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A Molecular Assessment of Speciation and Evolutionary History of the Globally Distributed Spotted Eagle Ray (*Aetobatus narinari*)

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The spotted eagle ray (*Aetobatus narinari*), a species of conservation concern (Near Threatened IUCN category) is commonly associated with coral reef ecosystems worldwide where it is likely to play an important predatory role. Currently described as a single, circumglobally distributed species, geographic differences in parasite diversity have led to suggestions that *A. narinari* may constitute a species complex. There has been no systematic evidence to support this suggestion, however. If multiple species of spotted eagle ray exist, each will likely possess decreased geographic ranges and population sizes, altering the impacts of threats and requiring separate assessments of conservation needs. We assessed the validity of *A. narinari* as a single cosmopolitan species using 1570bp of sequence data from two mitochondrial genes (cytochrome *b* and COI) and the nuclear ribosomal ITS2 locus. Individuals from four major geographic regions were examined: western north Atlantic, and western, central, and eastern Pacific. Phylogenies for each locus concordantly described three distinct lineages (western north Atlantic, western/central Pacific, and eastern Pacific) with no genetic exchange among regions. Genetic distances among the most divergent lineages were comparable to taxonomically uncontroversial batoid and teleost congener pairs. Using combined genealogical concordance and genetic distance results, we recommend 1) that the western/central Pacific lineage be recognized as a distinct species from the western north Atlantic and eastern Pacific lineages, and 2) the western north Atlantic and eastern Pacific lineages, separated by the Isthmus of Panama, be given subspecies status. Dramatically higher nucleotide diversity and sequence divergence coupled with a basal position in multiple phylogenetic analyses support an Indo-West Pacific origin for the *A. narinari* species complex, with subsequent migration into the Atlantic. Evolutionary relationships among lineages suggest a westerly migration around the southern tip of Africa, with intensification of the Benguela coldwater upwelling system a possible vicariant mechanism underlying speciation.