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Comment on Tuten Dal S et al

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Letter to the Editor

Comment on Tuten Dal S et al

To the Editor,

The article by Tuten Dal S et al on house dust mite molecular allergen (MA) sensitization among children appear to be consistent with previous studies in that: (1) sensitization levels and number of individual sensitizations increase with age; (2) certain MA mono-sensitizations are clinically relevant (e.g., Der p 20 and scabies, Der p 23 monosensitization) and (3) allergic sensitization to house dust mites can cause development of other allergies [1-3].

However, the hierarchical cluster analysis (HCA) employed in the study by Tuten Dal S et al were unable to address if a particular MA was associated with increased risk of development of allergic rhinitis, or if another MA was associated with decreased risk of atopic dermatitis. Hierarchical cluster analysis, although easy to employ and understand, relies on several arbitrary decisions (such as distance metric or linkage criteria, not provided by Tuten Dal S et al) that allocate the data into clusters and therefore not only prone to misinterpretation but also often a poor solution. In contrast, Bayesian Network Analysis such as latent class analysis provide separate probabilistic connections between individual MA and patient profiles thereby building the Bayesian directed acyclic graph and also a network [4, 5].

Considerable use of latent class analysis discussed in papers by Yuriev S et al (Ukraine, root node set to Der p 23 as it remained high in all age groups) and Hou X et al (China, whole allergen extracts) show the importance of understanding regional sensitization profiles and age groups before considering allergen immunotherapy products [2, 6]. Der p 7 was associated with development of allergic rhinitis while sensitization to Der f 2, Der p 2 and Der p 23 increased risk of developing atopic dermatitis. In contrast, Der p 10 sensitization reduced risk of atopic dermatitis [2]. Similarly, Hou X et al showed that patients in pollen sensitization clusters have increased risks of dermatitis and allergic conjunctivitis in contrast to those in Class 1 who were highly allergic to house dust mites and low rates of other allergens [4].

Such analysis is not possible using HCA and large datasets that are generated using microarray platforms should ideally be analysed using Bayesian statistics that employ prior/posterior probabilities and well-equipped to handle missing data.

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