**Introduction**

“The family Cervidae includes 40 species of deer distributed throughout the northern hemisphere, as well as in South America and Southeast Asia” (Gilbert, 2006). Based on the results of analyzing mitochondrial genes and two nuclear introns the family Cervidae is divided into two subfamilies and many tribes (Gilbert, 2006). The two subfamilies are Cervinae and Capreolinae, both of which were included in our study. Because this family is so wide spread across the globe, it provides an opportunity to discover interesting relationships between their phylogeny and environment. We chose to identify whether coat color is an autapomorphic trait or a synapomorphic trait.

**Methods**

Research analysis began with 21 complete mitochondrial DNA leaving us to search for at least 4 more individual species with two separate gene sequences. By using NCBI and searching for roughly 9 more species, we found sequences for the SRY gene along with the complete mitochondrial genome. We attempted to create a phylogenetic tree by using phylogeny.fr. With no success we continued on to PhyML, and T-Rex, all of which said that the complete mitochondrial DNA was too large. We then searched each species for the individual sequences of the SRY gene and the NADH Dehydrogenase gene. We were then successful in creating one tree but was having difficulty creating a second to combine the two. Come to find out that the sequences for the NADH Dehydrogenase gene also included 2+ other genes, the majority of which were the d-loop sequence, so alignment for the second tree was impossible. After attempting to BLAST the d-loop sequences from the rest of the individual species, searching NCBI specifically for the gene, and searching for other genes that would give us 25 individuals, we were unable to complete the required amount of sequences for the second gene. We completed the project with our first tree that gave us promising results.

![Phylogenetic tree](image)

**Results**

According to the tree that is represented by the SRY gene, it is apparent that there is no pattern when it comes to the coat color of the Cervidae family. This implies that coat color is an autapomorphic trait among the Cervidae family. The coat colors are distributed throughout the tree and it doesn’t appear that they all started as one particular color and branched from there. Mismatches are found among each monophyletic group which either indicates many distinct mutations in the genotype of many individuals, which isn’t likely, or their isn’t enough information given solely by the SRY gene sequence. It is also apparent that due to the large comb of individuals in the middle of the tree, there is not enough information that is different among these individuals to set them apart. This is possibly due to the fact that each gene sequence was either the same or indistinguishably similar. Now, if we were to have completed a second tree with a second gene sequence and combined the two of them, it would most likely have resulted in a more clear result as to exactly where these species are located on the tree, giving us more information on which to base our final conclusion.

**References**

- *FigTree*, tree.bio.ed.ac.uk/software/figtree/.