## Undergraduate

Science, Biology



Since the early 1980's, evolutionary pathway determination techniques have been used to investigate on different species and the factors that cause changes in their gene structures. The sex determination techniques used have been seen to be of importance in the development of molecular genetics (Haag & Doty, 3). However, though the research was well vested in the pathway determination genes, most of the sex determination genes are found to be conserved in the pathway determination that is specifically for mammals. Sex determination is referred to through either of the categories; the GSD sex determination and the ESD sex determination. While looking at evolution of mammals, keen focus will be set on the GSD, (Genetic Sex Determination). The purpose of this research is to dig deeper into the behavior of the conserved sex determination genes in mammals. By investigating on this, findings could be used to develop an evolution pathway. This way, analysis on patterns of the mammal and birds gene development can be determined. I have decided to use an approach that investigates every sex-determination gene in the different species.

Comparisons and behavior relations are observed to determine where each gene differs from each other (Haag & Doty, 3).

The project will first proceed by gene collection. Types of the collected genes will go further into the different sex determination genes. For instance, while studying the genes involved in the sex determination process, the somatics will be studied different from the germ-line, focusing on the behavior of each under its classification. Study of these genes will be conducted for mammals and birds and chosen vertebrates of interest.

For the vertebrates, the master genes for the sex determinants must be

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identified. In most of the mammals these genes are indicated in the Ychromosomes. Alongside this, the NM accession number is to be determined and the knowledge of the longest transcript. This way a sex determining loci can be observed. A complete nucleotide has significant impact on the study of evolutionary impact of sequential pathways. DNA sequences tend to have information about the background of a certain species' gene. Study on the rate of variations in genomes and relation to environment and population helps to draw a conclusion on the relation between the gene sequences and their evolution.

So as to effectively analyze the sequence alignments for quality control, analysis of the palms would be conducted. This type of analysis enables one to determine the protein sequences by modes of likeliness. After the study, molecular data of the gene sex determinants will be readily available and could be used in sex chromosomes selection mechanisms.

The research will thus look at the relational stages of the mammal genes, study various DNA sequence structures, behavior of genes in various environments and the interactions of genes with certain populations. This study will help to develop a flow of the evolution curve, thus identifying the decision pathway for sex determination chromosomes in mammals. This research will require a total budget of \$2500, where the individual studies will be waged a minimum of \$10 per hour, with a consistent working rate of 12 hours per week. The budget and period should be adequate to reach the results described in the proposal.

Works Cited

Haag, and Doty, " Sex Determination across Evolution: Connecting the Dots," PLoS Biol Journal. 3(1). January 18, 2005.