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QTL mapping for wood chemical properties and saccharification potential in black poplar (*Populus nigra*).

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Background

Lignocellulosic biomass from short-rotation coppice (SRC) poplar is a renewable resource of interest for producing second generation biofuels. However, current poplar varieties have not been bred for this purpose and, in order to optimize their biomass conversion into simple sugars (saccharification), we need to gain understanding into the genetic architecture of wood chemical properties. In this context, several genetic studies have been carried out over the last 5 years in various poplar species and genomic regions controlling lignin content and composition, and 5- and 6-C sugars from cellulose and hemicellulose have been identified either through QTL mapping in biparental crosses (Novaes et al., 2009; Yin et al., 2010) or association mapping in more complex crosses (Guerra et al., 2013) or natural populations (Wegrzyn et al., 2010). Despite the established relationships between wood chemical properties and saccharification yield (Davison et al., 2006; Studer et al., 2011), the impact of loci affecting chemical properties onto biofuel production has not been assessed. The present work aimed at specifically addressing this point by studying the genetic variability of wood chemical properties and saccharification potential and mapping the corresponding loci in a biparental cross of *Populus nigra*.

Methods

Near Infrared Spectroscopy (NIR) has been used as a high throughput phenotyping technique for predicting 12 phenotypes related to the chemical properties and saccharification potential of 479 *Populus nigra* samples. From these predicted values a genetic analysis was carried out in order to evaluate their broad sense heritability. Afterwards, we used a recently developed genetic map (El Malki et al., submitted) to identify loci that control the genetic variability of phenotypes related to chemical properties and saccharification potential.

Results

NIR spectra allowed the prediction of all phenotypes in the entire mapping population. From these predicted values, a significant genetic variability was found for all phenotypes, yielding medium to high broad sense heritabilities. A total of 10 QTLs located on 6 linkage

groups were detected. In addition, two genomic regions involved in an epistatic interaction were identified. These QTLs marginally explained between 2.2 and 16% of the phenotypic variance. Noticeably, one of them had opposite effects on lignin and solubilized sugars contents, and harbored genes from lignin and cellulose pathways. Another QTL, identified in the present study for the proportion of hydrolyzed glucose, collocated on linkage group XIII with a QTL previously detected in hybrid poplar for 5- and 6-C sugars (Novaes et al., 2009).

Conclusion

The present work shows that some genetic variability exists in *P. nigra* for saccharification potential. As a result, several genetic loci controlling this variability were detected, some of which being also detected for wood chemical properties. These QTL deserve further investigation in order to decrease their confidence intervals for example through association mapping in natural populations.

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