PROJECT PROFILE

Title: **Isolation and characterization of Cinnaomoyl coA reductase gene in *Casuarina equisetifolia***

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Start and Completion dates: **0**1.04.2016 to 31.03.2019 (Three years)

Objectives:

1. Isolation of full length CCR gene from *Casuarina equisetifolia.*
2. Expression profiling in tissues of *Casuarina equisetifolia.*
3. Identification of allelic variation in diverse population *of Casuarina equisetifolia.*

Funding Agency: Indian Council of Forestry Research and Education (ICFRE)

Summary

- Full length Cinnaomoyl coA reductase gene was isolated through whole transcriptome sequencing of developing wood tissue of *Casuarina equisetifolia*.
- The *de novo* assembly of raw transcriptome data showed the minimum and maximum transcript length ranged between 224 bp and 6627 bp with an average length of 609 bp and the N50 contig size was 780 bp.
- The raw paired - end sequence data was deposited in NCBIs Short Read Archive with the study accession number SRP136154.
- 26,985 unigenes were identified and 15,952 were annotated. Transcripts from *C. equisetifolia* showed highest similarity with *Prunus persica* (935), *Morus notabilis* (738), *Vitis vinifera* (663), *Citrus clementina*, *Jatropha curcas* (614), and *Populus trichocarpa* (587).
- A total of 2392 SSRs were identified from 2082 sequences, with 259 sequences containing more than 1 SSRs.

- Sixty putative Single Nucleotide Polymorphisms (SNPs) were identified among the international provenances. The identified alleles can be used for identifying markers tagging wood property traits in *Casuarina equisetifolia.*