

2007). We have tried to apply this method to quantification of the aquatic insect larvae respiration, particularly different species of bloodworms- Diptera, Chironomidae, Chironomus spp. and impact of the larval bioturbation on the oxygen uptake by sediment. First results are quite promising, showing linear relationships between larval density and speed of Resazurin decay. Method is quite promising and could be used as a complement to the traditional methods, used for aquatic invertebrates' respiration measurements.

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### **Dispersal is linked to habitat use in 59 species of water beetles on Madagascar**

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Lentic habitats (standing water, such as ponds and lakes) differ from lotic habitats (running water; streams and rivers) in their spatiotemporal persistence, with lentic habitats being more ephemeral in evolutionary time. This habitat instability is thought to select for dispersal, and several phylogenetic and macroecological studies have suggested that high rates of dispersal are more characteristic of lentic than lotic species. We tested this hypothesis using a comparative population genetic and phylogeographic approach based on mitochondrial DNA for 59 aquatic beetle species, sampled across Madagascar. Species were classified as lotic ( $n = 25$ ), lentic ( $n = 25$ ), or lotolentic (associated with both running and standing water;  $n = 9$ ). Hierarchical population genetic structure (AMOVA), nucleotide diversity ( $\pi$ ), and geographic structure were compared among habitat types. Lotic species had significantly greater population structure ( $F_{ST} = 0.55$ , hierarchical AMOVA) than lentic ( $F_{ST} = 0.13$ ) and lotolentic ( $F_{ST} = 0.19$ ) species using phylogenetic generalized least squares (PGLS) to correct for phylogeny. Body size was independent of habitat preference, and did not explain any of the intra-specific variation. A greater proportion of lotic species were endemic to Madagascar and lotic species had more pronounced geographic structure in their haplotype networks. The results indicate that dispersal is consistently lower among lotic species, independent of phylogenetic relatedness.

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### **Ecological characterisation of an unknown fauna using DNA taxonomy – An example with Himalayan Hydropsychidae (Insecta: Trichoptera)**

F. Hoppeler, R.D.T. Shah, D.N. Shah, S.C. Jähnig, J.D. Tonkin, S. Sharma & S.U. Pauls

In isolated regions like the Hindu Kush-Himalaya, taxonomic difficulties can obstruct studies on spatial and ecological patterns of diversity. We combined molecular tools and ecology in order to investigate the distribution of an unknown fauna of hydropsychid caddisflies along altitudinal gradients and explore potentially influencing factors. A total of 678 specimens (655 larvae and 23 adults) from 34 tributaries within four different Nepalese river systems were examined. Phylogenetic analysis of the mitochondrial cytochrome c oxidase I (COI-1 and COI-2) and the nuclear gene 28S RNA were used to delineate independently evolving lineages ("GMYC species") applying the general mixed Yule-coalescent (GMYC) model. Estimation of species diversity within the family of Hydropsychidae, based on 516 COI-2 mtDNA sequences, resulted in 29 GMYC species. High levels of species turnover among river systems indicate high site-to-site variation across geographical ranges in the Hydropsychidae community, and a great degree of regional endemism. Within each system, community composition was found to vary greatly along the altitudinal gradients, with many GMYC species associated with narrow specific altitudinal ranges. Overall, the results support the utility of DNA taxonomy approaches for biodiversity assessment of poorly studied groups or regions and highlight its further application to explore fundamental questions in freshwater ecology.

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### **Hidden diversity: revision of the Carpathian endemic semiaquatic *Pedicia staryi* Savchenko species group, Insecta, Diptera**

L. Keresztes, L.-P. Kolcsar & L.-A. Denes

Molecular data are especially useful to calibrate morphological characters for systematic purposes within homogeneous taxa. Here we applied phylogenetic methods to detect genetically coherent groups within the Carpathian endemic *Pedicia staryi* species group. The Maximum Likelihood and Bayesian Inference phylogenetic trees detect *P. staryi* complex sensu Savchenko as a monophyletic unit. The three Carpathian endemics, *P. apusenica*, *P.*

*lobifera*, *P. staryi*, forms a well-defined clade diverged about 8.56 million years ago from its most wide spread sister species, *P. straminea*. *P. staryi* and *P. apusenica* form a clade including *P. apusenica* and four well defined *P. staryi* lineages that have an insular-like distribution through the Carpathians. Morphological divergences are highly congruent with molecular data in the case of some genital structures and support these five cryptic groups as taxonomically well defined entities. The molecular clock however speculative, show these processes occurred during Miocene-Pliocene period as a result of an allopatric speciation process and were most probably connected to different aridification cycles of this region. These results show the importance of the Carpathians as "cumulative refugia" and an important genetic reserve of aquatic and semiaquatic organisms in Europe. This research was supported by a grant of the Ministry of National Education, CNCS – UEFISCDI, project number PN-II-ID-2012-4-0595.

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#### **Intern versus extern: Trigger für die Prä- und Postaugenfleck Entwicklung in der Embryogenese von Libellulidae, Odonata**

K. Koch

Temperatur und Photoperiode spielen eine große Rolle in der Ökologie von Insekten. Viele Insekten haben eine feste Temperatursumme (Ts) für die Embryonalentwicklung. Änderungen in der Photoperiode können Übergänge in das nächste Stadium im Lebenszyklus triggern. Gibt es bei Libelluliden eine feste Ts oder Lichtsumme (Ls) für die Embryogenese? Beeinflussen Temperatur und Photoperiode als externe Trigger die Entwicklung während der gesamten Embryogenese? Es wurden Eier von 5 europäischen und 3 afrikanischen Libellulidenarten unter verschiedenen variablen und konstanten Temperaturen aufgezogen.

Alle Arten wiesen weder für die Prä- noch für Postaugenfleckentwicklung eine allgemeine Ts oder Ls auf. Je höher die Temperatur, desto schneller entwickelten sich die Eier. Temperatur hatte einen größeren Einfluss auf die Embryogenese als die Photoperiode. Ts und Ls von der Postaugenentwicklung unterschieden sich zwischen den unterschiedlichen Umweltbedingungen stärker als von der Präaugenfleckentwicklung. Die Präaugenfleckentwicklung scheint eher intern getriggert zu werden, die Postaugenfleckentwicklung

eher extern. Dabei ist interessant, dass auch die afrikanischen Arten dies Muster auswiesen. Diese Plastizität in der zweiten Hälfte der Embryogenese könnte ein allgemeines Phänomen innerhalb der Libelluliden sein, um mit starken Variationen von Umweltbedingungen flexibel umgehen zu können

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#### **Distributions of European montane caddisflies in the wake of climate change: the Drusinae (Trichoptera)**

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The Drusinae subfamily consists of about 100 species distributed across Europe. Some species are widespread and common, while others are restricted to one of several regional centers of endemism, such as in the Alps or the Balkan Highlands. These local and rare species, along with some newly described ones, are known from few confirmed occurrences only. While the full distribution of some species thus remains uncertain, the majority of species in the group are micro and regional endemics. Moreover, and because of the predominantly montane habitats they occupy, Drusinae are particularly susceptible to climate change. These aspects make this larger, running water taxon an interesting group to assess their vulnerability to environmental change through species distribution models (SDMs). Models are applied for individual Drusinae species to describe their current distribution patterns in Europe at a spatial resolution of 1 km. Beyond the usual application of bioclimatic predictors, additional predictors enhance the model: (i) topographical properties are used to approximate position in the catchment (catchment size) and (ii) soil properties indicate the possible composition of the substrate. Distribution predictions are projected for the year 2080 to determine changes in range size, as well as shifts in altitude and latitude/longitude. Projections are based on 5 different future climate models and 4 different future climate scenarios. Results of the first SDM models show mostly shifts towards northern latitudes and higher altitudes, for most of the future climate scenarios.

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