

Isolation, molecular characterization, expression and phylogenetic analysis of NAC 025 like transcription factor (TF) in Coffee

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Introduction

- ✓ NAC constitute one of the largest group of plant specific transcription factors (TFs) which are associated with various developmental processes (Pereira-Santana et al., 2015).
- ✓ Unlike in coffee, the structural and functional characterisation of several NAC TFs has been reported in many plant species.
- ✓ Hence, molecular characterisations, phylogenetic and expression profiles of NAC 025 like genes was studied in Indian wild coffee species and two cultivated species.

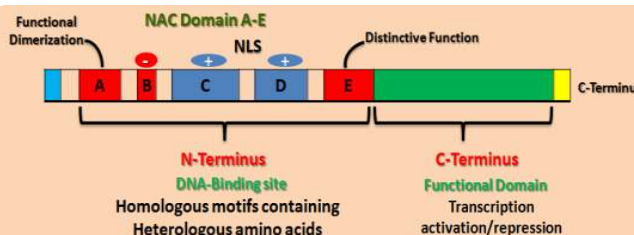


Figure 1: Structure of NAC transcription factor

Results/Discussion

1. The size of the NAC 025 like genes in seven coffee species varied from 2471bp in *Coffea jenkinsii* to 2528bp in *C. wightiana*.
2. In comparison to *C. canephora*, the frequency of SNP varied considerably among the species. Lowest (7) in *C. arabica* and highest (169) in *C. travancorensis*.
3. The frequency of non synonymous SNPs and frame shift mutation caused by indels was much higher in exonic region.
4. This has resulted in lower protein sequence homology among the species.
5. The sequence plasticity of the C terminal region of the NAC TF was confirmed both in the F₁ hybrids and *in-vitro* derived plants through somatic embryogenesis.
6. The expression profiling of NAC TF gene in different tissues of *C. canephora* revealed that the NAC 025 gene expresses in both vegetative and reproductive parts of plant with varying expression levels.

Materials/Methods

- The NAC 025 gene was cloned and sequenced from five wild Indian *Coffea species* such as *C. jenkinsii*, *C. wightiana*, *C. travancorensis*, *C. bengalensis*, and *C. khasiana* along with two cultivated species *C. canephora* and *C. arabica*.
- *In-silico analysis* of sequence data was carried out using BioEdit V 7.0.4.1.
- The expression profile of the NAC 025 TF was determined in the root, leaf, flower bud, flower and young fruit using QPCR analysis.

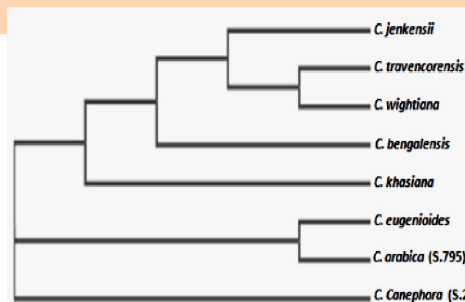


Figure 2: Clustering of coffee species based on sequence homology of NAC "C- domain"

Conclusion/Perspectives

The detail molecular analysis of NAC 025 like transcription factor and its structural architecture will greatly facilitate our understanding of the functional perspectives of the role of NAC gene in coffee

References:

Pereira-Santana A, Alcaraz LD, Castaño E, Sanchez-Calderon L, Sanchez-Teyer F, Rodriguez-Zapata L. Comparative Genomics of NAC Transcriptional Factors in Angiosperms: Implications for the Adaptation and Diversification of Flowering Plants. *PLoS One*. 2015;10(11):e0141866. Published 2015 Nov 16. doi:10.1371/journal.pone.0141866