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Poster Abstract – D.35

TIMING OF BUD SET IS ASSOCIATED TO POLYMORPHISMS WITHIN CANDIDATE GENES FOR FLOWERING TIME IN *POPULUS NIGRA*

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Natural populations of forest trees show adaptation to day- and seasonal-length of their local environment and their timing of bud phenology results to be correlated with the latitudinal and elevational origin of the trees. Bud phenology is also found to be under strong genetic control in forest trees, but very little is known about the identity of the genes responsible for genetic variation in bud phenology traits.

Association mapping, based on linkage disequilibrium (LD), offers an alternative method to dissect quantitative/adaptive traits in tree species, using ancestral recombination events in natural populations to make marker-phenotype associations. In a previous study, our group analysed sequence diversity and the linkage disequilibrium structure in a European poplar species, *Populus nigra*, as guidelines to design association studies. This research showed that in black poplar the levels of polymorphisms are not limiting for association studies and LD estimates are low but significant within few kbs, suitable for a candidate gene mapping approach.

In the present study, we identified a set of candidate genes for phenology based on the literature on flowering time pathway in *Arabidopsis thaliana*, with a particular interest on phytocromes, cryptochromes, signal integrators, vernalization factors and circadian clock factors. We then identified SNPs within those genes to be used as markers for the association. Identification of SNPs was possible by resequencing of amplified amplicons, taking benefit of the availability of the annotated genome sequence of *Populus trichocarpa*.

An association population of about 400 *P. nigra* genotypes, collected along 10 degree's latitude throughout Europe, was established in a common garden experiment. Bud set phenotypes were scored in the population and candidate gene SNPs genotyped. Despite the adaptive population differentiation of the bud set traits (Qst of 0.6), we observed low-to-moderate levels of genetic differentiation (Fst from 0.05 to 0.1) in the candidate genes analysed. We also found significant associations between a few candidate gene polymorphisms and bud set phenotypes.