MAPPING AND MOLECULAR CHARACTERISATION OF PARALOGS OF CANDIDATE GENES FOR CADMIUM TOLERANCE IN BLACK POPLAR


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Emissions of wastes from variable origins into the environment has led to soil contamination in many sites, mainly by heavy metals. The phytoremediation is emerging as a cost-effective and environmentally friendly technology to remove these pollutants. Poplar is a suitable candidate for phytoremediation because of its rapid growth, ease of propagation, and high biomass production. Moreover, poplar presents a high genetic variability inter- and intra-species and its genome has been entirely sequenced. The availability of the poplar genome sequence is a great progress for the identification of the genetic determinants of environmental adaptation.

The objective of this work is the identification of the allelic variation associated with the tolerance to heavy metals. The strategy is based on the comparison of two highly divergent Populus nigra genotypes that also present a different tolerance to cadmium stress. A mapping pedigree was obtained by controlled cross between these genotypes and used for the construction of genetic maps. The candidate genes characterised in this study are involved in metal sequestration (metallothionein 2a), ion transport (vacuolar H+-ATPase), and response to oxidative stress (ascorbate peroxidase 2, glutathione reductase, glutathione S-transferase). In a previous experiment, these genes presented a differential expression among two genotypes of Populus alba submitted to salt stress. They are likely involved in the intra-specific variability of stress tolerance. As the Populus genome is highly duplicated, for each candidate gene the presence of paralogs was checked in the Populus trichocarpa genome database. When paralogs were found, specific primers allowing their discrimination were designed in order to amplify and sequence a fragment of each gene copy. The sequences were used to identify allelic polymorphisms (SNPs), develop SNP markers, and map the genes by allele-specific PCR. The different gene paralogs were individually mapped on the expected linkage groups according to the Populus trichocarpa genome sequence. This strategy aims at obtaining a genetic map rich of candidate genes to dissect cadmium tolerance by QTL analysis. The next step will be to investigate the functional role of the candidate genes in response to cadmium stress. The availability of paralog-specific markers will allow to analyse separately their expression in the two Populus nigra genotypes under stress.