

Phylogeography of the semi-pelagic spotted eagle ray (*Aetobatus ocellatus*)

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Spotted eagle rays are large free-swimming batoids that trophically depend on the benthos. Although commonly occurring on coral reefs and associated habitats, they can undertake long pelagic migrations and are subsequently considered as semipelagic organisms (*i.e.* organisms that penetrate oceanic waters but concentrate close to continental landmasses). These life history traits, associated with the lack of clear biogeographical barriers to dispersal in marine environments, led to the long-held assumption that spotted eagle rays were comprised of well-connected population that formed a single circumtropically distributed species. However, molecular data has revealed high levels of genetic structure, possible due to their apparent dependency on coastal ecosystems. These genetic patterns have resulted in the sundering of spotted eagle rays into several allopatric species.

We herein attempt to link phylogenetic patterns with underlying ecological processes in a phylogeographic study of the Indo-Pacific spotted eagle ray (*Aetobatus ocellatus*). We firstly apply molecular species delimitation methods to sample data that we collected throughout the

Indo-Pacific therein revealing the presence of several hypothetical species units, suggesting that *A. ocellatus* is a complex that is comprised of several cryptic species. These data were then clubbed with public sequence data with high geographic coverage to recreate a time-calibrated phylogeny of the species complex. Our findings suggest that that the evolutionary history of Aetobatids is linked to shifts in biodiversity hotspots. We conclude that the migratory propensity of these semipelagic organisms is diminished by their dependency on coastal ecosystems.

Keywords

Biogeography; Phylogenetics; Species Delimitation; Conservation Genetics