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Initial seed proteomic study in *Opuntia* sp. for genotype differentiation

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Little is known about *Opuntia* seed storage proteins and their contribution to the differentiation and systematic of genotypes. The variation between 102 genotypes of Mexican *Opuntia* was investigates using electrophoretic patterns SDS-PAGE of their Seed Total Protein (STPs) and Seed Storage Proteins (SSPs). Albumins and globulins were the most abundant protein fractions with contents that oscillated between 2.6 and 11.9 mg/mL and between 2.6 and 9.5 mg/mL, respectively. These were followed by glutelins fraction (2.3-8.5 mg/mL) and prolamins as the lowest (1.1-7.9 mg/mL) of the four seed protein factions. Equally, STPs content varied between 1.13 and 7.12 mg/mL. Therefore, the total protein content and the different protein fractions were not found to be correlated with any of the seed morphological behaviors. However, regardless of variations in protein content estimated in seeds, the electrophoretic patterns of STPs and SSPs as revealed in their SDS-PAGE were not so variable. Furthermore, the individual analysis of each STPs or the SSPs analyses separately were not enough to differentiate *Opuntia* genotypes included in the study. The cluster and multivariate analyses indicated that there is no separation between accessions of species of the prickly pear (sweets fruits) and xoconostle (acidic fruits) even though the latter were grouped together. Based on biochemical markers analyzed herein, the need for revision of taxonomic assignment of genotypes belonging to the genus *Opuntia* was suggested.

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Identification, molecular cloning, and preparation of antigenic hepatitis C virus genotype 4a recombinant NS2 protein

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Hepatitis C Virus (HCV) infects around 185 million people around the world. In Egypt, HCV is number one infection estimated nationally at 14.7% and is one of the major causes of cirrhosis and hepatocellular carcinoma. Although new effective drugs are developing against HCV, late infection discovery and high cost of HCV therapies limit the efficacy of controlling the disease. Thus, the development and implementation of a preventive co valid vaccine is important. As NS2 protein plays a crucial role in protein-protein interactions needed for infectious HCV particle production, the aim of the present study was to clone and express NS2 of HCV genotype 4a and to investigate the protein antigenicity. Herein, we amplified NS2 DNA coding region from the Egyptian HCV4a strain ED43 that was previously inserted in PUC19 plasmid. Then, we successfully cloned, sequenced the PCR product and expressed the NS2 recombinant protein in E. coli M15 using pQE-30 vector. Antigenicity against pooled sera of Egyptian patients of the recombinant NS2 protein was confirmed by Western blotting. This study might help in the design of a vaccine against the predominant genotype 4a in the Egyptian population.

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