



<http://dx.doi.org/10.11646/zootaxa.3796.1.4>

<http://zoobank.org/urn:lsid:zoobank.org:pub:66323922-2C76-4AB7-98E6-59205AF86DBA>

Molecular parataxonomy as taxon description: examples from recently named Zoanthidea (Cnidaria: Anthozoa) with revision based on serial histology of microanatomy

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Abstract

Current taxonomic practices require corroboration from multiple lines of evidence to provide sufficient rigor for species discovery and description. However, many recently named taxa (species–families) are defined by nucleotide sequence with little or no description of the features that traditionally define higher taxa and link nucleotide-based information to the existing taxonomic system. Without knowledge of form, it may be impossible to identify conspecifics, congeners, and confamilials of new taxa among the hundreds of specimens and described species for which nucleotide sequencing is not now, and may never be, available. Additionally, some nucleotide sequences are invariant or inconsistently differentiated between congeners; severely limiting the utility of nucleotide-based taxon definitions. Here we use serial histology of paratypes to reveal the microanatomy of internal structures and revise the definitions of the Zoanthidea taxa *Corallizoanthus tsukaharai* Reimer, *Antipathozoanthus hickmani* Reimer & Fujii, *Parazoanthus darwini* Reimer & Fujii, *Terrazoanthus onoi* Reimer & Fujii, *Terrazoanthus sinnigeri* Reimer & Fujii, *Microzoanthus kagerou* Fujii & Reimer, and *Zoanthus kuroshio* Reimer & Ono; examination of *Mesozoanthus lilkweminensis* Reimer & Sinniger failed to produce interpretable sections. The results described here, with individual measurements documented in Morphbank (collection 829724) and Encyclopedia of Life (by taxon name), indicate a notably rich diversity of form for an order that is often characterized as depauperate in morphological diversity. One prominent example is a novel marginal muscle structure (cyclically transitional) that is not observable without serial sections. These findings may renew interest in morphological characters and provide the foundation for revision of Zoanthidea higher taxa, particularly now that phylogenetic relationships for these taxa can be inferred.

Key words: Coelenterata, DNA barcoding, DNA taxonomy, molecular parataxonomy, symbiosis

Resumen

Las corrientes prácticas taxonómicas requieren de la corroboración de múltiples fuentes de información para proveer con suficiente rigurosidad el descubrimiento y la descripción de especies. Sin embargo, muchos de los taxones (especie–familia) actualmente nombrados han sido definidos mediante la secuencia de nucleótidos con incompleta o la no descripción de características que tradicionalmente definen los taxones superiores y que pueden conectar la información basada en los nucleótidos con el sistema de taxonomía existente. Sin el conocimiento de forma, podría ser imposible identificar la misma especie, género y familia de taxones nuevos entre cientos de especímenes y de especies descritas, y cuya secuenciación de nucleótidos no existen, o jamás estarán disponibles. Además, algunas secuencias de nucleótidos son idénticas, o inconsistentemente diferenciadas entre géneros; limitando severamente la utilización de la definición de taxones basada en los nucleótidos. Para el propósito de ésta investigación, examinamos la histología en series de los paratipos que revelan la microanatomía de las estructuras internas y revisamos las definiciones de los taxones de Zoanthidea *Corallizoanthus tsukaharai* Reimer, *Antipathozoanthus hickmani* Reimer & Fujii, *Parazoanthus darwini* Reimer & Fujii, *Terrazoanthus onoi* Reimer & Fujii, *Terrazoanthus sinnigeri* Reimer & Fujii, *Microzoanthus kagerou* Fujii & Reimer, *Zoanthus kuroshio* Reimer & Ono; y al practicar el exámen a *Mesozoanthus lilkweminensis* Reimer & Sinniger fallamos en producir secciones histológicas que pudieron ser interpretadas. Los resultados que se describen aquí, con medidas individuales se documentan en Morphbank (colección 829724) y en la Encyclopedia of Life (buscar por el

Acknowledgements

We are grateful to S. Cairns, A. Collins, T. Coffey, and G. Keel of the USNM for permission to subsample specimens and assistance with loans. The Field Museum's Pritzker Laboratory for Molecular Systematics and Evolution and K. Feldheim provided acids and antidotes, and working space to use them, with support from the Pritzker Foundation; R. Bieler provided access to his histology lab and expendables, and the assistance of M. Prydzia. P. Sierwald and S. Ware provided access and expertise in the FMNH Collaborative Insect and Invertebrate Lab. The Biodiversity Synthesis Center and M. Westneat provided support and authorization for specimen loans. This work was supported in part by NSF CBET-0937987, Northwestern University, L. Marcelino, and V. Backman. L.O. Swain provided the abstract translation and A.K. Swain assisted with image analysis. Special thanks to Metra for providing the library-like environment of the Quiet Car, where most of this text was written.

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