FULL-LENGTH CDNA CLONING AND SNP DISCOVERY OF XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE (*XTH*) AND CELLULOSE SYNTHASE (*CESA*) GENES IN KELAMPAYAN (*Neolamarckia cadamba*)

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ABSTRACT: *Neolamarckia cadamba* or commonly known as kelampayan is one of the fast growing tropical tree species in Sarawak with high commercial value. Xyloglucan endotransglycosylase/hydrolase (XTH) and cellulose synthase (CesA) are proteins that play an important role in regulating wood formation. In this study, high integrity RNA was isolated from developing xylem for cDNA synthesis, RT-PCR and RACE-PCR amplification. Singletons of *XTH* and *CesA* genes obtained from *N. cadamba* EST database (Cadamomics or NcdbEST) were used to predict partial or full-length cDNA sequences using contig-mapping approach. The predicted hypothetical *XTH* and *CesA* cDNA were then used to designed full-length primer pairs and gene specific primer pair for 5'- and 3'-RACE amplification. Full-length *XTH* and *CesA* cDNA namely *Nc-XTH1* and *NcCesA1* were amplified from *N. cadamba* with nucleotide sequence 893 and 3,471 bp long encoding 858 and 3,126 bp open reading frame, respectively. Single nucleotide polymorphism (SNP) was discovered for the wood properties (basic density) association study of these two genes in *N. cadamba*. A total of 34 SNPs with 2.65% occurrence were found in full-length *Nc-XTH1* with two SNPs significantly associated with wood basic density ($p<0.05$). Three SNPs were found in the partial targeted region of *NcCesA1* (~778 bp) but no quantitatively significant association was proven. In conclusion, this study shows association between *XTH* and *CesA* genes with wood properties. In the future, further validation of gene-associated SNP can be carried out to benefit in the tree improvement programme for effective selection and plating of *N. cadamba*.

Keywords: Xyloglucan endotransglucosylase/hydrolase, cellulose synthase, *Neolamarckia cadamba*, full-length, gene association

INTRODUCTION

Wood is one of the most important renewable resources of energy which serves as a row material for global industry such as food, plastic, chemical products, textile products and constructions. Therefore, the study of wood biology is essential. Wood formation (xylogenesis) is an ordered and complex developmental process in plants, which mainly involves five stages: cell division, cell expension, secondary wall deposition, lignification and programmed cell death (Mellerowicz *et al.*, 2001). Xylogenesis is an open type of differentiation process of the meristematic cambium into specialized secondary xylem, which happens continuously as long as the tree grows by apical and lateral meristems (Rajangam, 2005; Aloni, 1989). Xyloglucan endotransglycosylase/hydrolase (XTH) and cellulose synthase (CesA) are two enzymes that play important roles in wood formation process.