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A Review of the Effects of Salt Stress on Cotton Growth and Germination at Various Stages

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ABSTRACT

Salinity is one of the most significant abiotic pressures in agriculture worldwide, with a salinity threshold of 7.7 dSm⁻¹; Cotton is a salt-tolerant crop. Salinity influences cotton growth, production, and fiber quality. The tolerance to salt stress varies according to the development stage and salt type. Cotton growth and seed output are significantly decreased at high saline levels, and various salts have varying effects on cotton growth. Salinity causes osmotic stress, lowering the leaf's water potential and turgor pressure. Salinity affects ion homeostasis and causes an increase in reactive oxygen species (ROS) in plant cells due to ion toxicity. Cotton salt tolerance has significant inter and intra-specific variation, which may be utilized through particular breeding and selection to increase plant salt tolerance. There are conflicting studies on crop reaction to salinity at various crop growth stages. Still, the majority of them show that the crop holds its level of salt tolerance during its developmental periods.

Salt stress causes delayed flowering, reduced fruiting positions, fruit loss, and decreased boll weight, all affecting seed cotton production. Improves abiotic stress tolerance, plant growth, and productivity by regulating ionic homeostasis, the photosynthetic apparatus, and antioxidant machinery, lowering heavy metal accumulations and oxidative damage. An effective strategy for enhancing cotton germination in soil salinity is seed priming. Additionally, a genetic approach could be a valid option for improving cotton yield in salt stress. Under salinity stress, the relative expression of GhSOS1 and GhNHX1 in leaves was substantially enhanced. It is suggested that the improvement of salt-tolerant cultivars may be pursued by combining traditional and advanced molecular technologies. The objective of this review was to describe the advancements in cotton biochemical and physiological characteristics and transgenic methods of salt stress tolerance in agricultural growth.

Keywords: Cotton; Salt Tolerance; Growth and Germination; Reactive Oxygen Species; Osmotic Stress

Abbreviations: LSB: Subtending Leaf of Cotton Boll; ROS: Reactive Oxygen Species; CAM: Choline Monooxygenase; SOS: Salt Overly Sensitive; ABC: ATP-binding cassette; TIPs: Tonoplast Intrinsic Proteins; PIPs: Plasma Membrane Intrinsic Proteins; SOD: Superoxide Dismutase; CAT: Catalase; POD: Peroxidases; GR: Glutathione Reductase; APX: Ascorbateperoxidase; QTL: Quantitative Trait Loci; DAPs: Differentially Abundant Proteins; GB: Glycine Betaine

Introduction

Climate change has altered ecosystem processes by enhancing abiotic and biotic stress (Robroek, et al. [1]). The agricultural land salt stress is predicted to have widespread negative consequences, leading to the loss of up to half of arable land by the middle of the 21st century (Kiriziy, et al. [2]). An increase in Na and Cl has been linked to the negative salinity effects, which are regarded as essential ions and have caused multiple abnormalities in the physiological processes of various plants (Tavakkoli, et al. [3]). The salinity of the soil has been a significant issue for global agriculture throughout human history (Hasanuzzaman, et al. [4]). Soil salinity is a severe issue impacting over half of the world's countries (Saddiqe et al. [5]). It is approximated that salts affect approximately 33% of irrigated agricultural lands and 20% of cultivated land globally and that this area is growing at a rate of 10 percent overall per year (Ayaz, et al. [6]).

Soil salinity decreases plant water availability, increases ion toxicity, inhibits nutrient absorption, and has an effect on crop quality and yield (GRATTAN [7]). Generally, saline conditions generate an excess of cellular ions, leading to osmotic stress, ion toxicity, and the generation of reactive oxygen species (ROS), all of which impair plant growth, morphology, and survival (USDA [8]). Cotton (Gossypium spp.) is the oilseed crop and most important fiber, providing 35% of the world's fiber and being used for biofuel and edible oil worldwide (USDA [9]). In 2016-2017 cotton crop grew around 29.5 million hectares worldwide, yielding a total of 106.49 million bales in 2017 (Rahaman, et al. [10]). In more than 80 countries, cotton crops are produced, with more than 30 of them considering it an economically significant crop. Cotton is cultivated in warmer regions like tropical and subtropical areas. China had the leading cotton in 2016–2017, followed by India, Pakistan, Brazil, and the United States, and 20.90, 8.25, and 6.50 million bales, respectively. More than two-thirds of the cotton fibers produced worldwide are produced in these five countries (Abd Ella, et al. [11]).

Throughout its existence, it has been confronted with various biotic and abiotic challenges, with salt being among the most significant risks to the sustainability of cotton production globally. Saline soils are characterized according to the electrical conductivity of their saturated paste extract (ECe), which must be more than four dS m1 at 25°C (Sharif, et al. [12]). With a salt stress threshold level of 7.7 dS m1, cotton is categorized as a crop with moderate salt tolerance. Salinity poses a significant danger to cotton's growth, productivity, and fiber quality. The type of salt and growth stage affects how sensitive someone is to salt stress (Maathuis [13]). This review provides information on biochemical parameters and physiological effects, which are used as stress indicators at the cellular level of the cotton plant. The overproduction of osmoprotectants increases the expression of antioxidant enzymes, which helps the plant prevent environmental stress.

Salt Transport in Cotton Plant

Salt stress has a global influence on agriculture. Soil salinity can be produced by either man-made factors, such as insufficient irrigation procedures that result in salt concentration buildup, or natural components, such as proximity to coastal areas. Although NaCl is the predominant salt, saline soils have significant quantities of other salts, including CaSO4 and Na2CO3 (Singh [14]). Salinity has two significant impacts on plants: (1) the osmotic effect, which causes a water deficit because of the high solute concentrations in the soil; and (2) ion-specific stressors, which cause a K+ shortfall because of changing K+/Na+ ratios (Blumwald, et al. [15]). Several plasma membrane channels allow sodium ions to enter cells at the cellular level. Plasma membrane Na/H antiports are operated by the plasma membrane ATPase's proton gradient and release cytoplasmic sodium, which is hazardous above a certain threshold level. Vacuolar Na/H antiports may also be used to categorize cytoplasmic Na. The proton gradient produced by the vacuolar H-ATPase and H-P Piase powers these transporters (Chen, et al. [16]).

Effect of Salinity on Cotton Plant

During the emergence and early growth stages of the cotton crop, it was more susceptible to salinity than in later developmental stages. Application of fertilizer may reduce growth inhibition in low to moderately saline soils (Loka, et al. [17]).

Physiological and Biochemical Mechanisms of Cotton in Response to Salt Stress

Numerous biochemical and physiological changes brought on by salt stressors harm cotton growth and yield. Abiotic stress generally significantly limits the growth and development of cotton (Ahmad, et al. [18]).

Germination Stage

Cotton germination, emergence, and young seedling stages are more vulnerable to saline stress than others (Wang, et al. [19]). Germination-stage seedlings are more susceptible to salt stress than seedlings in the juvenile stage (Khorsandi, et al. [20]). Beyond 10 dSm⁻¹, cotton germination percentage decreased dramatically. Cotton germination and emergence are both postponed indefinitely in response to salinity stress (Saqib, et al. [21]). Cotton crop emergence was delayed by up to 4 to 5 days compared to the average plant when exposed to 15-20 dS m⁻¹ salt stress. Poor germination reduces plant number, resulting in a significant reduction in cotton yield (Larcher [22]).

Seed Germination

Seed germination is a critical metric that is essential for total biomass and yield production. It is characterized by a complex series of physiological and biochemical processes that lead to embryo activation. There is a substantial negative association between seed germination %, germination time, and saline level. Salinity can disrupt seed germination by causing solute leakage, K+ efflux, and α -amylase activity. First, salinity limits moisture availability by producing osmotic stress, and second, it causes nutritional imbalance and ion toxicity. Cell membranes are key sites for governing active and passive solute transport and regulating plant nutrient absorption. An imbalance of mineral nutrients under salinity stress generally alters the structural and chemical composition of the lipid bilayer membrane, thereby controlling the membrane's ability to selectively transport solutes and ions inwards, and the membrane may become leaky to the solutes it contains.

Experiments were conducted to investigate the effects of salinity on seed germination of six rice cultivars with varying salt tolerances, using 0, 50, 75, 100, and 200 mM NaCl solutions. The results showed that salinity delayed rice seed germination by 36 days in treatments containing 100 and 200 mM NaCl, indicating a substantial negative association between salinity and seed germination. Rice farmers with little solute leakage had significantly greater germination rates under high salt stress of 100 and 200 mM NaCl than cultivars with higher solute leakage. Similarly, Jamil et al. (2012) examined the effects of salinity on seed germination in three distinct rice genotypes and discovered that the rice cultivars had varying germination responses to salt stress. Increased salinity from 0 to 150 mM reduced seed germination percentage and greatly delayed germination.

Effect on Root Growth

The root system is critical in reacting to abiotic stress since roots are typically the first organs to detect drought or salt stress. During the early phases of abiotic stress, certain plants can boost their root development, increasing the length of roots that can take water from deep soil. Crop abiotic stress-resistant has been linked to enhanced root development as evaluated by plant root length, weight, volume, and density. Cotton, among other crops, may grow tap roots that are ten times longer than the height of the aboveground plant (Luo, et al. [23]). It's significant, in cotton, a brief or moderate drought-enhanced root length (Abdelraheem, et al. [24]), but a longer or more extreme deficit decreased root weight and size. The root development and leaf thickness were boosted by moderate salinity under salt stress (Leidi [25]). Other studies that were either stressed by polyethylene glycol (PEG) or by circumstances containing NaCl supported similar findings (Ball, et al. [26]). In an experiment, Perez-Alfocea, et al. (1996) discovered an increase in root length after salinity stress and linked this to the plant's ability to maintain or even induce root extension at low water potential under salt stress. These data also revealed that plant roots have an adaptation mechanism under salinity stress, as well as the ability to reallocate photosynthetic components into roots while limiting their incorporation into shoot biomass.

Effect on Shoot Growth

A water shortage modifies the ratio of root-to-shoot weight accumulation by inhibiting shoot development more than root growth (Leidi, et al. [27]). Salinity was previously observed to decrease shoot mass, affecting the root/shoot ratio (McMichael, et al. [28]). However, research revealed that under abiotic stressors, the root-to-shoot ratio tended to significantly raise (Ashraf, et al. [29]). Therefore, when choosing cotton genotypes under abiotic stress circumstances, Longer shoots, root-and-shoot fresh and dry mass, and root-to-shoot ratios are all possible characteristics to consider (Basal, et al. [30,31]). Researchers assessed the root development of a few converted race stocks during a drought (Peng, et al. [32]).

Cotton Yield and Boll Development

The most significant cotton production byproduct, lint yield, has been the subject of several field research to ascertain the effects of salt or drought. There are inverse relationships between yield and morphological or physiological features. The weight and quantity of bolls were dramatically decreased in the cotton cultivars under salt stress. The number of bolls decreased, probably due to reduced development brought on by salt stress, toxicity from arbitrary intake of Na and Cl ions, and osmotic stress brought on by salt stress (Akhtar, et al. [33]). The increase in Na and Cl ions inside the cell damaged the integrity of the membrane, lowering the osmotic potential and resulting in reduced water absorption in the plant, which led to a decrease in boll weight. Vacuoles may have led to decreased boll weight in the cotton cultivars, possibly caused by the salt-induced shrinking of compartments to store undesirable harmful substances (Bublitz, et al. [34]).

Salt stress decreased cell division, which resulted in reduced leaf growth, smaller cells, and ultimately a considerable loss in photosynthate production inside the cell, which reduced the number of bolls (Yadav, et al. [35]). In cotton, the Subtending Leaf of Cotton Boll (LSCB), which plays a significant role in cotton output, transports 60–87 percent of produced sucrose to growing bolls. While sucrose buildup in LSCB reduces the damage caused by saline conditions, its effective delivery to developing bolls is delayed, resulting in reduced boll weight (Levi, et al. [36]). Additionally, in delayed irrigation circumstances, it was established that the decline in production owing to water shortage was 48.2% for seed cotton, 41.2% for lint yield, 40.0% for boll weight, and 21.0% for lint percentage (Longenecker [37]).

Fiber Quality

Under saline environments, the impact of ion deposition and fiber quality was examined (Manikandan, et al. [38]). Salt-sensitive genotypes have increased Cl- levels in their leaves and produced low-quality fiber. Cultivars that can tolerate salt have high leaf concentrations of Potassium ions and Calcium ion+. Salt stress increased ginning production and micronaire but a decline in staple length, fiber maturity, and fiber strength. It demonstrates the link between nutrient accumulation in plant parts and salt tolerance. Poor fiber quality is produced in salt and may be caused by individual fibers that are less mature (Peng, et al. [32]). Fiber length, strength, and fineness are reduced with increasing salt (Manikandan, et al. [38]). Although it is inherited, environmental variables can impact fiber quality. Water is primarily required for cotton fiber production to promote cell turgor and glucose digestion. As a result, under stressful conditions, cotton leaves lose turgor and reduce photosynthesis, which lowers the supply of glucose to developing bolls and prevents the creation of fiber (Yfoulis, et al. [39]). However, the properties of the fiber are known to be less susceptible to drought stress (Fernandes, et al. [40]). However, fiber length dropped during high drought stress (at a water potential of -2.8 MPa) (Peng, et al. [32]). Others claim that the impact of salt stress on micronaire is profound (KILIÇ, et al. [41]) (Figure 1).



Figure 1: Shows the salt-stress effect on cotton plant.

Seed Oil Content

Cotton seed oil content is commonly considered to decrease as salt concentration increases (Abdullah et al. [42]). Previously, (Ahmad, et al. [42]) discovered a rise in oil content at low salinity levels but a reduction at greater salt stress levels (1600 mg L1). They also found that a steady rise in salt enhanced the amount of oil, but a fast spike in salinity lowered the amount. Oil content decreased significantly as the salt level of the growing medium enhanced in 6 genetically different cotton lines with varying salt-resistant (Shah, et al. [43]). In soils damaged by salt, cotton is exceptionally susceptible to yield decline (30%) (Ouda, et al. [44]). Every 1 dS m⁻¹ rise in cotton salinity after the threshold salinity (7.7 dSm⁻¹) reduced the affected yield percentage by 5.2% (Maas [45]). Reduced yields were caused by potential solute variations (Ahmad, et al. [18]), salt accumulation on leaves, faster senescence, and decreased seed cotton production in highly salinized soil (Hu, et al. [46]).

A yield drop was also reported with more significant salinity water irrigated areas (Vulkan-Levy, et al. [47]). Under the impacts of climate change in saline regions, cotton production decreased by 9% (Reddy, et al. [48]). Similarly, the yield drop was 10–20% at 5 dSm⁻¹, and hybrids had seen the most reduction (Hebbar, et al. [49]). The yield decreased to 27% at 8 dSm⁻¹ genotypes (Manikandan, et al. [38]). On the other hand, the salt-tolerant lines contained a higher proportion of seed oil than the salt-sensitive lines. Inter- and intraspecific heterogeneity in salt stress in cotton with varying crop features indicates that cotton species or varieties respond differently to salt stress. Such variance would be of significant practical use in improving the salt the majority of this variability is gene clone based and natural.

Effect on Cotton Leaf

Salinity influences the growth of leaves by altering the osmotic potential, reducing plants' ability to absorb water and nutrients during the initial phase. During this period, a drop in leaf area indicates a reduction in water consumption to avoid salt stress. During the second phase of ion toxicity, Na+ accumulates in the leaf blade and transpiration stream, particularly in older leaves that do not expand and hence fail to dilute the ionic toxicity impact, whereas young leaves expand in response, reducing ion toxicity. The resulting situation results in the mortality of the elder leaves. When older leaves die at a rate faster than the development of new leaves, plants' ability to photosynthesis is dramatically diminished, resulting in an overall drop in growth rate (Munns and Tester, 2008). Ali et al. (2004) A study was conducted to investigate the impact of salt on the leaf and other yield metrics of cotton cultivars using an artificial saline soil medium. The results showed that as saline levels increased, the leaf area of cotton plants decreased significantly.

The size of the leaf is determined by cell division and elongation. Ali et al. (2004) ascribed the reduced leaf area to decreased cell division. By inhibiting the chlorophyll biosynthetic enzyme, which increases the efficiency of the chlorophyllase enzyme, decreases the leaf water potential, and restricts the absorption and allocation of nitrogen in Rubisco, an excess of sodium chloride lowers the production of photosynthetic pigments (Elkelish, et al. [50]). The indirect action of NaCl causes a decrease in chlorophyll and carotenoid concentration. Chlorophyll concentration, photosynthetic activity, and CO2 fixation all have a relationship. The reduction in net CO2 fixation is due to water scarcity, stomatal closure, apoplast salt buildup, mesophyll cell turgor loss, and direct toxicity of salt ions (Zhang, et al. [51]). These hostile conditions show that overall metabolic activity has reduced (Ayaz, et al. [6]). According to Abdul Qudos (Mishra [52]), when salt levels increased, total chlorophyll in pepper leaves reduced dramatically; this loss may be connected to increased activity of the chlorophyll-degrading enzyme, chlorophyllase (Guo-Wei, et al. [53]). The overall effects are summarized in Table 1.

 Table 1: Shows the effect of salt stress on the cotton plant at different growth stages.

Growth stages	Reasons Effects on Growth		References
Germination	Due to the response to salt stress, the germination stage is delayed.	Negative	(Guo-Wei, Hai-Ling, et al. [53])
Emergence	Due to the unavailability of nutrients, emergencies lead to delays of up to 4-5days	Negative	(Ahmad, Iqbal, et al. [18])
Seedling	Effect on plants height, leaf expansion, and root, shoot dry mass, and slow photosynthesis rate.	Negative	(Ahmad, Iqbal, et al. [18])
Root growth	It reduced the root's length and less fresh and dry mass of roots.	Negative	(Shaheen, Shahbaz, et al. [99])
Flowering & Boll development	Delayed onset flowering, less fruit, and yield decrease due to the reduction of boll and boll weight	Negative	(Peng, Liu, et al. [32])
Fiber length	Reduced activity of metabolic enzymes and sucrose and cellulose content.	Negative	(Peng, Liu, et al. [32])
	Fiber strength		
Fiber maturity			
Fiber Fineness			(Peng, Liu, et al. [32])

Mechanisms of Salt Tolerance

Organic Solutes

Organic solutes help to protect membranes and proteins from the degrading effects of salts and salutes, the maintenance of cell turgor, and the provision of gradient pressure for water absorption (Naidoo, et al. [54]). Glycine betaine is a significant organic solute that works as an osmoprotectant and accrues in dryness, salt stress, and acute heat stress (Rontein, et al. [55]). Several studies have found that glycine betaine helps with osmotic correction under salinity stress (Quan, et al. [56]). Found high levels of glycine betaine in genetically modified cotton lines that had the Choline monooxygenase (CAM) gene, which interacts in the catalytic route for converting choline into betaine aldehyde, which is It is subsequently transformed into genetically modified glycine betaine by a variety of enzymes. Proline has a significant role in stabilizing the RUBISCO enzyme and its functioning even in the presence of sodium chloride.

The levels of free proline in G. arboretum and G. hirsutum increased when treated with seawater. (Meloni, et al. [57]) following NaCl treatment, there was a 36% increase in proline content in treated crops' roots compared to the control, and a 121% increase in proline level in the leaves (Quan, et al. [56]). We have previously described inconsistent results, in response to salt stress, we observed inconsistent changes in proline or hydroxyproline concentrations in cotton. As a result, proline concentration is lower to achieve osmotic adjustment; however, if restricted to the cytosol, it may have a significant impact (Meloni, et al. [57]).

Ion Transport

In salt stress, ion flow control is required to maintain lower concentrations of hazardous ions while acquiring needed ions. Under control conditions, the plant cell cytosol maintains a high K/Na ions ratio with more significant potassium and lower sodium levels (Golan-Goldhirsh, et al. [58]). In saline conditions, the sodium/potassium ratio and Na+ concentration in plant roots rise, resulting in ionic imbalance, hyperosmotic stress, and toxic effects. The cause of this ionic imbalance is that under salt stress, the hydrated forms of K+ and Na+ become equal, making it difficult for the K inflow route to distinguish between sodium and potassium ions as a result in Na influx from the K inflow route, which resulting the sodium ions toxic effect in the cytoplasm. Salt-resistant crops minimize the inflow of sodium from roots, assortment the exciting sodium present in the cytosol to the vacuole, and produce an outflow of sodium from root cells to maintain the sodium/potassium ratio (Higinbotham [59]).

Plant cells use H-ATPases, channels such as K channel (AKT1), co-transporter such as increase affinity sodium transporter (HKTs) and high-affinity potassium transporter (HAK5), sodium/hydrogen antiporters such as sodium/hydrogen exchangers (NHX) for vacuolar assortment, Salt overly sensitive (SOS) pathway for sodium efflux and to maintain an increase potassium/sodium ratio in the cytosol (Conde, et al. [60,61]). Maintaining high Ca2/Na and potassium/sodium ratios in response to salinity is recognized as a primary selection criterion. The high absorption levels of K over Na in salt-tolerant cotton genotypes were maintained by the downregulation of GhSOS1, AKT1, and HAK-5 while simultaneously up-regulating GhHKT1 and GhNXH1. This demonstrates that salt-resistant in cotton genotypes is strongly associated with potassium and sodium ions control via an assortment of sodium ions into vacuole instead of potassium absorption (Zhao, et al. [62]).

ABC (ATP-binding cassette) transporters carry stress-related secondary metabolites such as guinines, terpenoids, alkaloids, and polyphenols (Wang, et al. [63]) and alter Na/K ion balance and salt stress (Theodoulou [64]). Upregulation of ABC transporters (gi|224130846) in cotton roots recommends a possible function in salt resistance. The response of the ABC transporters differs depending on the type of salt stress. Therefore, in addition to low cytosolic Na+ concentrations, maintaining a low cytosolic Na+/K+ ratio is critical for the normal functioning of plant cells. Transcriptome studies in cotton during Na2CO3, sodium chloride, and sodium hydroxyl stress revealed an up-regulation of 5 ABC genes (Gh A12G1090, Gh A10G0583, Gh A05G1089, and Gh Sca006272G01) and ABC2 (Gh A09G1286) to transports micro-molecules for ion homeostasis (Zhang et al. 2018). Aquaporin channel proteins, which aid in the passage of water, gases, and small neutral solutes across the intracellular and plasma membranes, have been related to stress tolerance in plants.

The two most prevalent aquaporin subfamilies are tonoplast intrinsic proteins (TIPs) and plasma membrane intrinsic proteins (PIPs). These biochemical changes from high uptake of Na+ and K+ leaking generally create an imbalance in the Na+ /K+ 1 ratio within the cytosol and affect enzymatic reactions in the cell. It has been observed that the expression of both PIPs and TIPs proteins was down regulated in cotton to minimize water loss under saline conditions (Lee, et al. [65]). The whole mechanism of ion transport are illustrated in Figure 2.

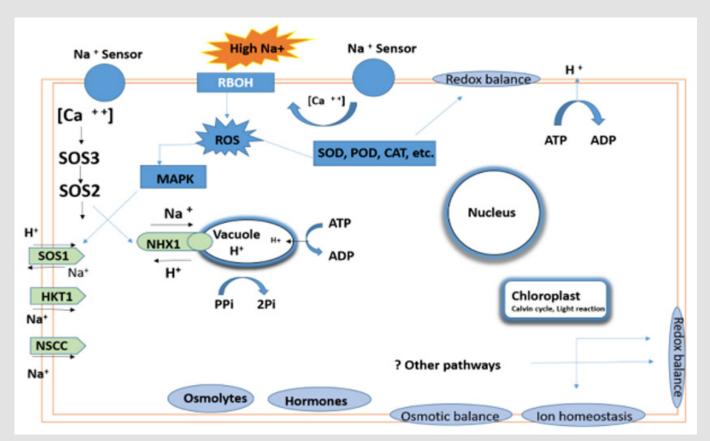


Figure 2: Shows the mechanisms of ions transport in cotton plant.

Antioxidant Response

Plants with higher antioxidant activity are more tolerant to salt (Zhang, et al. [66]). The generation of ROS, such as hydroxyl, superoxide radicals, and H2O2, was induced by salinity stress. During normal conditions, reactive oxygen species are neutralized by intracellular anti-oxidants; however, Increased ROS with salinity stress buildup causes ionic stress and significantly destroys normal metabolism, causing the breakdown of proteins and nucleic acid mutation (Noreen, et al. [67]). To prevent oxidative stress caused by salinity, crops contain two types of antioxidant systems: enzymatic and non-enzymatic. Glutathione peroxidase, superoxide dismutase (SOD), catalase (CAT), and peroxidases (POD) are all part of the enzymatic antioxidant system, as are ascorbate-glutathione peroxidase enzymes [glutathione reductase (GR) and ascorbateperoxidase (APX) because it controls 02- and hydrogen peroxides concentrations, SOD is recognized as a significant antioxidant enzyme. APX and CAT demonstrated effective hydrogen peroxide scavenging capabilities. In the presence of SOD, APX, and CAT performed critical roles in the scavenging process (Ashraf [68]).

Non-enzymatic antioxidants include ascorbic acid, glutathione, carotenoids, and tocopherols (Czégény, et al. [69]). It was discovered

in cotton that as the treatments of NaCl increased, so did the activity of SOD. POD activity was increased by up to 53% in resistant cultivars. Enhanced the POD and photo-synthetic activities, revealing the involvement of antioxidant defense mechanisms in reducing salt stress (Ashraf [68]). salt- resistance during fibers growth to enhance the enzymatic activities of anti-oxidants, such as glutathione reductase, ascorbate peroxidase, and superoxide dismutase (Rajguru, et al. [70]). The reactive oxygen species (ROS) are produced at a higher rate when plants are treated to salt stress, which leads to lipid peroxidation in cell membranes. The essential enzymes SOD and POD may detoxify excess ROS in cells and eliminate them. The primary byproduct of membrane lipid peroxidation is MDA, which indicates the extent of cellular membrane destruction (Ozgur, et al. [71]). The role and structure of cell membranes play essential roles in plant adaptability.

Plants respond to salt stress by boosting reactive oxygen species (ROS) scavenging and up-regulating defense enzymes such as SOD, POD, and CAT (Eraslan, et al. [72-75]). In normal physiological circumstances in plants, ROS's constant generation and absorption are preserved in dynamic balance. At the same time, salinity stress breaks that dynamic balance, leading to membrane lipid peroxidation and deacylation. Cell death occurs when the membrane system and metabolic processes are damaged and biological molecules like nucleic

acids and proteins (Mittler, et al. [76,77]). This analysis shows that antioxidation mechanisms, particularly the ascorbate glutathione cycle, may play a position in salt resistance. Another essential non-enzymatic antioxidant is ascorbate/ascorbic acids, whose content increases in chloroplast and cytosol during salt stress and can maintain photo-synthetic activity. In recent cotton development phases, resistant genotypes have higher ascorbic acid concentrations than sensitive genotypes (Aslam, et al. [78]).

Genetic Base Salt Tolerance

Salt tolerance is an extremely complicated quantitative trait controlled by several genes, each of which has little impact. With a single gene-based study, it is difficult to determine its genetic basis. QTL (quantitative trait loci) analysis has been used to explain gene-based salt tolerance in diverse plants. The majority of the studies on QTL mapping for salt resistance have been reported on rice crops and the SALTTOL locus, which is connected to QTLs for K and Na ions absorption and Na/K ratio maintenance (Wang, et al. [79]). Genes-mediated selection is a potential method for selecting salt-resistant genes in-

directly. An association study employing 145 SSRs was performed to map ten salt-resistant features in cotton. Of these 95 SSRs, 41 were connected to the generation stages physiological index, 37 to the biochemical index at four germination stages, and 17 to germinate index (Du, et al. [80]) 8 SSRs were connected to salt-resistance using association analysis, two of which were substantially combined with salt-resistance and reported phenotypic differences ranging from 7.82 to 6.26% [69]. Proteomic techniques can be used to discover proteins that are connected to salt-tolerant. In another report, iTRAQ found fifty-eight differently-sufficient salt-sensitive proteins in cotton seedling leaves. In salt stress, phosphor-related differentially abundant proteins (DAPs), N-methyltransferase 1, 14-3-3-like protein E, and phosphor-ethanol amine were upregulated. Twenty-nine salt-sensitive proteins were discovered to be genotype-specific, with 27.6% and 62.1% related to a defense response and chloroplast, respectively (Zhao, et al. [81]). The results evaluated show that marker-assisted selection may be used to identify and generate salt-tolerant genotypes, as summarized in Table 2.

Table 2: Shows different Genes and markers, their location on chromosomes & linked traits which are reported for salt stress in co	otton.

Gene name	Type of marker	Linked trait	Location on chromosome	Reference
BNL3103	SSR	Dry root weight & dry plant weight	D06	(Saeed, Wangzhen, et al. [98])
NAU478		Dry root weight & root shoot ratio	D08	
NAU2679		Fresh plant & shoot weight, shoot length	A06	
NAU1008(b)- NAU3608	QTL (qrl- Chr16-1)	Root length	16	(Oluoch, Zheng, et al. [97])
HAU2866-DPL0573	QRL-Ch22-1	Relative dry root	D09	(Cai, Wu, et al. [94])
EP1C356/C4	ILP	WARKY DNA binding protein	A12	(Cai, Wu, et al. [94])
EP1C09/C9 (MPK9)		Mitogen-activated protein kinase	A03	
i28278Gh, i31650Gh, i28055Gh	SNP	Relative survival rate	A10	(Sun, Li, et al. [100])
i12146Gh			D10	

Transgenic Methods

The transgenic method refers to the transformation of particular genes to get desired qualitative and quantitative features. This approach is applicable across genera or species; it is faster than traditional breeding and eliminates the transfer of undesired or extra genes. Genetically modified plants are not only for detecting genes to salt resistant but also for producing salt-resistant genetically modified plants. It has been effectively employed in cotton plants by introducing salt-sensitive genes from various sources. Glycine betaine (GB) is an essential osmoprotectant that assembles rapidly in different crops when exposed to salt stress. Choline monooxygenase is a critical catalyst in the production of glycine betaine. A CMO gene (AhCMO) was inserted into cotton by Agrobacterium to increase resistance to salt stress. Under normal and salt stress conditions, transgenic cotton seedlings transported 131% more GB than non-transgenic plants, and this increase was connected to AhCMO overexpression. Following salt stress exposure, transgenic plants showed enhanced photosynthesis capabilities Fv/Fm value and decreased leaf damage (Zhang, et al. [82]).

Co-expression of the AtNHX1-TsVP genes in transgenic cotton showed more fantastic seed cotton productions under saline conditions, which might be related to the buildup of K+, Na+, and calcium ions in the leaves of salt-affected crops. These cations' absorption increases ion homeostasis and osmotic potential, allowing the cell to maintain a tremendous water potential and carbon assimilation (Cheng, et al. [83]). The sodium/hydrogen ions antiporter gene (Gh-SOS1) was inserted from a salt-resistant cotton cultivator, and its expression was increased when exposed to sodium chloride salt stress in transgenic Arabidopsis. GhSOS1 overexpression in Arabidopsis improves salt tolerance, as evidenced by lower MDA levels and a lower sodium/potassium ratio in genetically modified plants than in wildtype plants. It was proposed that the GhSOS1 gene may be used to create genetically modified salt-resistant crops (Chen, et al. [84]). Cotton with AtEDT1/HDG11 overexpression had a more comprehensive root system, unique leaf proline content, and increased ROS scavenging enzyme activity (Yu, et al. [85]). Several investigations have shown that transgenic cotton with an over-expressed stress-related genotype involved in cell physiology has increased drought and salt tolerance (Ullah, et al. [86]).

Overexpression of the TsVP,aH+-PPase gene from Thellungiella halophile increased drought tolerance in cotton by increasing photosynthetic rates relative to non-modified crops (Lv, et al. [87]). Genetically modified cotton containing this H+-PPase demonstrated better salt resistance and cotton productivity under salinity (Lv, et al. [88]). The SUMO E3 ligase gene from rice, OsSIZ1, was recently (Mishra, et al. [89]) proven to be overexpressed in cotton, improving cotton's stress resistance to warm and dryness while also efficiently increasing fiber yields in drought regions. Drought also induces the minor heat shock protein GHSP2 in G. arboreum L. In G. hirsutum, overexpression of GHSP2 increases resistance to drought stress (Maqbool, et al. [90]). The gene LOS5/ABA3 encodes a molybdenum-binding co-factor necessary for the aldehyde oxidase engaged in ABA biosynthesis to operate correctly. Increased ABA levels in transgenic cotton caused it to overexpress the Arabidopsis gene AtLOS5, which in turn boosted its tolerance to drought. Comparing transgenic plants to non-transgenic cotton, transgenic plants generated around 13% fresher biomass recently, showing that overexpressing GhAnn1, which encodes for the greater activity of SOD in cotton plants, increased salt tolerance. (Zhang, et al. [85,91]).

Management of Nutrients and Seed Priming

Sub-optimal plant development due to poor germination is difficult for efficient crop yields under salinity stress. Due to osmotic pressure and the detrimental effects of sodium and chlorine, salinity stress slows and lowers cotton germination percentage (Sattar, et al. [92-100]). They have previously described a seed priming approach to overcome salt stress germination. It also needs to prepare the plants for prospective ecological problems and gives them an early advantage in terms of resistance. The impact of seed priming strategies on cotton development (Table 3).

Table 3: Three different seed priming techniques and their impacts on cotton under salt stress.

Priming agent	Significant improvement	References	
H ₂ O	Enhanced germination, emergence, root &plant dry mass, and plant length & leave area	(Ahmadvand, Soleymani, et al. [93])	
KNO ³	Enhanced germination, emergence, root &plant dry mass, and plant length & leave area		
Са	enhanced germination through down-regulation of ABA biosynthesis genes	(Kent and Läuchli [95])	
Hydrogen peroxide	adjust the shoot length	(Kong, Luo, et al. [96])	
bio	Germination improved		

Conclusion

Salt stress is a significant issue for maintaining agricultural production worldwide since it affects over half of the countries. Particular ion toxicities, somatically induced droughts, and nutritional imbalances are all brought about by salinity, which negatively impacts plant development and agricultural production. Cotton is susceptible to salt stress, which reduces growth, biomass production, and grain yields by suppressing a variety of morphological, physiological, biochemical, and genetic traits. In general, high salinity has an osmotic and toxic effect on plant growth. Salt stress has a negative impact on enzymatic metabolism, nutrient absorption, and nutritional disorders, resulting in lower yields and fiber quality. The development of salt-tolerant cotton varieties provides an effective management strategy for cotton under saline circumstances.

Maintaining high Ca+/Na+ and K+/Na+ ratios might be utilized as a basic selection criterion for selecting cotton genotypes that are salt resistant. The genome sequence variety might be efficiently used to develop salt-resistant genotypes. Moreover, as QTLs control the genetic basis of salt tolerance, gene-assisted selection is a viable strategy for the indirect selection of salt-resistant genotypes. Genetically modified techniques for salt tolerance in cotton have been effectively used with the development of molecular genetics. This method is more efficient than traditional breeding. Seed priming might enhance salt tolerance by overcoming germination difficulties and preparing crops for salt tolerance and other environmental challenges.

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