
Potassium ion (K⁺), an Inorganic Macro-Nutrient for Plant Growth

Potassium ion (K⁺) is one of the essential inorganic macro-nutrients for plant growth and the fourth abundant mineral on lithosphere. Although, plants constitute 2-10% of total dry weight and abundantly present cation in the cytosol with a narrow range (i.e. 60-150 mM) (Ashley, Grant, & Grabov, 2006). Plants utilize K⁺ ions for different fundamental processes like cell elongation, osmoregulation, control of membrane polarization and electrical neutralization of anionic groups. Potassium is also involved in maintainance the Ph of the cytosol, which is important for proper functioning of most of the enzymes. In addition to cytosol, potassium is also present in certain organelles i.e. vacuoles, nucleus and chloroplast (Wang, Zheng, Shen, & Guo, 2013).

Storage of potassium in vacuole is helpful for maintaining the concentration of K⁺ in cytosol through these two compartments. Despite its importance and abundance in the cell, optimum concentration of K⁺ is maintained for the proper functioning of the cell. For example, Plant tolerance to salinity (Shi, Ishitani, Kim, & Zhu, 2000) and drought stress (Gupta, Berkowitz, & Pier, 1989) correlated with maintainance of K⁺ ion concertation in the cytoplasm. Moreover, it is also important for the modulation of membrane potential and neutralization of anions. homeostasis of K⁺ in the cytosol is maintained by complex transport system consisting of transporters and channels (Leigh, 2001). This system mediates the absorption and translocation of K⁺ from soil into various part of plant. Almost 35 genes have been reported to code for K⁺ transport proteins (15 channels and 20 transporters) in *Arabidopsis thaliana*. (Mäser et al., 2001; Véry & Sentenac, 2003).

Potassium channels are multimeric proteins containing trans-membrane segments, that are quantified on the basis of pore (P) domains. To make a part of channel conduction pathway four P domains are associated with functional multimeric proteins. Highly conserved motif with an amino acid sequence "GYGD/E". is present in the P domain of potassium channel. Based on topology, 15 selective K⁺ channels are classified into three families in *Arabidopsis thaliana*, which includes one potassium inward rectifier, 9 voltage gated ion channels and, 5 Tandem-Pore K⁺ channels (TPK) (Gambale & Uozumi, 2006). Similarly, Potassium transporters are also classified into three families including KEA family of K⁺ efflux antiporters (six members), KUP/HAK/KT family of K⁺ uptake permeases (thirteen members) and Trk/HKT family of high-affinity K⁺ transporters (one member) (Rodríguez-Navarro & Rubio, 2006). However, various potassium channels and transporters are well characterized in *O. sativa* and *A. thaliana*, but there is no information is available on potassium transporters and channels in *Vigna radiata*.

Mung bean is an important legume crop, diploid (2n=2x=22) pulse crop, grown under tropical and subtropical regions. The seeds of mung bean are an excellent source of carbohydrates, fats, proteins and micronutrients (Nair et al., 2013). The production of mung bean is increase annually, mostly in Asia its center of diversity. Adaptation in extreme environmental conditions and long-term evolution make a mung bean a rich pool stress tolerance gene (Jain et al., 2013; Varshney et al., 2013). The availability of genomic and transcriptomics resources makes a valuable opportunity for the analysis of comparative and evolutionary analysis in mung bean. K⁺ is important micronutrient which greatly contribute to various physiological and biochemical

process correlate with biotic and abiotic stress tolerances in plants(Kant & Kafkafi, 2002). However, in mung bean our standing about the role of potassium in whole plant stress response mechanism is limited. This study was designed to explore the phylogenetic relation of various K⁺ transporters and channels in *Vigna radiata*, *Oryza sativa* *Cicer arietinum* and *Arabidopsis thaliana*. and to study the effect and possible role of potassium in abiotic stress responses.

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