

# EPIGENETIC REGULATION ON THE GENE EXPRESSION SIGNATURE IN BRONCHIAL ASTHMA WITH RHINITIS SYNDROME BY RNA SEQUENCE

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**Background:** Bronchial asthma with rhinitis syndrome is the global health problem that affects numbers of patients. This study was intended to identify the signature genes, which was helpful in understanding the potential molecule mechanism of bronchial asthma with rhinitis syndrome.

**Methods:** The blood samples of 3 patients with bronchial asthma (accompanied with rhinitis syndrome), 3 patients with rhinitis and 3 normal controls were obtained for the RNA sequence. Differentially expressed genes and miRNAs were identified by different software. MiRNA-gene target analysis was performed through prediction tools and the regulatory network was also constructed. Gene ontology and the Kyoto encyclopedia of genes and genomes were used to analyze the biological function of differentially expressed genes.

**Results:** A total of 353 differentially expressed genes and 59 differentially expressed miRNAs were obtained in bronchial asthma compared with that in rhinitis. And 4650 differentially expressed genes and 88 differentially expressed miRNAs were screened in rhinitis compared with that in the control. After targeting correlation analysis, 159 differentially expressed genes were not only the target genes but also negatively correlated with 39 differentially expressed miRNAs in bronchial asthma compared with that in rhinitis. And 2685 differentially expressed genes were not only the target genes but also negatively correlated with 88 differentially expressed miRNAs in rhinitis compared with that in control. Finally, 52 differentially expressed genes and 16 differentially expressed miRNAs were identified after merging the data in above three groups. Among which, five genes including *SLC14A1*, *SNCA*, *TNS1*, *KAT2B*, *PARP1* were target genes of differentially expressed miRNAs (*hsa-miR-93-5p*, *hsa-miR-92a-3p*, *hsa-miR-21-5p*) and were significantly associated with bronchial asthma with rhinitis syndrome. Additionally, functional analysis showed that phagosome was the significantly enriched signal pathway involving three important genes (*HLA-DOA*, *TUBB2A* and *MRC2*).

**Conclusion:** Taken together, eight genes including *TLR2*, *ICAM1*, *C1QB*, *HLA-DOA*, *ABL1*, *CASP3*, *CAV1*, *CD55*, *RPS26* and *TUBB2A* under the regulation of miRNAs played significant roles in the process of bronchial asthma with rhinitis syndrome.

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