Systematics and evolution of Syrphinae based on exon-capture sequencing

Ximo Mengual*[1], Christoph Mayer[1], Trevor O. Burt[1], Kevin M. Moran[2,3], Lars Dietz[1], Gaby Nottebrock[1], Thomas Pauli[4], Andrew D. Young[5], Marie V. Brasseur[1], Sandra Kukowka[1], Scott Kelso[2], Claudia Etzbauer[1], Sander Bot[6], Martin Hauser[7], Kurt Jordaens[8], Gil F. G. Miranda[2], Gunilla Ståhls[9], Wouter Van Steenis[10], Ralph. S. Peters[1], and Jeffrey H. Skevington[2]

[1]Zoologisches Forschungsmuseum Alexander Koenig, Leibniz-Institut zur Analyse des Biodiversitätswandels, Adenauerallee 127, 53113 Bonn – Germany

[2]Agriculture and Agri-Food Canada, Canadian National Collection of Insects, Arachnids and Nematodes, K.W. Neatby Building, 960 Carling Avenue, Ottawa, Ontario, K1A 0C6 – Canada

[3]Carleton University, Department of Biology, 1125 Colonel By Drive, Ottawa, Ontario, K1S 5B6 – Canada

[4]Institute of Medical Bioinformatics and Systems Medicine, Medical Center-University of Freiburg, Faculty of Medicine, University of Freiburg, Freiburg – Germany

[5]University of Guelph, School of Environmental Sciences, Guelph, Ontario – Canada

[6]Kerklaan 30E, NL-9751 NN, Haren – Netherlands

[7]California Department of Food and Agriculture, 3294 Meadowview Road, Sacramento, California – United States

[8]Royal Museum for Central Africa, 4Joint Experimental Molecular Unit, Leuvensesteenweg 13, Tervuren – Belgium

[9]University of Helsinki, Finnish Museum of Natural History Luomus, Pohjoinen Rautatiekatu 13, 00100, Helsinki – Finland

[10]Vrouwenmantel 18, NL-3621 TR, Breukelen – Netherlands

Abstract

In the present study, we used high-throughput sequencing to capture and enrich exonic regions. With the help of the BaitFisher software, we developed a new bait kit (SYRPHIDAE1.0) to target 1945 CDS regions belonging to 1312 orthologous genes. This new bait kit was successfully used to exon-capture the targeted loci in 121 flower fly species across the different syrphid subfamilies. We analyzed different amino acid and nucleotide data sets with the Maximum Likelihood and the Multispecies Coalescent approaches. Our analyses yielded highly supported similar topologies, although the degree of the SRH (global Stationarity, Reversibility and Homogeneity) conditions varied greatly between amino acid and nucleotide data sets. The sisterhood of subfamilies Pipizinae and Syrphinae is recovered in all our analyses, confirming a common origin of taxa feeding on soft-bodied arthropods. Based on our results, we redefine the tribe Syrphini **stat.rev.** and infer the origin of the Syrphidae using BEAST.

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*Speaker

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