Integrating Mitochondrial Genome Sequencing and Habitat Modeling to Inform Marine Protected Area Design for Deep-Sea Octocoral Conservation

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Deep-sea octocorals are critical ecosystem engineers that form biodiversity-rich habitats and support commercially and pharmaceutically valuable species, yet remain understudied and increasingly threatened by bottom trawling, deep-sea mining, and climate change. This study integrates molecular and ecological approaches to enhance octocoral conservation across the Eastern Pacific. Complete mitochondrial genomes for Leptogorgia and Paragorgia were assembled and annotated using Oxford Nanopore Technologies (ONT), expanding the Octocorallia mitogenome repository and demonstrating ONT's viability for genomic monitoring of non-model taxa. Phylogenetic analyses of 25 mitogenomes improved taxonomic resolution and revealed gene order variation consistent with family-level relationships. Population genetic analyses (FST, AMOVA, PCA) indicated minimal mitochondrial divergence between Hawaiian and Californian populations (FST = 0.0092), suggesting high connectivity and low spatial structuring. Habitat suitability modeling via MaxEnt (AUC = 0.98) identified bathymetry as the dominant predictor and revealed gaps in protection for moderate-suitability habitats (suitability = 0.5–0.7), many overlapping with areas targeted for seabed mining. These findings inform candidate areas for Marine Protected Area (MPA) expansion and underscore the importance of integrating genetic connectivity, modeling, and spatial planning in deep-sea conservation. This study contributes new genomic resources, sequencing benchmarks, and validates mitogenomic gene order as a diagnostic tool for resolving taxonomic uncertainty. Coupling genetic and habitat modeling, this research offers a scalable framework for identifying conservation corridors and expanding MPA coverage in data-limited deep-sea ecosystems.

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