University of Zabol
Graduate School
Faculty of Agriculture
Department of plant Breeding and Biotechnology

Dissertation for M.Sc Degree in Plant Biotechnology

Characterization, sequence and Molecular analysis of Quinoa Na^+/H^+ antiporter genes under Salinity Stress Conditions"

Supervisor:
Dr Barat-Ali Fakheri

Advisor:
Dr Nafiseh Mahdi-Nejhad

By:
Razie Nekouei

May, 2023

Title:

Characterization, sequence and Molecular analysis of Quinoa Na^+/H^+ antiporter genes under Salinity Stress Conditions"

Abstract:

Salt resistance is a complex trait that is controlled by several genes and includes various physiological and biochemical mechanisms. Exposure of plants to salt stress causes many molecular, biochemical and physiological changes, which are due to major changes in gene expression. Plants use different methods with the aim of preventing excess sodium accumulation, which include improving ion absorption by roots, loading in xylem for distribution over long distances, ion reabsorption by potassium transporting proteins and storage in leaf vacuoles. This storage prevents the toxic effects of sodium in the cellular reactions of the cytosol, which are the intracellular sodium/hydrogen transporters, such as NHX protein, SOS1, and... the most appropriate protein. are involved in this process. This research was aimed at identifying vacuolar membrane antiporters in quinoa plant and studying the obtained sequences through bioinformatics software. In this study, NHX and SOS1 genes from the quinoa plant with the scientific name Chenopodium quinoa were identified and sequenced using the Sanger sequencing method. This antiporter named CqNHX has a length of 520 base pairs and 172 amino acids with a molecular weight of 18 kilodaltons and an isoelectric point of 4.58. The results of the analysis with BLAST and Mega6 software showed that the sequence obtained in the quinoa plant is more than 95% similar to the sequence of this gene in Bassia scoparia and Oxybasis glauca. Multiple co-sequencing for this gene indicated a high percentage of similarity among the sequences used from different plants. It was also found that the NHX protein obtained from the quinoa plant of the Rahmat cultivar has a protected DNA binding region, and these transcription factors will be effective in salt stress tolerance through the identification of the promoters of induced genes during osmotic stress. Was. In addition, the investigation of the second structure of the NHX protein sequence using PSIPred program showed that this protein contains small beta sheets and alpha helices, so that this sequence has 81 alpha helices (42.25%), 14 beta helices (7.82%).), has 43 long strands (24%) and 41 random spirals (22.91%). These secondary structures are effective in the plant's tolerance to environmental stress conditions through the transmission of created messages. It seems that the proteins created in this way play a role in the repair of DNA damage and cause the activation of NHX proteins in the plant through the transmission of messages from the cytoplasm to the nucleus.

Key words: Na/H Anti porterT Sequencing, Quinoa, Vacouelar membrane, Open Reading Frame, Sanger Method**.**