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## The molecular basis of allergenicity

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Although a large number of allergens have been characterized, it is not known how such diverse structures could all lead to the stimulation of T cell helper type 2 responses and subsequent bias towards the synthesis of IgE. In the July issue of *Molecular Pathology*, Furmonaviciene and Shakib from the *University of Nottingham*, UK, show that various allergens have a common structural motif, which could potentially explain their ability to elicit powerful IgE antibody responses.

Furmonaviciene and Shakib analyzed the three-dimensional structures and examined multiple sequence alignments of diverse allergens such as the plant cysteine protease papain, the transport protein lipocalin Mus m 1 and the ragweed allergen Amb a 5. They found that these allergens have a similar structural motif; namely, an  $\alpha$ - $\beta$  groove resembling the substrate binding groove of house dust mite allergen Der p 1. The groove is located inside a  $\alpha$ - $\beta$  motif, an  $\alpha$  helix and an antiparallel  $\beta$  sheet (*J Clin Pathol: Mol Pathol* 2001, **54**:155-159).

An identical structural motif can also be found in some toxins and defensins. Defensins are natural antibiotics that give mammals innate resistance to invading bacteria, fungi and viruses. The authors speculate that comparable host defence functions can be activated by allergens using the  $\alpha$ - $\beta$  groove, enabling them to bind to a common ligand.

## References

1. Furmonaviciene R, Shakib F. The molecular basis of allergenicity: comparative analysis of the three dimensional structures of diverse allergens reveals a common structural motif. *J Clin Pathol: Mol Pathol* 2001, 54:155-159., [<http://www.molpath.com/cgi/content/abstract/54/3/155>]
2. University of Nottingham, [<http://www.nottingham.ac.uk/>]