Structure and Epitopes of Bet v 1

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The binding of human IgE to a foreign allergen represents a crucial step in the development of clinical symptoms of type I allergy. The binding of IgE occurs to B-cell epitopes composed of amino acid residues located on the molecular surface of the allergen. Detailed knowledge on the three-dimensional structure of the allergen is thus essential in order to identify and characterize its IgE-binding B-cell epitopes.

a Ribbon representation of the three-dimensional molecular structure of Bet v 1, the major allergen of birch pollen, which has recently been solved both in solution by NMR spectroscopy and in the crystalline state by X-ray crystallography [1,2]. The main feature of the structure is a seven-stranded anti-parallel β -sheet (orange) that wraps around a 25-residue-long C-terminal α -helix (red). The β -sheet and the C-terminal part of the long helix are separated by two consecutive α -helices. The structure reveals a most unusual feature, a large cavity that penetrates the entire protein with three openings on the molecular surface [2]. b The molecular surface of Bet v 1 is visualized by a space-filling model with surface-exposed amino acid residues in color. The areas in green, blue and red represent regions of exposed amino acid residues that are conserved among the major tree pollen allergens of Fagales. These areas are likely to harbor cross-reactive B-cell epitopes and provide a structural basis for the clinically observed allergic symptoms that birch-pollen-allergic patients experience when they encounter pollens from related trees such as hazel, alder and hornbeam. The structural determination represents a new and major step towards identifying and modifying IgE-binding B-cell epitopes of the major tree pollen allergens and will be invaluable to the future development of therapy and diagnosis of allergic diseases.

References

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