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EUROPEAN RESPIRATORY SOCIETY INTERNATIONAL CONGRESS 2023 MILAN Italy, 9-13 September

Cluster analysis to identify distinct clinical asthma phenotypes within ATLANTIS

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Introduction:

Better understanding of asthma phenotypes is crucial for understanding, characterizing and managing the disease. This post-hoc ATLANTIS study analysis aims to identify clinically distinct clusters including parameters of small airways disease and asthma associated gene-expression based on previous study.

Methods:

ATLANTIS included 773 asthma patients (mean age 44 years, 58% female, 76% never-smoker, GINA 1-5). Subjects were characterized using questionnaires, large and small airways disease, nasal brush RNA, blood and sputum samples, and chest computed tomography. Clusters were generated using the Self-Organizing Map-Ward's method.

Results:

We identified four groups: Cluster A (N=277) included predominantly male patients with well controlled symptoms and elevated levels of sputum neutrophils. Cluster B (N=228) characterized by normal lung function, low blood inflammatory cell counts and low sputum eosinophils. Cluster C (N=206) included mostly atopic patients with an early age of asthma onset, more severe bronchial hyperresponsiveness, uncontrolled symptoms and higher nasal epithelial expression of asthma related genes.

Cluster D (N=62) was characterized by frequent exacerbations, lower post-bronchodilator FEV1 %predicted and FEFs, small airways disease and hyperinflation. Cluster D patients also had higher sputum and blood eosinophil counts, and exhaled nitric oxide levels.

Discussion:

We identified four clinically distinct patient groups: Neutrophilic, Mild pauci-inflammatory, Atopic, and those with small airways disease, high eosinophil levels in blood and sputum and frequent exacerbations. Future research engaging the biology of these clusters may provide new options for precision medicine.