

The Impact of the Late Ordovician Mass Extinction on the Tree of Life. A. Z. Krug¹, C. Congreve¹ and M. E. Patzkowsky¹, ¹The Pennsylvania State University, University Park, PA 16802

Mass extinctions are important in shaping the history of advanced life on Earth due to their ability to remove high proportions of species and higher taxa in geologically short intervals, removing dominant taxonomic groups and allowing others to arise. The ecological or evolutionary impact of an extinction can vary, however, and does not appear directly connected to the proportion of species or higher taxa to go extinct during an event. Species are unevenly distributed within the modern tree of life, with many species-poor and few species-rich clades. As such, the internal branches of the modern tree are in some cases preserved by very few species, meaning extinctions that remove related species can remove much more of the internal branches (or evolutionary history) on the tree than predicted by species richness alone. Whether the loss of evolutionary history controls the long-term impact of extinction events has not been directly tested because of the absence of phylogenetic trees that focus on the relationships of species and genera within large clades in the geologic past.

Here, we present a preliminary tree of the evolutionary relationships of strophomenid brachiopod genera and use it to analyze whether extinctions are clustered phylogenetically during geologic intervals ranging from the Upper Ordovician through the Silurian, including the interval containing the Late Ordovician mass extinction. The phylogeny currently consists of 61 species representing 31 families/subfamilies, and will eventually be expanded to include the remaining strophomenid genera. The topology of the tree suggests that many of the traditionally defined families for this group are monophyletic, meaning all members of the family are descended from a common ancestor and therefore are evolutionarily distinct. The phylogeny also suggests that most major groups contain members that survive the Late Ordovician mass extinction. We tested this result using two metrics of the phylogenetic relatedness of taxa to go extinct or originate within intervals, mean pairwise distance and mean nearest taxon distance. Both suggest that extinctions in Ordovician intervals (the Lower Katian, Upper Katian and Hirnantian) are randomly distributed across the tree, whereas extinctions in the Early Silurian are clustered. Few sister taxa go extinct in the Ordovician intervals, and proportional extinction generally predicts the loss of phylogenetic diversity (the sum of the branch lengths within the tree) during this time. These results are consistent with previous analyses on the clustering of extinctions within families, and stand in stark contrast to results for the End-Cretaceous mass extinction, which was less intense but likely phylogenetically clumped. Incorporating phylogenetic relationships into studies of mass extinction can reveal how the loss of evolutionary history can impact recovery and evolution downstream of major extinction events.