



RESEARCH ARTICLE

Elucidating the role of osmotic, ionic and major salt responsive transcript components towards salinity tolerance in contrasting chickpea (*Cicer arietinum* L.) genotypes

Jogendra Singh¹ · Vijayata Singh¹ · P. C. Sharma¹

Received: 27 May 2017 / Revised: 23 January 2018 / Accepted: 31 January 2018 / Published online: 27 February 2018
 © Prof. H.S. Srivastava Foundation for Science and Society 2018

Abstract The growth of chickpea (*Cicer arietinum* L.) is extremely hampered by salt stress. Understanding of physio-biochemical and molecular attributes along with morphological traits contributing to the salinity tolerance is important for developing salt tolerant chickpea varieties. To explore these facts, two genotypes CSG8962 and HC5 with contrasting salt tolerance were evaluated in the salinity stress (Control and 120 mM NaCl) conditions. CSG8962 maintained lower Na/K ratio in root and shoot, trammed Na translocation to the shoots from roots compared to HC5 which ascribed to better exclusion of salt from its roots and compartmentation in the shoot. In chickpea, salt stress specifically induced genes/sequences involved at several levels in the salt stress signaling pathway. Higher induction of trehalose 6 phosphate synthase and protein kinase genes pertaining to the osmotic and signaling modules, respectively, were evident in CSG8962 compared to HC5. Further transcripts of late embryogenesis abundant, non-specific lipid transfer protein, HI and 219 genes/sequences were also highly induced in CSG8962 compared to HC5 which emphasizes the better protection of cellular membranous network and membrane-bound macromolecules under salt stress. This further suppressed the stress enhanced electrolyte leakage, loss of turgidity, promoted the higher compatible solute accumulation and

maintained better cellular ion homeostasis in CSG8962 compared to HC5. Our study further adds to the importance of these genes in salt tolerance by comparing their behavior in contrasting chickpea genotypes.

Keywords Gene expression · Glycinebetaine · Ionic homeostasis · Membrane leakage · Real-time PCR

Introduction

Salinity stress is an alarming problem in many regions of the world. Approximately 1 billion ha land in the world is prone to salt stress (FAO 2015). The quantum of the saline area is further added by arid and semi-arid areas associated with saline underground water. This saline underground water has to be used for irrigation due to unavailability or utilization of good quality water to the non-agricultural purpose that ultimately makes the soil unfit for crop cultivation (Munns and Tester 2008; Pons et al. 2011; Singh et al. 2014).

Chickpea is one among the very important legume crops, known for its nutritional benefits, soil enrichment properties (Arnoldi et al. 2014; Araujo et al. 2015) and is a key component of South Asian and Mediterranean diets. Chickpea is particularly sensitive to salt stress which reduces its productivity by 0–100% depending upon the level of salinity (Turner et al. 2013; Flowers et al. 2015). Even after a lot of research done to improve salt tolerance in chickpea, till date, only few salt tolerant varieties have been released for commercial cultivation across the world (Maliro et al. 2004). One major reason cited is the narrow genetic base of this crop which makes it difficult for breeders to produce new varieties with improved salt tolerance (Berger et al. 2003; Flowers et al. 2010).

✉ Jogendra Singh
jogendra.singh@icar.gov.in; jogendra82@gmail.com

Vijayata Singh
vijayatasingh.gpb@gmail.com

P. C. Sharma
pcsharma.knl@gmail.com

¹ ICAR-Central Soil Salinity Research Institute, Karnal, Haryana 132001, India