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GENOTYPING, PHYLOGENY, AND GENE EXPRESSION MEASUREMENT MODULE - THE DOOR TO HIGH-THROUGHPUT IN-SITU ANALYSES OF CLINICAL AND BIOLOGICAL SAMPLES IN SPACE.

Abstract

To date, limited high-throughput *in-situ* analyses of astronaut's samples and biological material from experiments carried out on the ISS could be performed without returning samples to Earth. In order to eliminate this drawback and create working conditions resembling those in a terrestrial setting, preserve sample integrity, increase efficiency, decrease costs and reduce requirements for down-mass, we propose to develop the Genotyping, Phylogeny, and Gene Expression Measurement Module (GEMM) - an automated, miniaturized, integrated fluidic system for *in-situ* measurements of mutation discovery and genotyping of biological samples (human included), microbial composition and diversity in human and environmental samples, and gene expressions in bacterial and tissue samples. The instrument is based on the GEMM that has been developed for deployment on nanosatellites. The integration and end-to-end technology validation of the latter instrument will be discussed.

The ISS version of the GEMM, the size of which is approximately 12x12x7 inches, will be capable of (1) lysing cell walls, (2) extracting and purifying nucleic acids released from cells, (3) hybridizing it on a microarray and (4) providing readout of hybridization signal. The new module will consist of a self-contained, disposable microfluidic cartridge and a companion, processing instrument that automatically controls all the processes on the cartridge and scans the resulting hybridized array. The key aspects of the instrument are its versatility, simplicity of use and modest costs of experiments.

Measurements of single nucleotide polymorphism (SNP), genotyping, and quantitative determination of allele frequencies in mixed samples will help us to understand the influence of the space environment on mutation rate and genomic instability in clinical and biological samples. Similarly, metagenomic analysis of astronaut's and ISS microbiomes will help us to adequately monitor the stressful influence of spaceflight mission on gut bacteria and minimize the threat from opportunistic contaminants from the ISS environment (surface, water and air). Finally, gene expression will assist in understanding acclimation and adaptation of terrestrial life to conditions beyond the planet of origin, identify deleterious effects of the space environment on a wide range of organisms, develop effective countermeasures against these effects, determine metabolic basis of microbial pathogenicity and drug resistance, test our ability to sustain and grow organisms in space that can be used for life support and *in-situ* resource utilization during long-duration space exploration, and monitor both the spacecraft environment and crew health. These and other applications hold significant potential for discoveries in space biology, biotechnology and medicine.