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DIFFERENTIAL PROTEIN EXPRESSION PROFILING BY ITRAQ-2DLC-MS/MS IN ARABIDOPSIS
THALIANA CALLUS UNDER MICROGRAVITY ON BOARD CHINESE SPACECRAFT SZ-8

Abstract

Plants can acclimate rapidly to environmental conditions. To evaluate the spaceflight –associated stress and the genetic responses that accompany cytoskeleton adaptation to spaceflight and identify molecular events important for acquired microgravity tolerance, we compared viability and proteomic profiles of *Arabidopsis thaliana* callus which grown under microgravitational conditions and its space 1g centrifugation control on board the Chinese spacecraft SZ-8. In order to investigate the influences of microgravity on the cellular proteome, the proteome alterations induced by microgravity have been comparatively analyzed by stable isotopic chemical labeling connected with mass spectrometry. The results revealed that 101 proteins showed quantitative variations that were significantly and reproducibly different between the microgravity and 1g space control samples. Of these proteins, fifty-one exhibited up-regulated expression level and the fifty display down-regulated expression level. Their functions were involved in stress response, primary and energy metabolism control, protein synthesis and degradation, cell wall biosynthesis, cytoskeleton, signaling pathway and transcript regulation. Among of them, eight proteins involved in cytoskeleton and cell wall biosynthesis respectively are particular interesting, because these proteins are important for plant cells to adapt the microgravity. The data presented in this study illustrate that the adaptation of plant cells to microgravity is accompany a serial protein expression alterations.

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