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Abstract

Identification of Allergenic Epitopes in The Sequences of Rapeseed Seed Proteins

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Abstract: Background: Australia annually produces around 3.5 million metric tons of rapeseed/Canola, and about half of this remains as de-oiled by-product, and largely consists of seed proteins. This rich source of proteins is primarily streamlined for animal feed as these proteins cannot be utilised for human consumption due to potential for triggering allergic reactions. When ingested these proteins are not digested in the stomach and therefore remain intact in the intestine where they trigger allergic reactions by binding with immunoglobulin E antibodies. Epitopes, the regions on the rapeseed seed proteins that bind these antibodies are yet to be characterised.

Methods: Rapeseed major seed proteins were probed by aligning the reported immunodominant linear epitopes of known allergens with respect to the sequences of rapeseed proteins to detect the corresponding epitope sites. Sequence alignment, evolutionary relations, allergen database surveys, and modelling of three-dimensional structure were performed to characterise the epitopes.

Results: The molecular surface epitope mapping identified epitopes in rapeseed proteins with high sequence coverage and identity to known food epitopes. This indicated conservation of allergenic epitope motifs, while the three-dimensional structure modelling allowed the prediction of ligand binding sites on human H1 Histamine receptors.

Conclusion: The epitopes identified in this study could be used in the development of recombinant proteins for diagnosis, to develop synthetic and recombinant vaccines for immunotherapy and therapeutic purposes against rapeseed allergy. This work enriches our existing knowledge on immunogenesis to seed proteins and provides a robust foundation and rational basis for protein bioengineering of seed storage proteins for human food.