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Salinity stress resistance in wheat

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ABSTRACT

Wheat is used as staple food worldwide and it ranked third in cereals. Its productivity a the global level decreases by many stresses mainly by salinity stress which is associated with different physiological and biochemical processes of plants. To overcome these growth and yield reduction issues, salinity resistance in wheat can be achieved. The introduction of resistance to salinity-induced water stress and ion toxicity in wheat lead to more reliable results. Salt tolerance mechanisms at tissues and whole plant levels along with sequestration of toxic ions can improve overall growth, yield, and salinity resistance capability in wheat. Different sources and measurements of salinity play important role in the production of salinity tolerant wheat. This article mainly reviews different physiological mechanisms, genetics, omics, and quality trait loci approaches for the production of salinity tolerant wheat.

Keywords: Salinity resistance, salt tolerance, wheat, NaCl, osmotic stress.

INTRODUCTION: Wheat (*Triticum aestivum*) is regarded as one of the major food components worldwide and is belonged to the family Poaceae. Its cultivation was reported from the Middle East about 8000 years ago which expanded readily throughout the world (De Vries *et al.*, 2018). The global production of wheat is categorized third following rice and maize and it produces 35% of total food grains in the world (Khan *et al.*, 2017). By virtue of different reasons including a reduction in cultivated land, heat, chilling, heavy metal, waterlogging, drought, chemical stress, and other abiotic and biotic stresses causes a reduction in wheat cultivation (Masuda, 2016). Large parts of the world are inclined to different levels of salinity stress from sodic saline-sodic to saline soils which cause adverse effects on plant growth, development, and yield. Osmotic components of salinity-induced cell reduced the hydration level of that cell which ultimately causes stomatal closure, photosynthesis inhibition, senescence, and cell expansion. Soil salinity is a major abiotic stress in the world. Around 20% of total agricultural fields are subjected to salinity which caused a 50% reduction in wheat yield along with the influence of other stresses (Miransari and Smith, 2019; Munns *et al.*, 2020). Wheat is not well tolerant to salinity stress as compared to its relatives, because at salinity level of 6-8dSm-1, causes a reduction in yield. To cope with this issue it is critical to developing methods and techniques for the production of salinity-resistant and tolerant wheat varieties (Miransari and Smith, 2019). Salt deposition with different amounts in the soil is the cause of different salinity levels. The main cause salt deposition is irrigation of soil with saline water (Iqra *et al.*, 2020). As wheat is used as staple food and salinity is increasing continuously in Pakistan and it may also be estimated that this rate of salinity will double in the incoming years. So to cope with these issues, there should be well aware of salinity resistance mechanisms and genetics to produce salinity resistant wheat plants, salinity affects all the physiological and biochemical functions of plants (Iqra *et al.*, 2020). So the development of salt-tolerant wheat and interpretation of salinity resistant mechanism in wheat is of great importance (Xiong *et al.*, 2017).

OBJECTIVES: The objective of the present study was to evaluate different mechanisms, sources, new proportions of salinity resistance, and, its improvement by different genetic and breeding approaches.

SALINITY RESISTANCE IN WHEAT: Salinity resistance may originate from resistance to osmotic stress and salinity-induced ion toxicity. Being a glycophytes crop, wheat responds in the saline environment at a different pace as compared with halophytes. The accumulation of saline water causes osmotic stress and thereby decreasing the water potential in plants which results in greater yield loss. SOS1 is a cell membrane Na^+/H^+ antiporter which is responsible for the exclusion of sodium from the cytoplasm. SOS_2; the serine-threonine type protein kinases (CIPK24) interact with SOS3 to regulate Na+/H+ exchanger SOS1, therefore this pathway is known as the salt resistance pathway (Xiong *et al.*, 2017). The wheat plant utilizes phenotypic plasticity to overcome the effect of salinity stress by upregulation of different salt responsive genes including ion transporters, signaling pathways, osmolyte production, transcriptional responsive genes, and antioxidant enzymes.

Resistance to salinity induced water stress: While wheat cultivation the quantity and quality of water is taken as an important parameter that affects wheat yield production. Saline water irrigation causes osmotic stress by affecting the level of organic solutes and inorganic ions (Na^+, Cl^-, K^+, etc.) and also causes more severe water deficiency in wheat. The results of a study indicate that the osmotic potential pressure significantly increases in salinity-resistant wheat genotypes as compared to sensitive ones. Osmoregulation is a common response and is an important mechanism in salinity-resistant wheat as it causes leaf desiccation avoidance and other consequences of turgor loss. In wheat, salinity stress is important to determine the osmotic adjustment of the plant under salinity. By determining the Na^+ toxicity and NaCl osmotic potential of wheat, it is confirmed that Na+ exclusion from leaves is an important mechanism to produce tolerant wheat varieties. The production of sugars under salt stress results in the adjustment of osmotic potential. Sugars, organic acids, Polyols, and many amino acids are also involved in the Osmoregulation mechanism in wheat and also protect the enzymes and cellular components during stress and make the plants more resistant to salinity (Guo *et al.*, 2015). Osmoregulation allows turgor maintenance by reducing water loss while maximizing water uptake and leaf desiccation avoidance and results in greater leaf growth and stomatal conductance which make wheat plants more resistant to salinity stress.

Resistant to salinity induced ion toxicity: Salinity stress causes hyper ionic and hyperosmotic stress in wheat which causes a nutrient disturbance, hormonal imbalance, and other negative impacts on wheat growth and yield (Daneshbakhsh *et al.*, 2013). Resistance to salinity-induced ion toxicity in wheat occurs by reduced ion uptake mechanism, ion exclusion mechanism, salinity tolerance, and by genetic engineering techniques (Wang and Xia, 2018). It has long been conferred that bread wheat is more salt-tolerant than tetraploid wheat. This difference is because of the maintenance of a higher ratio of K^+ concentration in leaves of bread wheat (Wang and Xia, 2018). Wheat plants have adapted several mechanisms to reduce ionic and osmotic stresses of salinity and tissue tolerance by Na+ exclusion from flag leaves.

Ion exclusion mechanism in wheat: There are different ion exclusion mechanisms in different plants. In the case of wheat HKT genes are involved in Na^+ exclusion and Na^+ transport regulation in wheat. These genes control Na^+ unloading from the xylem in root and sheath cells of wheat. In addition, these genes also involved in reduced Na^+ content in leaves. Some genes are involved in Na^+ exclusion from the xylem which is responsible for lesser uptake of Na^+ in leaves and results in an increase in wheat grains (Miransari and Smith, 2019). The result of a study also showed that the natural diversity of ancestral wheat germplasm also improves wheat tolerance against salinity by Na^+ exclusion. HKT transporters play important role in the vacuolar sequestration of Na^+ which is an important cost-effective strategy for wheat plants (Tiwari *et al.*, 2020).

Salt tolerance mechanism in wheat: Crops exhibit salinity tolerance in three ways, i.e., ion exclusion mechanisms; in which toxic ions are excluded from different plant parts, tissue tolerance in which toxic ions are compartmentalized into different plant tissues, the third is shoot ion- independent tolerance which is responsible for independent Na^+ accumulation in tissues as well as water uptake and growth of the plant (Munns *et al.*, 2020).

Na+ exclusion: Na^+ accumulation in the cytoplasm can be controlled by reduced Na^+ influx, increased Na^+ efflux, and vacuolar sequestration of Na^+ ions (Tiwari *et al.*, 2020). This process is controlled by SOS1, SOS2, SOS3 (salt overly sensitive) pathways and by the activity of different pumps such as H^+-ATPase pump. Na^+ and Cl^- require compartmentalization at the cellular and intracellular levels to avoid the harmful impact of salinity on wheat growth and yield. Na+ exclusion mechanism is also responsible for its storage root cell vacuoles. It was also investigated that the QTL for Na+ exclusion mechanism reduces negative effects of salinity of wheat grain quality. The introduction of the NaX2 gene in the durum wheat from the *Triticum monococcum* lead to the decreased Na+ content in the durum wheat which will produce more resistant wheat verities.

Salinity counter-mechanisms in wheat via different signaling pathways: The cell membranes in wheat plants are served with salinity Na+ receptors, which receive salinity stress signals and enhance the signaling molecules like Ca2+, hormones, ROS etc. By the elicitation of these molecules, three pathways will operate in wheat cells that ultimately regulate the SOS1 for pumping out of Na+ from the cytosol. For these mechanisms, all the SOS1 related genes were up-regulated. The activity of K+ and Na^+ transporters and proton pumps along SOS2 and SOS3 protein kinase pathways coordinate with SOS1 for sequestration and secretion of toxic Na+ out of cells (Shah *et al.*, 2017).

K+ retention in mesophyll cells: Potassium is an important nutrient which can control wheat development and growth under salinity stress. Potassium retention in mesophyll cells is an important strategy to control salinity stress by increasing tolerance capacity in wheat. A case study by using durum wheat and bead wheat genotypes was conducted and results showed that the ratio of K+/Na+ was a good indicator of salinity tolerance in bread wheat (Karthik *et al.*, 2014).

Salinity tolerance at whole-plant level: Salinity tolerance not only occurs at the tissue level but it also occurs at whole-plant level. At the whole plant level salinity tolerance can be achieved by alteration of flowering and fruiting times, retranslocation of photosynthates, allocation of leaf salt to leaf petiole or sheath, allocation of salts at epidermis instead of mesophyll cells, control of restoration of salts in the wheat stem, salt excretion via roots, salt removal from xylem and symbiotic association are the commonly studied phenomena in wheat plants (Isfahani *et al.*, 2018).

IMPROVEMENT OF SALINITY TOLERANCE IN WHEAT BY SILICON: Silicon is the second most abundant element on earth. It is not yet classified as an essential element but it plays important role in the improvement of salinity tolerance in wheat plants. Silicon has been reported to improve salinity tolerance mechanisms in wheat by application a small amount of soluble silicon (Miransari and Smith, 2019).

GENETICS OF SALINITY RESISTANCE IN WHEAT: Wheat exhibits multigenic traits which are more complex than other well-studied relatives. When wheat plants are exposed to different salinity stresses, many genes are activated to mediate different resistance mechanisms for the survival of plants. Some genes in wheat are activated for the synthesis of Phytohormones such as activation of TaAOC1 gene in wheat for the synthesis of jasmonic acid during salinity stress for regulation of resistance mechanisms (Zhao *et al.*, 2014). In the same way Overexpression of the TaBASS2 gene improves salinity tolerance in wheat via ABA signaling (Zhao *et al.*, 2016). Na+ exclusion conciliated by HKT genes has been playing a major salinity tolerance mechanism in wheat. The genes such as TaHKT1; 5-D were explored in salinity mediated mechanisms along with TaHKT1;5-B1 and TaHKT1; 5-B2 transcripts (Byrt *et al.*, 2014). Studies on wheat plants suggested that ROS homeostasis is the major biochemical factor for salinity tolerance. TaSRO1 gene play important role In ROS homeostasis in wheat and is predicted to affect PARP catalytic activity which is significant for DNA repair in salinity stress. TaCHP; a zink finger transcription factor that facilitates salinity tolerance in wheat through improved peroxidase leaf activity for the enhancement of ROS scavenging mechanisms. The salt tolerance gene SOS3 is indicated to encode calcium-binding protein with N-myristoylation signature sequence. The resultant gene products of SOS3 are predicted to use for the operation of SOS2 and SOS1 gene. It was also suggested that an increase in mRNA synthesis collaborates with the activation of the SOS3 gene in wheat during salinity stress (Tiwari *et al.*, 2020). In wheat, VHA-A transcripts are up-regulated in response to salinity stress. In the same way, NAC gene from wheat was also studied and considered to have possible physiological and morphological roles in salinity stress. The results of a study based on Nax genes associated with high sodium accumulation in wheat reveal that Nax genes play important role in osmotic stress (Genc *et al.*, 2019). The Overexpression of allene oxide cyclase in wheat causes an increase in jasmonate contents lead toward improved salinity resistance (Xiong *et al.*, 2017). Transcription factor families such as MYB, WRKY, bHLH, AP2/ERF, NAC, and bZIP are readily engaged in salinity stress responses (Karthik *et al.*, 2014). Recently some RNA sequencing techniques are used to elaborate transcriptomes of wheat under salt stress. It has also been found that the V-ATPase gene is involved in providing energy for the formation of a proton gradient to drive Na+ into vacuoles. In the same way, Cb1 interacting protein kinases proteins play role in salt tolerance signaling in wheat. MYB transcription factors and TARSL4 genes are involved with root development and play an important part in the salt tolerance resistance mechanism in wheat (Zhang *et al.*, 2016).

MEASUREMENTS AND SOURCES OF SALINITY RESISTANCE IN WHEAT: The successful breeding program of salinity-resistant wheat depends upon the reliable estimation of plants. This measurement depends upon reliable techniques and a controlled level of salinity. The sources of salinity resistance mainly consist of commonly cultivated varieties of wheat, germplasm collection, soma clones, transgenes, and related wild relatives of wheat which can be used in various patterns and combinations by the use of prevalent and modern techniques (Zhang *et al.*, 2016).

Gene	Group	specification	NaCl concentration	References
CBL2	Stress sensor	Ca sensor kinase	250mM	Goyal *et al.* (2016)
NHX1	Ion balance regulator	Na transporters	100mM-250mM	Formentin *et al.* (2018)
CLC	Ion balance regulators	Chloride anion channel	150-200mM	Formentin *et al.* (2018)
GLXR, ERD4	Ion balance regulators	Cation channels	200mM-300mM	Xiong *et al.* (2017)
GST	Ion balance regulators	Transferases	150mM-255mm	Goyal *et al.* (2016)
APX	ROS regulators	ROS scavengers	50mM-255mM	Hemida *et al.* (2014)
CAT	ROS regulators	ROS scavengers	25mM-255mM	Hemida *et al.* (2014)
SOD	ROS regulators	ROS scavengers	50mM-250mM	Hemida *et al.* (2014)
GR	ROS regulators	Redox enzymes	100mM-150mM	Hemida *et al.* (2014)
LOX	ROS regulators	Redox enzymes	300mM	Xiong *et al.* (2017)
PAO	ROS regulators	Redox enzymes	50mM-250mM	Zarza *et al.* (2017)
TASRO1	ROS homeostasis	Catalytic enzyme	-----	Liu *et al.* (2014)
TaBASS2	Salinity tolerance	ABA regulators	----	Zhao *et al.* (2014)
P5CR	Cell protectors	Proline synthesis	100mM-250mm	Nounjan *et al.* (2012)
ADC	Cell protectors	Polyamine synthesis	100mM-250mM	Xiong *et al.* (2017)

Table 1: list of genes which change their expression level under salinity stress in *Triticum aestivum.*

Breeding approaches for salinity tolerant in wheat: The genetic pool of wheat has a huge amount of genetic diversity for salinity resistance as well as tolerance. During the last few decades, different breeding approaches for confirmation of salinity resistance in wheat have progressed so far. The cDNA, microarray, proteomics, genomics, subtraction hybridization techniques, and many other new techniques are used in this regard. The other most useable techniques are improved genotype assays in form of SNP arrays, next-generation turn-over methods, gene editing tools to manipulate genetic effects, and other new phenomic platforms for elucidation of salinity effects in wheat. These techniques are used for the efficient utilization of salinity tolerance and resistance encoding genes in the wheat plant from different recourses (Wang and Xia, 2018).

NEW PROPORTION IN SALINITY RESISTANCE MECHANISM OF WHEAT: Omics web: The rapid increase in proteomics, transcriptomics, genomics, epigenomics, and other omics, and advances in whole wheat genomics will stimulate more gene discovery in wheat for improvement of salinity resistance. For the identification of salinity tolerance in wheat cDNA microarrays between salt-tolerant and salt-susceptible wheat, lines were performed with subtraction hybridization techniques (Wang and Xia, 2018). But the absence of the whole genome sequence of wheat srestricts discovery of new salinity tolerance encoding genes. By using high throughput transcriptome sequencing and wheat cultivars with different levels of salinity tolerance, allows global gene expression following salinity stress. The expression of tandem and homologous duplications contributing to various salinity tolerance mechanisms in wheat was also analyzed by analysis of transcripts via genome survey sequencing methods. In the same way, rapid improvement in the next-generation sequencing and genomic enrichment information allows epigenomics identification in the salinity tolerance mechanism of wheat. Moreover for the further investigation of population genetics, multiple omics, and salt-tolerant QTL analysis is essential for the better output of salinity-resistant wheat varieties (Wang and Xia, 2018).

Production of salinity resistant germplasm: Including salinity-resistant diploid germplasm and somatic hybridization interrogation along with much other specific germplasm for salinity, resistance is used with the elaboration of two main mechanisms (ROS homeostasis and ionic control mechanism). For the production of salinity-resistant germplasm for gene discovery and genetic breeding, there is a need for a more elegant system. There is another recent trend in functional genomics is the establishment of comprehensive mutant libraries of hexaploid and tetraploid wheat. Salinity tolerant involving genes are easily identified from these comprehensive mutant libraries which help in the formulation of more durable salinity resistant varieties (Wang and Xia, 2018). The salinity-resistant germplasm contains all the respective genes which enhance direct salinity tolerance mechanisms in wheat, or indirectly influence plant salinity tolerance by regulating different crosstalk pathways (Wang and Xia, 2018).

CONCLUSION: The present study illustrates importance of wheat as major food crop and different resistance mechanisms against salinity stress. It was also concluded that the salt tolerance mechanisms protect wheat plant by ion exclusion mechanism, tissue tolerance, and other salinity tolerance mechanisms. By using multi-genetic traits and different breeding approaches such as omics web and production of salinity-resistant germplasm salinity stress resistance can be achieved in wheat plants.

CONFLICT OF INTEREST: The authors declare no conflict of interest.

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