BIG4: Biosystematics, informatics and genomics of the big 4 insect groups- training tomorrow's researchers and entrepreneurs

> Kick-Off Meeting 14-18 September 2015 Copenhagen, Denmark





This project has received funding from the European Union's Horizon 2020 research and innovation programme under the Marie Sklodowska-Curie grant agreement No 642241



Morphology in insect systematics research

Martin Fikáček

National Museum & Charles University, Prague, Czech Republic

Faculty of Science CHARLES UNIVERSITY IN PRAGUE



NÁRODNÍ Muzeum



This project has received funding from the European Union's Horizon 2020 research and innovation programme under the Marie Sklodowska-Curie grant agreement No 642241

Morphology is problematic

• Morphological science is supposed as purely descriptive and uses "historical" data





Morphology is problematic

 Morphological science is supposed as purely descriptive and uses "historical" data

 Morphological characters are complex and time consuming to study



Charles D. Michener The Bees of the World SECOND EDITION

Morphology is problematic

 Morphological science is supposed as purely descriptive and uses "historical" data

 Morphological characters are complex and time consuming to study

 Morphology is prone to convergencies (i.e., problems with homology statements)





Morphology is problematic

 Morphological science is supposed as purely descriptive and uses "historical" data

 Morphological characters are complex and time consuming to study

 Morphology is prone to convergencies (i.e., problems with homology statements)







Cladistics 27 (2011) 341-355

Cladistics

10.1111/j.1096-0031.2010.00338.x

Morphological and molecular evidence converge upon a robust phylogeny of the megadiverse Holometabola

Rolf G. Beutel^{a,*}, Frank Friedrich^b, Thomas Hörnschemeyer^c, Hans Pohl^a, Frank Hünefeld^a, Felix Beckmann^d, Rudolf Meier^e, Bernhard Misof^f, Michael F. Whiting^g and Lars Vilhelmsen^h

^aEntomology Group, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, FSU Jena, Erbertstrasse 1, 07743 Jena, Germany; ^bBiozentrum Grindel und Zoologisches Museum, Martin-Luther-King-Platz 3, Universität Hamburg, 20146 Hamburg, Germany; ^cInstitut für Zoologie und Anthropologie der Universität, Berlinerstr. 28, 37073 Göttingen, Germany; ^dInstitute for Materials Research GKSS-Research Center, c/o GKSS at DESY, Notkestr. 85, 22607 Hamburg, Germany; ^eDepartment of Biological Sciences, National University of Singapore, 14 Science Dr 4, Block S2 #02-01, Singapore 117543; ^fZoologisches Forschungsmuseum Alexander König, Abteilung Molekulare Biodiversitätsforschung, Adenauerallee 160, 53113 Bonn, Germany; ^eDepartment of Biology, 693 Widtsoe Building, Brigham Young University, Provo, UT 84602, USA; ^hNatural History Museum of Denmark, University of Copenhagen, Universitetsparken 15, DK-2100, Denmark

Accepted 26 June 2010

Abstract

We present the largest morphological character set ever compiled for Holometabola. This was made possible through an optimized acquisition of data. Based on our analyses and recently published hypotheses based on molecular data, we discuss higher-level phylogeny and evolutionary changes. We comment on the information content of different character systems and discuss the role of morphology in the age of phylogenomics. Microcomputer tomography in combination with other techniques proved highly efficient for acquiring and documenting morphological data. Detailed anatomical information (356 characters) is now available for 30 representatives of all holometabolan orders. A combination of traditional and novel techniques complemented each other and rapidly provided reliable data. In addition, our approach facilitates documenting the anatomy of model organisms. Our results show little congruence with studies based on rRNA, but confirm most clades retrieved in a recent study based on nuclear genes: Holometabola excluding Hymenoptera, Coleopterida (= Strepsiptera + Coleoptera), Neuropterida excl. Neuroptera, and Mecoptera. Mecopterida (= Antliophora + Amphiesmenoptera) was retrieved only in Bayesian analyses. All orders except Megaloptera are monophyletic. Problems in the analyses are caused by taxa with numerous autapomorphies and/or inapplicable character states due to the loss of major structures (such as wings). Different factors have contributed to the evolutionary success of



Fig. 1. Single minumum-length cladogram with 1144 steps. Bremer support and bootstrap values mapped on branches.







Hebert et al. PNAS 2004;101:14812-14817 – Astraptes fulgerator complex in Costa Rica

ANNALS OF CARNEGIE MUSEUM

VOL. 77, NUMBER 1, Pp. 147-193

20 JULY 2008

SYSTEMATICS OF THE NORTH AMERICAN BEETLE SUBGENUS *PSEUDOPERYPHUS* (COLEOPTERA: CARABIDAE: *BEMBIDION*) BASED UPON MORPHOLOGICAL, CHROMOSOMAL, AND MOLECULAR DATA

DAVID R. MADDISON Department of Entomology, University of Arizona, Tucson, Arizona 85721 beetle@ag.arizona.edu

ABSTRACT

The subgenus Pseudoperyphus Hatch of Bembidion Latreille is revised. External structure, male genitalia, chromosome number, and DNA sequences from seven genes (28S rDNA, 18S rDNA, cytochrome oxidase I, wingless, CAD, arginine kinase, and RNA polymerase II) reveal the presence of nine species. Five of the species belong to the B. chalceum subgroup: B. chalceum Dejean. B. rothfelsi, new species (type locality: Bridgewater, Vermont), B. bellorum, new species (type locality: Tygart Valley River near Valley Head, West Virginia), B. antiquum Dejean, and B. louisella, new species (type locality: North Aspy River near Cape North, Nova Scotia). The remaining species belong to the B. honestum subgroup: B. honestum Say, B. arenobilis, new species (type locality: Danville, Virginia), B. integrum Casey, and B. rufotinctum Chaudoir. The group is most diverse in Vermont, where seven species live. The geographic ranges of many species overlap: of the 36 possible species pairings, 28 are found in sympatry. The morphological character system most closely correlated with species boundaries, as indicated by DNA sequences, is shape of the flagellum of the male genitalia, and it is likely involved in reproductive isolation. The shape of the pronotum is also implicated as important for species recognition. Two species, B. chalceum and B. rothfelsi, show derived haploid chromosome numbers distinct from the typical n=12 found in other Pseudoperyphus and most other Bembidion, with n=13 and n=17 respectively. Each of the nine species is inferred to be monophyletic in the Bayesian gene tree of at least one gene, but five of the species are paraphyletic for at least one gene, with two species (B. antiquum and B. arenobilis) being paraphyletic for as many genes as they are monophyletic. Evidence for nuclear copies of cytochrome oxidase I (COI) in several species makes inference of the COI gene tree difficult, and is one reason that COI is not the gene of choice to identify Pseudoperyphus specimens, contrary to standard DNA barcoding protocols. The best single gene for species identification is 28S rDNA; the two worst are COI and wingless. A key to species and geographic distribution maps are provided.

KEY WORDS: barcode, Bembidiini, Carabidae, chromosomes, cryptic species, gene tree, morphology, numts, Pseudoperyphus

INTRODUCTION

Members of the carabid genus *Bembidion* Latreille, subgenus *Pseudoperyphus* Hatch, are abundant beetles on gravel or cobble river shores throughout North America east of the *Pseudoperyphus* with a function of the pseudoperiod between the n=13 and n=17 specimens made it clear that two distinct species were involved, and that what has typically been called "*Bembidion chalceum*" is a mixture of at







Short & Fikacek (2013): Systematic Entomology 38: 723-752



Organized stridulatory file on sides of abdomen in hydrophilid beetles

> Short & Fikacek (2013): Systematic Entomology 38: 723-752



Understanding evolutionary history





Heliconius butterflies

Krzysztof M. Kozak et al. Syst Biol 2015;64:505-524

Understanding evolutionary history



Dasmahapatra et al. (2012) Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. *Nature* 487: 94–98

Integrating fossil data



Integrating fossil data





Solodovnikov et al. (2013) Cladistics 29: 360-403

Integrating fossil data







Outgroups Xyelidae Tenthredinoidea

Pamphilioidea

Cephoidea Siricoidea Xiphydriidae Orussidea

Apocrita





Ronquist et al. (2012) Syst. Biol. 61(6):973–999, 2012

Integrating museum specimens



Integrating museum specimens



Types of buprestid beetles from Obenberger collection



NÁRODNÍ MUZEUM



Historical specimens and types of carabid beetles from Jedlička collection

Integrating museum specimens





Tormissus guanicola (Hydrophilidae):

- described in 1904 from Bounty Islands
- in 1950s collected in masses in penguin colonies
- recent expeditions failed to find any single specimens



Additional benefits

e.g. saving your money and time for lab activities



honey bee (Apis mellifera)

Easy to present morphology data



ZooKeys 328: 47-57 (03 Sep 2013) doi: 10.3897/zookeys.328.5768



Rotational Scanning Electron Micrographs (rSEM): A novel and accessible tool to visualize and communicate complex morphology

David K-B Cheung¹, Adam J. Brunke¹, Nesrine Akkari¹, Carina Mara Souza², Thomas Pape¹

1 Natural History Museum of Denmark, Zoological Museum, Universitetsparken 15, Copenhagen, Denmark, 2100

2 Department of Animal Biology, Institute of Biology, State University of Campinas (UNICAMP), Barão Geraldo, Campinas, São Paulo, Brazil, P.O.B. 6109, 13083-970

Corresponding author: David K-B Cheung (David.Cheung@snm.ku.dk)

Academic editor: Pavel Stoev

Received 11 July 2013 | Accepted 5 August 2013 | Published 3 September 2013

(C) 2013 David K-B Cheung. This is an open access article distributed under the terms of the <u>Creative Commons Attribution License</u> 3.0 (CC-BY), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

For reference, use of the paginated PDF or printed version of this article is recommended.

Easy to present morphology data

Syrphidae Community Website



Description:	Sphecomyia vittata (Wiedemann) Male, dorsal view. Photographer: Mengual, Ximo. Publisher: Mengual, Ximo.
Taxonomic name:	Sphecomyla vittata (Wiedemann) (Syrphidae)
Licence:	(CC) BY-NC-SA
Creator:	© Mengual, Ximo



Photographer: Mengual, Ximo. Publisher: Mengual, Ximo.

Taxonomic name:	Sphecomvia vittata (Wiedemann) (Syrphidae)
Licence:	(CC) BY-NC-SR
Creator:	© Mengual, Ximo