

Institute: Institute of Botany

Topic: Taxonomy, phylogeny and population genetic diversity of high mountain species from the genus *Ptilagrostis* (Poaceae) in Central Asia

Name of supervisor: prof. dr hab. Marcin Nobis
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Background information:

Although the mountains of Central Asia have been recognised as one of the biodiversity hotspot, the factors driving their exceptional species diversity and endemism are poorly understood. Large differences in relative and absolute altitude, the isolation of individual mountain systems, as well as their considerable size, make the region unique in phytogeographic and phylogenetic analyses of high montane plant species (many of them being endemic to the region), studies of distribution patterns of species and vegetation, and potential threats associated with climate changes. Thus, genetic patterns of population and species diversity as well as the estimation of the potential changes in the number of species and area of endemic vegetation are a priority for conservation biology in this region.

The main questions to be addressed in the project:

We would like to know what is the floristic diversity and species richness of the alpine meadows vegetation in the Central Asian mountains as well as what are the patterns of genetic diversity and phylogenetic relationships of species representing the genus *Ptilagrostis* (Poaceae) – one of the main member of this vegetation.

Information on the methods/description of work:

Field research will be conducted in the mountains of Central Asia (Tian-Shan: Kyrgyzstan, Kazakhstan; Pamir-Alai: Kyrgyzstan, Tajikistan, Altai: Kazakhstan) in localities with alpine meadows. During fieldwork, environmental data as well as plant materials for morphological, molecular, syntaxonomic and phytogeographic examinations will be collected. Phylogenetic analyses will be based on amplification and Sanger sequencing of plastid DNA, whereas analyses of genetic diversity of *Ptilagrostis malyshevii*-*Ptilagrostis mongholica* agg. populations will be done by genotyping of DNA using DArTseq methods. A database on the distribution and ecology of selected species will be based on available bibliographic data, herbarium data, and data obtained during field studies conducted by the project team. SNP genotyping by high-density sequencing will be done by using the DArT method, which represents a combination of complexity reduction method and next-generation sequencing. Statistical analysis will be performed in R.

Special requirements from the student:

A potential candidate should possess knowledge and experience in designing and conducting interdisciplinary research. The candidate needs to have the ability to work in the research team. Oral skills in Polish and excellent written and oral skills in English language are required.

Name of potential foreign collaborator:

Dr Wen-Lee Chen, Beijing, China, and Dr. Polina Gudkova, Tajikistan.

References

- [1] Agakhanjanz, O. & Breckle, S.-W. 200). Plant diversity and endemism in high mountains of Central Asia, the Caucasus and Siberia. In Ch. Korner, & E. Spehn (Eds.), Mountain Biodiversity – A Global Assessment. Boca Raton, New York: Parthenon Publ. Group.
- [2] Romaschenko, K., P. M. Peterson, R. J. Soreng, N. Garcia-Jacas, O. Futorna & A. Susanna. 2012. Systematics and evolution of the needle grasses (Poaceae: Pooideae: Stipeae) based on analysis of multiple chloroplast loci, ITS, and lemma micromorphology. *Taxon* 61: 18–44.
- [3] Tzvelev N.N. 1976. *Zlaki SSSR*. Nauka, Leningrad.