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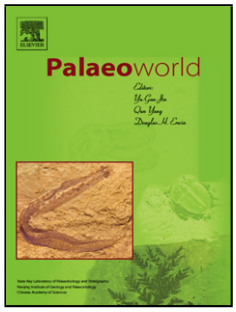

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A preliminary phylogenetic study of late Palaeozoic spiriferoid brachiopods using cladistic and Bayesian approaches

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Abstract

The brachiopod Superfamily Spiriferoidea diversified greatly and was widely distributed in the late Palaeozoic (Carboniferous–Permian), and yet its phylogeny has been seldom investigated with analytical methods. This is reflected in the current flux of very different classification schemes for this superfamily. This paper provides the first attempt to investigate the phylogenetic relationships of spiriferoid brachiopods through both cladistic and Bayesian analyses involving 24 discrete and continuous characters. The continuous characters, from morphometric data, have been separately discretized using the gap weighting method, and the 'as such' option in TNT. Our results highlight the potential significance of continuous characters in reconstructing and elucidating phylogenies, as much as qualitative characters. Building on the outcomes of the analyses, we also briefly evaluate existing classification schemes of Spiriferoidea. We found that none of the existing classifications fully reflect the phylogeny properly; major families within the superfamily, such as Spiriferidae, Choristitidae, and Trigonotretidae, turned out to be polyphyletic. Although this study is considered preliminary, due to the selection of and restriction to certain taxa, combined with the use of a relatively small number of characters, it nevertheless demonstrates that potentially the true phylogenetic relationships of spiriferoid taxa sharply contrast with any of the existing classification schemes. This highlights the need to develop an alternative scheme that takes into account a more comprehensive range of phylogenetic variables.

Keywords: Spiriferoid brachiopod; Late Palaeozoic; Classification; Continuous characters; Cladistics; Bayesian analysis

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