

How and why to achieve more objectivity in taxonomy, exemplified on a fossil ostracod from long-lived Lake Pannon

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Taxonomists are commonly confronted with poor descriptions. The situation is exacerbated for fossil taxa which display few homologue landmarks useful for defining morphological traits. These latter are either necessary for building a clear taxonomic diagnosis or for further phylogenetic analysis.

Amplocypris abscissa was briefly described by A. E. Reuss (1850) from several outcrops near Vienna and Sopron (Vienna Basin; Upper Miocene, Pannonian). Subsequently, it was mentioned all around the Pannonian Basin respectively the Palaeo-Lake Pannon, which covered this area at that time: from the western sites in Austria and Slovakia, to eastern and southern ones (Romania, Serbia and Croatia). This geographic distribution contrasts with the high number of fossil species belonging to this genus, which are considered to be endemic in Lake Pannon. Our project on fossil ostracods from Hennersdorf (Vienna Basin, Pannonian "D") document *A. abscissa* as a polymorphic taxon. Moreover the genus *Amplocypris* Zolanyi 1944, displays an elusive diagnosis and an unsecured phylogenetic position. We demonstrate, using a precise protocol, how the taxonomic status of both of the genus *Amplocypris* and of the species *A. abscissa* can be achieved in an accurate and reproducible way: (a) A comparative morphological study of the valves, for fossil *Amplocypris* species and Recent representatives of genera belonging to higher-rank taxa, using both TL- and SE-microscopy, is absolutely necessary for developing a clear differential diagnosis of this genus and its allocation to one of the Cyprididae subfamilies (i.e. the Eucypridinae). (b) *Amplocypris* displays few homologue landmarks. Geometric morphometrics for outlines, combined with an original algorithm, which resemble a semi-landmark approach, offers the possibility to create morphological traits: Linhart's B-spline Approach (cf. the web site "Methods in Ostracodology" at <http://palstrat.uni-graz.at>). (c) Data expressed as pair-wise resemblance matrix of Euclidean distances are further analysed using techniques specific to numerical taxonomy, like UPGMA-cluster analysis, Principal coordinate analysis and the SIMPER exploratory analysis (cf. the computer package PRIMER v6 and PERMANOVA+ for PRIMER). (d) A matrix of dissimilarity values of the traits, expressed as arithmetic means with their 99% CL, allow to produce a new diagnosis of *A. abscissa* and to separate it from two other unnamed taxa. Together they form a phylogenetic lineage.