



INDIAN INSTITUTE OF TECHNOLOGY GUWAHATI
SHORT ABSTRACT OF THESIS

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SHORT ABSTRACT

Pongamia pinnata is a species of tree in Leguminosae family that grows over the different agro-climatic condition of India, Southeast Asia, Australia and Pacific islands. The tree is a source of seeds containing non-edible oil for biodiesel preparation and industrial uses. However, very little is known about the genetic and genomic organisation of *Pongamia*. Repetitive elements in eukaryotes occupy a significant portion of the nuclear and organellar genome. In the present investigation, *reverse transcriptase* (RT) fragment of *copia*, *gypsy* and *long interspersed nuclear element* (LINE) was identified in *Pongamia* genome. The annotation of *Pongamia* EST libraries yielded more than 400 TEs, confirming that some class of transposons are still transcriptionally active. With a view to understand the contribution of transposable elements (TEs) distribution and insertional orientation in *Pongamia* transcriptome, unigenes were screened with the RepeatMasker program. Analysis revealed that most of the unigenes were found with TE insertions, with an average of 1.42 insertions per unigene. The significant population of identified TE insertions were from retrotransposons and less with DNA transposons. Along with TEs, simple sequence repeats (SSRs) were successfully mined from transcriptome libraries of *Pongamia*. Among isolated repeats, dinucleotide repeat SSRs were abundant in *Pongamia*. Primers were successfully designed and amplified to expected size of amplicons in 14 accessions of *Pongamia*. All the amplified SSRs showed transferability among different families of plants. The newly designed SSR markers were found to be helpful in diversity analysis, as they successfully differentiated the accessions of *Pongamia*.