Proceedings of the XLIX Italian Society of Agricultural Genetics Annual Congress
Potenza, Italy – 12/15 September, 2005
ISBN **88-900622-6-6**

Poster Abstract – C.66

MULTILOCUS LINKAGE DISEQUILIBRIUM SCAN IN *POPULUS* GENOME

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linkage disequilibrium, poplar genome, association mapping, Populus alba, Populus nigra

Linkage disequilibrium (LD) is currently the focus of many studies for its application in association mapping of quantitative or adaptive traits in natural populations of outcrossing long-lived plants. The extent of LD across the genome under study determines the feasibility of two different association approaches, whole genome scan and candidate gene approach, since it affects the number of markers that should be genotyped.

At the moment, no studies on LD across extensive regions of the genome are available for forest trees. The recent release of the genome sequence of *Populus trichocarpa* offers a unique opportunity to analyse the structure of the poplar genome and map important genes.

Preliminary analysis on sequence variation and linkage disequilibrium in *Populus nigra* showed that LD extends over 5 Kb, but definitely decays within 100 Kb. On the basis of these data, LD has been measured (R^2 measures) at four genomic regions, each 100 Kb in length and composed of different consecutive sequence tracts spaced 1 – 3 Kb apart. These four regions are considered unlinked as distant more than 6 Mb or located on different chromosomes, *i.e.* linkage groups II, VIII, XIV on the *P. trichocarpa* genome. 24 unrelated genotypes of *P. nigra* belonging to a French and an Italian populations and 24 of *Populus alba* belonging to European and Northern Africa populations were analysed in this study. At each genomic tract SNPs were identified and SNP haplotypes determined. We used different softwares (Haplotyper, Phase, LDanalyzer) to infer haplotypes, as a requirement for LD estimation, and we eventually selected LDanalyzer (http://www.chgb.org.cn/lda/lda.htm) after comparison of the haplotype inferences to cloned sequences (known gametic phase).

We first analyzed patterns of LD within the chromosomal regions under study in the two species by considering triangle plots of LD between SNPs (minor allele frequency greater than 0.1), where we observed variable patterns of LD across the four genomic regions surveyed. We next estimated the extent of LD in the two poplar genomes considering the overall LD decay plot for SNP pairs within each chromosomal region. The distribution of R^2 values had a similar trend in the two species with an higher average value in *P. alba* (average R^2= 0.20) than in *P. nigra* (average R^2= 0.14) and in both species the LD slowly decayed to R^2= 0.1 at a distance of 90 kb. Since LD is a property of the natural population under study, we also evaluated LD extent in the two populations (French and Italian) of *P. nigra* considered in this work. The distribution of R^2 values across the four chromosomal regions suggested a slightly more extensive LD in the Italian population than in the French one, even though no significant differences ($P > 0.05$) were detected between the two distributions.

Our results suggest that LD in poplar is not extensive enough for a whole genome association approach, as too many markers should be genotyped for an efficient mapping. On the other hand, the candidate gene approach emerges as a promising approach for association mapping in poplar, since LD extends over distances that span one or a few genes.