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

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Received February 21, 2010
Accepted March 20, 2010
Published June 11, 2010
DOI 10.4238/vol9-2gmr804

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.

**Keywords:** Bamboo; Expressed sequence tag; Flowering; Mechanism