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De Novo sequencing and hybrid assembly of biofuel crop *Jatropha curcas* Ls Insights on gene annotation, comparative genomics and transcriptome analysis with identification of quantitative trait loci for geminivirus resistance

Nagesh Kancharla

Reliance Industries Limited, India

J*Jatropha curcas* is an important perennial, drought tolerant plant identified as a potential biodiesel crop. We report here the hybrid de novo genome assembly of *Jatropha curcas* generated using Illumina and PacBio sequencing technologies and identification of quantitative loci responsible for geminivirus resistance. In this study, we generated scaffolds of 265.7 Mbp in length which is corresponding to 84.8% of the gene space using BUSCO analysis. Additionally, 96.4% of predicted protein-coding genes were captured in corresponding tissues transcriptome data, which reconfirms the accuracy of the assembled genome. The genome was utilized to identify 12,103 dinucleotide repeat SSR markers, which were exploited in genetic diversity analysis to identify genetically distinct lines. A total of 250, polymorphic SSR markers were employed to construct a genetic linkage map for Jatropha Mosaic Virus (JMV) resistance using

interspecific F2 mapping population involving *Jatropha curcas* and *Jatropha integerrima* as parents. QTL analysis showed the identification of three minor Quantitative Trait Locus (QTL) for JMV resistance and validated in an alternate recipient genetic background F2 mapping population. These validated QTLs were utilized in Marker Assisted Breeding (MAS) for developing *Jatropha Mosaic Virus* resistance hybrids in *Jatropha*. Comparative genomics of oil-producing genes across selected oil producing species revealed 27 conserved genes and 2,986 orthologous protein clusters in *Jatropha*. This reference genome assembly gives an insight into the understanding of the complex genetic structure of *Jatropha* and serves as source for the development of agronomically improved virus resistant and oil producing species.