

Salt stress tolerance in Rice Plants: Latest Findings

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Short Communication

High salinity of the soil hinders the plant germination, growth and development. Salt stress causes osmotic stress, nutritional stress, stomatal closure, ion stress, reactive oxygen species accumulation. Nearly one third of the irrigated land is affected by salinity. More than half of the world population depend on rice as staple food source. Soil salinity affects the rice planting and yield. Better understanding of the morphological, physiological and biochemical properties of the rice plant towards the salt stress provide us regulatory mechanisms that control salt stress tolerance. As of now more than 85 QTLs and genes that are associated with salt stress tolerance in rice are identified so far. SKC1 is the first isolated salt stress related QTL in rice that encodes sodium ion transporter. OsNHX1 encoding vacuolar Na⁺/H⁺ antiporter aids in the transport of Na⁺ that accumulates in the cytoplasm to the vacuole. OsSOS1 is the Na⁺ efflux transporter that is activated by OsCBL4-OsCIPK24 complex. OsKAT1 and OsAKT2 encode potassium channel proteins that play a role in the absorption of the potassium ions⁺ by rice roots. Several of the QTLs and the genes are characterized for understanding of the salt stress mechanism. Several studies were conducted in genomics, transcriptomics, proteomics, metabolomics, and epigenetics that enhance our understanding of the salt stress. The data obtained from these studies can be integrated for precise breeding for the development of the salt stress [1].

One of the recent studies screened OsPM1 containing nearly 30 amino acid residues by using the microarray technology. The analysis of the promoter region revealed that this gene contains multiple cis-regulatory elements that respond to the abiotic stress. QT PCR and promoter GUS transgenic plant analysis revealed that OsPM1 was induced by multiple abiotic stress. GFP analysis revealed that OsPM1 was localized in the cell membrane. Overexpression of the OsPM1 resulted in the hypersensitivity of the rice plants to the salt stress but enhanced drought stress. Alternately the plants expressing antisense OsPM1 were hyposensitive to salt stress and weak to the drought stress [2].

One of the recent studies showed that foliar application of the 24-epibrassinolide replenished the negative effect of the salt stress in the rice seedlings. It also improved the plant growth and the physiology, reduced the oxidative injury, enhanced the antioxidant enzyme and phenolic compounds in ice plants by reducing the endogenous levels of the ABA. It also resulted in the upregulation of the carotenoids and flavonoids genes [3].

The methylation of the N6-methyladenosine (m6A) represents the new layer of epitranscriptomics regulation of the plant development and growth. One of the studies performed methylated RNA immunoprecipitation sequencing analysis under salt stress conditions. It was found that salt stress led to increased m6A methylation in the shoot tissue. More than two thousand m6A sites were identified in the shoots under salt stress. The upregulation was mediated by the certain transcription factors, antioxidants, auxin-responsive proteins. The m6A changes regulates the gene expression that are responsible for the plant growth, stress response and ion transportation [4].

During the salt stress the transcription factors get involved in the

absorption, transport, compartmentation of sodium and potassium to resist salt stress. One study used the CRISPR/Cas9 technology for inducing gene editing mutant for deciphering the role of the OSbHLH024 in rice under salt stress with A nucleotide deletion. The results revealed that exposure of the A91 resulted in the higher shoot weight, high chlorophyll content, chlorophyll fluorescence, high antioxidant activity, less reactive oxygen species and stabilization of the malondialdehyde levels. Mainly the balancing of the ions in the shoot and the root allowed the salt stress tolerance. Also resulted in the upregulation of the ion transporter genes [5].

Salt stress induces the synthesis of the osmolytes including the proline and glycine betaine. It was observed that salt stress resulted in the significant reduction in plant growth parameters. It was found that salt sensitive genotypes and the salt tolerant genotypes increased the total proline and glycine betaine accumulation. However, inoculation of the B. linens RS16 has resulted in the improvement of the plant growth parameters in salt sensitive and tolerant genotypes enhancing the proline and glycine betaine accumulations. Both proline and glycine betaine are compatible osmolytes in rice under salt stress [6].

Monogalactosyldiacylglycerol is regarded as the most abundant lipid on the earth constituting the polar lipids in the thylakoid membranes of the higher plants. The study revealed that under salt stress OsMGD overexpression in the rice seedlings led to higher biomass with lower Na⁺ content. These plants also had higher content of chlorophyll a and carotenoids and photosynthetic capability such as higher photosynthetic ability, the electron transport rate. Therefore it was concluded that the OsMGD improves the salt tolerance in the plants by protecting the photosynthetic capabilities and balancing the ion ratio [7].

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