

## IUFRO SYMPOSIUM ON POPULATION AND EVOLUTIONARY GENETICS OF FOREST TREES

Stará Lesná, Slovakia, August 25–29, 2002

A Symposium dedicated to the topics of population and evolutionary genetics of forest trees was held from August 25 to 29, 2002, in the Congress Centre of the Slovak Academy of Sciences in Stará Lesná, Slovakia. The Symposium was hosted by the Faculty of Forestry of the Technical University in Zvolen and organised by the IUFRO RG 2.04.00 "Genetics". The Symposium was a part of the festivities organized on the occasion of the 195<sup>th</sup> anniversary of the higher forestry education in Slovakia and the 50<sup>th</sup> anniversary of the Technical University in Zvolen (former College of Forestry and Wood Technology).

In total, 132 scientists who participated in the Symposium (including 10 accompanying persons) represented 31 countries of Europe, North and Central America, Africa, Asia and Australia. In addition, in the opening ceremony participated Heinrich Schmutzenhofer, the Secretary General of the International Union of Forest Research Organizations, Jozef Turok, Director of the European Office of the International Plant Genetic Institute, Rome, and Professor Mikuláš Šupín, Rector of the Technical University in Zvolen.

The tradition of the IUFRO Symposia on Population Genetics of Forest Trees started in 1984 in Göttingen. After that followed successful IUFRO symposia aimed at the same or similar topics organized between 1986 and 1996 in Porano (Italy); Corvallis (USA); Mauboussin (France); Gent (Belgium), the last conference was organized in 1999 in Freising (Germany). Roughly counting (there were also some other smaller IUFRO events) this is the seventh event of the Research Group 2.04.00 Genetics.

The last IUFRO Conference held in Freising (Germany) was focussed mainly on forest tree populations impacted by air pollution and changing environments. Although forest tree populations are still significantly impacted by global changes and, at least in Europe, by air pollution, this symposium has been mainly aimed at natural populations and the evolution-

ary processes and phylogeny.

This Symposium was divided into five indoor sessions, two poster sessions and excursions. The main sessions of the symposium were:

- (1) Gene diversity and differentiation of natural populations
- (2) Gene flow in natural and breeding populations
- (3) Introgressive hybridization and phylogeny of forest trees
- (4) Gene diversity as the basis for adaptation
- (5) Genomics, gene mapping, QTLs and gene markers as biomonitoring tools.

Symposium started with invited key-note address by Cs. Mátyás "Allochthony and autochthony in the perspective of evolutionary genetics" in which he outlined the impact of forestry practices on the make-up of the European forests.

In five sessions 10 invited papers and 26 voluntary papers were presented.

In two poster sessions, 48 posters were presented which covered the complete range of the five symposium sessions, although individual sessions were unequally represented.

A half-day excursion within the Tatra National Park (Slovakia) was aimed at *in situ* gene conservation practices combined with natural regeneration of mixed silver fir and Norway spruce stands as well as the nature conservancy strategy of the Tatra National Park. Excursion was combined with the cable car trip to Skalnaté Pleso (1500 m a.s.l.) at the upper tree limit and the visit of the Museum of the Tatra National Park.

Three full-day excursions were aimed at the *in situ* gene conservation practices linked with the visit of the Dobroc virgin forest in Central Slovakia and the Cierny Váh valley with a unique occurrence of the European larch forests, the visit of the Polish Tatra National Park in Zakopane aimed at the nature conservation and sightseeing and the visit of Pieniny National Park (canyon of the Dunajec river).

Session	Invited speakers	Number of	
		voluntary contributions	posters
1 Gene diversity and differentiation of natural populations	G. G. Vendramin W. Ratnam	9	17
2 Gene flow in natural and breeding populations	J. Burczyk	4	5
3 Introgressive hybridization and phylogeny of forest trees	A. E. Szmidt	5	12
4 Gene diversity as the basis for adaptation	A. Kremer O. Savolainen	4	4
5 Genomics, gene mapping, QTLs and gene markers as biomonitoring tools.	D. Neale F. C. Yeh G. Müller-Starck	4	4
Others			6

