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Mirzaei, K.^{a, b}, Bahramnejad, B.^b, Fatemi, S.^b

Genome-wide identification and characterization of the bZIP gene family in potato (*Solanum tuberosum*)

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^a Biodiversity Research Centre, Earth and Life Institute, UCLouvain, Croix du Sud 4 box L7.07.04, Louvain-la-Neuve, B-1348, Belgium

^b Department of Agronomy and Plant Breeding, Faculty of Agriculture, University of Kurdistan, Sanandaj, Iran

Abstract

The basic leucine zipper (bZIP) transcription factors, as members of the family of transcription regulators, play a role in multiple developmental and biological processes such as organ and tissue development and responses to diverse stresses. However, knowledge of the bZIP genes in potato, which is one of the most valuable crops, is still limited. In this study, 56 bZIP genes in total were identified from the *Solanum tuberosum* genome and classified into 10 main groups. The classification of potato bZIP genes into ten groups was endorsed by the sets of conserved motifs present and gene structure of bZIP genes. The locations of the bZIP genes on the chromosomes were unevenly scattered over the potato genome, as in other studied plants. Investigation of promoter sequences revealed that *Solanum tuberosum* bZIP genes possessed variable sets of cis-regulatory elements, such as MYB, MYC, and ABRE elements, which may play roles in response to various stresses. Expression analyses of the potato bZIP genes based on transcriptome data showed that these genes have broad expression patterns in different tissues. Three distinct gene expression patterns observed for potato bZIP genes were similar to other plant species. Overall, this first and broad investigation of bZIP genes in the potato will provide useful insights into stress-responsive potato genes and pave the way for high-stress tolerance potato breeding. © 2020 Elsevier B.V.

Author Keywords

bZIP transcription factor family; Drought response; Potato

Correspondence Address

Mirzaei K.; Biodiversity Research Centre, Croix du Sud 4 box L7.07.04, Belgium; email: Khaled.Mirzaei@uclouvain.be

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