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Topotype Phylogenomics Restores Species Status to 12 Overlooked Staghorn Corals on the Great Barrier Reef

Ecology & Evolution * Marine Biology * Coral Reefs

Branching staghorn and table-forming corals of the genus Acropora serve as the primary structural architects of Indo-Pacific coral reefs, constructing the complex three-dimensional calcium carbonate frameworks that shelter thousands of marine fish and invertebrate species [1, 3] . Yet for more than a century, coral biologists have wrestled with a fundamental taxonomic dilemma: do subtle variations in branch thickness, radial corallite spacing, and colony symmetry represent environmentally induced phenotypic plasticity within a single widespread species, or do they mask distinct, reproductively isolated evolutionary lineages [1, 2] ?

In a landmark taxonomic revision published in Invertebrate Systematics , researchers led by Augustine J. Crosbie, Tom C. L. Bridge, Peter F. Cowman, and Andrew H. Baird at James Cook University and the Queensland Museum -- working as part of the CoralBank initiative -- resolved decades of synonymy across eastern Australia's reefs [1, 2] . By integrating historical museum type collections with genome -wide phylogenomic sequencing of freshly collected topotypes across 369 specimens, the team reassessed 53 nominal Acropora (Scleractinia: Acroporidae) species [1, 2] . Their results confirm 47 genetically distinct lineages and formally restore valid species status to 12 overlooked corals previously dismissed as mere morphological variants, alongside four formerly unresolved taxa [1, 2] .

The Bleached-Skeleton Dilemma and Topotype Phylogenomics

Revising coral taxonomy poses a unique technical hurdle compared to birds, mammals, or insects [1, 2] . When 19th- and early 20th-century naturalists described new stony corals (Scleractinia) from the Great Barrier Reef and Coral Sea, they preserved only bleached aragonite ($CaCO_3$) skeletons [1, 2] . Boiling, bleaching, and decades of dry museum storage completely destroy extractable nuclear DNA, rendering historical holotypes inaccessible to standard ancient- DNA sequencing [1, 2] .

To bridge century-old museum morphology with modern genomics , Crosbie and colleagues deployed a topotype-anchored phylogenomic framework [1] :

* Resampling Historical Type Localities: Researchers navigated to the exact reefs, bays, and depth zones across eastern Australia recorded in historical taxonomic monographs to collect fresh living coral fragments matching the original holotype morphologies, assembling 369 genetically verified specimens [1, 2] .

* Ultraconserved Element (UCE) and Exon Capture: Applying an enhanced Hexacorallia target-enrichment bait set pioneered by Cowman and colleagues, the team sequenced thousands of orthologous nuclear ultraconserved elements and exonic loci per specimen [1, 4] . Unlike traditional single-marker mitochondrial barcoding -- which famously fails in anthozoan corals because anthozoan mitochondrial genomes evolve 10

to 100 times slower than those of bilaterian animals -- genome-wide UCE phylogenomics resolves fine-scale speciation events even among rapidly radiating Acropora clades [1, 3, 4] .

* Morphological Re-Verification: Once phylogenomic clustering separated true evolutionary lineages from environmental variants, taxonomists re-examined fine-scale skeletal micromorphology -- such as axial corallite wall thickness, radial corallite shape, and coenosteum spinule texture -- confirming consistent diagnostic traits that match the genomic clades [1, 3] .

Untangling Synonymy Across Eastern Australia's Reefs

Historically, sweeping late-20th-century taxonomic monographs lumped dozens of regional Australian coral names into broad, pan-Indo-Pacific "catch-all" species, assuming that wave exposure, turbidity, and light depth alone sculpted colony geometry [1, 2] . Evaluating 40 nominal Acropora species described from eastern Australia alongside 13 widespread Indo-Pacific senior synonyms overturned that consensus [1] :

| Taxonomic Category | | Count in Assessment | | Phylogenomic & Systematic Outcome |

| Total Nominal Species Reassessed | | 53 named taxa | | 40 eastern Australian nominal species + 13 putative Indo-Pacific senior synonyms evaluated across 369 specimens [1] . |

| Genetically Supported Distinct Species | | 47 valid species | | Confirmed as monophyletic, evolutionarily independent lineages via nuclear UCE phylogenomics [1, 2] . |

| Resurrected from Synonymy | | 12 overlooked species | | Previously lumped as ecomorphs of widespread species; restored to full species status [1, 2] . |

| Newly Resolved Taxa | | 4 species | | Previously unresolved or ambiguous lineages confirmed as distinct taxa [1, 2] . |

Crucially, the genomic trees demonstrated that morphological differences long dismissed as trivial reef-flat versus reef-slope plasticity frequently track deep reproductive isolation [1, 3] . Colonies growing side by side on the same reef crest often belonged to separate evolutionary clades that fail to interbreed despite synchronous annual mass-spawning events -- maintained by subtle temporal offsets in gamete release or pre-zygotic sperm-egg recognition barriers [1, 3] . This mirrors similar recent genomic revisions in the Acropora hyacinthus table-coral complex across the Indo-Pacific, where apparent single widespread species dissolved into regionally structured cryptic lineages [3] .

Hidden Extinction Risk and Great Barrier Reef Conservation

Restoring species status to 12 overlooked Great Barrier Reef corals carries immediate consequences for marine conservation, climate-vulnerability modeling, and reef restoration [1, 2] :

* Shrinking Perceived Geographic Ranges: When a cryptic regional endemic is mistakenly lumped under a wide-ranging Indo-Pacific species name, conservation databases assume the coral is abundant and buffered against local catastrophe [1, 2]

. Splitting those composite taxa into their true constituent species reveals that many restored corals occupy far narrower geographic ranges and smaller effective population sizes than previously assumed [1, 2] .

* Thermal Bleaching and Disturbance Triage: Following recurrent marine heatwaves, severe mass coral bleaching events, and crown-of-thorns starfish (Acanthaster) outbreaks across the Great Barrier Reef, cryptic species with localized distributions face disproportionate extinction risk [1, 3] . Accurate genomic species delimitation allows marine managers to pinpoint distinct thermal-tolerance traits across sister species and update International Union for Conservation of Nature (IUCN) Red List assessments [1, 2] .

* Biobanking and Assisted Reef Restoration: Initiatives such as CoralBank and reef-restoration cryopreservation programs rely on precise taxonomy to ensure that larval seeding, coral gardening, and genetic biobanks preserve true species diversity rather than inadvertently propagating a single dominant lineage while letting overlooked sister species vanish [1, 2] .

By pairing classical museum scholarship with genome-wide phylogenomics, the Invertebrate Systematics revision proves that even on the world's best-studied coral reef system, foundational biodiversity remains hidden in plain sight [1, 2] . Resolving these taxonomic boundaries also strengthens environmental DNA (eDNA) metabarcoding surveys, coral reef resilience modeling, and algal-symbiont (Symbiodiniaceae) host-specificity studies, ensuring that marine monitoring programs measure genuine species turnover rather than masking silent local extinctions behind outdated, overly broad species names [1, 3, 4] .

References & Primary Sources

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