

Protein Profiles of Seedy and Mutant Seedless Lemon Cultivars

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Aim of the study: Seedlessness is one of the most desired characters for citrus fruits and can be obtained through several methods. 'Alata', 'Uzun' and 'Gülşen' varieties were rendered seedless by exposure of budwood to gamma radiation (⁶⁰Co). In the present study, it was aimed to determine the proteins responsible from seedlessness through comparisons of seedless lemon cultivars with the seedy control (Küttdiken) cultivar.

Material and Methods: The whole fruit of the 'Alata', 'Gülşen', 'Uzun', and 'Küttdiken' lemon cultivars were crushed and homogenized in extraction buffer and protein extractions were carried out by phenol extraction method. The quantitation analysis was performed by modified Bradford method and the amounts of proteins in samples were equalized. Subsequently, the samples were subjected to 2D gel electrophoresis. Spot differences were determined by comparing the protein spots of the varieties with the Delta2D DECODON software. Spots seen in one sample but not in others, and also differentially expressed ones were excised from the gels and stored for further dual spectrometric mass analysis using Eksigent ekspert™ nano LC 400 system.

Results: In the current study, immature fruit tissues of seedless 'Alata' and seedy 'Küttdiken' were compared in terms of protein expression profiles. Approximately 400-425 different protein spots ranging from 5-150 kDa with pH range of 3.0-10.0 were observed. The 2D gel protein profiles of varieties were localized in 4 specific locations in general. The majority of the spot differences among the varieties were observed at high molecular weight proteins in the range of 4 to 7 isoelectric point. Of these, five spots were observed only in seedy 'Küttdiken' but not in seedless 'Alata' variety. Although few protein spots were observed as up regulated, most of the others aroused mainly in the form of down regulation in seedless 'Alata' variety. The results were confirmed by repeating the processes with proteomics grade chemicals. It is suggested to conduct more detailed studies to reveal the identification of these interesting proteins in order to better understanding of the major protein/s responsible for seed formation by using the mass spectroscopic analysis. In case of clearly identifying peptide/s responsible for seedlessness, they can be used in breeding programs through biotechnological methods.

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