

PHYLOGENETIC CONGRUENCE BETWEEN HARD AND SOFT PART DATA SETS: HOW DOES TAPHONOMY AFFECT PHYLOGENETIC RESOLUTION OF AN OSTRACODE CLADE?

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Taphonomic bias against soft tissue preservation is a barrier to understanding evolutionary relationships and diversification patterns among fossil and recent organisms. While many theoretical studies have been conducted to assess the impact of the omission of certain taxa or random parts of the data sets in a quantitatively modeled phylogenetic analysis, few case studies using actual data have been performed to determine the impact of the removal of specific characters in a phylogenetic analysis and none have been undertaken for ostracodes.

We conducted a phylogenetic analysis using 70 morphological characters (both hard and soft parts) for 17 extant taxa of a monophyletic clade of lacustrine podocopid ostracodes from the Lake Tanganyika system of East Africa. We used the phylogenetic program PAUP (ver. 3.1) to compare the effect of the types of information that can be lost when hard skeletal features are not used in a phylogeny or when the soft anatomical details are lost. This analysis provides an approximation of the effect of taphonomic bias on the phylogenetic resolution of an ostracode clade. Separate analyses were made using the entire data set, followed by subsequent analyses using only soft part characters and then hard part characters.

Eliminating the 36 hard part characters caused the collapse of many branches to polytomies and decreased the agreement of the hard part trees. Although some of the subclades still exist with the exclusion of the soft part data, there is more ambiguity in the specific relationships within these subclades. Still, many of the components of the subclades are supported in the hard part only analysis. The "stable islands", which could include parts of subclades from the composite analysis, are partially supported in the hard part only analysis, but with limited resolution. By re-introducing characters back into the analysis one at a time, we found that inclusion of certain sexual-specific characters provided a closer approximation of the composite analysis, suggesting that the absence (i.e. due to lack of preservation) of certain sexual characters in the fossil record of ostracodes could reduce the resolution within their phylogeny reconstruction.

Excluding the 34 soft part characters increased the number of most parsimonious trees, and decreased the resolution of the trees by creating many unresolved polytomies, but produced similar islands of stability as the complete analysis. The overall effect of eliminating all hard part characters in the analysis of this clade was to decrease the resolution of the phylogeny while retaining, by a much higher degree than the hard part only analysis, the important islands of stability. The close affinity that the soft part tree had to the composite tree suggests that the soft parts are more stable and are more phylogenetically conservative than the hard parts in the ostracode group studied (e.g. *Gomphocythere*). The hard part only tree may be less well-resolved because those features are more likely to be ecophenotypic and therefore more plastic, which would be consistent with previous studies on ecologically promoted variation in ostracode carapaces.

It is not surprising that our study verifies that the loss of soft and hard part characters reduces the resolution of the analysis of diversity. It is significant, however, that more resolution was lost with omission of the soft parts in comparison to the hard parts, although an approximately equal number of characters were used in each analysis, suggesting that the soft part preservational bias present in the ostracode fossil record may have an appreciable (loss of ~20%) effect on the analysis of their biological diversity.