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MICROBIOLOGICAL GENETIC INVENTORY WITHIN THE NASA AMES RESEARCH CENTER  
HIGH BAY CLEANROOM

**Abstract**

Space exploration goals over the coming decades place a high priority on the search for life in the universe, and space agencies have set in place ambitious endeavors to investigate environments relevant to possible past, or even present life on Mars. A broad diversity of microorganisms have been detected in cleanrooms where spacecraft are assembled, and these contaminants can be broadly divided into two different types, those that are human commensals and/or pathogens, and those that simply thrive in the harsh cleanroom environment. The latter, depicted as oligotrophs, are of special concern, as they are capable of colonizing inorganic surfaces like metal, and have been shown to be a concern for forward contamination of other planets, and by complicating testing for extraterrestrial life forms. Subsequently, information on microbial diversity is essential for making data-based decisions about the implementation of bioburden reduction measures and interpretation of life detection experiments. Comprehensive, DNA sequence based surveys of spacecraft assembly, integration, and test (AIT) facilities are needed to identify all microorganisms present; as has been suggested by the National Research Council. The NASA Ames Research Center High Bay Clean Area (HBCA) and Clean Room (HBCR) certification to ISO class 8 and 7, respectively, has recently been performed prior to the arrival of the Lunar Atmosphere and Dust Environment Explorer (LADEE) spacecraft for final assembly. This provided a unique opportunity to assess the total bioburden and perform a genetic microbiological inventory of the HBCA prior to (where limited maintenance has been performed), and after its certification. In order to assess the changes induced by the cleaning and recertification of the HBCA on microbial diversity, samples were collected and analyzed by hybridizing target sequences to a universal 16S rRNA gene microarray (Phylochip) that provides a rapid and comprehensive view of prokaryotic community composition. Preliminary results comparing the genetic profile of the clean room pre- and post-certification will be discussed. To our knowledge, this will be the first such study. This assessment will be extremely valuable in our understanding of how the environment and cleaning procedures impact microbial diversity in NASA spacecraft AIT facilities. Supported by the NASA Planetary Protection and the Exobiology Programs.