

A COMPARISON OF CRUSTACEAN DISPARITY AND PHYLOGENY THROUGH TIME

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Morphospace analyses comparing the disparity of all Cambrian and Recent arthropods have already proved invaluable for investigating the magnitude of the Cambrian explosion. However, a time series analysis for a major clade of arthropods through the phanerozoic has yet to be produced. The Crustacea provide the ideal subject, since the group contains diverse fossil taxa with a relatively extensive record. A morphological data base of discrete characters at the subordinal level was compiled for this purpose.

As with several major groups (e.g. blastoids, trilobites, crinoids), the framework of crustacean morphospace was defined relatively early in the history of the clade. Subsequent evolution involved the differential filling of morphospace, and the variation on existing themes. Several major clades and higher taxa have no fossil representatives until long after the initial Cambrian arthropod radiation. These include the Enantiopoda (Visean), Brachypoda (Pragian or Recent) and Eumalacostraca (Givetian). However, preservational factors aside, the absence of even relatively deep branches of crustacean evolution in the fossil record does not imply that large areas of morphospace were vacant, particularly where the groups involved are minimally differentiated from their sisters. Numbers of higher taxa and major clades may be only a loose correlate of disparity, and morphospace analysis therefore contributes greatly to understanding the systematics of the group.

Several key fossils show affinities with more than one crustacean group, and may occupy markedly different positions in cladograms with subtle reinterpretations of the data. Among these are *Canadaspis*, *Perspicularis*, *Waptia* and *Branchiocaris*, from the Burgess Shale, and several genera from the Upper Cambrian Orsten fauna of Sweden. Morphospace analyses are typically more stable, and shed light on evolutionary questions from a consideration of the phenetic proximity of nearest neighbors.

All cladograms for the Crustacea, whether deduced from morphological or molecular data, have a branching order incongruent with the sequence of appearance of groups in the fossil record. Hence, a given cladogram can be used to deduce the existence of ghost ranges for the later occurring members of sister group pairs, and a modified picture of morphospace filling produced as a result. This is of particular interest, since many of the groups believed to be most basal in the clade appear comparatively late in the record (e.g., Remipedia, Brachypoda, Branchiopoda). A rapid initial burst of crustacean evolution is implied as a result.