

NASA GeneLab Computomics Reveal Horizontal Gene Transfer on International Space Station Environmental Metagenomes

Nicholas Bense¹, Nitin Singh², Mike Lee³, Afshin Beheshti⁴, Egle Cekanaviciute⁵, Sylvain Costes,⁶ Jonathan M. Galazka⁶, Kasthuri Venkateswaran²

¹Blue Marble Space; ²Jet Propulsion Laboratory; ³Bay Area Environmental Research Institute; ⁴Wyle Laboratories; ⁵Universities Space Research Association; ⁶NASA Ames Research Center

Prokaryotic lifeforms can be observed to demonstrate many keen adaptive advantages, perhaps facilitated by a nature simplistic relative to divergent domains of life. In particular, de-compartmentalized gene expression facilitates adaptation by allowing free exchange of genetic material, albeit at the cost of increased susceptibility to genetic damage. Thus, these lifeforms must compensate by embracing diverse investment strategies in an attempt to “brute force” the evolvability equation through precipitous genesis, lean metabolic efficiency, and sheer population. This prokaryotic archetype also enables symbiotic relationships with secondary mobile genetic elements known as plasmids, which have been shown to drive evolution on rapid temporal scales through processes such as conjugation and transformation. This study attempts to decipher whether these mechanisms of horizontal gene transfer (HGT) are major factors in determining prokaryote fitness within a unique isolated environment, the International Space Station (ISS). The ISS Microbial Tracking (MT) project has generated a wealth of data concerning the successive reigns of microbial genera that appear to thrive amidst harsh conditions for life. Despite relatively higher doses of ionizing radiation as compared to Earth, complications associated with microgravity, and the anti-microbial mélange deployed, microbial life still persists in this environment. The NASA GeneLab serves as a data repository and analysis platform to enable researchers to access space flight factor related data. With the use of GeneLab’s modern computational suites (computomics), phylogenetic and functional genomic investigations of HGT events were conducted on the data generated from the MT-1 project. The putative data concerning the plasmid population (plasmidome) of the ISS was algorithmically derived and compared to those of habitats with similar environmental dynamics- such as living quarters and hospitals- to investigate whether these HGT elements may play crucial role(s) in shaping the microbiome of this closed habitat that serves as the only inhabited structure in space.