



Category: Plant Genomics

Dynamic transcriptome profiling of the floral buds in the dioecious cucurbit *Coccinia grandis* using RNA-Seq

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Abstract

Angiosperms exhibits diversified sexual systems encompassing bisexual, monoecious and dioecious conditions. Dioecy offers opportunities to explore separately, the male and female systems giving an insight into the evolutionary, developmental and molecular processes of sex expression in plants. *Coccinia grandis* (Family: Cucurbitaceae) with small genome size and heteromorphic sex chromosomes is often considered a model dioecious plant for sex evolution. However, the information relating to its genetic orientation, physical state and sex determining factors is highly ambiguous and limited. In the present study we have attempted to identify the molecular basis of sex determination in *C. grandis* through genome wide transcriptome profiling of the floral buds. About 75 million clean reads were generated resulting in 72,479 unigenes for male library and 63,308 unigenes for female library with a mean length of 736 bp. 1410 unigenes were differentially expressed (DEGs) between the male and female buds as identified from the RNA-Seq pattern and qRT-PCR validation. Functional annotation using BLAST2GO and KEGG revealed high enrichment of DEGs in phytohormone biosynthesis, hormone signaling and transduction, transcriptional regulation and methyl transferase activity. Manifold up-regulation of genes phytohormone responsive genes such as *ARF6*, *ACC synthase1*, *SNRK2* and *BR11-associated receptor kinase 1 (BAK1)* suggest that a signaling crosstalk is implicated in the sex determination of this species. Besides, a wide range of transcription factors including zinc fingers, homeodomain leucine zippers and MYBs were recognized as major determinants of male specific expression in the dioecious plant. Additionally, *C. grandis* transcriptome revealed 48 target genes for many miRNAs sequences with established role in floral development and sex determination. Overall, our study resulted in the identification of a large amount of molecular resources that could be critical to the mechanism of sexual dimorphism in dioecious plants in general and *C. grandis* in particular.

Citation: Mohanty, J.N. and Joshi, R.K. Dynamic transcriptome profiling of the floral buds in the dioecious cucurbit *Coccinia grandis* using RNA-Seq [Abstract]. In: Abstracts of the NGBT conference; Oct 02-04, 2017; Bhubaneswar, Odisha, India: Can J biotech, Volume 1, Special Issue, Page 210. <https://doi.org/10.24870/cjb.2017-a195>