



Understanding bamboo flowering based on large-scale analysis of expressed sequence tags

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ABSTRACT. Unlike other plants, bamboo (Bambusoideae) flowering is an elusive physiological phenomena, because it is unpredictable, long-periodic, gregarious, and uncontrollable; also, bamboo plants usually die after flowering. The flowering mechanism in *Arabidopsis thaliana*, a eudicot model species, is well established, but it remains unknown in bamboo species. We found 4470 and 3878 expressed sequence tags in the flower bud and vegetative shoot cDNA libraries, respectively, of the bamboo species, *Bambusa oldhamii*. Different genes were found expressed in bamboo flower buds compared to vegetative shoots, based on the Munich Information Center for Protein Sequences functional categorization; flowering-related genes were also identified in this species. We also identified *Arabidopsis* flowering-specific homologs

that are involved in its photoperiod in this bamboo species, along with autonomous, vernalization and gibberellin-dependent pathways, indicating that bamboos may have a similar mechanism to control floral transition. Some bamboo expressed sequence tags shared high similarity with those of rice, but others did not match any known sequences. Our data lead us to conclude that bamboo may have its own unique flowering genes. This information can help us understand bamboo flowering and provides useful experimental methods to study the mechanisms involved.

Key words: Bamboo; Expressed sequence tag; Flowering; Mechanism