**Introduction:** Research on molecular evolution of microbes can help us better understand microevolutionary changes, even in humans, since we share a common molecular origin with them [1-14]. Bacteria and fungi are documented to thrive in manned space stations, some of which are closely related to pathogenic forms. The accurate identification, sound classification, and better understanding of the pattern of molecular change in microbial genome are important in the management and control in enclosed environments such as the International Space Station. Moreover, they can provide clues to mutational patterns in the human genome under extra-terrestrial conditions.

**Discussion:** Microbial colonization of NASA equipment in space poses risks to both man and machine. Prior to decommissioning in 2001, the Russian space station Mir was reported to have been ‘eaten alive’ with plastics, metal, and quartz glass windows deteriorating from fungal and bacterial growths. [15-17]. Due to the potential health risks to astronauts and long-term damage to space stations, the understanding of molecular and genomic changes that can happen in space are important. Microbial life have been documented to have relatively faster rates of mutation due to ionizing radiation. Organisms around Chernobyl power plant were found to have mitochondrial, nuclear and chromosomal mutations hundreds of times greater than normal [18-20].

In order to better understand the diversity of microorganisms, we are evaluating genes to serve as unambiguous markers of identity. Fungi are especially challenging. Recent estimates of fungal diversity suggest that known and described species represent less than 5% of the actual number of distinct taxa on Earth [21-23]. Thus, molecular approaches that could identify operational taxonomic units with high fidelity, and provide information to patterns of molecular change are imperative for environmental management of microorganisms on Earth as well as in space.

Our current studies involve 1) the assessment of various mitochondrial and nuclear genes, such as cytochrome oxidase 1 (cox1) and ITS genes, as DNA barcode to accurately identify fungal taxa and track the phylogeographic origins of fungal communities, and 2) estimating the rates and patterns of molecular differences within and among *Aspergillus* and other fungi to test the validity and stability of fungal taxonomy.

For our initial analyses, alignments were done using GeneiousAlign program within Geneious Pro (Biomatters, Ltd., New Zealand). We are also currently augmenting our dataset with reliable data from GenBank. Figure 1 shows a preliminary analysis of COI sequences obtained from GenBank. Final alignments were exported in nexus file format. Using PAUP*4b10 [24] we conducted phylogenetic analyses using Maximum Parsimony (MP), distance method using Neighbor-Joining, and Maximum Likelihood (ML). Additionally, Bayesian analysis were done using the MrBayes program [25].

Support for nodes were estimated using nonparametric bootstrap [26] and were done for MP, distance and ML analyses with 500 fast-addition replicates (200 for ML due to time constraints). The MP analysis was conducted using the heuristic search option. To determine the best-fit model of molecular evolution we used ModelTest program using the Akaike Information [27].

**Figure 1:** Preliminary maximum likelihood analysis of cytochrome oxidase 1 sequence.

**Concluding Remarks:** Our preliminary analysis suggested the following observations. 1) The conflict
The use of single locus marker such as COI, for identification, diagnosis and design of probes for DNA chips may be limited as it may reflect the evolution of the gene, rather than the evolution of the organism. We are currently looking at the comparative performance of various genes such as elongation factor 1-alpha, beta-tubulin, ITS, and other single-copy nuclear genes for identification and barcoding of microorganisms.