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229-4: SPECIES AS TESTABLE HYPOTHESES: A CASE STUDY FROM TEREBRATELLIDINE BRACHIOPODS

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In paleontology, setting species boundaries is a difficult task. With few lines of evidence for delimiting species available, paleontologists rely mainly on morphology and stratigraphy. Considering the challenges posed by the fossil record, it is essential to understand how species are delimited in extant close relatives in order to set species boundaries that are comparable in both extinct and living species, thereby building a bridge between neontology and paleontology. The objective of our research is to understand how species are delimited in both fossil and living brachiopods by quantifying ranges of morphological variability and implementing next-generation sequencing techniques to analyze species boundaries using genomic DNA. We focused on named species in three exemplar genera distributed in the North Pacific: *Laqueus, Terebratalia,* and *Dallinella*. We first analyzed one of the most conspicuous morphological features in terebratellidine brachiopods, the long loop—the calcareous structure that supports the lophophore. Given the geometric complexity of this structure, we generated 3D models from CT scans of extant specimens and analyzed them using 3D geometric morphometrics to quantify variability and test current taxonomic assignments of species. Since loops are rarely preserved in the fossil record, we then analyzed shell outline variation to determine if loop shape and shell outline covary. Outline analysis was performed using an Elliptical Fourier method, and patterns of variability of both outlines and long loops were compared using a Procrustes analysis. Finally, to test species boundaries, we are sequencing DNA using RADSeq and analyzing the resulting sequences using a phylogenetic and species delimitation approach (e.g. using BPP: Bayesian Phylogenetics and Phylogeography). Preliminary results show that extant named species can be reliably recognized based on morphology; distinct named species are statistically different from one another. We predict that genetic data will show similar results, recovering the same species named on the basis of morphology. It is essential to treat morphologically-described species as working hypotheses to be tested, particularly in paleontology where many macroevolutionary studies depend on the accurate assessment of named species.

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