EVALUATION OF GENETIC DIVERSITY IN MAPPING POPULATIONS AS A BASIS FOR CONSTRUCTING A GENETIC MAP OF *SALIX* SPP.

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Abstract

Ongoing climate change and the extraction of fossil fuels which depletes their reserves, thus increasing the costs of energy and fuel production, as well as adverse environmental changes are observed in all countries in the world. Therefore, attempts are being made to develop and implement modern technologies, and alternative (including renewable) energy sources are being searched for. Over the past few decades, particular attention has been paid to short rotation coppice (SRC) that in the future can become one of the major sources of biomass for energy generation. Plants of the genus *Salix* have also gained increasing interest in this respect. Interspecific and intraspecific diversity of *Salix*, and the availability of molecular biology techniques support the implementation of breeding programs aimed at increasing the productivity of new varieties, which is a highly interesting research topic. The breeders of new varieties, which will be characterized by improved biomass quality and increased productivity, must face numerous challenges, including those related to the flowering biology of *Salix* species. The selection of suitable forms for crossing must be preceded by a thorough analysis of flowering in males and females, observation of inflorescences of both sexes, and evaluation of stigma receptivity and pollen viability. Postzygotic barriers must also be overcome in order to obtain a sufficiently large population of progeny characterized by high genetic diversity. In vitro embryo rescue is an efficient method that supports embryo growth and development outside the ovule.

The optimization of the processes aimed at deriving mapping populations is very important and plays a decisive role in the construction of high-resolution genetic maps as a basis for the detection of QTLs linked with yield-related traits.

In view of the above, two populations were derived which could be regarded as mapping populations based on the parameters of genetic diversity. A sufficient number of repetitive DNA markers, characterized by high polymorphism, were used to construct

a genetic map of *Salix* based on each of the analyzed mapping populations. The values of yield-related traits were determined in field experiments. As a result, QTLs linked with individual traits could be identified.