

PHYLOGENETIC ANALYSIS OF ASPERGILLUS AND OTHER RELATED FUNGI BASED ON MITOCHONDRIAL CYTOCHROME OXIDASE 1 Shaunte Abdin¹, O. Jejelowo² and H. C. Miranda, Jr³, ¹Texas Southern University NASA URC Center for Bionanotechnology and Environmental Research, Houston TX 77004, huletsn@tsu.edu, jejelowo_oa@tsu.edu, mirandahc@tsu.edu,

Introduction: Microorganisms are hypothesized to endure reasonably rapid rates of mutation in space due to microgravity and ionizing radiation. As an initial effort to test the relative rates to which certain genes evolve under space-like conditions, we reviewed the usefulness and reliability of mitochondrial cytochrome oxidase 1 (COI) gene in resolving the evolutionary relationships within *Aspergillus* and related fungi. The objectives of this study were 1) to characterize the mitochondrial COI gene of *Aspergillus* and related fungi, 2) conduct phylogenetic analysis using parsimony, distance methods, maximum likelihood, and Bayesian statistics.

Most recently, the 600 bp region of the 5' end of the COI gene was proposed to be the ideal marker for barcoding eukaryotes. However, several investigators have suggested potential problems associated with the use of COI gene as a universal marker for fungi. The universality of the gene is also questioned by reports of the prevalence of mobile introns across many fungal groups. However, the pervasiveness and pattern of occurrence of this observation have yet to be investigated thoroughly.

We are sequencing at least 10 species from ATCC, plus unknown cultures obtained from environmental samples. For the analyses, alignments were done using Geneious Pro (Biomatters, Ltd., New Zealand). Final alignments were exported in nexus file format. Using PAUP*4b10 [1], we conducted phylogenetic analyses thru Maximum Parsimony (MP), distance method using Neighbor-Joining, Maximum Likelihood (ML) and Bayesian statistics using the MrBayes program [2]

Support for nodes were estimated using nonparametric bootstrap [3] and were done for MP, distance and ML analyses. To determine the best-fit model of molecular evolution we used ModelTest program using the Akaike Information [4].

Concluding Remarks: Our preliminary analysis suggested the following observations. 1) The conflict in the utility of COI as barcoding marker reflects the lack of taxonomic stability within Fungi at the intra- and inter- species level. There is a need to expand geographic sampling of taxon to further test the validity of current classification. 2) No intron was observed within the short barcode region (600 bp) among the samples we investigated.

References: [1] Swofford, D. (1999) PAUP 4.0. Sinauer Associates, Sunderland, MA. [2] Huelsenbeck, J. P. and F. Ronquist. (2001) *Bioinformatics* 17, 754-755 [3] Felsenstein, J. (1985) *Evolution* 39, 783-791. [4] Posada, D., and K. A. Kranda. (1998) *Bioinformatics* 14, 817-818.