Phylogenetic and Evolutionary Patterns of the P53 Gene in Mammals

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P53 is an important tumor suppressor protein, that when mutated will lead to much higher cancer rate. This project constructed a phylogenetic tree using the mRNA sequences for p53 gene in 20 mammals and performed evolutionary pattern analysis. This study is a preliminary step in the identification of potential mechanisms to target in therapeutic cancer investigations. mRNA sequences used in this project were collected from National Center for Biotechnology Information (NCBI) Gene Bank. MEGA 7.0.26 was used to construct the tree and perform the statistical analysis. The phylogenetic tree of the genes constructed in this project generally resembles the species tree, but there are some differences in a primate branch and a rodent branch, suggesting a special evolutionary pattern. Data analysis was aimed to find evolutionary patterns at molecular levels. Types of selection on every site were detected by comparing the synonymous mutations and nonsynonymous mutations. Most of the sites (n = 88%) undergo purifying selection. The rate of evolutionary change of amino acids of the branches was calculated and analyzed for the two branches selected, and each was found to have a constant evolutionary rate different from each other. The combination of methodologies used in this research may be able to apply to preliminary research of other genes. The long-term goal of the study is to find the relationship between evolutionary patterns and the functions, as well as the importance of certain series of sequences or amino acids, which may serve for future therapeutic cancer investigations.

Awards Won:

University of Arizona: Tuition Scholarship Award