

P. 105

PLANT PROTEOMICS IN RESPONSE TO IONIZING RADIATIONS

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The effects of ionising radiations (IR) on organisms are mainly caused by the water radiolysis phenomenon which produces a significant amount of hydroxyl ions, generating a specific oxidative stress in cells. Our interest is focused on the IR effects on plant metabolism and changes occurring in cellular and tissue functioning after exposure to IR. Global plant responses to IR have been studied at transcriptional level, but studies dealing with IR stress on plant proteome are missing

To complete the knowledge on changes occurring in plants exposed to IR, we proposed to analyze *Arabidopsis thaliana* proteome on a short- and long-time scale after exposure (or not) to sub-lethal doses of IR obtained from X-Rays. In order to facilitate the differential analysis, plant roots and aerial part proteomes will be separately studied. We are interested in exploring by this way different ecotypes or mutants owning special characteristics or genes involved in the glucosinolate pathway, the latter potentially having an antioxidative effect.

Our model are 10-days old plants of *Arabidopsis thaliana*, ecotype Col-0, which are grown on petri dishes, in sterile conditions, in a 16h-light, 8h-dark photoperiod. The treatment stage corresponds to a 2-leaves-spread-out stage. Irradiation will be performed in a X-rays chamber Faxitron at a dose rate of 1.6 gray.min⁻¹. Plants will be treated in the petri dishes and will receive a total dose of 10 and 40 grays (Gy). After the irradiation treatment is applied, leaves and roots will be separately frozen at 2, 6, 24, 48 and 72 hours after irradiation.

Results of this program work, dealing with optimization of extraction protocol, realization of 2D-electrophoresis proteomic gels, and MS analysis of proteins will be presented.