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Population Genetics and Genomics of Forest Trees: From Gene Function to Evolutionary Dynamics and Conservation

A joint conference of IUFRO Working Groups **2.04.01** (*Population, ecological and conservation genetics*) and **2.04.10** (*Genomics*), and COST Action **E-28** (*Genosilva: European Forest Genomics Network*)

PROGRAMME and CONFERENCE ABSTRACT BOOK

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Heritabilities out of the beaten test site: looking at the perspectives of in situ inferences for forest tree species with a preliminary study in *Quercus* species.

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With non domesticated species, like most forest trees, the assessment of heritability for traits of adaptive relevance represents one of the first steps granting future conservation and breeding programs. This essential step, however, is lengthy to conduct on long-lived species, implying mostly ex situ experiments and little environmental resemblance to the original populations. A major obstacle for in situ genetic studies has been the difficulty in grasping the extent of family interrelations in natural populations. Recent developments in molecular biology, however, are making genetic markers readily available and more efficient for measurement of relatedness. Theoretical improvements have also been proposed to infer the heritability and the evolution of genetic variance from the joint analysis of natural relatedness and the in situ quantitative trait variation. Here we propose one of the first evaluations with forest tree species of this in situ approach. The studied population comprised 280 trees of two interbreeding species: Quercus petraea and Quercus robur. This study considered as many as 60 different traits: foliar morphology, growth, phenology, wood properties, wood defects and wood biochemical compounds, some of which with no published records of heritability estimations. A total of 17 highly polymorphic microsatellite markers were studied in the sample. The genetic markers revealed low levels of relatedness and variance of relatedness, which are in principle unfavourable conditions for the detection of heritability. We proceeded by ranking the estimates among traits, and carried out randomization test to setup confidence intervals. We found that those traits known to be highly heritable in the species or at least in related taxons (i.e. phenology, wood physical and biochemical properties) appeared at the top of the trait ranking for the two species, with highly significant associations between the genetic distance revealed by the genetic markers and the phenotypic resemblance. On the opposite, other traits known to have moderate heritabilities, like growth, showed positive but no significant associations. Moreover, the two species exhibited different heritability patterns for leaf morphology traits, known to discriminate Quercus species. Although this in situ methodology cannot substitute its more precise ex situ counterpart, it could become an excellent exploratory tool of the natural occurring variation, and the detection of valuable populations for conservation purposes. We discuss the role of some useful add-ons that might further improve this in situ approach, like spatial statistics and simulation studies.

NOTES:

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