Contribitions to Zoology

Phylogenetics and taxonomy of the scleractinian coral family

Euphylliidae

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Supplementary material

TABLE S1. List of the analysed samples with sample number, species identification, family, locality, date, collector, repository number, and NCBI accession numbers. Sequences obtained in this study are in bold. IRD (Institute de Recherche pour le Développement), KAUST (King Abdullah University of Science and Technology), UNIMIB (University of Milano-Bicocca), TO (Tara Ocean Expedition), ZPAL (Institute of Paleobiology, Polish Academy of Sciences).

TABLE S2. List of species and relative sequences downloaded from GenBank and used for the molecular phylogenetic analyses in this study.

TABLE S3. List of the 23 morphological characters and states analysed in this study.

TABLE S4. List of specimens analysed from a morphological point of view and their character states for the 23 investigated morphological characters. NA = not applicable.

DATA S1. Morphological character matrix used for maximum parsimony tree searches in TNT.



FIGURE S1. Bayesian inference phylogeny reconstruction of Euphylliidae based on COI. Numbers at nodes indicate Bayesian posterior probabilities (\geq 50), maximum likelihood bootstrap supports (\geq 50), and maximum parsimony supports (\geq 50), respectively. Colours and clade names refer to Luzon et al. (2017, 2018).



FIGURE S2. Bayesian inference phylogeny reconstruction of Euphylliidae based on 12S rRNA. Numbers at nodes indicate Bayesian posterior probabilities (\geq 50), maximum likelihood bootstrap (\geq 50), and maximum parsimony supports (\geq 50), supports, respectively. Colours and clade names refer to Luzon et al. (2017, 2018).



FIGURE S3. Bayesian inference phylogeny reconstruction of Euphylliidae based on 16S rRNA. Numbers at nodes indicate Bayesian posterior probabilities (\geq 50), maximum likelihood bootstrap supports (\geq 50), and maximum parsimony supports (\geq 50), respectively. Colours and clade names refer to Luzon et al. (2017, 2018).



FIGURE S4. Micromorphological/microstructural skeletal characteristics of representatives of other coral families and genera closed to Euphylliidae used in this study. (a–d) *Acropora horrida* (ZPAL H.25/110), (e–h) *Pachyseris speciosa* (ZPAL H.25/99), (i–l) *Gardineroseris planulata* (ZPAL H.25/17), (m–p) *Pavona cactus* (ZPAL H.25/103). Rapid Accretion Deposits (RADs) form clusters

along the straight or undulated zone at distal margin of septa (f, j, n, *Acropora* not illustrated) and form fast growing tips of skeletal spines (e.g., b). RADs are recognised in SEM in etched sections (c, g, k, o) as hollowed out regions or as typically darker areas in transmitted optical images (white-red-outline arrows). Lateral surfaces of septa show shingled (b, n) or granulated (f, j) textures; this is reflected in microstructural organization of thickening deposits (TDs) that are typically composed of well-delineated bundles of fibers. Longer bundles of fibers (red arrows; such as those in shingled TDs of *Acropora*) suggest spatially confined formation of microstructural units within skeleton/calicoblastic epidermis interface. Left 1st-2nd columns: SEM images of corallum surface; 3rd column: etched sections (SEM); 4th column: transmitted light optical images.