

diversity.

POSTER 117.

‘Bad’ species? RADsequencing, DNA barcoding, and a role for *Wolbachia* in the evolutionary history of the *Erebia tyndarus* species complex

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The *Erebia tyndarus* species complex is a cluster of closely related alpine butterflies. Members of this group have been characterized so far by morphological and ecological characters, cross-breeding experiments, karyology, and molecular data from allozymes and mitochondrial DNA (mtDNA). However, the delimitation of species, their relationships, as well as the origin of their peculiar geographic distribution, are still largely unclear. We employed restriction sites associated DNA (RAD) sequencing in order to clarify the systematic and genetic relationships among taxa of the *E. tyndarus* “Alpine” clade. Our results showed, for the first time, that the four species traditionally recognized in this clade (*E. tyndarus*, *E. calcaria*, *E. nivalis*, *E. cassioides*) indeed correspond to very well defined genetic units, which can be easily identified even by analysing small subsets of 15-20 of polymorphic markers. A species tree analysis based on a subset of 400 SNPs indicate that the four species gradually diverged from each other within the last 150,000 years. In contrast to the neat delimitation provided by nuclear RAD data, we did not find any species-specific synapomorphies at 2100 bp of mtDNA (Figure 1b), despite a clear intraspecific geographic structure. Moreover, our RADsequencing approach allowed to reveal the presence of *Wolbachia* endosymbionts in all of the species and geographic regions. We thus used coalescent simulations to compare the probability of the observed mtDNA data under a ‘neutral’ scenario of divergence fitted to our RAD-SNPs data and under a non-neutral scenario involving mtDNA replacement driven by *Wolbachia* infection. Results clearly indicate that a neutral scenario is extremely unlikely, and that the lack of interspecific mitochondrial differentiation in the *E. tyndarus* ‘Alpine’ clade is most probably due to a *Wolbachia*-driven mitochondrial replacement occurred ca. 15,000 – 40,000 years BP.

POSTER 118.

Cytogenetic mechanisms and evolutionary dynamics of chromosome number evolution in butterflies (Insecta: Lepidoptera)

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The order Lepidoptera is generally characterized by a stability of karyotypes, and between-species variation in chromosome number is usually very low or absent. Most species have the same haploid number of chromosomes, $n = 30$ or 31 . However, several complexes of closely related species of butterflies demonstrate high level of chromosome number variation. For instance, the subgenus *Polyommatus* (*Agrodiaetus*) of the family Lycaenidae is characterized by one of the highest variation in chromosome numbers across invertebrates (from $n=10$ to $n=134$). The variability is not associated with polyploidy and is caused by multiple chromosome fusions and fissions. Chromosome stability, on one hand, and high variability in the chromosome numbers, on the other hand, suggest that in the evolution of butterflies periods of chromosome conservatism can be interrupted by periods of fast karyotype changes. In our research we addressed the questions of cytological and evolutionary mechanisms underlying the rapid change of chromosome number. First, using methods of classic and molecular cytogenetics (such as fluorescent in situ hybridization), we conducted a comparative study of karyotypes in groups with a high level of interspecific karyotype diversity. A special attention was paid to *Polyommatus* (*Agrodiaetus*) phyllis species group, in which closely related or even sister species were discovered to have extremely different chromosome numbers. Second, we applied comparative phylogenetic methods to check different hypotheses about rapid chromosomal evolution. It has been tested whether chromosomal numbers possess a phylogenetic signal. We also checked the compliance of karyotype evolutionary dynamics to the models of complex trait evolution. Based on phylogenetic data and distribution of traits across the phylogenetic tree, our approach allows defining rapid karyotype evolution in terms of Brownian motion model. Thus, karyotype diversity evolutionary dynamics can be explained by a stochastic process without implication of natural selection.

POSTER 119.

Hidden diversity of Caucasian blues of the *Polyommatus* (*Agrodiaetus*) *ripartii* species complex (Lepidoptera, Lycaenidae): Assessing species taxa by chromosomal and molecular data

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The butterflies of the Western Palearctic *Polyommatus* (*Agrodiaetus*) *ripartii* species complex are model systems in evolutionary research, and are important in conservation. Despite this fact, their taxonomy is poorly elaborated since