



Deutsche Botanische Gesellschaft
Tagung der Sektion
Biodiversität & Evolutionsbiologie

**19th International Symposium
“Biodiversity and Evolutionary
Biology”
of the German Botanical Society
(DBG)**

Vienna, 16. - 19. September 2010

Program & Abstracts



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All events take place in the Biodiversity Centre if not indicated otherwise.

Thursday, September 16th

- 16.00 - 19.00 Registration onsite (Aula)
- 19.00 - 22.00 Welcome (Biodiversity Centre and Botanical Garden)

Friday, September 17th

- 08.00 - 08.30 Welcome Address** (Lecture hall)
- Prof. Dirk Albach, Oldenburg, Chair section Biodiversity and Evolution of German Botanical Society
- Prof. Georg Grabherr, Wien, Speaker of Faculty Centre of Biodiversity, Head of Department of Conservation Biology, Vegetation- and Landscape Ecology
- Prof. Tod Stuessy, Wien, Head of Department of Systematic and Evolutionary Botany
- 08.30 - 09.30 Opening Lecture: Integrating molecular and morphological data in phylogenetic analysis: the water-lilies as model group** - Thomas Borsch, Berlin (Lecture hall)
- 09.30 - 10.30 Symposium: Trends in Systematics** (Lecture hall)
- Chair: Dirk Albach, Oldenburg
- 09.30 – 09.50 Radiation of *Hypochoeris* (Asteraceae) in South America after long-distance dispersal from northwestern Africa - Tod F. Stuessy et al.
- 09.50 – 10.10 Molecular phylogenies of European members of *Euphorbia* subg. *Esula* - Božo Frajman and Peter Schönswetter
- 10.10 – 10.30 Chemodiversity: biodiversity beyond chemical structures - Karin M. Valant-Vetschera

Molecular phylogenies of European members of *Euphorbia* subg. *Esula*

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Euphorbia (Euphorbiaceae) is with over 2150 species one of the largest genera of flowering plants. In Europe, it is represented by more than 100 species with highest diversity in the Mediterranean area. The majority of the European taxa belong to the species-rich subgenus *Esula* Pers. The few available phylogenetic studies of *Euphorbia* showed that most members of subg. *Esula*, along with some additional taxa, form a monophyletic clade, but the phylogenetic relationships within the clade remain poorly understood.

We have sampled DNA sequences of nuclear ribosomal ITS and the plastid *trnT-trnF* region from about 80, predominantly European taxa of subg. *Esula* in order to infer its phylogenetic history. The phylogenies inferred do largely not corroborate the traditional sectional delimitations and the relationships among and within them are often incongruent between both DNA regions used. The clades receive better support in the plastid tree, the ITS region being less informative. Molecular dating of the *trnTF* data set in a Bayesian framework, using a relaxed clock model and published substitution rates indicates that the diversification within subg. *Esula* begun roughly 5.3 million years ago, when the main groups started to diverge. The character state reconstruction illustrates that the annual life form developed several times in different clades of subgenus *Esula*, and that combining several annual taxa in one taxonomic group as traditionally practised is highly artificial.