Abstract:

Background: Der p 5 is an important allergen of Dermatophagoides pteronyssinus that plays a key role in allergic airway diseases. Its three dimensional structure (PDB 3MQ1) consists of three anti-parallel α-helices arranged in a helical bundle. Aggregation of Der p5 can modulate its allergenicity. This study aimed to identify the key residues of IgE binding epitopes of Der p 5.

Methods: IgE binding epitopes of Der p 5 were characterized as follow. An in silico prediction of the epitope was performed with the help of SEPPA program. We also made a mapping of the epitope by using an overlapping library of peptides that encompass the sequence of mature Der p 5. Finally, an alanine scanning mutagenesis allowed us to define the key residues of the allergen involved in its interaction with IgE. The integrity of the structure of the different protein's mutants was assessed by far UV circular dichroism.

Results: The presented data indicate that the major epitope sequence of Der p 5 is 90DRLMQRKDLDIFEQYNLEM108. Residues L98, D99, I100, F101, E102 and Y104 appear to be important for IgE binding.

Conclusion: This study highlighted the residues of Der p 5 essential for IgE binding. The identification of the major residues epitope of Der p 5 allergen may participate in the selection and engineering of new hypoallergens used in immunotherapy.