

IAF/IAA SPACE LIFE SCIENCES SYMPOSIUM (A1)
Biology in Space (8)

Author: Dr. Yao Mu
China, ymhtgcu2020@126.com

COMPARATIVE GENOMICS ANALYSES OF SPACE MICROBES

Abstract

Space microbes are a major safety issue for long-term manned spaceflight, which seriously threatens the life and health of astronauts and the long-term safe operation of spacecraft. The microbiological risks of space shuttles mainly come from humans (astronauts and ground assembly workers), food, water, Air, equipment and structural surfaces may even come from the mounted animals and plants. The study of microbes is of great significance for human well-being and future space manned missions, and the evolution and adaptability of microbes is essential for studying the physiological requirements of space survival. We obtained genomic data of *Bacillus subtilis*, *Deinococcus geothermalis*, and *Deinococcus radiodurans* bacteria in different flight cultures, simulate extreme environment cultures and ground control cultures. *B. subtilis* strain 168 flew with BRIC-21 and BRIC-23 respectively, and after comparative-genome analyses of flight cultures with the ground control cultures, we find some genes were rearranged and inverted, which provided relevant knowledge for the evolutionary trend of Gram-positive bacteria running in orbit for a long time. *D. geothermalis* and *D. radiodurans* are typical highly radiation-resistant bacteria. After a comparative-genome analyses of simulate extreme environment cultures with the ground control cultures, we find that the genes in their genomes have also been rearranged and inverted. Some functional genes seem to be affected, and these effects will be further verified in the future. The gene rearrangement and inversion of these two strains are not as obvious as *B. subtilis*. It is speculated that because of their tolerance to high radiation, and their DNA repair system is more effective. Scientists tend to study changes in transcriptomics of microorganisms during long-term flight, but the transcriptome results were easily affected by experiments, like utilizing different hardware, media, incubation times, and transcript measurement technologies. In contrast, although comparative genomics is often overlooked, the results are relatively stable and can well reflect the long-term changes of orbiting microorganisms, and have great reference value in the study of the evolution and adaptation of orbiting microorganisms.