

Genetic Assessment and Phylogenomics of *Stenella* species stranded in Philippine Waters, Inferred from Mitochondrial and Whole Genome Sequences

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ABSTRACT

Marine mammal strandings represent unique opportunities for obtaining biological material from highly vagile marine organisms that are otherwise difficult to sample. In the Philippines, *Stenella* species, dolphins belonging to the Delphinidae family, are endangered species and very frequent to moderately frequent stranders, with more than 18 stranding events occurring in the country every year. *Stenella* species include the spinner dolphin (*Stenella longirostris*), striped dolphin (*S. coeruleoalba*), Pantropical spotted dolphin (*S. attenuata*), Atlantic spotted dolphin (*S. frontalis*), and Clymene dolphin (*S. clymene*). Despite frequent strandings, endangered status, and vulnerability to anthropogenic threats, studies that have used tissue samples from stranded *Stenella* dolphins for genomic research are lacking. In this study, DNA material collected from five stranded individuals consisting of three species (*S. longirostris*, *S. coeruleoalba*, *S. attenuata*) will be used to conduct mitochondrial and whole genome analyses through bioinformatic tools. Sequence data from the Philippine samples will be analyzed together with 37 publicly available genome sequences from other Pacific and Atlantic *Stenella* populations. Through this, the study aims to conduct a phylogenomic analysis of Philippine *Stenella* species, screen for introgressive hybridization or incomplete lineage sorting, and infer genetic connectivity and population structure of Philippine samples in relation to global samples. Findings from this study can serve as a baseline for genomic studies on Philippine *Stenella* species and an essential tool for formulating and implementing conservation policies that protect genetic diversity and population abundance in these vulnerable species.

Keywords: *Stenella*, mitochondrion, nuclear, phylogenomics, genetic assessment