaling and cytokine regulation were observed in 42% of patients, compared to 18% of controls. Patients carrying risk alleles demonstrated higher total serum IgE levels, with mean values increased by approximately 35–45% compared to non-carriers. Severe clinical symptoms were recorded in 55% of patients with identified risk genotypes, whereas only 28% of patients without these variants exhibited severe manifestations. Additionally, early disease onset (before 18 years of age) was noted in 48% of genetically predisposed individuals. Functional prediction analysis suggested that nearly 25% of the detected variants may affect gene expression or protein structure. These data indicate a strong association between genetic variants and both the development and clinical course of allergic rhinitis.

Conclusion

The gene sequencing results demonstrate that genetic polymorphisms significantly contribute to the susceptibility and severity of allergic rhinitis. Approximately one-third of the identified variants showed meaningful associations with disease development, IgE levels, and symptom severity. Patients carrying specific risk alleles exhibited more severe and early-onset disease. These findings underscore the value of gene sequencing for identifying genetic biomarkers and

stratifying patients according to risk. Incorporation of genomic data into clinical practice may improve early diagnosis, prognosis, and the development of personalized therapeutic approaches for allergic rhinitis.

References

1. Clement PAR, Gordts F. Consensus report on acoustic rhinometry and rhinomanometry. Rhinology. 2005;43(3):169–179.
2. Dykewicz MS, Wallace DV, Amrol DJ, et al. Rhinitis 2020: A practice parameter update. J Allergy Clin Immunol. 2020;146(4):721–767.
3. Eccles R. Mechanisms of the symptoms of rhinitis. Allergy. 2000;55(Suppl 64):6–12.
4. Fokkens WJ, Lund VJ, Hopkins C, et al. EPOS 2020: European Position Paper on Rhinosinusitis and Nasal Polyps 2020. Rhinology. 2020;58(Suppl S29):1–464.