



Microarray-based Identification of Novel Biomarkers in Asthma

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Bronchial asthma is a complicated and diverse disorder affected by genetic and environmental factors. It is widely accepted that it is a Th2-type inflammation originating in lung and caused by inhalation of ubiquitous allergens. The complicated and diverse pathogenesis of this disease yet to be clarified. Functional genomics is the analysis of whole gene expression profiling under given condition, and microarray the echnology is now the most powerful tool for functional genomics. Several attempts to clarify the pathogenesis of bronchial asthma have been carried out using microarray technology, providing us some novel biomarkers for diagnosis, therapeutic targets or understanding pathogenic mechanisms of bronchial asthma. In this article, we review the outcomes of these analyses by the microarray approach as applied to this disease by focusing on the identification of novel biomarkers.

<u>存档文本</u>

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