Mitogenomic Assessment of *Kogia sima* (Dwarf Sperm Whale) and *Kogia breviceps* (Pygmy Sperm Whale) in the Philippines: Insights into Genetic Diversity, Population Connectivity, and Conservation

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The dwarf sperm whale (*Kogia sima*) and pygmy sperm whale (*Kogia breviceps*) are among the least studied cetacean species in the Philippines. The species have limited genetic and genomic data constraining assessments of their population structure, connectivity, and conservation. Therefore, this study aimed to generate and analyze the first complete mitochondrial genomes of the *K. sima* and *K. breviceps* from the Philippines, and to benchmark them against the global datasets to provide baseline insights into their genetic diversity, population connectivity, and conservation. To achieve this, a bioinformatics-based comparative mitogenomic approach was employed using datasets generated by the Philippine Genome Center from whole-genome sequencing of four tissue samples obtained by the Marine Mammal Research and Conservation Laboratory (MMRCL) of the Institute of Environmental Science and Meteorology (IESM), University of the Philippines Diliman (UPD). The mitochondrial genomes were assembled and annotated, followed by a comparative analysis, haplotype reconstruction, and phylogenetic inference to situate Philippine samples in a broader evolutionary context. Results showed that all four Philippine *Kogia* samples yielded complete, circularized mitochondrial genomes with high coverage and no structural errors. The assembled mitochondrial genomes also exhibited conserved gene content, organization, and base composition, which is consistent with a typical vertebrate mitochondrial architecture. Within the Philippine *Kogia* dataset, *K. sima* exhibited mitochondrial diversity, with multiple haplotypes observed, indicating the presence of more than one maternal lineage within the Philippine population. *K. breviceps*, on the other hand, was represented by a single sample, which limits local genetic diversity estimates. Phylogenetic analysis on the Philippine *Kogia* samples revealed a clear species-level separation between *K. sima* and *K. breviceps,* supported by a relatively high interspecific divergence (~9.8%) and a low intraspecific variation (~0.52%) within *K. sima*. At the global scale, comparative analysis revealed a contrasting pattern between *K. sima* and *K. breviceps*. The global datasets showed weak mitochondrial differentiation across *K. breviceps* populations, suggesting broad population connectivity or limited resolution of the mitochondrial marker used. In contrast, the global *K. sima* population exhibited stronger genetic structuring, characterized by high haplotype diversity and population differentiation (Fst = 0.62669) across ocean basins. For the Philippine population, unique and shared haplotypes were observed, highlighting preliminary evidence of local genetic variation within the Philippines and the broader Indo-Pacific context. Overall, this study establishes the first mitochondrial genomic baseline information for *Kogia sima* and *Kogia breviceps* in the Philippines, addressing a critical knowledge gap in marine mammal genetics. The findings of this study provide initial insights into the genetic diversity and population connectivity of *Kogia* populations in the Philippines and globally, with implications for conservation and management. Despite limitations in sample size and the reliance of this study on mitochondrial markers (i.e., cytochrome b and control region), this study underscores the value of integrating molecular approaches into cetacean research and offers a foundation for future population genomic and conservation studies in the region.

Keywords: *Kogia sima*, *Kogia breviceps*, Dwarf sperm whale, Pygmy sperm whale, Mitochondrial Genomics, Population connectivity