

Broad data from nrDNA spacers fill the gap between population studies and phylogenetics – a case study of *Lathyrus* and *Oxytropis* (Fabaceae)

Matthias Schlee (University of Tübingen, Center for Plant Molecular Biology, ZMBP, Auf der Morgenstelle 28, 72076 Tübingen, Germany)

Co-authors:

Guido W. Grimm (University of Tübingen, Institute of Geosciences, IFG, 72076 Tübingen, Germany)

Wilhelm Sauer (University of Tübingen, Special Botany & Mycology, 72076 Tübingen, Germany)

Vera Hemleben (University of Tübingen, Center for Plant Molecular Biology, ZMBP, 72076 Tübingen, Germany)

Intra-individual and intraspecific genetic variability can be detected by cloning and sequencing a large number of tandemly repeated nrDNA spacers (internal transcribed spacers, ITS1 and ITS2, and 5' external transcribed spacer, 5'ETS). The organisation and molecular evolution of nrDNA spacers (biparentally inherited, multi-copy, undergoing concerted evolution as well as frequent recombination) allows us to trace back population dynamics evaluating various molecular signals. Here, we report on strategies of two rare species, *Oxytropis pilosa* and *Lathyrus pannonicus*, originating in Eastern Eurasian steppes and exceeding to distinct and endangered relict (post-) glacial sites in Central Europe, where they often share the same xerothermic refuges. *Oxytropis pilosa* is morphologically highly conserved, and two general sequence types, an Eastern and a Western type with a transition zone in Central Europe, can be distinguished; additional unique mutations characterize outermost populations. *Lathyrus pannonicus* shows a higher morphological and genetical diversification due to a) an ecological shift from xerothermic to even moisture habitats as traced by accompanying phytosociologic studies, and b) a broader spectrum of biogeographic glacial refuges and (re-) migrations between these regions. Especially, in the case of *L. pannonicus* the complex pattern of intra-individual variability and differentiation reflects on-going speciation (in course of an ecological shift) and migratory pathways, which are partly independent from each other. Our detailed analyses demonstrate the value of nrDNA sequencing for inter- and intrageneric taxonomy, filling the gap between sequence-based phylogenies and genetic analyses at population level.