

Photosynthesis Metabolism Affects Yield Potentials in *Jatropha curcas* L.: A Transcriptomic and Physiological Data Analysis

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Abstract : *Jatropha curcas*, a well-described bioenergy crop has been extensively accepted as future fuel need especially in tropical regions. Ideal planting material required for large-scale plantation is still lacking. Breeding programmes for improved *J. curcas* varieties are rendered difficult due to limitations in genetic diversity. Using a combined transcriptome and physiological data, we investigated the molecular and physiological differences in high and low yielding *Jatropha curcas* to address plausible heritable variations underpinning these differences, in regard to photosynthesis, a key metabolism affecting yield potentials. A total of 6 individual *Jatropha* plant from 4 accessions described as high and low yielding planting materials were selected from the Experimental Plot A, Universiti Kebangsaan Malaysia (UKM), Bangi. The inflorescence and shoots were collected for transcriptome study. For the physiological study, each individual plant (n=10) from the high and low yielding populations were screened for agronomic traits, chlorophyll content and stomatal patterning. The *J. curcas* transcriptomes are available under BioProject PRJNA338924 and BioSample SAMN05827448-65, respectively Each transcriptome was subjected to functional annotation analysis of sequence datasets using the BLAST2Go suite; BLASTing, mapping, annotation, statistical analysis and visualization Large-scale phenotyping of the number of fruits per plant (NFPP) and fruits per inflorescence (FPI) classified the high yielding *Jatropha* accessions with average NFPP =60 and FPI > 10, whereas the low yielding accessions yielded an average NFPP=10 and FPI < 5. Next generation sequencing revealed genes with differential expressions in the high yielding *Jatropha* relative to the low yielding plants. Distinct differences were observed in transcript level associated to photosynthesis metabolism. DEGs collection in the low yielding population showed comparable CAM photosynthetic metabolism and photorespiration, evident as followings: phosphoenolpyruvate phosphate translocator chloroplast like isoform with 2.5 fold change (FC) and malate dehydrogenase (2.03 FC). Green leaves have the most pronounced photosynthetic activity in a plant body due to significant accumulation of chloroplast. In most plants, the leaf is always the dominant photosynthesizing heart of the plant body. Large number of the DEGS in the high-yielding population were found attributable to chloroplast and chloroplast associated events; STAY-GREEN chloroplast, Chlorophyllase-1-like (5.08 FC), beta-amylase (3.66 FC), chlorophyllase-chloroplast-like (3.1 FC), thiamine thiazole chloroplast like (2.8 FC), 1-4, alpha glucan branching enzyme chloroplast amyliplastic (2.6FC), photosynthetic NDH subunit (2.1 FC) and protochlorophyllide chloroplast (2 FC). The results were parallel to a significant increase in chlorophyll a content in the high yielding population. In addition to the chloroplast associated transcript abundance, the TOO MANY MOUTHS (TMM) at 2.9 FC, which code for distant stomatal distribution and patterning in the high-yielding population may explain high concentration of CO₂. The results were in agreement with the role of TMM. Clustered stomata causes back diffusion in the presence of gaps localized closely to one another. We conclude that high yielding *Jatropha* population corresponds to a collective function of C3 metabolism with a low degree of CAM photosynthetic fixation. From the physiological descriptions, high chlorophyll a content and even distribution of stomata in the leaf contribute to better photosynthetic efficiency in the high yielding *Jatropha* compared to the low yielding population.

Keywords : chlorophyll, gene expression, genetic variation, stomata

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