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# COSPAR 2018

42ND ASSEMBLY | 60TH ANNIVERSARY

## Scientific Assembly Abstracts

July 14 – 22, 2018 Pasadena, California, USA



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### **F3.1-0011-18 THE BIOMEX EXPERIMENT ON-BOARD THE INTERNATIONAL SPACE STATION: BIOMOLECULAR AND BIO-GEOCHEMICAL CHANGES OF LICHENS EXPOSED TO SPACE AND TO MARS-LIKE CONDITIONS**

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Exploration of the solar system is a priority research area of the AstRoMap European Astrobiology Roadmap (Horneck et al., 2015) [1], focusing on several research topics, such as "Life and Habitability" and another one is "Biomarkers for easy detection of life". Therefore, "space platforms and laboratories", as the EXPOSE setup installed outside the ISS, are essential to gain more knowledge of space and planetary environments, which might be an essential basis for improvement of the robotic and human interplanetary exploration (Space, Moon, Mars, Enceladus, Titan, Europa). At the exposure platform EXPOSE-R2 on the ISS (2014-2016), samples of the astrobiological model lichen *Circinaria gyrosa* [3,4,5,6], a species which was exposed 18 months to space and simulated Mars-like conditions during the BIOMEX experiment

[2] (Biology and Mars Experiment, ESA), was investigated, to study Mars' habitability and resistance to space conditions. The data obtained by this biomarker-study after being exposed to Mars-like conditions will support the analysis of data obtained during future instrumental detection operations in future space missions on Mars (i.e. ExoMars or Mars 2020). After the return of the samples in June 2016, the first preliminary analysis showed a quick and complete recovery of metabolic activity of the control samples exposed to space vacuum and Mars-like atmosphere. In contrast, the samples directly exposed to solar UV radiation showed slow recovery, in reference to their observed original activity. Recent

results will be presented that show biomolecular changes of the DNA analysed by PCR-based [7, 8] and complementary sequencing techniques, in correlation with the previous results showing changes in metabolic activity and changes in viability (Electron and fluorescence microscopy techniques), as well as in morphology/ultrastructure - a potential effect due to space vacuum and Mars atmosphere. In addition, the biogeochemical variations have been examined with spectroscopic analyses (Raman) to look for possible degradation of cell surfaces and pigments which were in contact with terrestrial rocks, and Martian analogue regolith. Moreover, differences were observed between samples irradiated directly with solar UV radiation and samples positioned in the shielded area as dark control. These experiments will contribute to answer questions of the habitability of Mars, on the likelihood of the Lithopanspermia Hypothesis, on the capability to detect biomolecules by life-detection instruments exposed to an extraterrestrial environment and will be of relevance for planetary protection issues.

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### **F3.1-0012-18 GENE EXPRESSION MEASUREMENT MODULE (GEMM)- THE DOOR TO HIGH-THROUGHPUT IN-SITU ANALYSES OF BIOLOGICAL SYSTEMS**

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A central, long-standing goal of the astrobiology program that holds promise for both major scientific discoveries and exciting the general public is to understand life in outer space and on other celestial bodies. One strategy towards achieving this goal is to determine the potential for terrestrial microbial life to adapt and evolve in space environments. Identifying the limits of terrestrial life in space and the accompanying molecular adaptations is a prerequisite for developing predictions and hypotheses about life on other worlds. The ability of microorganisms to survive in a wide range of conditions encountered in space would support the hypothesis that terrestrial life might not be a local planetary phenomenon, but instead could expand its evolutionary trajectory beyond its planet of origin. This would, in turn, support the notion that terrestrial life may not be unique and similar life forms might exist elsewhere in the Universe. In order to facilitate studies on the impact of the space environment on biological systems, we have developed GEMM (Gene Expression Measurement Module) - an automated, miniaturized, integrated fluidic system for in-situ measurements of gene expressions in bacterial samples. The project has been funded through the ASTID program. The GEMM instrument is capable of (1) lysing bacterial cell walls, (2) extracting and purifying RNA released from cells, (3) hybridizing it to probes attached to a microarray and (4) providing electrochemical readout, all in a microfluidics cartridge. Its first application on a nanosatellite platform is to cultivate and measure gene expression of the photosynthetic bacterium *Synechococcus elongatus*, a cyanobacterium known for its metabolic diversity and resilience to adverse conditions, under light and dark cycles exposed to polar orbit for a period of 6 months. The integration and end-to-end technology validation of this instrument will be discussed. In particular, results demonstrating that the instrument properly measures gene expression after cellular lysis, nucleic acid extraction, its purification, and hybridization to an electrochemical array will be presented and compared to commercial microarray