

Molecular Phylogenetics

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Comparative genital and molecular genetic analysis of blue butterflies (Lepidoptera: Lycaenidae) of Rostov-on-Don area

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The application of DNA markers allows getting an objective picture of the phylogenetic relationships of various groups of organisms, particularly Lepidoptera. However, the classical approach to taxonomy is based on the application of morphological methods, and the analysis of genitals in this case plays the crucial role. The results of molecular-genetic and genital analysis of the blues (Lycaenidae) phylogeny have been compared. As the objects, 43 species living in the Rostov region have been used.

Minimum Evolution algorithm was used for the complex phylogenetic analysis of nucleotide sequences of the mitochondrial COI gene and nuclear loci ITS2. Using the Jaccard similarity coefficient (software "Cluster Analysis," version 5.0.1), cladogram of genitalia similarity was obtained, constructed based on their 28 morphological characteristics. Comparison of these two cladograms shows their significant similarity. In the subfamily of Polyommatinae, it is necessary to distinguish between the tribes of Lampidini and Polyommatini, irrespectively separated by both methods (molecular-genetic analysis and genital analysis) into individual monophyletic sister branches, thus increasing the reliability of the authors' conclusion.

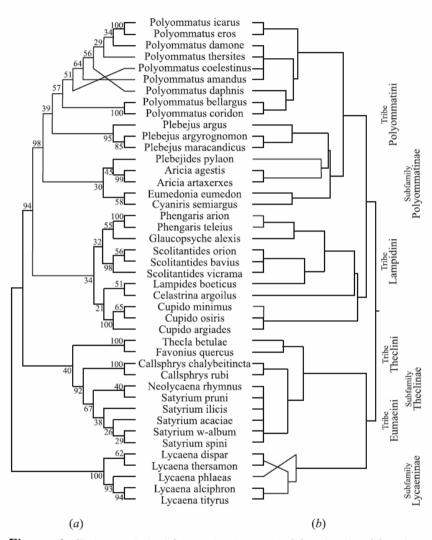


Figure 1 Cladogram derived from molecular-genetic (a) and genital (b) analyses