

Introducing the 1KITE Project and First Results on Phylogenomics of Apterygote Hexapods Based on Thousands of Orthologous Genes*

Karen MEUSEMANN^{1, 2)}, Daniela BARTEL³⁾, Nikola SZUSCICH³⁾, Alexander BOEHM³⁾, Manfred WALZL³⁾, Gerald TIMELTHALER³⁾, Guenther PASS³⁾, Alexander BLANKE²⁾, Malte PETERSEN²⁾, Peter RUEHR²⁾, Ryuichiro MACHIDA⁴⁾, Kaoru SEKIYA⁴⁾, Yasutaka NAKAGAKI⁴⁾, Shigekazu TOMIZUKA⁴⁾, Makiko FUKUI⁵⁾, Bernhard MISOF²⁾, on the behalf of the 1KITE Consortium

¹⁾ CSIRO Ecosystem Sciences, Australian National Insect Collection, Canberra, Australia

²⁾ Zoologisches Forschungsmuseum A. Koenig / Zentrum für Molekulare Biodiversitätsforschung, Bonn, Germany

³⁾ Department of Integrative Zoology, Universität Wien, Vienna, Austria

⁴⁾ Sugadaira Montane Research Center, University of Tsukuba, Ueda, Nagano, Japan

⁵⁾ Ehime University, Graduate School of Science and Engineering, Matsuyama, Japan

E-mail: mail@karen-meusemann.de (KM)

Insects are the most species-rich lineage of metazoans on Earth. Detailed knowledge of the phylogeny of major insect lineages is mandatory to reveal how changes of the atmosphere, mass extinction events, and the shaping of different ecosystems forged insect evolution and gave rise to today's amazing diversity.

However, inferring the origin, phylogenetic relationships of major insect groups, in particular relationships of primarily wingless (so called apterygote) hexapods including the orders Protura, Diplura, Collembola (entognathous insects), and Archaeognatha and Zygentoma turned out to be notoriously difficult. With regard to entognathous insects, the first phylogenomic studies including transcriptome data from few apterygote hexapods yielded contradictory results, *e.g.*, by either supporting or rejecting the clade "Entognatha".

In this talk, we introduce the 1KITE initiative including more than 80 scientists from nine countries. In 1KITE we have finished sequencing transcriptomes of more than 1,000 insect species, to infer a robust molecular phylogeny. The final aim of experts from palaeontology, embryology, morphology, bioinformatics, scientific computing and molecular biology is to understand the origin and evolution of insects. We will present preliminary results from the 1KITE "Basal hexapod subgroup". Our analyses, focusing again on entognathous insects, based on transcriptome data from ~40 species revealed more than 2,000 orthologous single copy genes. We will point out challenges and pitfalls of large phylogenomic datasets, and present advanced methods developed and used during our analyses. See <http://www.1kite.org/subprojects.html>.

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