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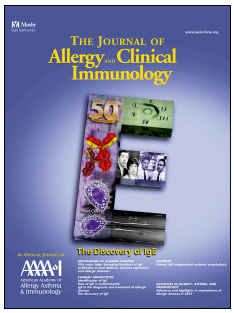

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Incorporating the airway microbiome into asthma phenotyping - moving towards personalized medicine for non-eosinophilic asthma

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Asthma is highly heterogeneous in severity and in patterns of airway immune responses[1, 2]. This heterogeneity, expressed as differences in asthma phenotypes, challenges the effectiveness of uniform management strategies. It is clear, for example, that current therapies, directed largely at ameliorating bronchoconstriction and airway inflammation with bronchodilators and inhaled corticosteroids (ICS), do not work for all patients. A promising approach to this clinical dilemma lies in stratifying patients by markers of underlying airway inflammation, in particular neutrophilic and eosinophilic phenotypes. Such strategies have already identified patients with eosinophilic or type 2-driven inflammation as more likely to respond to corticosteroids or recently approved biologics, and have prompted research on phenotypes unresponsive to such treatments, such as those with non-eosinophilic inflammation or eosinophilic inflammation that persists despite high-dose ICS treatment. Whilst many mechanisms underlying eosinophilic asthma have been delineated, the mechanisms driving neutrophilic or persistent eosinophilic inflammation remain poorly understood.

Severe asthma itself is heterogeneous based on differences in clinical, demographic, and inflammatory features. Recent findings indicate this heterogeneity extends also to the