

Reevaluating species number, distribution and endemism of the coral genus *Pocillopora* Lamarck, 1816 using species delimitation methods and microsatellites

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Species delimitation methods based on genetic information, notably using single locus data, have been proposed as means of increasing the rate of biodiversity description, but can also be used to clarify complex taxonomies. In this study, we explore the species diversity within the cnidarian genus *Pocillopora*, widely distributed in the tropical belt of the Indo-Pacific Ocean. From 943 *Pocillopora* colonies sampled in the Western Indian Ocean, the Tropical Southwestern Pacific and Southeast Polynesia, representing a huge variety of morphotypes, we delineated Primary Species Hypotheses (PSH) using two mitochondrial markers and one nuclear marker (Internal Transcribed Spacer 2). Then, we confronted identified PSHs to the results of clustering analyses using 13 microsatellites to determine Secondary Species Hypotheses (SSH). We defined at least 18 SSHs among 14 morphotypes, confirming the high phenotypic plasticity in *Pocillopora* species and the presence of cryptic lineages. We also identified three new genetic lineages never found to date, which could represent three new putative species. Moreover, the biogeographical ranges of several SSHs were re-assessed in the light of genetic data, which may have direct implications in conservation policies. Then, focusing on *Pocillopora eydouxi* corresponding to PSH09, we assessed the genetic structure from a large sampling (2507 colonies) using 13 microsatellites loci and assignment tests (Structure and DAPC). We confirmed the three SSHs previously identified (SSH09a, SSH09b and SSH09c). SSH09a is restricted to the Western Indian Ocean, and SSH09b and SSH09c are almost exclusively in the Tropical Southwestern Pacific, suggesting that gene flow is extremely rare between the Pacific Ocean and the Western Indian Ocean. Moreover, genetic structuring analysis revealed a fractal partitioning for each SSH separately. Thus the cryptic diversity within this genus should be taken into account seriously, as neglecting its importance is source of confusion in our understanding of ecosystem functioning.