



**INSTITUTE OF ZOOLOGY and BIOMEDICAL RESEARCH
JAGIELLONIAN UNIVERSITY**

On behalf of our Institute we invite you to join us for the next
Distinguished Lecture.

On January 26th 2018 (Friday) we welcome

Dr Marianne Espeland

from the Zoological Research Museum
Alexander Koenig in Germany for a lecture

Butterfly phylogenomics at multiple levels

Location: Institute of Zoology and Biomedical Research,
Gronostajowa 9, lecture hall 014 (ground floor)

Time: 2PM

Duration: approx. 45 min.



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Marianne Espeland received a BSc in biology from the Norwegian University of Science and Technology in 2003. In December 2004 she was awarded a MSc in systematic biology from the same university. Her thesis dealt with systematics and melanization of *Pieris napi* in lowland and mountain populations in Norway. Following this she moved to the Swedish Museum of Natural History and Stockholm University where she first worked as a curatorial assistant and then spent 4.5 years working on her PhD thesis on caddisfly (Trichoptera) diversification and evolutionary history in the Pacific. She switched back to butterflies for her first postdoc at the Museum of Comparative Zoology at Harvard University (Pierce lab). Funded by a grant from the Research Council of Norway she used tools from phylogenomics and transcriptomics to study evolution, diversification and ant attendance in lycaenid butterflies. Then she followed 1.5 years as a postdoctoral research associate at the Florida Museum of Natural History where she worked on phylogenomics and diversification of the subtribe Euptychiina (Satyrinae, Nymphalidae) and Riodinidae. Currently she is the Curator of Lepidoptera and Head of the Lepidoptera Section at the Zoological Research Museum Alexander Koenig in Germany.

More information on the lecturer on her official website:
marianneespeland.weebly.com.



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Abstract

Next generation sequencing approaches within Papilionoidea (butterflies and skippers) are mostly limited to very closely related species. Currently, most higher-level phylogenetic studies of Papilionoidea utilize 4 to 10 'standard' loci, and these genes often do not provide robust support for deeper relationships within the superfamily. We used a target enrichment approach and Illumina sequencing to sequence 425 loci of length 300-2200bp for 170 taxa covering all butterfly tribes and the Hedylidae. To assess phylogenetic signal at a lower taxonomic level, we also sequenced 96 members of the subtribe Euptychiina (Satyrinae, Nymphalidae) which has been difficult to resolve using Sanger sequencing. This probe kit contains the most commonly used mitochondrial and nuclear loci (COI, Ef1-a, wg, GAPDH, Rps5, Rps2, IDH, MDH, CAD, ArgK, DDC), and can readily be combined with available sequence data. Preliminary results show that these 425 loci provide robust support for both higher and lower taxonomic levels. At an even lower taxonomic level a second probe kit with 600 loci has been designed and used to infer a phylogeny of the closely related genera in the *Euchrysops* section (Polyommatainae, Lycaenidae) to study the evolution of ant association and diversification of the group.

Selected publications

- Espeland M**, Hall JPW, DeVries PJ, Lees DC, Cornwall M, Hsu Y-F, Wu L-W, Campbell DL, Talavera G, Vila R, Salzman S, Ruehr S, Lohman DJ, Pierce NE. 2015 Ancient Neotropical origin and recent recolonization: Phylogeny, biogeography and diversification of the Riodinidae (Lepidoptera: Papilionoidea). *Molecular Phylogenetics and Evolution* 93: 296-306
- Peña C, **Espeland M**. 2015. Diversity dynamics in Nymphalidae butterflies: Effect of phylogenetic uncertainty on diversification rate shift estimates. *Plos One* 10 (4): e012028. doi: 10.1371
- Boyle JH, Kaliszewska ZA, **Espeland M**, Suderman TR, Fleming JE, Heath A, Pierce NA. 2015. Phylogeny of the Aphnaeinae; myrmecophilous African butterflies with carnivorous and herbivorous life histories. *Systematic Entomology* 40: 169-182
- Hawliitschek O, Heinrich L, **Espeland M**, Toussaint EFA, Genner MJ, Balke M. 2012. Pleistocene climate change promoted rapid diversification of aquatic invertebrates in South-East Australia. *BMC Evolutionary Biology* 12: 142.
- Johanson KA, Malm T, **Espeland M**, Weingartner E. 2012. Phylogeny of the Polycentropodidae (Insecta: Trichoptera) based on protein-coding genes reveal non-monophyletic genera. *Molecular Phylogenetics and Evolution* 65: 126-135.
- Espeland M**, Johanson KA. 2010. The diversity and radiation of the largest monophyletic animal group on New Caledonia (Trichoptera: Ecnomidae: *Agmina*). *Journal of Evolutionary Biology* 23: 2112-2122
- Espeland M**, Irestedt M, Johanson KA, Åkerlund M, Berg J-E, Källersjö M. 2010. Dichlorvos exposure impedes extraction and amplification of DNA from insects in museum collections. *Frontiers in Zoology* 7: 2
- Espeland M**, Johanson KA. 2010. The effect of environmental diversification on species diversification in New Caledonian caddisflies (Hydropsychidae: Trichoptera: Insecta). *Journal of Biogeography* 37: 879-890
- Johanson KA, **Espeland M**. 2010. Phylogeny of the Ecnomidae (Trichoptera). *Cladistics* 26: 36-48
- Espeland M**, Johanson KA, Hovmöller R. 2008. Early *Xanthochorema* (Trichoptera, Insecta) radiations in New Caledonia originated on ultrabasic rocks. *Molecular Phylogenetics and Evolution* 48: 904-917
- Espeland M**, Aagaard K, Balstad T. & Hindar K. 2007. Ecomorphological and genetic divergence between lowland and montane forms of the *Pieris napi* species complex. *Biological of the Linnean Society* 92: 727-745.