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Molecular Systematics of Odonata

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Abstract
Dragonflies and damselflies are insectivorous, occupying a crucial niche in aquatic communities. When they are present in communities, it’s an indicator of ecosystem health. Because of their comparatively large size and bright colors, they are often popular insects with the public and can thus serve as a flagship group in conservation initiatives. Dragonflies and damselflies together compose the order Odonata. This study analyzed paraphyletic families and the deepest nodes of evolutionary divergence within the order Odonata. Sequences accessed from GenBank within NCBI were used to build the taxa data set with ribosomal 18S genes. The results of the most parsimonious tree analysis in SeaView reflected Anisoptera and Zygoptera as sister groups. The maximum likelihood analysis positioned the clade of Anisoptera as paraphyletic with four nested clades, but the bootstrap support for that topology hypothesis was low. Future analyses should incorporate more taxa and genes to increase accuracy of resulting phylogenies.

Introduction and Goals
Odonate systematics has been greatly debated in the literature over last hundred years, but there are still many unanswered questions. Therefore, the goals were to:
1) Reconstruct the evolutionary history of damselflies and dragonflies
2) Test the deepest nodes of evolutionary divergence in Odonata using molecular characters
3) Resolve paraphyletic nodes at the suborder and family level

Materials and Methods
• 56 taxa representing 3 suborders and 29 families were selected to test the deepest nodes of evolutionary divergence within Odonata
• Ribosomal 18S sequences of these taxa were retrieved from GenBank within NCBI
• The molecular dataset was assembled and aligned using SeaView v4.6.1
• Most parsimonious and maximum likelihood trees were generated within SeaView v4.6.1 and configured using FigTree v1.4.3

Results
Figure 1. Most parsimonious tree with 100 bootstrap replicates for ribosomal 18S Odonata dataset. Parentheses indicate paraphyletic groups.

Figure 2. Maximum likelihood tree for ribosomal 18S Odonata dataset. Utilized GTR model of evolution with no invariable sites, no across site variation, and 500 bootstrap replicates. Parentheses indicate paraphyletic groups.

Conclusions and Recommendations
• Anisoptera and Zygoptera are sister groups which aligns with the consensus in the literature
• Incorporating additional taxa and genes into future analyses would reduce paraphyly at the family level
• Future analyses could integrate fossil records and biostratigraphy methods to date nodes of molecular diversification and reconstruct spatial distribution of Odonates through deep time