

Immunological behavior of cysteine containing apple allergen isoforms

Jana Unterhauser^a, Reiner Eidelpes^a, Linda Ahammer^a, Christina Meisenbichler^a,
Bettina Nothegger^b, Claudia Covaciu^c, Valentina Cova^d, Thomas Letschka^d,
Klaus Eisendle^c, Norbert Reider^b, Thomas Müller^a, Martin Tollinger^a

^aInstitute of Organic Chemistry, University of Innsbruck, Austria

^bDepartment of Dermatology, Venereology and Allergology,
Medical University of Innsbruck, Austria

^cDepartment of Dermatology, Hospital of Bolzano, Italy

^dDepartment of Molecular Biology, Laimburg Research Centre for Agriculture and
Forestry, Italy

Apple allergy in central and northern Europe is predominantly the result of initial sensitization to birch pollen, followed by subsequent development of allergic reactions after apple consumption. This allergic cross-reaction arises due to the presence of proteins in apple fruit (Mal d 1), that are similar in their structure to the sensitizing protein in birch pollen (Bet v 1).

To understand the immunological cross-reactivity on a molecular basis, it is thus necessary to determine the three-dimensional structure of these proteins in solution at high resolution. Therefore, different isoforms of the apple allergen with variation in their amino acid sequence were examined with NMR spectroscopy. Structure models for six isoforms of Mal d 1 could be obtained, all showing a highly conserved fold consisting of a seven-stranded antiparallel β -sheet wrapped around one long and two short α -helices, which is similar to the structure of the sensitizing protein Bet v 1.

Nevertheless, the differences in the amino acid side chains might potentially influence the allergenicity of the isoforms. In addition, recent immunological data indicate that other food constituents, like vitamin C or polyphenolic compounds, can affect the allergenicity of the proteins, presumably due to chemical modification of the protein surface of the allergen itself. After incubation with Vitamin C and different polyphenols an increase in mass for Mal d 1.01 isoforms was confirmed with ESI-MS, indicating a site-specific covalent modification of the protein.