

Decoding the Genome of *Bambusa tulda*: Implications for Floral Development and Lignocellulose Biology

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Abstract: *Bambusa tulda* Roxb., is an ecologically and commercially important bamboo broadly distributed across the Indian subcontinent. We recently have sequenced the first bamboo genome from India by using the long-read PacBio HiFi sequencing platform. The *de novo* haploid genome assembly of *B. tulda* predicted 43 contigs, distributed across three subgenomes, with a total sequenced length of 1.37 Gb. Functional annotation predicted 56,890 protein-coding genes in the genome. This high-quality draft genome assembly is currently being utilized as an invaluable resource to unravel the genetic regulation controlling unusually extended flowering time of bamboos, which may be up to 120 years. The study has already identified and functionally characterized important photoperiod, integrator and organ differentiating genes such as *LATE ELONGATED HYPOCOTYL (LHY)*, *TIMING OF CAB EXPRESSION1 (TOC1)*, *ZEITLUPE (ZTL)*, *GIGANTEA (GI)*, *CONSTANS A (COA)*, *CONSTANS B (COB)*, *FLOWERING LOCUS T1, 2, 3, 4 (FT1, 2, 3, 4)*, *FD1*, *FD2* and *APETALA1* from *Bambusa tulda*. Many of these genes have been found to be duplicated and demonstrate divergence with respect to expression and possible developmental function. We also focus on the lignin biosynthetic pathway with an intention of future genome engineering for improved biomass utilization. Discussions will be held in the context of utility of bamboo as a sustainable lignocellulosic feedstock, advancing biofuel production, and clean energy solutions for India.

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