Title

Comparison of Nucleotide Diversity Across Five Different Species of Sea Ducks

<u>Authors</u>

Melanie Sosa¹, Philip Lavretsky², Jonathon Mohl^{1,3,4,5}
¹Bioinformatics Master Program, ²Biological Science, ³Computational Science Program, ⁴Department of Mathematical Sciences, ⁵Border Biomedical Research Center The University of Texas at El Paso, El Paso, TX

Abstract

The goal of this study is to analyze genetic variation and differentiation among five species of sea ducks: Long-tailed Duck (LTDU), Spectacled Eider (SPEI), Steller's Eider (STEI), Common Eider (COE), and King Eider (KIEI). Using a combination of nanopore long-read and Illumina short-read sequencing data, we assembled the genomes and evaluated them using QUAST. Python and R were used for data processing and statistical analysis, with the assemblies compared against reference genome, LTDU, to evaluate genetic diversity across the species. In short, the top 100 scaffolds were analyzed to calculate Fixation Index (FST) metrics and other nucleotide diversity metrics which were then used to assess genetic diversity and evolutionary relationships. Our analysis revealed close evolutionary relationships between KIEI, SPEI, and COE, as indicated by their lower FST values, while LTDU and STEI exhibited higher FST values, suggesting more distinct evolutionary trajectories. These findings provide insights into the genetic structure and potential hybridization events among sea duck species. This study contributes to our understanding of evolutionary relationships within the sea duck family and provides a framework for future research on species conservation and hybridization.