

Genome-Wide Analysis of BES1/BZR1 Gene Family in Five Plant Species

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Abstract : Brassinosteroids (BRs) regulate cell elongation, vascular differentiation, senescence and stress responses. BRs signal through the BES1/BZR1 family of transcription factors, which regulate hundreds of target genes involved in this pathway. In this research a comprehensive genome-wide analysis was carried out in BES1/BZR1 gene family in *Arabidopsis thaliana*, *Cucumis sativus*, *Vitis vinifera*, *Glycin max*, and *Brachypodium distachyon*. Specifications of the desired sequences, dot plot and hydropathy plot were analyzed in the protein and genome sequences of five plant species. The maximum amino acid length was attributed to protein sequence Brdic3g with 374aa and the minimum amino acid length was attributed to protein sequence Gm7g with 163aa. The maximum Instability index was attributed to protein sequence AT1G19350 equal with 79.99 and the minimum Instability index was attributed to protein sequence Gm5g equal with 33.22. Aliphatic index of these protein sequences ranged from 47.82 to 78.79 in *Arabidopsis thaliana*, 49.91 to 57.50 in *Vitis vinifera*, 55.09 to 82.43 in *Glycin max*, 54.09 to 54.28 in *Brachypodium distachyon* 55.36 to 56.83 in *Cucumis sativus*. Overall, data obtained from our investigation contributes a better understanding of the complexity of the BES1/BZR1 gene family and provides the first step towards directing future experimental designs to perform systematic analysis of the functions of the BES1/BZR1 gene family.

Keywords : BES1/BZR1, brassinosteroids, phylogenetic analysis, transcription factor

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