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413 Amino Acid Positions Involved in the Formation of IgE-binding Epitopes of Api g 1 and Mal d 1 Allergens*Fatima Ferreira***Daniel Hebenstreit***Bettina Kramer***Martin Himly***Heimo Breiteneder†**Otto Scheiner†**Peter Briza***Christof Ebner†**M Breitenbach****Inst f Genetik u Allg Biologie, Universität Salzburg, Salzburg, Austria†Inst f Allg u Exp Pathologie, Universität Wien, Vienna, Austria*

In a previous study, we found that six amino acid positions/ residues influenced IgE binding to Bet v 1. To investigate if the same residues are also involved in IgE binding to Api g 1 and Mal d 1 homologous allergens, the corresponding amino acid positions in these sequences were identified. Amino acid substitutions in the Api g 1 and Mal d 1 sequences were engineered using a PCR-based site-directed mutagenesis approach. The mutant Api g 1 and Mal d 1 proteins were expressed in *E. coli* and tested for their IgE-binding properties using sera from celery and apple-allergic patients, respectively. All celery-allergic patients tested showed extremely low or no detectable IgE binding activity to the Api g 1 mutant. Similarly, apple-allergic patients tested displayed significantly reduced IgE binding activity to the Mal d 1 mutant.

Our results indicate that amino acid positions 10, 30, 57, 112, 113, and 125 shown to be important for the IgE-binding activity of Bet v 1, also seem to play a substantial role in the formation of IgE-binding epitopes of the homologous allergens in celery and apple. Use of these engineered allergens for immunotherapy could substantially decrease the risk of anaphylactic (IgE-mediated) side effects during treatment.