Molecular allergen sensitization drives phenotypes of severe asthma in children: evidence from a megacity cohort (SAMP)

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Abstract

Background: Several major sensitization profiles have been described in children with asthma, but it remains unclear how these profiles relate to asthma phenotypes. The aim of this study was to determine allergenic sensitization profiles in a megacity cohort (SAMP). Methods: This was a cross-sectional analysis performed from 2011 to 2015 including preschool and school-age children with severe and moderate asthma from the SAMP cohort. We performed ALEX multiplex array and carried out cluster analysis. Results: Data from 367 children were analysed: 224 of preschool age and 143 of school age, respectively 84 (38%) and 114 (80%) presented at least one allergic sensitization. At preschool age, three clusters were identified: Cluster 1, Few sensitizations to inhaled allergen molecular families and non-type 2 (T2) inflammation (n=61); Cluster 2, Predominant sensitization to HDM molecular families. (n=16); Cluster 3, Severe asthma with multiple sensitizations to inhaled and food allergen molecular families (n=7). At school age, five clusters were identified: Cluster 1, Few sensitizations to inhaled allergen molecular families and non-T2 inflammation (n=43); Cluster 2, Predominant sensitization to HDM molecular families (n=31); Cluster 3, Predominant sensitization to PR-10 family (n=25); Cluster 4, Severe asthma with predominant sensitization to tropomyosin family (n=11); Cluster 5, Severe asthma with multiple sensitizations to inhaled and food allergen molecular families (n=4). Conclusion: These results underline the heterogeneity of sensitization profiles in severe allergic childhood asthma. The most severe asthma phenotypes were associated with multiple sensitizations to both inhaled and food allergen molecular families as expected, and to the tropomyosin molecular family, a novel finding.

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