



Category: Plant Genomics

Transcriptome profiling of floral development in *Dendrocalamus hamiltonii* uncovers floral transition mechanism in bamboos

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Abstract

Bamboos are the giant woody grasses belonging to family Poaceae. The plants have versatile utilities including rural and industrial applications. Bamboos are indeed major players in the economies of many Asian countries. They support an international trade worth more than US\$ 2.5 billion per year and this is expected to increase further. Bamboos have long juvenile phase and unique flowering behavior - the major deterrents to their conservation and propagation. Most genera/species have a long intermest period of juvenile stage that varies from 40-120 years after which bamboos flower gregariously, irrespective of geographical locations. The entire culms of all clonal individuals from a single mother, flower simultaneously and die *en masse*. This results in huge loss of valuable germplasm, and is a continuous but unpredictable threat to all standing populations of bamboos. Besides gregarious flowering, some culms of bamboos flower sporadically, set a few seeds annually and die. Although the process of flowering in bamboos demands attention, it is poorly understood. Therefore, an attempt was made to elucidate the molecular mechanism of floral transition in *Dendrocalamus hamiltonii*, a multipurpose bamboo native to Himalayan region using a transcriptomic approach in an *in vitro* system. The Illumina paired-end sequencing was conducted, and a total of 37862456, 35040478 and 35017513 reads were obtained after filtering by RNA-seq of the vegetative, about-to-flower and flowering stages. These were assembled into 191575 transcripts with mean length of 1005.68 bp. A total of 98,782 unigenes were annotated in the NCBI non-redundant protein database and 86,665 in the Swiss-Prot database. Also, 73,802 annotated unigenes were allocated to gene ontology (GO) categories. In them most of the unigenes were categorized into biological process followed by molecular function and cellular component. By searching against the Kyoto Encyclopedia of Genes and Genomes Pathway database (KEGG), 7,222 unigenes were assigned to 372 KEGG pathways and in addition 28905 simple sequence repeats (SSRs) were identified. In total 7439 differentially expressed floral specifiers representing the three floral developmental stages were identified.

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