Isolation and Characterization of Bacterial Communities in the Clean Room Environment of NASA’s Jet Propulsion Laboratory-Spacecraft Assembly Facility in Pasadena, CA

Timothy Eberl
Faculty: Mark Schneegurt
Department of Biological Sciences, Fairmount College of Liberal Arts and Sciences

NASA’s Jet Propulsion Laboratory-Spacecraft Assembly Facility (JPL-SAF) in Pasadena, California is known for its work in the assembly of spacecraft capable of traversing the harsh environments on extra planetary bodies, like Mars. Facilities like JPL-SAF, which use “clean rooms” to assemble these craft, are concerned with the presence of microbial populations in these environments and in the assessment of risk microorganisms may pose in the contamination of equipment during assembly. Because of the supposed lack of organics for use as microbial nutrition, these clean room environments are typically considered to be “extreme” conditions for microbial growth. In recent years, research has shown that species of both archaea and bacteria can be isolated from samples taken from various clean rooms currently in use in the fields of medicine, manufacturing, and chemistry. Understanding the microbial communities that live in these environments may shed some light on methods for control and the prevention of contamination.

Multiple samplings collected from various distinct locations inside and outside the JPL-SAF location in Pasadena, CA were cultivated, morphologically studied, and subjected to various biochemical and phenetic tests to assess their ability to survive in these clean room environments. Special attention was paid to subjecting isolates to halophilic tolerance tests, due to the relatively high percentages of salt that is thought to exist on the surface of extra planetary bodies NASA is interested in sending craft to study, particularly Mars. These salts include magnesium sulfate, sodium chloride, and perchlorates, which have been found in differing concentrations in Martian soils. Fresh DNA was extracted from the bacterial isolates and 16S rRNA genes were amplified using universal bacterial primers. Sequences were then screened, aligned, and phylogenetic trees were generated using parsimony analysis. Growth of bacteria in clean rooms, particularly those involved in spacecraft assembly, has implications with regards to the possible forward contamination of extra-planetary bodies during exploration.