MOLECULAR IDENTIFICATION AND PHYLOGENETIC SYSTEMATICS OF ASPERGILLUS AND RELATED FUNGI BASED ON ITS AND EF1-ALPHA GENES Tiarra Spencer[1], O. Jejelowo[2] and H. C. Miranda, Jr[3], [1]Texas Southern University NASA URC Center for Bionanotechnology and Environmental Research, Houston TX 77004, spencer2@prodigy.net, jejelowo_oa@tsu.edu, mirandahc@tsu.edu,

Introduction: Barcoding genes, or molecular markers, are those segments of DNA that have unique characteristics which can be used in the identification processes of organisms. The criteria for a good barcode for identification is that the gene must be conservative, have differences between species, and have few or no copies of the gene. There have been major difficulties in obtaining a reliable barcode for fungi. This difficulty has been mostly due to the natural inhibitors of the fungal genome that hinder the process of polymerase chain reaction (PCR) and DNA sequencing. However, internal transcribed spacer (ITS) gene has been recently proposed as a barcode in fungal species identification. However, using a single gene for barcoding and phylogenetics has pitfalls due to presence of unrecognized multiple copies, or differential substitution rates across the clade. As a result of this, the search has continued on finding a more reliable set of genes for barcoding. We are currently evaluating the rates and patterns of substitution, as well as the phylogenetics of Aspergillus using ITS, and compare with other genes such as cytochrome oxidase 1 or COI (in conjunction with the work of Shaunte Hulett), and elongation factor 1 alpha (EF1-alpha). We obtained multiple samples of known species from ATCC, extracted DNA from each species, performed amplification of DNA by using PCR, purification of DNA, DNA sequencing, and DNA analysis using various optimality criteria.

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 using Maximum Parsimony (MP), distance method using Neighbor-Joining, and Maximum Likelihood (ML). Additionally, Bayesian analysis were done 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].

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