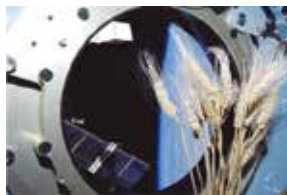
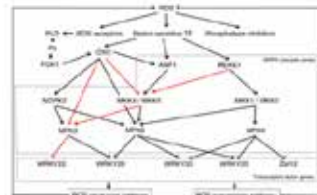


Genome-wide expression analysis of reactive oxygen species gene network in plants grown in long-term spaceflight

Spaceflight environment have been shown to generate reactive oxygen species (ROS) and induce oxidative stress in plants, but little is known about the gene expression of the ROS gene network in plants grown in long-term spaceflight. The molecular response and adaptation to the spaceflight environment of plants harvested after 27 days of cultivation onboard the International Space Station (ISS) have been measured using genome-wide mRNA expression analysis.



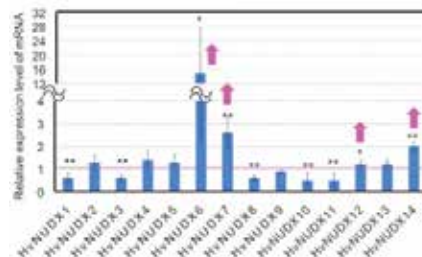
Crop grown in International Space Station (©NASA)



ROS network induced in plants grown in space (red arrows)

Gene expression analysis in plants exposed to UV irradiation

Plants should be necessary to self-supply foods when astronauts would stay during long-term space travel and habitation on the Moon and Mars. Though the sunlight is the most importance to plants, UV presenting the sunlight can damage many aspects of plant processes at the physiological and DNA level. Especially UV-C, which is eliminated by the stratospheric ozone layer, is suspected to be extremely harmful and give a deadly injury to plants in space. The molecular response to UV irradiation of plants have been analyzed.



Expression level of genes in plants exposed to UV-C irradiation

Assoc. Prof.
SUGIMOTO Manabu

