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SALINITY STRESS IN PLANTS

Abstract: *Plants are influenced by various biotic and abiotic factors. One of the most critical abiotic stressors is salinity, which significantly reduces the growth and yield of cultivated crops. To achieve high productivity under saline conditions, it is necessary to develop salt-tolerant varieties adapted to such environments. This*

article discusses the responses of plants to salt stress and highlights several genes responsible for salt tolerance, including transcription factors and QTL loci.

Keywords: *salinity, transcription factors, genes OsERF48, OsERF922, OsDREB1A, AP37, AP59, PsAP2, GhWRKY17, QTL loci.*

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СОЛЕВОЙ СТРЕСС У РАСТЕНИЙ

Аннотация. На растения воздействуют различные биотические и абиотические факторы. Одним из наиболее важных абиотических стрессов является засоление, которое значительно снижает рост и урожайность сельскохозяйственных культур. Для получения высоких урожаев в засоленных условиях необходимо создавать сорта, адаптированные к таким условиям и устойчивые к засолению. В данной статье рассмотрены реакции растений на засоление, а также приведены некоторые гены, отвечающие за устойчивость к солевому стрессу (включая транскрипционные факторы и локусы QTL).

Ключевые слова: засоление, транскрипционные факторы, гены OsERF48, OsERF922, OsDREB1A, AP37, AP59, PsAP2, GhWRKY17, локусы QTL.

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O‘SIMLIKLARDA SHO‘RLANISH STRESSI

Annotatsiya. *O‘simliklarga turli biotik va abiotik omillar ta’sir ko‘rsatadi. Ulardan eng muhimlaridan biri bo‘lgan sho‘rlanish – abiotik stress omili sifatida madaniy o‘simliklarning rivojlanishi va hosildorligini sezilarli darajada pasaytiradi. Sho‘rlangan muhitda yuqori hosil olish uchun bu sharoitga moslashgan, sho‘rga chidamli navlarni yaratish zarur. Ushbu maqolada o‘simliklarning sho‘rlanishga javob reaksiyasi, sho‘rga chidamlilikka javobgar ayrim genlar (jumladan, transkripsiya omillari va QTL lokuslar) keltirib o‘tilgan.*

Kalit so‘zlar. *Sho‘rlanish, transkripsiya omillari, OsERF48, OsERF922, OsDREB1A, AP37, AP59, PsAP2, GhWRKY17 genlari, QTL lokuslar.*

Introduction. Plants are affected by a variety of abiotic and biotic stress factors. Among abiotic stresses, salinity is one of the most widespread and detrimental, severely limiting plant growth and productivity. Soil salinization refers to the accumulation of water-soluble mineral salts in the soil. Soils with more than 0.1% harmful water-soluble salts or more than 0.25% dry residue in the soil solution are considered saline. Saline soils are further categorized as slightly saline (0.1–0.2%), moderately saline (0.2–0.4%), strongly saline (0.4–0.8%), and very strongly saline (>0.8%) [27].

According to the Food and Agriculture Organization (FAO) of the United Nations, approximately 1.4 billion hectares of land are currently affected by salinization, with an additional 1 billion hectares at risk [27]. The impact of salinity is further exacerbated by climate change and unsustainable irrigation practices.

Physiological and morphological effects of salinity. Salinity affects almost all stages of plant development, including seed germination, vegetative growth, and reproductive development. Key effects include osmotic stress, ion toxicity, and oxidative stress [19, 22]. Salinity reduces leaf area, increases leaf thickness and succulence, causes premature leaf drop, and leads to necrosis in roots and shoots. Shortened internodes and decreased biomass are commonly observed symptoms [10, 15, 17, 26].

In saline environments, hormonal balance is disrupted. Stress conditions induce the accumulation of abscisic acid (ABA) and ethylene [14]. ABA is a central hormone in the plant response to abiotic stress, including drought, high temperature, cold, and salinity [3, 5, 8]. It promotes stomatal closure and helps in osmolyte accumulation, such as potassium, calcium, proline, and soluble sugars [7].

Mechanisms of salinity tolerance. Salinity tolerance mechanisms in plants are classified into two main categories:

1. Restriction of salt entry into the plant.
2. Reduction of cytoplasmic salt concentration through compartmentalization.

Halophytes, or salt-tolerant plants, typically possess both types of mechanisms [13]. Key molecular processes include ion homeostasis, osmotic regulation, and activation of antioxidant defense systems. Na^+/H^+ antiporters, particularly those located in the tonoplast, help in vacuolar sequestration of excess Na^+ to maintain cellular ion balance.

Role of transcription factors in salinity tolerance. Transcription factors (TFs) play essential roles in regulating gene expression under salt stress. Important TF families include AP2/ERF, bHLH, bZIP, DREB, NAC, WRKY, and MYB [2, 8, 28]. The AP2/ERF family regulates various developmental and stress-responsive genes. For instance, in rice, OsERF48 enhances root growth and yield under drought, while OsERF922, when overexpressed, reduces salt tolerance due to increased Na^+/K^+

ratios [8]. DREB genes such as OsDREB1A, AP37, and AP59 enhance drought and salinity tolerance in rice [11]. WRKY transcription factors like GhWRKY17 in *Gossypium hirsutum* are upregulated by drought, salinity, H₂O₂, and ABA [24]. Other salt-responsive TFs in cotton include GhERF2–GhERF6 (ERF family), GhZFP1 (zinc finger protein), GhNAC1–GhNAC6 (NAC family), GhMT3a (metallothionein), GhMPK2, GhMKK1 (MAP kinases), and GhDREB1 (DREB family) [4].

bZIP (basic leucine zipper) transcription factors are present across all eukaryotic organisms [29]. bZIP (basic leucine zipper) transcription factors (TFs) are widely distributed in plants and play crucial roles in various biological processes, including plant growth and development, photomorphogenesis, signal transduction, resistance to pathogenic microorganisms, tolerance to biotic and abiotic stresses, and regulation of secondary metabolism [30]. bZIP transcription factors consist of a conserved domain comprising 60–80 amino acids [31, 32].

In *Arabidopsis*, the AtbZIP36 (ABF2/AREB1), AtbZIP37 (ABF3), and AtbZIP38 (ABF4/AREB2) genes are involved in ABA signaling and play key roles in the plant's response to dehydration and salinity stress [2, 33].

In rice (*Oryza sativa*), 89 genes encoding bZIP transcription factors have been identified. These genes were analyzed under drought, salinity, and cold stress conditions. Among them, 37 genes exhibited differential expression based on microarray analysis [34].

In cotton species, 228 bZIP genes were identified in *Gossypium hirsutum*, 91 in *G. arboreum*, and 86 in *G. raimondii*. Transcriptome analysis conducted under drought (water stress), salinity (salt stress), and temperature stress conditions in *G. arboreum*, *G. herbaceum*, and *G. hirsutum* cultivars revealed differential expression of several bZIP genes, including *bZIP11*, *bZIP17*, *bZIP37*, *bZIP47*, *bZIP53*, *bZIP55*, *bZIP60*, and others [35]. Furthermore, *GhABF2* enhances drought and salt tolerance

by regulating genes associated with ABA signaling and responses to drought and salinity [36].

Genetic mapping and QTLs related to salinity tolerance. Quantitative trait loci (QTLs) mapping plays a crucial role in identifying genomic regions associated with salt tolerance in plants. In *Arabidopsis*, eleven QTLs have been identified in a recombinant inbred line (RIL) population, which influence both germination and vegetative growth stages under salinity stress [16]. Similarly, in rice, twenty-seven QTLs associated with salt tolerance were discovered using backcross inbred lines (BILs) derived from the Nipponbare and Kasalath cultivars [20]. In barley, important QTLs located on chromosomes 1H, 4H, 5H, 6H, and 7H contribute to salinity tolerance during both germination and seedling development stages [12]. In tomato, thirteen and twenty QTLs were found in F8 populations developed from crosses between salt-sensitive and salt-tolerant parental lines. These QTLs are associated with key salt-tolerance genes such as *SlSOS1*, *SlSOS2*, *SlSOS3*, *LeNHX1*, and *LeNHX3* [23]. In cotton, several simple sequence repeat (SSR) markers, including BNL3103 on chromosome D6, NAU478 on D8, and BNL3140 on D9, have been linked to salinity tolerance and are currently being used in marker-assisted breeding programs [18].

Genetic engineering and molecular breeding approaches. To enhance salt tolerance, researchers have introduced genes from halophytes and microbes into crop plants. For example, overexpression of the *ST7* gene from *Thellungiella halophila* in cotton has been shown to improve germination and seedling growth under NaCl-induced stress. Similarly, microbial genes such as *K2-NhaD* from *Alkalimonas amylolytica* have been used to confer improved resistance to both salinity and drought conditions in transgenic cotton. Furthermore, the *GhDREB* gene, when introduced into wheat, enhances the plant's tolerance to drought, salt, and cold stress [6]. In addition to transgenic approaches, marker-assisted selection (MAS) offers a powerful strategy for indirectly selecting traits using molecular markers. This technique

significantly accelerates breeding programs by linking QTLs and key stress-responsive genes to observable phenotypic traits [1].

Conclusion. Salinity is a major abiotic stress that limits plant growth and agricultural productivity worldwide. Cotton, a key industrial crop, is highly sensitive to salinity. Understanding the physiological, molecular, and genetic mechanisms underlying salt tolerance is crucial for developing resilient cultivars. Recent advances in molecular biology, genomics, and biotechnology offer promising tools to accelerate the breeding of salt-tolerant cotton varieties. Integrating these tools with conventional breeding and sustainable agricultural practices will be vital in mitigating the adverse effects of salinization on crop productivity.

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