



Exploring the GRAS gene family in common bean (*Phaseolus vulgaris* L.): characterization, evolutionary relationships, and expression analyses in response to abiotic stresses

Parbej Laskar¹ · Saswati Bhattacharya² · Atreyee Chaudhuri³ · Anirban Kundu¹

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Abstract

Main conclusion Genome-wide identification reveals 55 *PvuGRAS* genes belonging to 16 subfamilies and their gene structures and evolutionary relationships were characterized. Expression analyses highlight their prominence in plant growth, development and abiotic stress responses.

Abstract GRAS proteins comprise a plant-specific transcription factor family involved in multiple growth regulatory pathways and environmental cues including abiotic/biotic stresses. Despite its crucial importance, characterization of this gene family is still elusive in common bean. A systematic genome-wide scan identified 55 *PvuGRAS* genes unevenly anchored to the 11 common bean chromosomes. Segmental duplication appeared to be the key driving force behind expansion of this gene family that underwent purifying selection during evolution. Computational investigation unraveled their intronless organization and identified similar motif composition within the same subfamily. Phylogenetic analyses clustered the *PvuGRAS* proteins into 16 phylogenetic clades and established extensive orthologous relationships with *Arabidopsis* and rice. Analysis of the upstream promoter region uncovered *cis*-elements responsive to growth, development, and abiotic stresses that may account for their differential expression. The identified SSRs could serve as putative molecular markers facilitating future breeding programs. 37 *PvuGRAS* transcripts were post-transcriptionally regulated by different miRNA families, *miR171* being the major player preferentially targeting members of the HAM subfamily. Global expression profile based on RNA-seq data indicates a clade specific expression pattern in various tissues and developmental stages. Additionally, nine *PvuGRAS* genes were chosen for further qPCR analyses under drought, salt, and cold stress suggesting their involvement in acclimation to environmental stimuli. Combined, the present results significantly contribute to the current understanding of the complexity and biological function of the *PvuGRAS* gene family. The resources generated will provide a solid foundation in future endeavors for genetic improvement in common bean.

Keywords Abiotic stress · Common bean · Expression · Genome-wide · miRNA · Transcription factor

Abbreviations

FPKM	Fragments per kilobase per million mapped reads
SSR	Simple sequence repeats
TF	Transcription factor
TFBS	Transcription factor binding site

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Parbej Laskar and Saswati Bhattacharya have contributed equally to this work.

✉ Anirban Kundu
discoveranirban@yahoo.co.in

¹ Plant Genomics and Bioinformatics Laboratory, P.G. Department of Botany, Ramakrishna Mission Vivekananda Centenary College (Autonomous), Rahara, Kolkata 700118, India

² Department of Botany, Dr. A.P.J. Abdul Kalam Government College, New Town, Rajarhat, India

³ Aquatic Bioresource Research Laboratory, Department of Zoology, University of Calcutta, Kolkata, India



PUBLISHING

Phylogenetic, structural, functional characterisation and effect of exogenous spermidine on rice (*Oryza sativa*) HAK transporters under salt stress

Jayita Saha^{A,B,*}, Dwaipayan Chaudhuri^B, Anirban Kundu^C, Saswati Bhattacharya^D, Sudipta Roy^E and Kalyan Giri^{B,*}

For full list of author affiliations and declarations see end of paper

*Correspondence to:

Jayita Saha
Department of Botany, Rabindra Mahavidyalaya, Champadanga, Hooghly, West Bengal, India
Email: ijayita@gmail.com
Kalyan Giri
Department of Life Sciences, Presidency University, 86/1 College Street, Kolkata 700073, West Bengal, India
Email: kalyan.dbs@presiuniv.ac.in

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ABSTRACT

The HAK (High-affinity K⁺) family members mediate K⁺ transport that confers normal plant growth and resistance against unfavourable environmental conditions. Rice (*Oryza sativa* L.) HAK transporters have been extensively investigated for phylogenetic analyses with other plants species with very few of them functionally characterised. But very little information is known about their evolutionary aspects, overall structural, functional characterisation, and global expression pattern of the complete HAK family members in response to salt stress. In this study, 27 rice transporters were phylogenetically clustered with different dicot and monocot family members. Subsequently, the exon–intron structural patterns, conserved motif analyses, evolutionary divergence based different substitution matrix, orthologous-paralogous relationships were studied elaborately. Structural characterisations included a comparative study of secondary and tertiary structure, post-translational modifications, correspondence analyses, normal mode analyses, K⁺/Na⁺ binding affinities of each of the OsHAK gene members. Global expression profile under salt stress showed clade-specific expression pattern of the proteins. Additionally, five OsHAK genes were chosen for further expression analyses in root and shoot tissues of two rice varieties during short-term salinity in the presence and absence of exogenous spermidine. All the information can be used as first-hand data for dissecting the administrative role of rice HAK transporters under various abiotic stresses.

Keywords: HAK transporters, Indica rice, MEGA, normal mode analyses, phylogenetic tree, real-time PCR, salt stress, spermidine, synteny analyses.

Introduction

Potassium is an essential macronutrient that plants accumulate in huge quantities accounting for about 2–10% of their total dry weight (Cai *et al.* 2021). However, their cytosolic concentrations are kept at approx. 100 mM (20–200 mM in the vacuoles) (Sharma *et al.* 2013), providing an optimum environment for the functioning of enzymes. K⁺ ions are involved in several fundamental biochemical processes that include enzyme activation, osmoregulation, protein synthesis, metabolism of carbohydrates, stomatal movement, and photosynthesis. (Hasanuzzaman *et al.* 2018; Cheng *et al.* 2018; Ou *et al.* 2018). Additionally, K⁺ ions play a pivotal role in abiotic stress tolerance (Wang *et al.* 2013; Véry *et al.* 2014; Hasanuzzaman *et al.* 2018). In plants, the root absorbs K⁺ ions against a concentration gradient (since soil K⁺ concentration ranges from 0.1–1 mM) facilitated by K⁺ transporters and channels (Wang and Wu 2011). While the K⁺ channels demonstrate low-affinity transport operating in higher K⁺ concentrations (>0.5 mM), the K⁺ transporters are capable of functioning in much lower K⁺ concentrations (<0.2 mM) (Cheng *et al.* 2018).

K⁺ uptake by roots and its transport to different plant parts are mediated by various [K⁺] transporters. The plant K⁺ transporters are quite conserved and can be broadly categorised in four basic types: (1) TrK/HKT1 family; (2) KT/HAK/KUP family (HAK family); (3) CHX

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Nanoparticles regulate redox metabolism in plants during abiotic stress within hormetic boundaries

Saswati Bhattacharya^{A,#}, Sumanti Gupta^{B,#} and Jayita Saha^{B,*}

For full list of author affiliations and declarations see end of paper

***Correspondence to:**

Jayita Saha
Department of Botany, Rabindra
Mahavidyalaya, Champadanga, Hooghly,
West Bengal, India
Email: jjayita@gmail.com

[#]These authors contributed equally to this paper

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ABSTRACT

Abiotic stress management remains under scrutiny because of the unpredictable nature of climate, which undergoes abrupt alterations. Population pressure, loss of cultivable lands, environmental pollution and other anthropogenic disturbances add to the problem and grossly hinder ongoing management strategies. This has driven increasing effort to find better performing, eco-friendly and reliable alternatives that can contribute to sustainable agricultural practices to manage abiotic stress. Nanotechnology and its implementation in agriculture have emerged as a promising option to cater to the problem of abiotic stress. Induction of reactive oxygen species (ROS) is an inevitable phenomenon linked to stress. Nanoparticles (NPs) perform dual actions in regulating ROS biology. The bidirectional roles of NPs in modulating ROS generation and/or ROS detoxification is tightly coupled within the hormetic boundaries. Nonetheless, how these NPs control the ROS metabolism within hormetic limits demands extensive investigation. This review focuses on the details of ROS metabolism under normal versus stressed conditions. It shall elaborate on the types, modes and process of uptake and translocation of NPs. The molecular dissection of the role of NPs in controlling transcriptomic expressions and modulating molecular crosstalks with other growth regulators, ions, reactive nitrogen species and other signalling molecules shall also be detailed. Throughout, this review aims to summarise the potential roles and regulation of NPs and consider how they can be used for green synthesis within a sustainable agricultural industry.

Keywords: abiotic stress, antioxidative system, hormetic zone, molecular crosstalk, nanoparticles, reactive oxygen species, signal transduction, transcriptional gene expression.

Introduction

Technological advancement and availability of knowledge databases have caused steady improvement in the understanding of stress biology of plants over the past few decades. Even so, the unpredictable nature of abiotic stress factors remains a major threatening factor limiting crop production worldwide (Kumari *et al.* 2022). In addition, incremental population pressure and associated anthropogenic disturbances have resulted in drastic reduction of cultivable land area causing substantial losses in agricultural output (He *et al.* 2018; Mustafa *et al.* 2019). Various abiotic stresses, such as drought, salinity, heavy metals, flooding, cold and heat, are known to constantly challenge plant productivity. These stress factors elevate levels of intrinsic reactive oxygen species (ROS), which cause cellular toxicity beyond tolerance limits. However, plants are known to possess an efficient intrinsic antioxidative system (AOS) that rescues the plant's metabolism from the ill effects of ROS (Khan *et al.* 2017; Denaxa *et al.* 2020). Under normal conditions inherent metabolic ROS generation and AOS-mediated scavenging machinery work in tandem to maintain the cellular homeostasis. Similar results are found when plants are exposed to short term and/or minimal quantities of abiotic stress agents (Jalil and Ansari 2021). Quite often however, because of their immobile nature, plants fail to escape from long term and high intensity exposures to abiotic stresses that cause imbalance in ROS generation versus ROS detoxification. Thus, these accumulated ROS cause cellular toxicity and growth inhibition, eventually leading to plant death (Saha *et al.* 2023).

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