



**Universitatea *Transilvania* din Braşov**

**HABILITATION THESIS  
SUMMARY**

**Evaluation of genetic diversity in forest tree species in Romania**

**Domain: Forestry**

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**BRAŞOV, 2016**

Genetic diversity is essential to the adaptive potential and long-term survival of species. The purpose of this thesis was to evaluate the patterns of genetic diversity of forest tree species in Romania by using various types of genetic markers (enzyme coding genes, PCR-RFLPs, genomic SSRs, EST-SSRs). The focus was on the understanding of the evolutionary forces responsible for causing the current distribution of genetic diversity within and among tree populations.

A lot of research has been devoted to determine the patterns of genetic diversity within and among species belonging to genus *Quercus* (oaks) that is well known for its taxonomic complexity. Differences in leaf morphology and genetic structure between *Q. robur* and its closest relative, the drought tolerant *Q. pedunculiflora*, were evaluated. The analysis of seven enzyme coding gene loci revealed a very low level of nuclear divergence and an incomplete sorting of *Q. robur* and *Q. pedunculiflora* populations according to their physical appearance. All DNA chloroplast haplotypes observed in *Q. pedunculiflora* have been detected in the *Q. robur* sample or have been previously reported in *Q. robur*. However, the two taxa were genetically separated by means of 22 highly polymorphic gSSR and EST-SSR markers. One population of each taxon was sampled at three geographic locations. In accordance with the assumption that *Q. pedunculiflora* and *Q. robur* are separate taxonomic units, all populations of the same taxon grouped together. The Bayesian analyses indicated that a genetic structure with two clusters, corresponding to *Q. pedunculiflora* and to *Q. robur*, respectively, best fits the molecular data. As expected, EST-SSR markers showed lower diversity within oak populations and higher divergence among populations and species than gSSRs. The results suggest that *Q. pedunculiflora* is an incipient species or subspecies of *Q. robur*, and that the process of ecological speciation is not yet completed.

A high and significant genetic differentiation was observed between *Q. frainetto* and *Q. pubescens*, two species of section *Dascia* that reach in Romania the margins of their natural distribution range. By using a combined set of only seven gSSR and EST-SSR markers, the vast majority of sampled individuals were genetically assigned to the cluster corresponding to their phenotype. The higher degree of admixture in *Q. frainetto* compared to *Q. pubescens* may be explained by different rates of introgressive hybridization.

The presence of fine-scale spatial genetic structure (SGS) was tested in a four-oak-species forest with contrasting species abundances and hybridization rates. A weak but significant SGS was observed in each of the four oak species, with *Q. frainetto*, the species with the lowest density in the sampling plot, exhibiting the strongest SGS. The spatial correlogram of the total population

was significantly different when hybrids were removed from the analysis, which suggests that hybridization has weakened the SGS.

A high genetic differentiation among Romanian oak species ( $F_{ST}$  values up to 0.91) was revealed at a dehydrin gene (*Dhn-3*) that is involved in plant response to environmental stress. Frequencies of the two major alleles varied markedly between four oak species (*Q. robur*, *Q. petraea*, *Q. frainetto* and *Q. pubescens*) but not among populations within species. Only the closely related *Q. robur* and *Q. pedunculiflora* were not significantly differentiated at *Dhn-3* locus.

To test for genetic differences between the two pubescent oak species of Romania, *Q. pubescens* and *Q. virgiliana*, seven highly polymorphic gSSRs were used. A very low level of genetic differentiation was found and no statistical support for two distinct genetic entities was obtained.

Chloroplast DNA diversity was analyzed in 61 populations of *Q. robur* and *Q. petraea* in Eastern Romania. A high number of chloroplast DNA haplotypes were observed and shared by both species. Different dispersal abilities may explain the higher value of genetic differentiation among populations in *Q. petraea* than in *Q. robur*.

The level and distribution of genetic diversity at enzyme coding loci was analyzed in the most important coniferous species of Romania (*Picea abies*). Extensive gene flow may explain the very low genetic divergence among populations across Carpathians and pairs of low and high elevation populations. Genetic diversity of drought-tolerant and sensitive individuals from an ecologically marginal population of *Abies alba* was assessed using newly characterized EST-SSR markers.

My future research directions will focus on using the new genotyping and analytical tools to infer the evolutionary history of forest tree (and wild animal) populations and to address future evolution of populations in the context of environmental changes.