




Epigenetics and pulmonary diseases in the horizon of precision medicine: a review

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Network medicine approaches, supporting the integrative analysis of global epigenetic changes, clinical features and environmental factors, provide new hypotheses for pathogenesis of chronic lung diseases and lead to new interventions for prevention <https://bit.ly/3kHND9m>

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ABSTRACT Epigenetic mechanisms represent potential molecular routes which could bridge the gap between genetic background and environmental risk factors contributing to the pathogenesis of pulmonary diseases. In patients with COPD, asthma and pulmonary arterial hypertension (PAH), there is emerging evidence of aberrant epigenetic marks, mainly including DNA methylation and histone modifications which directly mediate reversible modifications to the DNA without affecting the genomic sequence. Post-translational events and microRNAs can be also regulated epigenetically and potentially participate in disease pathogenesis. Thus, novel pathogenic mechanisms and putative biomarkers may be detectable in peripheral blood, sputum, nasal and buccal swabs or lung tissue. Besides, DNA methylation plays an important role during the early phases of fetal development and may be impacted by environmental exposures, ultimately influencing an individual’s susceptibility to COPD, asthma and PAH later in life. With the advances in omics platforms and the application of computational biology tools, modelling the epigenetic variability in a network framework, rather than as single molecular defects, provides insights into the possible molecular pathways underlying the pathogenesis of COPD, asthma and PAH. Epigenetic modifications may have clinical applications as noninvasive biomarkers of pulmonary diseases. Moreover, combining molecular assays with network analysis of epigenomic data may aid in clarifying the multistage transition from a “pre-disease” to “disease” state, with the goal of improving primary prevention of lung diseases and its subsequent clinical management.

We describe epigenetic mechanisms known to be associated with pulmonary diseases and discuss how network analysis could improve our understanding of lung diseases.