# 149-11 - EXPLORING RATES OF CHANGE AND MODES OF EVOLUTION IN BLASTOZOAN ECHINODERMS

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*301 / 302 (3, David L Lawrence Convention Center)*

## Abstract

Studies assessing shifts in rates and modes of anatomical evolution have been a critical component of paleobiology for nearly half a century. However, many fossil groups lack a rigorous phylogenetic framework to assess rates of character change and modes of evolution in an iterative and repeatable manner. Blastozoans, a diverse, globally distributed, and morphologically disparate clade of Paleozoic echinoderms, are one such group with few phylogenetic frameworks. Recently, advances have been made in understanding echinoderm homologies, allowing for the development of more reliable character states, and therefore, the development of phylogenetic frameworks upon which to test hypotheses of rates and modes of character evolution. Herein, we focus on three groups of blastozoans: diploporans, paracrinoids, and eublastoids. We evaluate character group evolution within and across each of these groups, using time-stratified phylogenetic trees. We also consider character group rates of change in context with major climatic and biotic shifts, and explore possible relationships between different character groups to understand if rate shifts in some character groups might trigger rate shifts in others. We use reversible jump Markov Chain Monte Carlo (rjMCMC) model averaging to test these hypotheses. Characters were partitioned into categories (e.g., feeding characters or attachment characters). rjMCMC allows us to test different combinations of functional group partitions and assess support for which sets of characters are evolving according to similar mechanisms and to co-fit other model components (such as the fossilized birth-death tree model) at the same time. This is a more computationally tractable approach than previous more iterative methods utilizing the stepping stone analyses.This work provides the first exploration of this framework to fossil organisms and provides new insights into the connections between different character groups' evolutionary patterns within extinct echinoderms.

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## Author

S

**Sarah Sheffield**
Binghamton University

## Authors

L
Maggie Limbeck
The University of South FloridaSchool of Geosciences

B
Jennifer Bauer

W
Peter J. Wagner
University of Nebraska-Lincoln

W
April Wright
Southeastern Louisiana University

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