

## INVESTICE DO ROZVOJE VZDĚLÁVÁNÍ

Centrum teorie vzdělávání přírodovědných oborů  
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## Zahraníční konference v rámci projektu ESF

Mgr. Kristýna Janišová, Katedra biologie PdF UP Olomouc

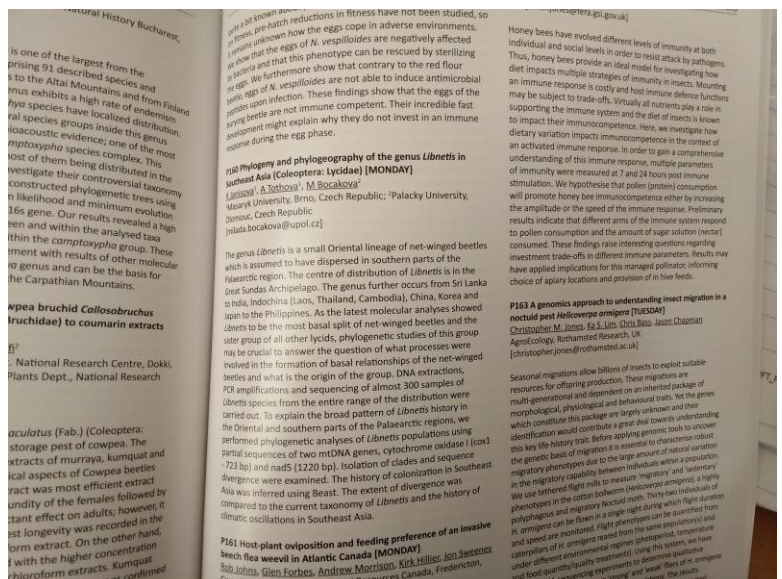
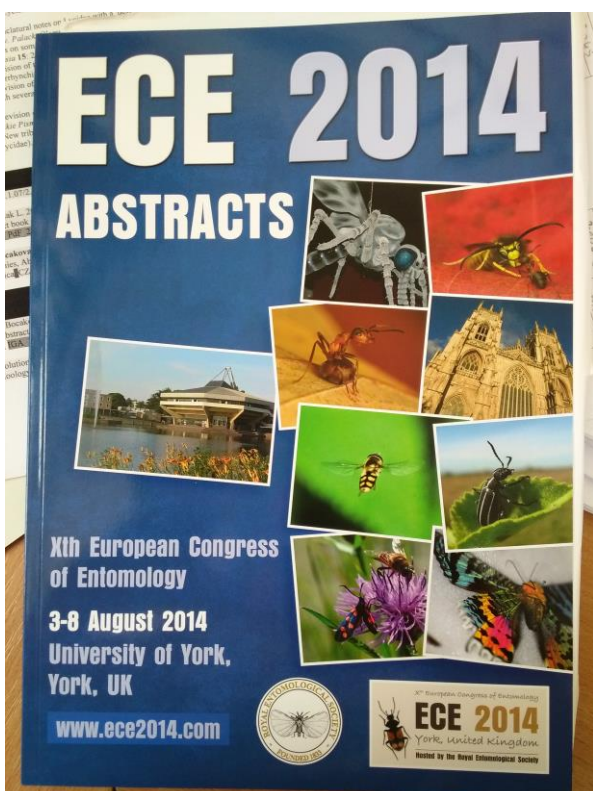
Cílová instituce: X<sup>th</sup> European Congress of Entomology, York, Velká Británie

Termín konání: 3.-8. 8. 2014

Cílem pracovní cesty byla prezentace výzkumných výsledků formou posteru „*Phylogeny and phylogeography of the genus Libnetis in Southeast Asia (Coleoptera: Lycidae)*“. Prezentované výsledky jsou součástí výzkumu probíhajícího v rámci projektu CeTPo CZ.1.07/2.3.00/20.0166 a z interního grantu PdF UP v Olomouci IGA\_PdF\_2014019.

Kromě prezentace posteru je také výstupem publikovaný abstrakt: Janisova K., Tothova A., Bocakova M. 2014: Phylogeny and phylogeography of the genus *Libnetis* in Southeast Asia (Coleoptera: Lycidae), Abstract book, X<sup>th</sup> Congress of Entomology, 3.-8. 8. 2014, p. 107.

V průběhu konference jsme se účastnili plenárních přednášek a výstupů ve vybraných sekcích.



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Phylogeny and phylogeography of the genus *Libnetis* in Southeast Asia (Coleoptera: Lycidae)

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INTRODUCTION

*Libnetis* is a small predominantly Oriental lineage of net-winged beetles. The genus consists of approximately 60 described species and many other species undescribed yet. Several *Libnetis* lineages also occur in southern parts of the Palearctic region. Therefore, we hypothesize they have probably dispersed from Oriental clades. The center of distribution of *Libnetis* is in the Greater Sunda Islands (Sumatra, Java, Borneo) while missing in Sulawesi. The genus further occurs from Sri Lanka to India, Indochina (Laos, Thailand, Cambodia), Malay peninsula, China, Korea and Japan to the Philippines. Members of the genus *Libnetis* can be found in different habitats but most species prefer humid tropical rainforests. Several species are adapted to deciduous forests on the slopes of the Himalayas and in the eastern Palearctic. *Libnetis* includes small, yellow to brown species (Fig. 1, 2) with a slight median longitudinal carina in the anterior half of the pronotum and each elytron with four longitudinal costae. In contrast to most other net-winged beetles, the reticulate cells on elytra are absent. The genus *Libnetis* was shown to be a relatively old lycid clade. Unfortunately, there are no known *Libnetis* fossils. Therefore, dating the age of *Libnetis* was previously inferred using relative age of branches (Bocak et al. 2008). In accordance with Coleoptera phylogeny (Hunt et al. 2007) the age of *Libnetis* clade was shown as 58.5 My. As the latest molecular analyses showed *Libnetis* to be the most basal split of net-winged beetles (Bocak et al. 2008), phylogenetic studies of this group may be crucial to answer the question of what is the origin of *Libnetis* clade and what processes were involved in the formation of basal relationships of the net-winged beetles.

MATERIAL AND METHODS

As an ingroup we sampled 248 specimens of the genus *Libnetis* from the entire range of its distribution - Sumatra, Java, Borneo, India, Laos, Thailand, Cambodia, Malay peninsula, China, Japan, and the Philippines (except Sri Lanka, Nepal and Korea). These specimens represent 77 *Libnetis* species. Seven outgroup exemplars included representatives of other elateroid families (Phengodidae, Rhagophthalmidae, Lampyridae, and Cantharidae) whose sequences were published in previous studies (Bocakova et al. 2007, Bocak et al. 2008). We sequenced two mitochondrial gene fragments (*cox1* - 723 bp) of 248 *Libnetis* samples. The *cox1* is a protein coding gene and therefore is length invariable, and the sequences were used unaligned after visual inspection for errors. Phylogenetic analyses of the concatenated dataset were performed using maximum parsimony (MP), maximum likelihood (ML) and Bayesian approaches (BA). Isolation of clades and sequence divergence were examined. The estimation of divergence times was conducted under the Bayesian framework implemented in BEAST v2.0.2 (Drummond and Rambaut, 2007) using the GTR+I+G model selected by ModelTest 3.7 (Posada & Crandall, 1998) and relaxed uncorrelated lognormal clock (estimate). We used S-DIVA and BBM analyses implemented in RASP 2.1 (Yu et al. 2012) to reconstruct the possible ancestral ranges of *Libnetis* on the phylogenetic trees of 77 *Libnetis* species and to infer the history of colonization in Southeast Asia. The extent of divergence was compared to the morphological diversity and the history of climatic oscillations in Southeast Asia.

RESULTS AND DISCUSSION

The aligned COI sequences for all individuals formed an alignment of 723 homologous positions. MP analysis using TNT resulted in 78 equally parsimonious trees with CI = 0.15, RI = 0.78 (Fig. 4). The majority of clades (including five basal dichotomies) were present in the strict consensus tree showing 100% support. MP analysis proposed that *Libnetis* originated in peninsular Malaysia and continental Asia with Malaysian and Yunnan (China) species as the earliest splits. In contrast, the ML results of RAxML fast bootstrap procedure analyses showed one species from Yunnan as the most basal split suggesting continental Asiatic origin of the genus *Libnetis*.

We believe that the present distribution of the genus is the result of several dispersal and vicariant events. S-DIVA analysis applied on the first of the set of 78 MP trees suggests four possible ancestral ranges, AM (continental Asia + Malaysia), ABM (continental Asia + Borneo + Malaysia), ABCM (continental Asia + Borneo + Sumatra + Malaysia), ACM (continental Asia + Sumatra + Malaysia). Optimal area reconstruction assumed that *Libnetis* ancestors originated in continental Asia and Malaysia. Most of the *Libnetis* clade (represented by 74 of 77 analyzed species) originated in Sumatra as S-DIVA proposed Sumatra as ancestral range for node 156 with 100% frequency of the range occurrence. Then, *Libnetis* diverged in two clades: the first with Sumatranese + Javanese origin (clade 155) that dispersed to Borneo and Okinawa (Japan), while the other diversified in Sumatra (node 144) and later dispersed multiply to Java and several times through Borneo to the Philippines.

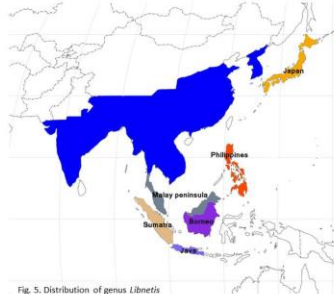


Fig. 5. Distribution of genus *Libnetis*



Fig. 1. *Libnetis basilianus*

Fig. 2. *Libnetis* spp.

*Libnetis* spp.

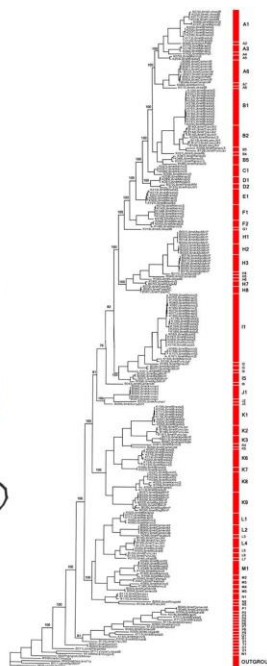


Fig. 3. One of the 78 maximum parsimony trees based on the analysis of *cox1* sequences. Values above branches refer to the majority rule support values. Bars (A1-W1) on the right designate individual *Libnetis* species.

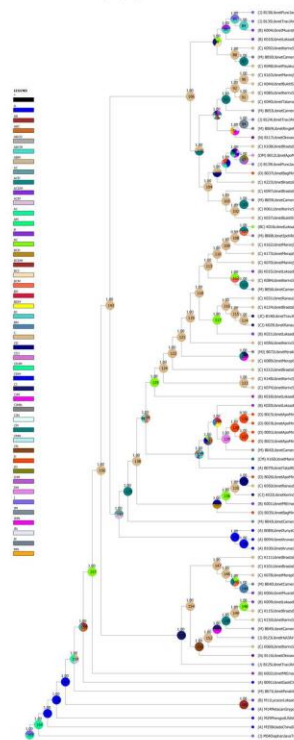


Fig. 4. The result of statistical dispersal-vicariance analysis using S-DIVA as implemented in RASP 2.1. MP reconstructions of ancestral distributions were inferred using the phylogenetic hypothesis of the genus *Libnetis*.

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