In Silico Allergenicity Assessment of Novel Proteins Derived from GMHR Crops

Najaf Allahyari Fard¹, Zarrin Minuchehr¹, Amir Mousavi¹

¹National Institute of Genetic Engineering and Biotechnology (NIGEB), Bioinformatics Group, 14965/161, Tehran, Iran allahyar@nigeb.ac.ir

Abstract. Genetically modified herbicide resistant (GMHR) crops have transformed weeds management. Today, HR traits are used on >80% of the estimated 134 million hectares of transgenic crops grown annually in 25 countries. Transgenic herbicide traits are five events, including two transgenes code for glyphosate resistance and insensitive 5- enolpyruvylshikimate-3-phosphate synthase (EPSPS), the cp4 epsps gene from Agrobacterium tumefaciens strain CP4 that causes shikimate pathway in another manner as the process mediate by phosphoenol pyruvate (PEP) and the mutated zm-2mepsps from corn (Zea mays L.), and three transgenes code for metabolic inactivation. One gene from Ochrobactrum anthropi strain LBAA encodes for glyphosate oxidoreductase (GOX), and two genes pat and bar from Streptomyces viridochromogenes and Streptomyces hygroscopicus, respectively, encode N-acetyltransferases that inactivate glufosinate. In this research, allergenicity of EPSPS, CP4 epsps, zm-2mepsps, GOX, pat and bar proteins was studied. Protein encoded by EPSPS, CP4 epsps, zm-2mepsps, GOX, pat and bar genes contains 427, 455, 431, 183, 183 amino acids respectively. These sequences were aligned using the FASTA program in allergen databases FARRP, SDAP, Algpred. Sequence alignment was implemented with the allergen proteins in three matches including: the full sequence matching sequence, matching the 80 amino acids and eight amino acids. The results showed no similarity between EPSPS, CP4 epsps, zm-2mepsps, GOX, pat and bar proteins and allergen proteins in the full sequence matching. Matching the 80 amino acid (Domain) in the SDAP database showed three little similarity (35, 36 and 37.25) for CP4 epsps that was not confirmed in the Algpred for Mapping of IgE epitopes search. Matching 8 amino acids showed no similarity to determine the epitope potential. Therefore, we conclude that EPSPS, CP4 epsps, zm-2mepsps, GOX, pat and bar proteins probably has nonallergenic potential at bioinformatics level.