Genomic and Transcriptomic Analysis of Deinococcus aerius after exposure on the ISS Exposed Facility

Özgen Natalie*[1], Emanuel Ott[1], Yuko Kawaguchi[2], Denise Kölbl[1], Wolfram Weckwerth[3,4], Akihiko Yamagichi[5], and Tetyana Milojevic†[1]

[1]Department of Biophysical Chemistry, University of Vienna – Austria
[2]Planetary Exploration Research Center (PERC), Chiba Institute of Technology (CIT)E, Chiba, Japan – Japan
[3]Department of Ecogenomics and Systems Biology, University of Vienna, Vienna, Austria – Austria
[4]Vienna Metabolomics Center (VIME), University of Vienna – Austria
[5]Tokyo Institute of Technology, Department of Life Science, Nagatsuta, Yokohama, Japan – Japan

Abstract

The members of the genus *Deinococcus* are polyextremophile and gram-positive bacteria that can withstand the harsh conditions of the outer space environment. Air-born member of the genus, *Deinococcus aerius,* isolated from the stratosphere above Japan, exhibits strong resistance to desiccation, UV-C, and gamma radiation. In the course of the Tanpopo orbital mission to explore the possibility of interplanetary transfer of life, dehydrated cells of *D. aerius* were exposed to Low Earth Orbit (LEO) conditions outside the International Space Station (ISS) to assess their viability. To deepen our understanding of the molecular mechanisms underlying *D. aerius* effective protection against environmental stress factors at LEO we employed a transcriptomic approach. For our transcriptomic analysis we used cells that were placed on the ISS Exposed Facility for 3 years and respective ground control cells. In order to investigate cellular integrity after long-term LEO exposure, the surface of dehydrated clustered cell layers of *D. aerius* deposited on aluminum plates was examined with scanning electron microscopy (SEM). Dehydrated LEO-returned cells of *D. aerius* were recovered in complex medium and harvested after 5 hours and 15 hours to capture molecular alterations after the ISS exposure. We extracted RNA from harvested exposed and ground control cells. Followed by rRNA depletion, the extracted RNA was sequenced via Illumina sequencing. To enable application of –omics approaches, the genome of *D. aerius* was *de novo* assembled employing the software Trinity. The annotation of *D. aerius* coding sequences was performed using the rapid prokaryotic genome annotation software tool Prokka. Overall, combining the analysis on protein and metabolite levels with gene expression alterations, we strive to identify molecular key players in the stress response of *D. aerius*, thus elucidating the mechanisms behind the extraordinary regenerative abilities of this organism.

*Speaker
†Corresponding author: