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W245: Forest Trees

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### Sequence And Polymorphism Map Of The *Populus Nigra* Genome From A *de novo* Assembly Approach

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Progress in applying new methods to forest tree breeding has been slow considering the difficulty to acquire genomic data in the major commercial species. The situation has improved rapidly through whole genome sequencing in *Populus trichocarpa*, and EST sequencing in poplar.

Nevertheless, the genomic tools to develop molecular markers for advanced breeding are still inadequate, in particular for the native European poplar species, *Populus nigra*.

In the framework of a joint resequencing effort undertaken by the EU projects Evoltree, Noveltree, and EnergyPoplar, we first obtained the sequence of the *P. nigra* genome using Illumina technology and a *de novo* assembly approach. Our strategy was based on assembling together sequences from three libraries from a single genotype with different insert sizes that provided a total coverage of 60X. Then, we resequenced two individuals at high coverage and an additional fifty *P. nigra* genotypes representing the European latitudinal range at lower coverage (2X), and aligned their reads to the assembled sequence in order to detect SNPs and structural variants to produce a

whole-genome map of markers. The utility of the *P. nigra* assembly as reference for variant discovery in place of the *P. trichocarpa* sequence will be evaluated.

This *Populus* sequencing effort provides a valuable resource for population genetics and genomics. It will also be exploited to introduce the concept of the pan-genome, which includes core genomic features common to all individuals and a dispensable genome composed of non-shared DNA elements that can be individual- or population-specific and important for explaining phenotypic variation.