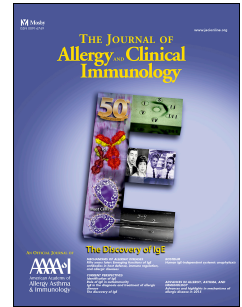


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Incorporating the airway microbiome into asthma phenotyping - moving towards personalized medicine for non-eosinophilic asthma

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

33
34 Severe asthma itself is heterogeneous based on differences in clinical, demographic, and
35 inflammatory features. Recent findings indicate this heterogeneity extends also to the

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