Accademia Italiana
di Scienze Forestali

RIASSUNTI DEI CONTRIBUTI ORALI

ABSTRACT BOOK OF ORAL CONTRIBUTIONS

Sessioni / Sessions 1-4

Key words: *Quercus suber*, *Quercus ilex var rotundifolia*, flowering/fruiting, phenology, genetic variability

Background and Aims
Flowering and fruiting studies at cork oak and holm oakperformed at various plots in Portugal during several years aim to evaluate the population effective size (Ne), the flowering synchronisation, the possibilities of inter-specific hybridization and the occurrence of mast seed years for assessment of genetic variability in seed sources and conservation of genetic resources.
The cork oak and holm oak ability for clonal stump/root propagation, frequently used by forest owners and managers after fire and to propagate interesting phenotypes reaching old age, has been estimated in various stands. The consequences for genetic variability and the possibility of genetic senescence are discusseddue to aging of the root system.
Results are a contribute for assessment of genetic variability for further use on seed collection guide lines on afforestation programmes, animal grazing in silvopastoralism, seed stands/orchard management and management of conservation of genetic resources.
Key Results
The resultson flowering and fruiting ability show that holm oak is more precocious, has a more stable and predictable reproductive behaviour and has less frequently poor seed years than cork oak.
The reproductive capacity is site-quality and tree-vigour dependent. For cork oak at Quinta da Serra plot (good site) the Ne ranges from 40%-80% while at the poor site plot ÁguaFerrenha it varies from 10%-20%.
For the same year at mixed plots of cork oak and holm oak at Quinta da Mitra and Coudelaria de Alter holm oak always exhibits a considerable high Ne.
In mixed stands and years of odd weather the flowering suffers phenological changes that lead to overlap, opening possibilities for intersections and inter specific hybridization
The ability of *Quercus* species to sprout from dormant buds at the stump and roots after a cut/torn down tree is being extensively used as after-fire or decline stand recovery and to propagate interesting phenotypes. This type of clonal propagation often gives origin to various individuals that are a clone set from the the treethat existedand in various stands it is exceeding recruitment from seed origin.
Evaluation of the rate of extensive clonage has been done in 2012 and 2013 at two stands with decline and one stand that suffered a fire hazard in 2003.
On mild situation of decline and fire thenumber of stumps/root signsstillvisible the clone sprouting is minor upon seed origin, while on strong fire situation more than 2/3 of the trees are from clonal origin
This clonal propagation is liable to induce decrease in the number of genetically unrelated individuals upon the natural stands. Over the years when the traces of the stump are not visible it is no longer possible to differentiate trees from clonal origin from seed.
Clonal propagation at cork oak and holm oak shall be used sporadically and scattered either in time and space. Lturning stands less able to respond to changing environmental conditions and adaptation to biotic and abiotic factorsPoor rate of sexual recruitment and the associated low genotypic diversity can further affect the population’s long-term ability to reproduce sexually.
On stands where extensive clonal propagation is being favoured the levels of kinship should be assessed by means of molecular markers. If the level of relationship proves high actions to increase genetic diversity through sexually originated plants should be put in place.

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Characterization of the international network FAIR 202 of provenance and progeny trials of cork oak on multiple sites for further use on forest sustainable management and conservation of genetic resources

Keywords:*Quercus suber*, genetic variability, genetic improvement, selection, adaptation under climate change

The international network of provenance and progeny trials was established in 1998 in France, Italy, Portugal, Spain and Tunisia under the EU Commission financed concerted action FAIR 202 benefiting from homogeneous plant raising and standardize experimental design.

The trials include 34 provenances that are being characterised using quantitative genetics and molecular genetics to study survival, growth, morphological and physiological traits in relation with geographical origin.

France 2008– Provenance were assess using survival, growth (height) and vigour parameters. Provenance PT 23 and PT+ES 25 had the lowest survival rate respectively 79,2% and 77,8% while ES 8, ES 7, MA 31 and PT 19 had 94,4%. In 2008 the mean height at Les Maures was 48.73 cm and the form keeps plagiotropic.

Italy- Sardinia, Grighine, 2010

The average mortality was 7%, ranging from 13-14% at the provenance IT LA-VT; IT SI-CT; MO I-1 and 0-2% for FRII, ES 3-V, ES F-PAR, PT IV-03, TU I; TU II. Mean height and trunk DBH over cork were respectively 273cm and 5.1cm.

MO I-2, TU II, ES 4-CR are above mean on height (302-309 cm), and the Italian provenances are under mean (237-249cm). The maximum DBH was reached by MO I-2 (6 cm) followed by ES-4 CR and MO III-2 (5.8 cm) and the minimum is at IT PU-BR (3.8 cm), followed by the other Italian provenances (4-4.6cm) and PT V-01 (4.5 cm).

Portugal

Results from field trials show significant differences among populations on survival, growth and adaptive traits (phenology, water use efficiency - WUE).

Mogadouro trial, 2011 -provenance variation was assessed using growth, vigour and survival. The bud burst as adaptive characteristic was observed during 2011-2013. The Moroccan provenances show good adaptive characteristics in terms of growth, vigour and stem form. There was no significant differences ($p<0.05$) in provenances bud burst. The mean height is not correlated with survival. Italian provenances present lower height but higher survival. The overall mortality is around 26%.

The highest growth is being observed in the Moroccan provenances and French ones showed lowest survival.

Results from field trials at Italy (continent), Spain and Tunisia are also referred.

Genotype by environment interaction (G x E) is discussed.

Due to the large variability of responses between cork oak provenances we emphasise the importance to use these results when considering the seed origin aiming for large scale planting programs for adaptation, cork quality, pest and diseases susceptibility and for conservation of genetic resources,

Progeny trials provide key information for genetic improvement programmes on estimates of breeding values on economic characteristics such as cork quality and an approach on inbreeding problems.

Perspectives

Used in synergy the results from provenance and progeny trials are likely to provide insights for balancing the conflicting objectives such as maximising selection intensity while maintaining variation. Taking into consideration that the cork from the second striping made 3-4 years after the first gives information about the quality liable to be used on selection for afforestation guide lines we enhance the need of concerted criteria on debarking season and procedures.

The results from these trials will contribute to the knowledge on genetic variation and are a privileged living material to study climate change effects and adaptation to biotic and abiotic factors and for sustainable management of this long living species.

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Molecular signatures of climate adaptation in Mediterranean conifers

Understanding range-wide patterns and interactions among environments, demography and evolution is essential in the face of impending climate change. Species from the Mediterranean Basin, inhabiting highly heterogeneous environments, are particularly at risk because of the predicted increase in aridity and recent land-use change in this area, which fosters fragmentation. Conifers are ecologically and economically important tree species and it is hence of great interest to assess their adaptive potential to foreseen climate changes. In this talk, we review our studies on population genomics and association genetics in maritime and Aleppo pines, two relevant elements of Mediterranean landscapes. In maritime pine (*Pinus pinaster*Aiton), 17 SNPs (Single Nucleotide Polymorphisms) were found to be strongly correlated with climate, once population genetic structure was removed from environmental association models. The utility of these SNPs to predict climate maladaptation of forest stands was further tested in a common garden showing that genetic distance to optimal allele frequencies resulted in reduced survival. At the same time, some of these loci were correlated with both fire-related and drought traits using association genetic approaches. In Aleppo pine (*Pinus halepensis* Miller), we are studying the genetic signatures of range expansions, from refugia populations in Turkey and Greece towards its large western Mediterranean distribution. This species showed signatures of selection while expanding its range in a previous study based on drought-response candidate genes. However, new SNP data showed signals of recurrent bottlenecks in the colonized range and ‘gene surfing’ in the expanding wage of colonization appears now as a feasible alternative explanation. These studies at large spatial scales are accompanied by research at local scales aiming at detecting the role of micro-environmental variation in creating and maintaining genetic diversity within populations. The combination of approaches and spatial scales gives an integrated view to understand the quantitative genetic and molecular mechanisms responsible for adaptation as well as the drivers of selection (both climatic and ecological) in Mediterranean conifers. Furthermore, it will also provide a basis to identify population differences that may help the species to survive future environmental changes, as well as insights on optimal management strategies for the future European forests.

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Monitoring of genetic diversity - an early warning system to aid the assessment of a species response to environmental change at a long-term temporal scale

Keywords: monitoring, genetic diversity, indicator, LIFEGENMON