

Expression of stress response genes in barley *Hordeum vulgare* in a spaceflight environment

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Abstract

The transcriptome of barley *Hordeum vulgare* grown aboard the International Space Station was studied using microarray analysis. In the spaceflight environment, mRNA levels of over 500 genes were changed more than twofold; among them, genes of stress response proteins, in particular, heat shock proteins, pathogenesis-related proteins, and antioxidant proteins. Further analysis by real-time PCR confirmed enhanced transcription of reactive oxygen species scavenging genes. The superoxide dismutase (sod) mRNA level in the space environment was 6-fold higher than in earth conditions. The transcript levels of glutamyl transferase (gst), catalase (cat), and ascorbate peroxidase (apx) were increased in spaceflight 24, 18, and 3 times in comparison to ground control, respectively. For the first time, it has been shown that spaceflight environment can induce oxidative stress in plants. © 2010 Pleiades Publishing, Ltd.

<http://dx.doi.org/10.1134/S0026893310050080>

Keywords

antioxidant defense, gene expression, *Hordeum vulgare*, microgravity, real-time PCR