REPEATABILITY ASSAY FOR PROTEOMIC ANALYSIS OF POTATO SAMPLES

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Plant breeding techniques may cause significant changes in characteristics of vegetables used for human consumption. Currently, the procedures for detection of unintended effects often involve targeted analysis. Nevertheless, more detailed evaluation is needed for commercial approval of these new varieties. “Omics” techniques are suggested as effective tools for identification of unintended effects in plant metabolism. In the present work, proteomics was applied using two dimensional electrophoresis technique (2-DE). For a reliable comparative proteomic analysis, the methodology needs to be validated. Repeatability test is essential as parameter for further proteomic analysis in different samples. With this purpose, the impact of extraction procedure and 2-DE on the repeatability of the protein profile was investigated by comparing the quantitative (spot quantity) variability of the protein profile among extracts of the same sample. Samples of freeze-dried potato tubers (variety Fontane) were submitted to four independent protein extractions (Coll, 2011), which generated four 2-DE gels. For each gel, 250 µg of protein were applied in 13 cm IEF strips pH 4-7. The mean number of total spots in each gel was 245 ± 38, and the coefficient of variation (CV) of 15.7%. The gel-to-gel comparison of matching spots ranged from 81.16% to 90.55%, and the correlation coefficients (r²) were 0.98 in all cases. This experiment presented adequate repeatability as the CV was lower than 19% and the r² was higher than 0.90 (Valledor, 2011). The present repeatability assay will be used as parameter for further proteomic analysis of five potato varieties.