ID: 217

In silico genome-wide comparative analysis of Auxin Response Factors (ARFs) from *Brassica oleracea* and *Arabidopsis thaliana*

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Abstract

Auxin, a crucial phytoharmone, governs gene expression via plant-specific Auxin Response Factors (ARFs) which regulate diverse processes. Auxin profoundly shapes growth from embryogenesis to senescence. At molecular level auxin prompt gene transcription shifts within cell nuclei, steering particular gene activation or suppression. These changes steer auxin-governed developmental plants. The auxin response factor gene family in *Brassica oleracea* is poorly understood, unlike in other species. For comparison, 17 non-redundant genes of *Brassica oleracea* (BolARF) and 22 genes of *Arabidopsis thaliana* were analyzed from a total of 49 genes. Phylogenetic revealed auxin response factor relation across *Brassica* species and *Arabidopsis thaliana*. Chromosomal mapping showed 17 genes spread over *Brassica oleracea*'s 9 chromosomes, with 3 genes on chromosome 5 and 8. Intron/exon and domain analyses offered insights into auxin response factor homology along comparative phylogenetic trees and synteny analysis also echoed homology. Promoter analysis uncovered 44 cis-elements, with 11 displayed. Conserved domains showed three auxin response factor transporting proteins. This study deepens *Brassica oleracea* auxin response factor gene family understanding.

Key Words: *Auxin, Auxin response factor, Brassica oleracea, Comparative analysis, Phylogenetic analysis, Promotor analysis*