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Identification of asthma-associated microRNAs in bronchial biopsies

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Shareable abstract (@ERSpublications)
Using small RNA sequencing on bronchial biopsies of asthma patients and healthy controls, this study identified microRNAs associated with clinical and inflammatory features of asthma that are potential regulators of asthma-associated gene expression https://bit.ly/3rZXMDf

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Abstract

Background Changes in microRNA (miRNA) expression can contribute to the pathogenesis of many diseases, including asthma. We aimed to identify miRNAs that are differentially expressed between asthma patients and healthy controls, and explore their association with clinical and inflammatory parameters of asthma.

Methods Differentially expressed miRNAs were determined by small RNA sequencing on bronchial biopsies of 79 asthma patients and 82 healthy controls using linear regression models. Differentially expressed miRNAs were associated with clinical and inflammatory asthma features. Potential miRNA–mRNA interactions were analysed using mRNA data available from the same bronchial biopsies, and enrichment of pathways was identified with Enrichr and g:Profiler.

Results In total, 78 differentially expressed miRNAs were identified in bronchial biopsies of asthma patients compared with controls, of which 60 remained differentially expressed after controlling for smoking and inhaled corticosteroid treatment. We identified several asthma-associated miRNAs, including miR-125b-5p and miR-223-3p, based on a significant association with multiple clinical and inflammatory asthma features and their negative correlation with genes associated with the presence of asthma. The most enriched biological pathway(s) affected by miR-125b-5p and miR-223-3p were inflammatory response and cilium assembly/organisation. Of interest, we identified that lower expression of miR-26a-5p was linked to more severe eosinophilic inflammation as measured in blood, sputum as well as bronchial biopsies.

Conclusion Collectively, we identified miR-125b-5p, miR-223-3p and miR-26a-5p as potential regulators that could contribute to the pathogenesis of asthma.