Analisis kladistik berdasar karakter morfologi untuk studi filogeni: contoh kasus pada conidae (Gastropoda: Mollusca) / Ucu Yanu Arbi

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Abstrak

ABSTRACT
Phylogenetic taxonomy or cladistics is a classification system based on evolutionary history of an organism with other organisms, so that the process of evolution can be reconstructed. The main principle of the classification system is that only the unique characters of the adjacent group owned by descendants of an ancestor that was used in classifying organisms and secondly the reconstruction is based on group monophyly. So, the purpose of the use of this method is to classify organism and reconstruct the phylogenetic relationship based on the character encoding. Similarities and differences in the characters shown by a certain code lead to a tracing ancestors of each species. Several methods to reconstruct the phylogeny tree using qualitative data base are Maximum Parsimony and Maximum Likelihood. Study phylogeny based on morphological characters has a fundamental weakness which ultimately requires molecular characters to cover up these weaknesses.