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# DNA Barcoding Confirms the First Record of the Coral *Pocillopora acuta* in Sri Lankan Reefs, which was Previously Misidentified as *P. damicornis*

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## Abstract

Accurate species delineation is essential for effective coral reef management and conservation. However, phenotypic plasticity and introgressive hybridization in scleractinian corals, particularly in morphologically variable genera like *Pocillopora*, often obscure species boundaries. As a result, morphological taxonomy alone is insufficient, underscoring the need for molecular approaches. This study aimed to verify the taxonomic identity of *P. damicornis*-like corals in Sri Lanka using the mitochondrial open reading frame (mtORF) as a molecular marker. Coral fragments (1-2 cm) were collected from 11 sites along northwest, west, south, east and northeast coasts in 2023, maintaining a minimum distance of 5 m between mature colonies to minimise the risk of clonal sampling. A total of 423 samples were successfully amplified and sequenced. Preliminary BLAST searches against GenBank produced ambiguous matches to both *P. damicornis* and *P. acuta*. To resolve this, phylogenetic relationships were inferred using maximum parsimony based on a 590 bp alignment of 118 unique haplotypes, together with reference sequences from GenBank of different *Pocillopora* species verified by skeletal data. Bootstrap statistics were conducted based on 1,000 replicates. In addition, a median-joining haplotype network was constructed to visualise genetic relationships among haplotypes and to complement the tree-based results. In the phylogenetic analysis, none of the Sri Lankan samples clustered with the *P. damicornis* clade, which had a bootstrap support of 97%. Two haplotypes grouped with the *P. verrucosa/P. bairdi* clade, while six haplotypes formed a more divergent subclade closely related to that group. Two additional haplotypes did not cluster with any recognised *Pocillopora* lineage. The remaining 108 haplotypes could be assigned to *P. acuta*, marking the first confirmed record of this species in Sri Lanka. The haplotype network showed consistent results: two haplotypes grouped with the *P. verrucosa/P. bairdi* haplogroup, six were more divergent but still associated with that haplogroup, and the remaining 110 haplotypes grouped with *P. acuta*. This difference illustrates how tree-based and network-based approaches combined can help to resolve ambiguous species identification. Overall, these results indicate that *P. acuta* is the dominant *P. damicornis*-like lineage present in Sri Lanka, while *P. damicornis* itself was not detected. These findings highlight the value of incorporating molecular data for accurate coral taxonomy, which is essential for clarifying species boundaries, understanding their ecology, and informing effective conservation strategies in Sri Lanka.

**Keywords:** *Conservation genetics, Coral biodiversity, Cryptic species, Molecular taxonomy, Phylogenetic analysis*