
A new approach to the delineation of taxa at the species and higher levels

Irina Kaygorodova^{*†1}, Alexander Bolbat¹, and Yuriy Bukin^{1,2}

¹Limnological Institute (LIN SB RAS) – 3, Ulan-Batorskaya st., Irkutsk, Russia

²Irkutsk State University (ISU) – 5, Suhe-Batora st., Irkutsk, Russia

Abstract

The study of ecological interactions within biological communities requires a thorough understanding of biodiversity which is inseparable from taxonomy. Despite centuries of dispute and controversy, the guidelines for assigning organisms to certain taxonomic levels have not been established. Admittedly, all human attempts to systematize living organisms are artificial, and there are no strict cut-off boundaries between taxa in nature. However, accounting for inaccurate taxonomic variables may lead to misguided estimates of ecological effects. Unfortunately, there are no clear guidelines for taxonomic assignment at levels above species. Here, we present a novel approach to the use of genetic divergence to evaluate the taxonomic position of certain samples with the simultaneous estimation the correctness of current systematics. This approach includes measuring raw and model-adjusted distances between samples' genetic sequences and attributing them to the lowest taxonomic levels that are common in sample pair to reveal distance distributions matching different taxonomic levels (species, genus, family etc.). This approach facilitates the reassessment of the taxonomic position of the samples, whose genetic distances relative to other samples in the dataset did not match their taxonomic divergence. A set of molecular data of segmented worms was chosen to test this approach. As a result, numerous inconsistencies in the systematics of Clitellata were pointed out. These inconsistencies included both oversplitting and over-lumping of specimens into the taxa of different levels and clear cases of misidentification. Our approach sparks re-evaluation of current systematics where traditional methods fail to provide sufficient resolution. Getting insights into a real degree of taxonomic divergence between inferred samples provides better opportunity to account for taxonomic variables in ecological research by comparing the same level taxa.

Keywords: genetic divergence, high level taxa delimitation, molecular based systematics, oligochaetes, leeches, leechlike parasites

^{*}Speaker

[†]Corresponding author: irina@lin.irk.ru