

貝殻の異質性の綱を越えた比較は可能か

How to compare disparity across the molluscan classes?: refinement of theoretical morphospace and beyond

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Study on global biodiversity through geologic time has been a leading paleontological science over the past few decades. The biodiversity is commonly estimated by taxonomic richness through compilations of the fossil records. On the other hand, disparity, a morphological aspect of biodiversity, has attracted less attention despite its significances. It may be partly because assessment of disparity is not so easy as counting the number of taxa. Measurement of disparity is defined through accommodating a variety of taxonomic groups into an integrated morphospace; in other words, it cannot be described without common morphological traits across all taxa of interest. The affair does matter when we try to compare morphological diversity between disparate organisms. For instance, disparity in bivalves is rarely compared with that in gastropods, notwithstanding a great success in theoretical morphology of molluscan shells. Indeed, even the number of parameters necessary for defining shell form is prone to differ between theoretical models designed for clams and snails. An integrated model and morphospace, as well as an appropriate measure of disparity itself, is required for future development of study on long-term disparity patterns in mollusks.

Here, I would propose a method to compare disparity across the different classes of the Conchifera described as follows. The shell form is represented by the five parameters; tightness of shell coiling, translation rate of the aperture along the coiling axis, the relative size of the aperture, the orientation of the aperture with respect to the coiling axis, and the angle of the aperture to the radial direction. The parameters are log-transformed and normalized to give data with standard normal distribution. Distance for each morphological trait between a pair of shell forms is defined as a difference in parameter value between them. Disparity is assessed by the mean distance between all pairwise combinations. If the parameters approximate normality, the mean pairwise distance does not depend on sample size. Relation of the morphological distance defined herein to the taxonomic unrelatedness was analyzed in more than a thousand conchiferan species to find a disparity measure which is independent of taxonomic distinctness.

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