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05 – 29 Poster

PHYLOGEOGRAPHY, PHENOLOGY AND MORPHOLOGY OF BALKAN SNOWDROPS (*GALANTHUS SPP.*)

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The genus *Galanthus* L. (Amaryllidaceae) comprises 22 species, which are perennial bulbous petaloid monocots, commonly known as snowdrops. It is distributed throughout Europe, Asia Minor and the Near East. *Galathus spp*. are cherished garden plants and the world's most traded wild-sourced ornamental bulb genus, threatened by illegal collecting and habitat destruction and thus listed in Appendix II of the CITES. However, species delimitation is problematic and the infrageneric classification uncertain, mainly due to the overall morphological similarity within the genus, and lack of easily discernible distinguishing characters. In order to shed light on taxonomy and evolutionary history of *Galathus* species from the Central Balkans, we analyzed variability of three plastid regions (*rps16-trnK, trnL-trnF* and *trnE-trnT*) in 119 individuals from 40 populations representing six species (*G. nivalis*, *G. elwesii* and *G. reginae-olgae* occurring naturally in this region and three allochthonous species, phenology in 21 populations representing two species (*G. nivalis* and *G. elwesii*), and variability of 13 quantitative characters in 510 individuals from 17 populations belonging to one species (*G. nivalis*). Although evolutionary relationships among species were not fully resolved, they were concordant with those based on morphological data (sensu Davis), with the exception of *G. gracilis* which was not grouped with *G. elwesii* and *G. woronowii*. Interspecific hybridization between *G. nivalis* and *G. reginae-olge* was detected. We observed a phylogeographic structure in the Balkans, with eight lineages distributed throughout this region. The most recent common ancestor of *G. nivalis* lineages was dated to the 1.683 Mya (1.089 Mya - 2.376 Mya), and diversification of more or less all *G. nivalis* lineages took place during the past 0.500 Mya. Phenological differences were observed among six *G. nivalis* lineages, of which one was characterized also by specific morphological traits.

CITES, *GALANTHUS SP.*, MOLECULAR DATING, MORPHOLOGY, PHYLOGEOGRAPHY, PLASTID GENOME, PHENOLOGY

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05 – 30 Poster

POSSIBLE EVOLUTIONARY PATHWAY OF B CHROMOSOMES IN YELLOW-NECKED MOUSE, *APODEMUS FLAVICOLLIS*

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B chromosomes (Bs) are supernumerary chromosomes in standard karyotype, unnecessary for normal growth and development. Bs are present in 3% of all analyzed eukaryote species. The most specific characteristic of those elements is great heterogeneity considering: origin, morphology, size, number and molecular content. This heterogeneity goes from individual to population level. Our recent studies, revealed the molecular structure and potential origin of these supernumeraries from sex chromosomes in yellow-necked mouse, *Apodemus flavicollis*. Here, we analyse structure of Bs in specimens from geographically distant populations. Our findings indicate that regions of almost all chromosomes from standard karyotype can be found on Bs. Detected differences among Bs from distant populations are unexpectedly small. In this content we consider possible evolutionary scenario in order to explain this lack of Bs' heterogeneity in *A. flavicollis*.

B CHROMOSOMES, *APODEMUS FLAVICOLLIS*, EVOLUTION