



Leaf transcriptome analysis and development of SSR markers in water chestnut (*Eleocharis dulcis*)

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ABSTRACT. Water chestnut (*Eleocharis dulcis*) is an important aquatic crop in China; however, transcriptomic and genomic data in public databases are limited. To identify genes and development molecular markers, high-throughput transcriptome sequencing was applied to generate transcript sequences from water chestnut leaf. More than 24 million reads were obtained, trimmed, and assembled into 40,796 contigs with an average length of 616.6 bp. Sequence similarity analyses against 4 public databases (NR, GO, KEGG, KOG) revealed 17,628 contigs that could be annotated with gene descriptions,

conserved protein domains, or gene ontology terms. Among the important metabolic pathways, 27 genes were related to starch synthesis and 13 genes were in the steroid synthetic pathway. In addition, 2570 cDNA simple sequence repeats were identified as potential molecular markers in our contigs. One hundred pairs of polymerase chain reaction primers were designed and used for validation of the amplification. The results revealed that 87 primer pairs were successfully amplified in initial screening tests. Overall, this transcriptome dataset and these markers can serve as a platform for further gene expression studies, functional genomic studies, and marker-assisted selection in *E. dulcis*.

Key words: *Eleocharis dulcis*; High-throughput sequencing; Simple sequence repeat; Transcriptome