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Abstract

Isolation and Characterization of Full-Length Phenylalanine Ammonium Lyase and Cinnamyl Alcohol Dehydrogenase Genes Involved in Lignin Biosynthesis of Erianthus Arundinaceus †

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Abstract: Lignocellulosic biomasses available in abundance is the most promising raw material for alternate energy production considering the issues of dwindling oil prices, and global warming. Recently, *Erianthus arundinaceous* has been identified as a potential target for second generation biofuel crop due to its high biomass production, and adaptability to extreme growth environments. Lignin is a major plant cell wall polymer indispensable for plant growth and development, however it hinders the saccharification of lignocellulosic biomass. Based on the previous transcriptome studies in a set of sugarcane genotypes differing for lignin content, genes encoding cinnamyl alcohol dehydrogenase (CAD), and Phenylalanine ammonia lyase (PAL) genes playing major roles in genetic regulation of lignin production have been cloned and characterized from an *Erianthus* clone IK 76-81. The genomic region of EriCAD was 3524 bp sequence containing four exons and three introns, among which the exon 1&2 of 88 and 80 bp were conserved with sorghum and Miscanthus CADs. The coding region of CAD was identified with 1086 bp open reading frame (ORF), a 68 bp 5′ untranslated region (UTR), and a 86 bp 3′ untranslated region (UTR). In the PROSITE analysis, a zinc-containing alcohol dehydrogenase signature (GHEVVGEVVEVGPEV) and an NADP-binding domain motif (GLGGLG) was identified. Similarly sequence analysis of PAL showed an ORF of 2106 bp encoding for 702 amino acid residues. It was flanked by 172 bp of 5′ UTR and 121 bp of 3′ UTR. This sequence information on PAL and CAD from *Erianthus* might be useful for subsequent research on lignin modification for improved biomass conversion.

Keywords: lignocellulosic biomass; Erianthus; lignin modification