

A molecular phylogeny of the spiny lobster *Panulirus homarus* supports a new species from the Southwest Indian Ocean

S. Singh, J.C. Groeneveld & S. Willows-Munro
Oceanographic Research Institute, South Africa
sohanasng@gmail.com

Accurate species description in the marine environment is critical for estimating biodiversity and identifying genetically distinct stocks. Analysis of molecular data can potentially improve species delimitations, because they are easily generated and independent, and yield consistent results with high statistical power. We used classical phylogenetic (maximum likelihood and Bayesian inference) and coalescent-based methods (divergence dating with fossil calibrations and coalescent-based species delimitation) to resolve the phylogeny of the spiny lobster *Panulirus homarus* subspecies complex in the Indo-West Pacific. Analyses of mitochondrial data and combined nuclear and mitochondrial data recovered *P. h. homarus* and *P. h. rubellus* as separately evolving lineages, while the nuclear data trees were unresolved. Divergence dating analysis also identified *P. h. homarus* and *P. h. rubellus* as two distinct clades which diverged from a common ancestor during the Oligocene, approximately 26 million years ago. Species delimitation using coalescent-based methods corroborated these findings. A long pelagic larval life stage and the influence of ocean currents on post-larval settlement patterns suggest that a parapatric mode of speciation drives evolution in this subspecies complex. In combination, the results indicate that *P. h. rubellus* from the Southwest Indian Ocean should be acknowledged as a separate species. Consequently, conservation and management efforts should focus on *P. h. rubellus* as being endemic to south east Africa and Madagascar.