

## Abstract of Contribution 200

### Radiation and Speciation

#### Ecological adaptation leading to speciation in *Lathyrus*: Combining nuclear spacer data and phytosociologic surveys using phylogenetic networks

Schlee M.<sup>1</sup>, Göker M.<sup>2</sup>, Grimm G.<sup>3</sup>, Sauer W.<sup>2</sup> and Hemleben V.<sup>1</sup>

<sup>1</sup>University of Tübingen, Center for Plant Molecular Biology (ZMBP), Germany; <sup>2</sup>University of Tübingen, Special Botany & Mycology, Germany; <sup>3</sup>University of Tübingen, Institute of Geosciences (IfG), Germany; [matthias.schlee@uni-tuebingen.de](mailto:matthias.schlee@uni-tuebingen.de)

Extreme intraindividual and intraspecific variability has been detected by cloning and sequencing a large number (290) of nrDNA spacers (internal transcribed spacers, ITS1 and ITS2, and 5' external transcribed spacer, 5'ETS) of >30 specimens of *Lathyrus pannonicus*. The degree of variability can not be handled with standard phylogenetic approaches to reconstruct evolutionary pathways. Therefore, we use phylogenetic networks in combination with (novel) distance functions (based on morphological and molecular data) to model the radiation and migration of *Lathyrus pannonicus*, originating in Eastern Eurasian steppes and exceeding to distinct and endangered relict (post-) glacial sites in Central Europe. Patterns of morphological and genetical diversification in *Lathyrus pannonicus* can be attributed to an ecological shift from xerothermic to even moisture habitats, evidenced by accompanying phytosociological studies, and to a wide spectrum of potential glacial refuges and (re-) migrations between temporarily isolated populations. The complex pattern of intraindividual nuclear spacer variability reflects both, on-going speciation (in course of the ecological shift) and migratory pathways. These processes are partly independent from each other and, hence, result in an agglomeration of competing phylogenetic signals. Our detailed analyses demonstrate the potential of nrDNA sequencing for modelling radiation in the legume family at the species level as a source of phylogenetic signal originating from incongruent evolutionary processes.