# Evolutionary Relationships of Hammerhead sharks (Sphyrnidae): Reconciling signals across anatomical and molecular data

In the current study we reassessed the conflicting hypotheses that have been forwarded to account for the evolution of hammerhead sharks. First, skeletal anatomical features of seven species of hammerhead sharks (Sphyrnidae) and two species of requiem shark (Carcharhinidae) were used to estimate a phylogenetic hypothesis for the group. Specimens were CT scanned and segmented to create virtual 3-D models of the sharks. A character matrix was derived from the segmented CT scans and subjected to phylogenetic analysis. The phylogenies created using the anatomical data gathered from the CT scans were consistent with the former phylogeny derived from anatomical data. They showed that the hammerhead shark most closely related to the outgroup sharks from the Carcharhinidae family was *Sphyrna tiburo*, the “bonnethead” shark, which has one of the least developed cephalofoils among all of the hammerhead family. The data suggests that cephalofoil size has increased over the course of evolution and may confer some evolutionary advantage. However, an analysis of both nuclear and mitochondrial DNA sequence data using a newly developed cross species gene capture approach was conducted and yielded a tree that was concordant with previous hypotheses based on molecular data, but strongly discordant with the tree created based on the anatomical data. We attempted to reconcile these two conflicting hypotheses and pinpoint the causes underlying the conflict between the analyses. Initial indications suggest that the way the trees are rooted may account for the apparent conflict.