RESEARCH PAPER

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Promoter analysis of an unknown gene in *Populus trichocarpa* x *Populus deltoides*, exposed to *Malacosoma disstria* Hubner

MAMTA SAGAR

Department of Bioinformatics, University Institute of Engineering and Technology, Chhatrapati Shahuji Maharaj University, KANPUR (U.P.) INDIA

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Several duplicated genes are present in populus genome and have multiple roles in transporting metabolite and synthesis of lignin and cellulose. Duplicated chs genes in *Populus* genome have been identified to be involved in defense mechanism due to production of flavonoid derived compound with pathogens interaction and sequences of the genes are available in the databases. In this work, one unknown gene (Accession No. EF148325,GI:118488982), expressed due to continuous feeding by *Malacosoma disstria* Hubner (forest tent caterpillar) in *Populus trichocarpa* x *Populus deltoids,* was analyzed by pattern searching and sequence comparison methods. Regulatory sequence analysis tool was used to identify regulatory site using sequence motifs of Arabidopsis *thaliana* and *Zea maize*. Using pattern matching approach the consensus pattern was predicted in Populus *hybrid,* to characterize the function of gene. DNA pattern search program was used to predict the patterns CNGTTR, CANNTG, AC like element, GCCTACC, GCCTACC, ACCTACA, ACCTAAC in upstream sequences of 7 chs genes of *P. trichocarpa* and one gene (EF148325) of *P. Trichocarpa* x *P. deltoides*. CNGTTR, CANNTG, known as b HLH pattern flanked by AC like element, have been predicted in the gene EF14325, which is the promoter for MYB134 regulatory protein which regulate phenylpropanoid metabolism and is involved in activating defenses in herbaceous plants. The gene sequence is compared with chs gene sequences of *Populus trichocarpa*, β-ketoacylcoa synthase from *Populus trichocarpa*; Acyltransferase from *Ricinus communis*; fiddlehead-like protein from *Pisum sativum*, were close homologs which share 97%, 83%, 77% identity, respectively with protein encoded by target gene and share same product binding site for coumaryl-CoA and malonyl-CoA, a critical step of flavonoid biosynthesis pathway.

Key words : *Populus trichocarpa*, *P. trichocarpa* x *P.deltoides*, Proanthocyanidine, Chalcone synthase, Flavonoid, *Malacosoma disstria,* EF148325

INTRODUCTION

Genome duplications followed by sequence divergence can create new gene in addition to gene with original function. *Populus* genome has duplicated genes that might be particularly useful for protection from pathogens. These genes are involved in synthesizing lignin and cellulose, transporting metabolites, and bringing about programmed cell death. Chalcone synthase (CHS), a key enzyme of plant flavonoid biosynthesis, is generally encoded by a multigene family. CHS plays multiple roles in the production of diverse flavonoid derived compounds under complex developmental and environmental regulation, and with pathogen interaction. *chs* genes have been cloned from a wide range of plant species. Studies have shown that specific patterns of expression of four *chalcone synthase* genes in a Hunnegem poplar clone have been identified *(Populus trichocarpa* x *Populus deltoides*) (Claire Lurin 1 and Lise Jouanin). Melampsora leaf rust, a destructive disease of poplar, causes premature leaf drop, loss of biomass and vigor, and even death in poplar plantations (Newcombe *et al.,* 1994). Some of the PR proteins have been detected in many species, which may be directly inhibitory to pathogens (Van Loon *et al.,* 2006).

In a comparative analysis with insect-induced defenses in leaves of the same hybrid poplar, Ralph *et al.* (2006) found that *M.medusae* infection down regulates many of the major herbivor-inducible defenses genes. *M.medusae* rust infection strongly induced genes for enzymes of flavonoid and proanthocyanidin (condensed tannin) biosynthesis late in the infection process. This study indicates that this pathway is closely related to the pathogen defense response in poplar**.** Myb and WRKY proteins are regulatory proteins involved in activating defenses in herbaceous plants (Eulgem, 2005). This study provided the fundamental basis to do the research analysis of expression pattern of an unknown gene in *P.*

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