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### ABSTRACT

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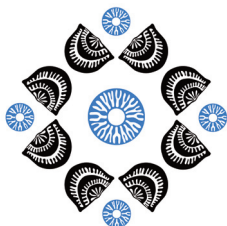
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# Developing a phylogenetic framework for tiny Ordovician brachiopods (Atrypida: Anazyginae and Catazyginae) from the eastern United States

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Elucidating how environmental change can facilitate the differentiation of evolutionary lineages and the establishment of new species is a critical issue for understanding both the history of life and modern biota. Notably, speciation events are known to be the main drivers of biodiversity; thus, generating well-constrained phylogenetic hypotheses to investigate speciation processes and facilitators can provide key data on links between biogeography, speciation, and diversification. During the Great Ordovician Biodiversification Event (GOBE), articulate brachiopods were a key group on the rise. By the Middle to Late Ordovician, the brachiopod order Atrypida was no exception. The atrypids diversified greatly and established evolutionary novelties such as helical and calcite-supported lophophores. The Ordovician epicontinental seas in eastern Laurentia provided an excellent environment for reproductive isolation and speciation, with sea-level fluctuations, ideal climate conditions, and active tectonic settings. However, speciation patterns and drivers within two widely-distributed atrypid subfamilies, Anazyginae (*Anazyga* spp. and *Zygospira* spp.) and Catazyginae (*Catazyga* spp.), remain poorly known. In this project, we seek to develop a robust phylogenetic framework for these clades and use that framework to evaluate speciation processes and facilitators during the Late Ordovician.

Morphological data will be collected from published literature and museum collections for a target group of 18 species, five recently reviewed species of *Zygospira*, seven species of *Anazyga*, and five species assigned to *Catazyga*. *Protozyga exigua* will be included for outgroup comparison. Specimens will be assessed at the Smithsonian National Museum of Natural History, which houses the comprehensive Cooper Collection, and specimens loaned from other museums. A morphological matrix will be created using more than 40 characters, including both external and internal characters. The resulting character matrix will be analyzed via Bayesian phylogenetic inference using the MrBayes software package. The Bayesian framework assesses the posterior probability in a generated tree by incorporating likelihood models and uncertainties, such as data insufficiency. Hence, given the incompleteness of the nature of morphological data for these clades, Bayesian inference is an ideal and efficient method to reconstruct phylogenetic relationships. Speciation mode and biogeographic patterns will then be analyzed using the BioGeoBears software package. Through this process, we aim to understand the speciation relationships within a monophyletic clade (Anazyginae and Catazyginae) and ancestor forms.

Systematic revision results in more precise species identities, through which it is possible to track character evolution within the genera. The results include (1) consistency in morphological traits within genera, such as shell ribs and the number of lophophore whorls, and (2) articulated differences among the three genera, evidencing derived states from a common ancestor. Combining phylogenetic and biogeographic analyses within the Atrypida provides essential information for understanding the impacts of geological and biotic changes on marine species across the Middle and Upper Ordovician. Thus, incorporating unique characters such as the number of whorls, shell ribs, and size in phylogenetic frameworks can elucidate evolutionary trends and phylogenetic relationships within the clade and provide evidence of how those factors impacted atrypids' distribution and abundance throughout the Paleozoic.