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Poster Abstract – D.16

STRUCTURAL AND NUCLEOTIDE VARIATION AMONG *POPULUS* GENOMES

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Structural variation has been defined as genomic alteration involving DNA segments longer than 1 kb. These generate genomic variants which can contribute to phenotypic differences between individuals, populations and species.

Here, we report a structural variation study within the *Populus* genus carried out through the sequence comparison of allelic chromosomal regions (totaling more than 800 kb) among the three poplar species *P. deltoides*, *nigra* and *trichocarpa*, which are interfertile and, when intercrossed, produce F1 hybrids with improved performances ("hybrid vigour"). Such a study is attractive in this genus, considered a model system for biological studies on trees, as a huge amount of genetic and genomic resources are steadily accumulating within single species of the genus, but there is a lack of information on inter-species comparative analyses.

In the present analysis, allelic pairs of BAC inserts have been detected within the library *Populusxeuramericana* cv. 'Ghoy', an F1 hybrid of *P. deltoides* x *P. nigra*, then sequenced to 10-times coverage, annotated and compared over distances of 90 to 130 kb between the two poplar species and the *P. trichocarpa* reference genomic sequence.

Surprisingly, especially when considering that we are comparing different species, so far the levels of homology and co-linearity resulted to be very high. As in the *P. trichocarpa* reference genome, the other sequenced genomic regions showed a high gene density (putative genes and gene relics considered), where genes are shared and conserved. On the contrary, transposable elements were rarely present, mainly represented by transposable element remnants and classI-retrotransposons, which resulted to be not shared but corresponding to the major insertion tracts. Insertion/deletions represented the main source of genomic variants among the three species, concerning 15% of the whole sequences and spanning few bases to about 10 kb, while no evidences were found for major translocations, duplications or inversions. In this scenario, still microsatellites, especially AT-rich stretches, and SNPs, with a inter-species frequency of 4,5 % on average, represented abundant classes of variants at the nucleotide level.