PB-60

# High Quality Genome Sequence of Physic Nut (*Jatropha curcas* L.), a Biodiesel Plant

Jungmin Ha[1,2], Sangrea Shim[1], Taeyoung Lee[1] and Suk-Ha Lee[1,2]*

[1]Department of Plant Science and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea
[2]Plant Genomics and Breeding Institute, Seoul National University, Seoul 08826, Republic of Korea

**[Introduction]**

Physic nut (Jatropha curcas) is one of the most promising alternative energy source for fossil fuels because of its high seed oil content, rapid growth and adaptability to a wide range of climatic and soil condition. As non-edible oilseed crop, physic nut does not threaten food security. Physic nut belongs to Euphorbiaceae family consisting of rubber tree, cassava and castor bean which are economically important crops.

**[Materials and Methods]**

Genomic DNA was prepared from young Jatropha curcas CN leaves using the CTAB method. RNA samples were prepared from the leaf tissue of nine Jatropha accessions, including J. aconitifolia, J. cinerea, J. curcas CN, J. curcas M10, J. gossypiifolia, J. integerrima, J. macrantha, J. multifida, and J. podagrica, as well as Ricinus communis and from stem, root, male flower, and female flower tissue, as well as seed endosperm tissue from fruit at four different developmental stages (immature, green, yellow, and brown fruit), of J. curcas CN, and sequenced on the Illumina HiSeq2000 platform.

**[Results and Discussions]**

We sequenced J. curcas var. Chai Nat and the assembled genome has in total 339 Mbp (N50 = 15.4 Mbp). The genome assembly was anchored to a genetic map consisting of 1,188 markers resulting in 11 pseudo-chromosomes. Among 3,352 differentially expressed genes (DEGs) between female and male flowers, transcription factors activity was the most enriched GO term and ~82% differentially expressed transcription factors were up-regulated in female flower. Triacylglycerol biosynthesis genes were the most representative DEGs of putative acyl lipid genes in endosperms among four different stages of fruit development. RNA-seq from eight Jatropha species revealed J. aconitiforia was closer to cassava than other Jatropha species. This work will contribute to functional genomics in the Euphorbiaceae family and breeding elite cultivar for Jatropha smallholders.

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*Corresponding author: Tel. +82-880-4545, E-mail. sukhalee@snu.ac.kr