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Genome-Wide Structural Variation In Poplar

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GENOME-WIDE STRUCTURAL VARIATION IN POPLAR

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Background:

In the last few years, researchers realized that single nucleotide polymorphisms (SNPs) identified by genome wide association scans explained only a small proportion of the heritability of complex and quantitative traits. Several authors suggested that a substantial part of the missing heritability might reside in structural variants, such as copy number variants (CNVs).

Aim:

In the framework of the EU funded project EnergyPoplar and with the support of Evoltree and Noveltree EU funded projects, we set out with the aim of determining genome-wide structural variation in poplar, and of correlating structural variants (SVs) with heterotic behavior.

Results:

We performed next generation sequencing of 16 plants obtained from a factorial design composed by two *P. nigra* males, two *P. deltoides* females and 12 hybrids offspring (*P. nigra* × *P. deltoides*), three for each of the possible crosses. Average coverage was 20x in the parents and 10x in the offspring, for a cumulative coverage of about 200x.

As a first step, we used methods based on depth of coverage to identify 68 large deletions, 47 of which were confirmed by additional evidence, such as family structure, SNP heterozygosity, and signatures from paired-end mapping.

Perspectives:

Algorithms based on paired-end mapping will be used to detect smaller indels and copy number invariant polymorphisms such as inversions and translocations.

Genotype-phenotype association will be evaluated for all the identified variants, to provide a list of candidate SVs involved in hybrid vigor in poplar.