GSA Connects 2024 Meeting in Anaheim, California

Paper No. 29-1
Presentation Time: 8:00 AM-5:30 PM

GROWTH VARIATION AND DEVELOPMENTAL SEQUENCE POLYMORPHISM IN THE MIDDLE CAMBRIAN TRILOBITE *ELRATHIA KINGII* (MEEK)

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Developmental sequence polymorphism (variation in the timing of developmental events) is a neglected form of variation, and whether it is correlated with other forms of variation, what role it plays in shaping a species' evolutionary trajectory, and the overall extent to which it characterizes and can be measured in extinct species remain open questions. Intraspecific variation constitutes the raw material with which natural selection shapes phenotypes over the course of evolutionary history. A complete understanding of the mechanisms underpinning biological evolution therefore requires detailed knowledge of the different forms of variation by which species are characterized. Intraspecific developmental variation is an important source of phenotypic variety because minor differences in developmental pathways can result in significant differences among adult phenotypes.

The fossil record provides representatives of past species, the most direct evidence we have of evolutionary change across geologic time. However, one limitation of studying fossils is that they are generally uncommon and sample sizes are often small. Intraspecific variation of any kind is therefore rarely quantified for fossil species. Here, continuous growth and discrete developmental timing data for the well-studied and abundant trilobite species *Elrathia kingii* are presented. 116 specimens representing a range of growth stages were photographed, measured, and coded for the expression of discrete developmental transformations. The fossils are reposited at the AMNH and were collected from a narrow stratigraphic interval in the Wheeler Formation of west central Utah. Linear measurements were plotted in multivariate space to construct growth series, a common practice in trilobite ontogenetic research. In addition to this, however, phenotypic characters associated with abrupt developmental transformations are documented for each specimen and coded into the growth series to illustrate the timing of these transformations relative to continuous changes in size and shape. The result is a series of plots in which overlap in developmental character states represents variation. This novel technique indicates that sequence polymorphism is present in *E. kingii* and future work will use this result as a starting point for the application of Ontogenetic Sequence Analysis.

Session No. 29--Booth# 58

D16. Recent Advances in Phylogenetic/Morphological Patterns (Posters)
Sunday, 22 September 2024: 8:00 AM-5:30 PM

Hall D (Anaheim Convention Center)

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Back to: D16. Recent Advances in Phylogenetic/Morphological Patterns (Posters)

Previous Abstract | Next Abstract >>