



# Identification and analysis of expressed sequence tags present in xylem tissues of kelampayan (*Neolamarckia cadamba* (Roxb.) Bosser)

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Received: 20 November 2013 / Revised: 16 February 2014 / Accepted: 3 April 2014 / Published online: 24 May 2014  
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**Abstract** The large-scale genomic resource for kelampayan was generated from a developing xylem cDNA library. A total of 6,622 high quality expressed sequence tags (ESTs) were generated through high-throughput 5' EST sequencing of cDNA clones. The ESTs were analyzed and assembled to generate 4,728 xylogenesis unigenes distributed in 2,100 contigs and 2,628 singletons. About 59.3 % of the ESTs were assigned with putative identifications whereas 40.7 % of the sequences showed no significant similarity to any sequences in GenBank. Interestingly, most genes involved in lignin biosynthesis and several other cell wall biosynthesis genes were identified in the kelampayan EST database. The identified genes in this study will be candidates for functional genomics and association genetic studies in kelampayan aiming at the production of high value forests.

**Keywords** cDNA library · Expressed sequence tags (EST) · Developing xylem · *Neolamarckia cadamba* · Wood formation · Lignin biosynthesis

Forest trees represent the majority of terrestrial biomass production and are a vital component of biodiversity. However, slow growing trees are unable to meet current global demand for wood, resulting in the loss and degradation of forests. Plantation forests of fast growing species have the potential to supply the bulk of wood needs on a long-term basis, and

thus reduce the harvest pressure on natural forests for wood production to an acceptable level. In Sarawak, the state government has set a target of 1 million hectares for forest plantations to be established within 15 years. *Neolamarckia cadamba* (Roxb.) Bosser, locally known as kelampayan, has been identified as a promising fast growing species for planted forest development in Sarawak. Kelampayan is a large, deciduous and fast-growing tree species, thus with characteristics which guarantee early economic return within 8 to 10 years. Under normal conditions, it reaches a height of 17 m and a diameter of 25 cm at breast height (dbh) within 9 years. It is one of the best sources of raw material for the plywood industry, besides pulp and paper production. Kelampayan can also be used as a shade tree for dipterocarp line planting, whilst its leaves and bark have medical application (Joker 2000). The dried bark can be used to relieve fever and as a tonic, whereas a leaf extract can serve as a mouth wash (World Agroforestry Centre 2004).

Despite the high economic value of tropical wood, little is known about the genetic control of wood formation or xylogenesis for this species compared to loblolly pine (59,797 ESTs, Whetten et al. 2001), poplar (25,218 ESTs, Sterky et al. 2004) and spruce (16,500 ESTs, Pavy et al. 2005). Wood or secondary xylem is produced through the process of cell division, cell expansion and secondary cell-wall formation, the latter involving cellulose, hemicellulose, cell-wall proteins and lignin biosynthesis and deposition, and finally programmed cell death (Li et al. 2009). These processes are strongly interlinked, and the modulation of any one aspect may affect several others. Thus, the careful use of a functional genomics approach could rapidly provide information on the regulation of not just one gene, but of an entire pathway or several pathways at the same time. As of July, 2009, no kelampayan EST information was available in the NCBI GenBank. Therefore, we applied genomics approaches to explore the molecular basis of wood formation in

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