International Journal of
Molecular Sciences

MDPI

Article

Genome-Wide Identification, Expression Profile, and Alternative Splicing Analysis of the Brassinosteroid-Signaling Kinase (BSK) Family Genes in *Arabidopsis*

Zhiyong Li [1,2,*], Jinyu Shen [3] and Jiansheng Liang [2,*]

1 Academy for Advanced Interdisciplinary Studies, Southern University of Science and Technology (SUSTech), Shenzhen 518055, China
2 Department of Biology, Southern University of Science and Technology (SUSTech), Shenzhen 518055, China
3 Co-Innovation Center for Modern Production Technology of Grain Crop, Yangzhou University, Yangzhou 225000, China; shenjinyu20160710@outlook.com
* Correspondence: lizy6@sustc.edu.cn (Z.L.); liangjs@sustc.edu.cn (J.L.); Tel.: +86-0755-8801-5711 (Z.L.); +86-0755-8801-0303 (J.L.)

Received: 17 February 2019; Accepted: 2 March 2019; Published: 6 March 2019

Abstract: Brassinosteroids (BRs) are steroid hormones essential for different biological processes, ranging from growth to environmental adaptation in plants. The plant brassinosteroid-signaling kinase (BSK) proteins belong to a family of receptor-like cytoplasmic kinases, which have been reported to play an important role in BR signal transduction. However, the knowledge of BSK genes in plants is still quite limited. In the present study, a total of 143 BSK proteins were identified by a genome-wide search in 17 plant species. A phylogenetic analysis showed that the BSK gene originated in embryophytes, with no BSK found in green algae, and these BSK genes were divided into six groups by comparison with orthologs/paralogs. A further study using comparative analyses of gene structure, expression patterns and alternative splicing of BSK genes in *Arabidopsis* revealed that all BSK proteins shared similar protein structure with some exception and post-translation modifications including sumolyation and ubiquitination. An expression profile analysis showed that most *Arabidopsis* BSK genes were constitutively expressed in different tissues; of these, several BSK genes were significantly expressed in response to some hormones or abiotic stresses. Furthermore, reverse transcription-polymerase chain reaction (RT-PCR) assays showed that *BSK5*, *BSK7*, and *BSK9* underwent alternative splicing in specific stress induced and tissue-dependent patterns. Collectively, these results lay the foundation for further functional analyses of these genes in plants.

Keywords: brassinosteroid-signaling kinase; gene family; expression profile; alternative splicing; intron retention

1. Introduction

As sessile organisms, plants need to proceed in a coordinated manner to adapt to the constantly changing environment and react to stress conditions for growth and development. Phytohormones play a crucial role during these processes. Among them, brassinosteroids (BRs) are generally known as important plant hormones that play fundamental roles in various cellular, physiological, and developmental processes during plant life cycle [1,2].

To date, the BR signaling pathway has been well established and a number of the intracellular components of this pathway have been identified by genetic, genomic and proteomic studies. In the current model of the BR signaling pathway, the BR signal is perceived by BRASSINOSTEROID