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Salinity Stress and Its Alleviation in Plants: A General Review

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ABSTRACT

Agricultural salinization is one of the major and long-lasting abiotic stresses, as it hinders plant growth and development leading to physiological abnormalities that endanger global food security. This is primarily the result of salt build-up in the soil caused by human activities, including irrigation, inadequate growing, and excessive fertilization. Nearly 147 million ha of land are at the risk of soil degradation, with water erosion contributing to 94 million (ha), salinity/alkalinities/acidification for 23 million (50%), water depletion/flooding for 14 million (60%); wind erosion for 9 million and 7 million ha of a combination of factors arising from different forces. In order to ensure food security for the increasing population, the Indian government has set a goal to restore 26 million hectares of degraded land, including those affected by salt, by 2030. It is estimated that almost 10% of the added land becomes saline every year, and by 2050, about 50% of the arable land would be caused by salt. High levels of Na+ and Cl- ions in the soil subdues overall plant growth through ion imbalance, osmotic stress, oxidative stress, reduces nutrient uptake, reduction in yield, and damage to lipids, protein and DNA. In response to salinity stress, plants have developed a range of adaptive mechanisms such as ion homeostasis, osmoprotection, polyamines, nitric oxide, phytohormones and antioxidative defence system. This reviews tells about epigenetic regulation of salinity stress and various mitigation process to combat salinity stress like physical method (leaching, flushing and scrapping), chemical methods (Gypsum, zeolites, biochar, compost, and organic amendments) and biological methods (phytoremidation, bioremediation by use of PGPR, salt-tolerant bacteria, mycorrhiza, cynobacteria, use to various nanoparticle and some biotechnical tools like use of genome wide-association studies, salt-tolerant genes, proteomics, metabolomics and transcriptomics).

Keywords: Phytoremidation,Proteomics, Metabolomics, Transcriptomics, Osmoprotection, Polyamines, Nitric oxide, Nanoparticle.

I. INTRODUCTION

Abiotic and biotic restrain cut downs plant's biomass and its overall development and this is known as plant stress. Plant's development, quality and quantity of yield is affected by biotic and abiotic stress (Shi-Ying et al., 2018). Biotic stress includes damage by pest and various types of pathogens that cause harm to plants. Abiotic stress includes drought, temperature (heat and cold), salinity, heavy metal and organic contaminants. Of all abiotic stress salinity is the major and affects major crop productivity (Zorb et al., 2019). The salt content of the soil is one of the main issues that adversely affect agricultural productivity in arid and semi-arid regions of the world (Halima et al., 2019). 20% of all cultivated areas and 30% of irrigated agricultural lands globally already have salinity in their soil, and by the year 2050, this percentage is predicted to rise rapidly (Srivastava and Kumar, 2015). Due to increasing in salinity in the agricultural land, the increasing food demand is unable to fulfil requirement and the expected elevation of salt is by 8.5 billion in next 25 years. In current scenario, about 1125 ha of land is constrained by salinity stress out of which 76 million ha is owing to anthropogenic activities. Salinization of soil has significant impacts on agricultural productivity and quality, crop selection, biodiversity, water quality (including binding on minerals to produce hydrocarbons), water supply for human and industrial needs, as well as long-term agriculture.

The value of soil salinity, which measures the salt concentration in the soil, is commonly referred to as the electrical conductivity (EC). The salinization of the soil, or salt accumulation, has an impact on agricultural production, environmental health, and soil quality, which is known as 'soil salinability'. The process of salinization of soil involves multiple processes, including salt transport, ion exchange and evaporation as well as precipitation/dissolution of salts. A lack of leaching of base cations leads to salts having too high concentrations of either soluble s alt, exchangeable sodium or both. The stellar soluble mineral salts are the cations like sodium (Na^+), calcium (Ca^{2+}), magnesium (Mg^{2+}), potassium (K^+) and the anions like chloride (Cl^-), sulfate (SO_2^{-4}), bicarbonate (HCO^{-3}), carbonate (CO_2^{-3}), and nitrate (NO^{-3}). Both natural and anthropogenic causes may lead to soil salinization. The extent of human caused salinization is 76.6 in 932.2 million ha global salt contaminated soils (Shahid et al., 2018). Gupta and Abrol (1990) have solely reviewed processes of soil salinization:

1) **Natural process (Primary salinization):**
    I. Weathering of parent material: When rock minerals or sediments are subjected to physical, chemical and biological weathering, they release salts that can be soluble in water. They are carried away from their source by surface or groundwater motions. In arid regions, the concentration of salts increases little by little until they begin to deposit in the soil due to limited natural precipitation and leaching, high evaporation and evaporation rates. In areas with low elevation, high water table, and locked topography, salinization is more favourable.

II. Fossil salts: In arid regions fossil salt deposits of marine and lake deposits are responsible for salinization. The dissolution of fossil salts under reservoirs or water transfer structures can result in salinization.

III. Salinization in coastal areas: Seawater intrusion along the coast increases salinity in coastal areas. Sea spray and salt winds are responsible for the accumulation of ocean salts along coastlines, leading to the formation of salt. Marine sprays can contain salinities up to 14.2μg m^{-3}, and can affect depths up to 80 kilometers inland or even more. Coastal regions face the risk of soil salinization, which can be triggered by storms, cyclones or cycles, tides and floods.

IV. Transport of salt in rivers: Salinization can also occur on the plains due to salinizing salts brought by downstream rivers, sediments from deposits, flood materials, and rock erosion.

2) **Anthropogenic activities (secondary salinization):**

I. Land clearing for farming: The salinization of soil can be caused by the replacement of perennial plants with annual crops, which are replaced by salt water. Changing land use from native forest vegetation to annual food plants reduces evapotranspiration and increases leaching. Salinization can occur in low-lying areas due to the presence of impermeable subsurface layers that prevent saline infiltration through sediments, which causes lateral percolation.

II. Improper irrigation: The selective use of brackish and saline irrigation water, inadequate drainage conditions and groundwater surge etc. are cause of secondary salinization of land and water resources. Proper soil management and water management can lead to salt accumulation, even if good quality irrigation water is used for a prolonged period. Approximately 20-33% of the 310 million hectares of land in the world that is currently irrigated is estimated to be salt-imperious (Shahid et al., 2018). Irrigation with sea water is one of the major causes of salinity in coastal areas.

III. Over extraction of groundwater: Salts are left at the surface as water evaporates due to excessive extraction of groundwater. This causes salt to deposit.

IV. Over-usage of agro-chemicals: Excessive use of chemical fertilizers and soil amendments (lime and gypsum) can also lead to soil salinization.

V. Canal water seepage: A significant issue is the rise in salinity and groundwater on canal banks. Water logging and soil salinization in the Indira Gandhi Nahar Priyojna (IGNP) region of India's a vivid example of this process. Roughly half of the IGNP control zone was affected by water-logging.

VI. Use of water effluents: Using industrial brine and untreated sewage, as well as using sludge and other unprocessed waste, etc. can also cause soil salinization. Heavy metals' infiltration into the soil is of particular concern.

3) **Depending on the nature and concentration of salt present in soil it is classified into three groups:**

a. **Saline soil**: It is also known as "white alkali" or "solonchak" soils. At 25ºC saline soil is defined as having an electrical conductivity (EC) above 4 dS/m, while salt mass ratio (SAR) and ESP are below 13 and 15 respectively. Mineral salts such as for example NaCl, $MgSO_4$, $NaHCO_3$, Na_2CO_3, $CaSO_4$, $CaCO_3$, precipitation is the main characteristic of saline soil.The presence of a white crust on the surface caused by salt crust causes it to turn white, and it is prone to salt problems. It can be found in arid or semi-arid regions with less rainfall for better plant growth, where high evaporation rates lead to the concentration of salts in the soil, but not in humid areas.

b. **Sodic soil:** It is also known as non-saline sodic soils" or "alkali soils," or "solonetz". The proportion of exchangeable sodium percentage (ESP) in sodic soil is above 15%. The EC of sodic soil can differ, but it is typically less than 4 dS/m at 25ºC at pH 8.2 to 10.5. Soils formed by the exchange of Ca^{2+} and Mg^{2+} ions with Na^+ ion poses some problems, including black coloration, inability to withstand water and air, and sodium-related issues.

c. **Saline-sodic soils:**This soil is intermediate between saline and sodic soils. EC of this soil is more than 4dS/m at pH greater than 8.5. The exchangeable sodium percentage (ESP) and salt mass ratio (SAR) of saline-sodic soil is more than 15 and 13 respectively. Salt formation and alkalization lead to the development of sodic soils that are prone to leaching due to their sodium and other salt content. The permeability of air and water is also influenced by the concentration of sodium.

A significant amount of research has recently focused on the concerning influence of climate change on soil salinity. The likelihood of climate change isinfluenced by many factors such as high atmospheric greenhouse gases concentrations, warmer air temperature, and reduced humidity, as well as excessive rainfall, which can have a significant impact on development due to soil salinity (Haj-Amor and Bouri, 2019). The rise in sea levels can be a result of climate change, which can also lead to the faster absorption of saltwater into fertile soils, and an overabundance of groundwater in dry areas that contribute to higher soil and ground water levels (Dasgupta et al., 2015). About 600 million individuals residing in coastal regions around the world are potentially susceptible to salinization (Dasgupta et al., 2015). By restoring salt-contaminated soil, millions of tons of food can be produced globally. Therefore, it is imperative to have a comprehensive set of climate-smart technologies capable of recovering soils that are subject to salt.

Soil salinity is a contributing factor to increased EC_e, poor soil structure, and low soil water potential (ψ_w). The salt stress in plants can be characterized as occurring in either the osmotic phase or the other ionic phase. The osmotic phase is initiated within minutes of salt accumulation in the root zone. In the osmotic phase, plants exhibit significant features such as stomatal closure, increased leaf temperature, and reduced shoot length due to the low water potential of the soil and the presence of a thick inner wall of guard cells. On the contrary, in different cases of adding salt, the ion phase starts from a few minutes to a few hours, accompanied by the accumulation of salt in the shoots for a long time, leading to leaf senescence and premature abscission. Salt stress can be referred to as "hyperosmotic stress" because it reduces the ability of the roots to absorb water and increases the amount of water that evaporates from the leaves. During the first phase of osmotic stress, plants undergo several physiological changes, including membrane disruption, nutritional imbalances, and decreased ability to detoxify from ROS. Additionally, photosynthesis and antioxidant enzyme activity also decrease. Elevated Na^+ levels inhibit the K^+ uptake pathway, resulted in low productivity and may even lead to cell death (Ahmad and Umar, 2011).

Saline soils are posing a threat to India's national food security and economic development. Therefore, it is imperative to alter the country's food production policy and methodology. Food security efforts must focus on both expanding agricultural sectors and increasing crop productivity. Restoring food security in the country could be possible through the reclamation of degraded land, such as those damaged by salt. In order to achieve this objective, the Government of India has established a target to restore 26 million damaged lands by 2030.

II. GLOBAL SCENARIO OF SOIL SALINIZATION ACROSS THE WORLD:

A rise in soil salinity poses a significant threat to global agriculture production.Morethan 100 countries have affected billions of hectares, and the number is continuously increasing (Ivushkin et al., 2019). 7-8% decrease in productivity is due to the presence of 954 million ha of saline soils in 120 countries worldwide (Meena et al., 2019).Salinity currently affects about 1,125 million hectares of land, of which 76 million are hampered by anthropogenic salinization and oxidation, and 1.5 million hectares become unfavourable for agricultural practices each year due to boosting salinity in soil(Hossain, 2019).A recent FAO data from 2021 revealed that saline land covers a wide area of the globe, with measurements in topsoil (0-30 cm) and subsoil (30-100 cm). Globally, Australia and Asia-Pacific have the highest levels of salinity. The two continents havea total of 2016.63 million ha of agricultural land, of which 27% (549.30 million ha) are affected by salinity. In Africa, salinity affects 72.2 million hectares of land, which is approximately 6.40% of the total agricultural sector. In America, 130.5 million ha out of 1,223.41 million ha of agricultural land are saline.In Europe, 17.30% of land is affected by salinity (FAO, 2019; World Bank, 2019). (Figure: 1).

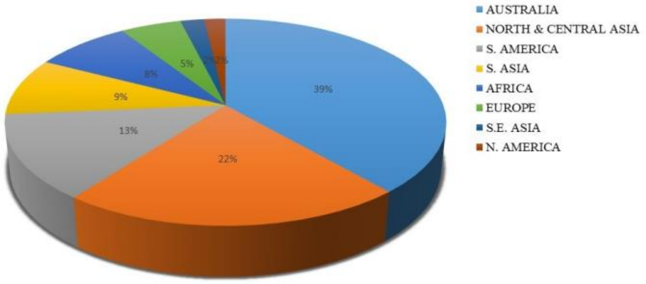

Figure 1: Salinity percentage in continents

Roughly 60% of the India's total area is covered by arable land, with crops accounting for almost 80% (141 million ha) and rangeland for approximately 6% (10 million ha) (Mythili and Goedecke, 2016). Almost 147 million ha of land are vulnerable to soil degradation, including 94 million ha to water erosion, 23 million ha to salinity/alkalinity/acidification, 14 millionhato irrigation/flooding, 9 million ha to wind erosion and 7 million ha from the combination of many factors (Mythili and Goedecke, 2016).The Indo-Gangetic plains of the country have about 2.347 million hectares of saline soils, of which 0.56 million ha are saline and 1.787 million ha are sodic soils (Arora and Sharma, 2017). Almost 75% of the country's saline soils are found in the states of Gujarat (2.23 million ha), Maharashtra (0.61 million ha),Rajasthan (0.38 million hectares),Uttar Pradesh (1.37 million ha)and West Bengal (0.44 million ha) (Mandal et al., 2018). The salt affected area is shown in India Map in (Figure 2).

The agriculturally important ecological regions in 15 states of India and the Andaman and Nicobar Islands are saline soils that are classified into four major categories:

a) **Semi-arid Indo-Gangeticalluvial tract** of Delhi, Haryana,Punjab, UP, parts of Bihar and West Bengal.
b) **Arid and semi-arid regions** of Gujarat, Madhya Pradesh, MaharashtraandRajasthan.
c) **Peninsular regions** of Andhra Pradesh, Karnataka, Maharashtra, Orissa and Tamil Nadu.
d) **Costal-Alluvial regions** of Andhra Pradesh, Gujarat, Island of Andaman& Nicobar, Karnataka, Kerala, Maharashtra,Orissa and Tamil Nadu.

Major percentage of sodic soil is found in Indo-Gangetic plains of India. According to Mandal et al., (2018), about 19% is costal-saline soil, 25% is saline soil and 56% is sodic soil of total area of India. Uttar Pradesh covers highest percentage of saline soil of about 71.2%. Gujarat and West Bengal covers about 72% of costal-saline soil. About 35.6% of sodic soil occurs in Gujarat. (Figure: 2).

Lack of proper drainage in canal irrigation projects, has led to increased salinity. Considerable salt-affected area occurs indifferently in canal, e.g., Sharda Sahayak in Uttar Pradesh; Tungabhardrain Karnataka; Indira Gandhi Nahar Pariyojana (IGNP), Chambaland Tawa in Rajasthan and Madhya Pradesh; and Mahi and Ukai command area in Gujarat. Continuous percolation from canals has caused an increase in groundwater and subsequent rise of salts to the surface, watering, formation of swamps, increase in soil salinity,and decrease in biological diversity. Two striking examples are: (i) The salinization of an area of about 0.37 million in the Sharda Sahayak Canal Command area in Uttar Pradesh over three decades; (ii) Salinization of an area of about 0.18 million hectares in the Indira Gandhi Nahar Priyojana (IGNP) area of Rajasthan after the irrigation project is launched in a few years.

Approximately 17% of the country's irrigated lands have been secondary salinized due to the use of brackish water (Shahid etal.,2018). As of rising needs for production of more food per unit of arable (cultivated) land there is immense use of brackish groundwater for irrigation. Studies on groundwater demonstrate that low-quality water is utilized in various states for 32 to 84% of the total development of ground waters. The introduction of irrigation systems in new areas is leading to a growth in the number of saline areas in India every year. And this growth of saline areas is with rate of 10% each year. Soil salinization will cause 50%crop loss by 2050 if it continues to grow at current rates (Kumar and Sharma, 2020). Unless preventive/remedial measures are taken for salt affected areaswill triple from about 6.74 million to 16.2 million ha by 2050. (Table: 1).

Table 1: State-wiseshare(%)ofsalt-affectedsoilsinIndia

STATE	SODIC SOIL	SALINE SOIL	COSTAL-SALINE SOIL	TOTAL
Andaman & Nicobar Island	-	-	1.6	0.3
Andhra Pradesh	5.2	-	6.2	4.1
Bihar	2.8	2.8	-	2.3
Gujarat	14.3	71.2	37.1	32.9
Haryana	4.8	2.9	-	3.4
Jammu & Kashmir	0.5	-	-	0.3
Karnataka	3.9	0.1	-	2.2
Kerala	-	-	1.6	0.3
Madhya Pradesh	3.7	-	-	2.1
Maharashtra	11.2	10.4	0.6	9.0
Orissa	-	-	11.8	2.2
Punjab	4.0	-	-	2.2
Rajasthan	4.7	11.4	-	5.6
Tamil Nadu	9.4	-	1.1	5.5
Uttar Pradesh	35.6	1.3	-	20.3
West Bengal	-	-	35.4	6.5
TOTAL	**100 (3.78)**	**100 (1.71)**	**100 (1.25)**	**100 (6.74)**

Figures in parentheses indicate total area in million ha.

Source: Adapted from Mandal et al., (2018).

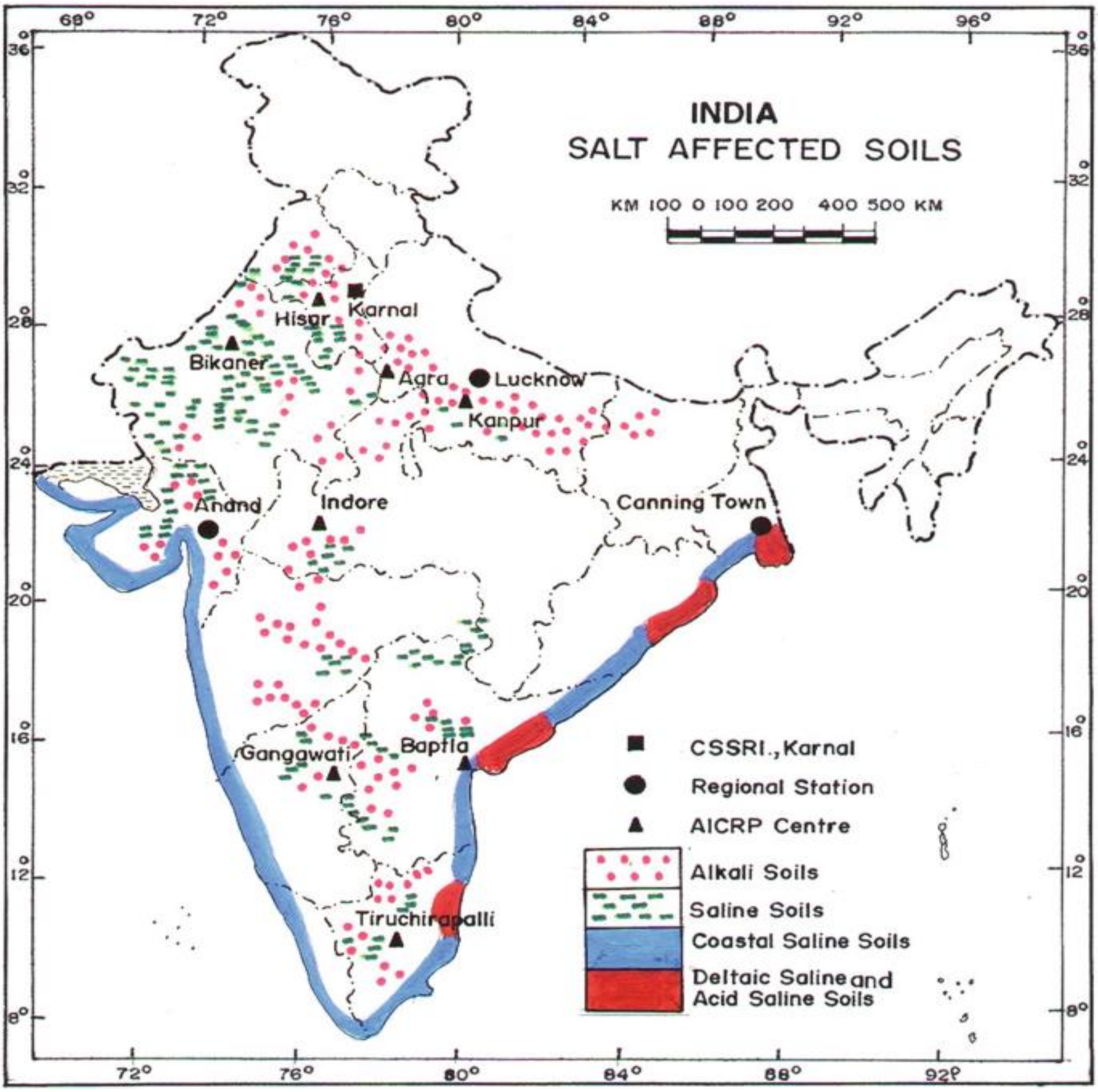

Figure 2: Map of India showing salt-affected soil regions (Source: Chhabra, 2021)

III.PHYSIOLOGICAL AND BIOCHEMICAL CONSEQUENCES OF SALINITY STRESS IN PLANT:

1. EFFECT ON SEED GERMINATION:

Under conditions of salinity stress, the absorption of water and the decreased activity of α-amylase, a starch hydrolyzing enzyme effects seed germination. Due to salinity, the soil's osmotic potential is lower than the internal osmotic Potential of the seed, which prevents water absorption during seed imbibition (Munns et al., 2020). This results in reduced seed germination and delayed subsequent seed germinating. Despite germination, salinity can still affect the viability of embryos due to the accumulation of Na^+ and Cl^- ions (El Sabagh et al., 2021).

Generally, seed germination occurs in three phases. Dry seeds quickly absorb water (imbibition) during the germination phase I. During phase II, metabolic activities are restored and water consumption is restricted. The post-germination phase is Phase III, which involves continuous water absorption until full germination. Seed germination can be delayed or prevented by the onset of salinity stress, which is typically followed by phase I osmotic stress and phase II ionic stress. The development of embryonic organs, growth, and vigour of seedlings in the phase III is affected by both ionic and osmotic stress after seed germination (El-Hendawy et al., 2019). Seed germination is hindered by salinity, which lowers gibberellic acid levels, increases abscisic acid level in seeds, alters membrane permeability and decreases water retention. The main reasons for the extended time required for germination may include slower water intake, decreased -amylase activity, with increased NaCl concentration. Those with salt-sensitive genotypes were found to have lower α-amylase activity than those with salt-tolerant genotypes. This decrease in α-amylase activity has important implications for the translocation of sugars, which is crucial for embryonic development (Ucarli, 2020).

2. EFFECT ON PLANT GROWTH:

The rate at which growth slows down depends on several factors, such as plant species, stage of development, and salinity (Yadav et al., 2019). The adaptive adaptation of stunted growth enables plants to cope up with salt stress. Key regulatory genes involved in cell cycle progression, such as cyclin and cyclin-dependent kinase, can be suppressed by salt stress, leading to reduced numbers of cells within the meristem and growth inhibition, which affects the plant's ability to absorb nutrients and water effectively.

The plant cell shrinks and dries immediately after being exposed to salt stress, but it will recover later. Despite the recovery, there are effects on cell elongation and cell division, which result in lower growth rates among roots and leaves. After exposure to salinity stress, it affects shoot lateral expansion, resulting in apparent differences in overall growth and damage between salt-stressed plants and their unstressed controls. The osmotic effect reduces the water absorption capacity of plants. The effect of salinity on plant growth is largely studied in many plants including *Eruca sativa* Mill (Petretto et al., 2019) and *Fragaria ananassa* Duch (Denaxa et al., 2022).

3. EFFECT ON PHOTOSYNTHESIS:

Photosynthesis, the process of converting solar energy into chemical energy, is one of plants' most significant and important features. Several factors, including impaired chlorophyll biosynthesis (Qin et al., 2020), altered enzymatic activity (Al Hinai et al., 2022), stomatal closure, reduced carbon dioxide uptake (Orzechowska et al., 2021), and impaired photosynthetic apparatus (Zahra et al., 2022), are correlated with salt-induced photosynthetic reduction. Chlorophyll and carotenoids are said to reduce under salt stress due to increased oxidation and degradation of chlorophyll and carotenoids by reactive oxygen species (ROS), and this reduction is proportional to the salinity gradient (Taibi et al., 2016). Overproduction of ROS is caused by a reduction in the electron transport chain, which leads to pseudocyclic electron transport (Zahra et al., 2021).

Salt stress experienced at higher concentrations leads to disruption of chloroplast ultrastructure, resulting in increased swelling and starch accumulation (Goussi et al., 2018). Total chlorophyll content was found reduced by 9% in rice (*Orzya sativa* L.) (Khan et al., 2016), 11% in Soybean (*Glycine max* L.), 13% in Maize (*Zea mays* L.) (Li et al., 2017) and 14% in Cucumber (*Cucumis sativus* L.) seedlings. Some studies have showed the decrease in carotenoid content of about 16 % in Ginseng (Sukweenadhi et al., 2018); 19% in Mung bean (Shahid et al., 2021) and 49% in tomato (Akram et al., 2019) seedling.

4. EFFECT ON PLANT NUTRIENT:

Plant growth in the absence of salinity is typically depicted by a "general dose-response curve"that measures the concentrations of essential nutrients in their root medium. The absorption of Na^+ and Cl^- ions from soil by plants, which accumulate in tissues at high concentrations, leads to cytotoxicity, leading to leaf burns that stunt growth and ultimately plant death. Nutrient deficiency can be caused by cation competition between high Na^+ levels and nutrient ions such as K^+, Ca^{2+} and Mg^{2+} and thus reduces their availability (Atta et al., 2021). Under salt stress, the excessive Na^+ influx leads to an increase in ion channel damage, decreases membrane depolarization, and increases the amount of nutrients uptake (Gaikwad et al., 2022). In a study conducted by Farooq et al., (2022) in rice plan showed that the concentration of the essential nutrients (K, Mn, Fe, Mg, P and Zn) was found to be decreased in root and shoot under salinity stress. The reduction of root surface area caused by salinity stress is directly linked to the decrease of nutrient uptake, leading to decreased root hair density and rooting length (Arif et al., 2019).

Increased assimilation and accumulation of Cl^- in saline solutions can result in decreased total nitrogen uptake by shoots due to the antagonism between Cl^- andNO3. Salt stress also affects the absorption of phosphorus essential for photosynthesis, energy storage, and transfer. If the soil contains too much Cl^- and SO_4^{2-}, phosphorus uptake decreases, which may be due to the high ionic strength of the environment and the low solubility of Ca P minerals. Na^+ and K^+ compete for the root uptake sites, resulting in a decrease in K^+ and Ca^{2+} concentration. A significant amount of literature, including *Manihot esculenta* and *Zea mays*, indicates that salinity is responsible for crop failure due to nutrient imbalance and crop yield reduction (Hasana et al., 2017).

5. SALINITY LEADS OXIDATIVE STRESS:

During the growth and development of plants, ROS serves as a key mediator in regulating plant growth by seed germination (Ishibashi et al., 2015), cell differentiation, root primary growth (Tognetti et al., 2017), and stem cell function (Zeng et al., 2017). Contrary, increased accumulation of ROS in plant tissues also causes oxidative damage to proteins, DNA, lipids and Chlorophyll biosynthesis (Huang et al., 2019). The presence of reactive oxygen species (ROS) can cause plant oxidative damage by reacting with other essential components of plant cells, such as DNA damage caused by salinity, lipid peroxidation, enzyme inactivation during high salinability, protein degradation, oxidative, hormonal and nutritional disorders (Hasanuzzaman et al.,2021). ROS are predominantly generated in chloroplasts, mitochondria, endoplasmic reticulum, cytosol, and peroxisomes. Chloroplast photoreactions are the primary source of ROS compounds, including superoxide ($O_2^{\cdot-}$), hydrogen peroxidation (H_2O_2), hydroxyl radical ($OH^{\cdot}$), and singlet oxygen ($^1O_2$)(Khorobrykh et al., 2020).

ROS homeostasis plays a crucial role in keeping plant growth relatively stable under harsh environmental conditions. An enzymatic defence mechanism in plants is responsible for countering salinity-induced oxidative stress by synthesis an array of antioxidant enzyme (AEs) and non-enzymatic antioxidant (NEAs) to neutralize and detoxify ROS (Santoset al., 2018). Free radical chain reactions are broken by NEAs, while AEs perform their function as scavengers by breaking free radicals (Nimse et al., 2015). Accelerating synthesis and accumulation of osmolytes (OS) are common responses in plants to achieve osmotic adjustments, which also protect cell membrane integrity (Per et al., 2017).

Under stressful conditions, Pro is produced through the glutamate pathway or the ornithine pathway and accumulates in the cytosol and vacuole. Under normal conditions, in plants Pro accounts about 5% of total free amino acids. Contrary to this in stress condition, Pro content rise up to 80% of total amino acids, and thus, plays vital role in ROS homeostasis and plant water balance. Pro was found to protect against damage caused by $^1O_2$ or OH (Hossain et al., 2014). Plants can respond to stresses like wounding, salinity, and drought by utilizing ethylene as a stress hormone. Systemic plant resistance can be triggered by a small amount of ethylene that is formed immediately after stress, and an excess of this ethylene can hinder growth or even cause cell death in plants (Gamalero et al., 2015).

Studies conducted in the past have revealed salt-induced oxidative damage to various crops such as *Vigna radiata*(Moong bean) (Nahar et al., 2016), *Oryza sativa*(Rice) (Rahman et al., 2016), *Zea mays*(Maize), and *Solanum lycopersicum*(Tomato). They also found reduced ascorbate (AsA) to dehydroascorbate (DHA) ratio, superoxide dismutase (SOD) and catalase (CAT) activity, along with an increase of methylglyoxal (MG) content, which collectively contribute to oxidative damage. Salt-stressed rice seeds had higher MDA and MG, as well as increased lipoxygenase (LOX) and SOD activities, while CAT activity was reduced (Rahman et al., 2016).

6. SALINITY LEADS LIPID PEROXIDATION:

The plasma membrane of the cell is mainly composed of lipids that serve to shield it from environmental stresses. Lipid peroxidation, a consequence of salinity, is an extremely destructive process that destroys lipids by chain reaction mechanism which leads to the formation of fatty acids radicals, which later harm other biomolecules. Peroxidation of membrane lipids due to salinity leads to the destruction of fluidity and elasticity, disrupting normal cell function, or hijacking the cell. Malonaldehyde (MDA) is a significant component of lipid peroxidation and serves primarily as an indicator of the adverse effects on membrane lipids caused by ROS and oxidative stress, which can impair membrane stability (Awasthi et al., 2018). The membrane-bound phospholipids are highly susceptible to free radicals, and ROS targets polyunsaturated fatty acids (PUFA) in the membrane. Hydroperoxides, lipid peroxy radicals, and conjugated dienes are produced by the reaction of free radical and methylene groups of PUFA.

MDA content was remarkably increased by 36% in ginseng (Sukweenadhi et al., 2018) root seedlings, 39% in corn (Li et al., 2017), 47% in peanuts (Alexander et al., 2020), 70% in chickpeas (Abd_Allah et al., 2018), 131% in oats (Sapre et al., 2018), 153% in mung beans (Shahid et al., 2021) and 300% in rice seeds (Sarkar et al., 2018), indicating severe damage to cell membrane integrity and/or membrane permeability by salinity (Khalid et al., 2017).

7. SALINITY CAUSED DAMAGE TO PROTEIN AND DNA:

The presence of ROS affects proteins either directly or indirectly. The synthesis of disulfide bonds, carbonylation, S-nitrosylation, and glutathionylation are direct modifications that occur in proteins when exposed to ROS. The markers for protein oxidation can be identified by using these modifications. The interaction between proteins and lipid peroxidation products leads to the indirect modification of proteins to ROS. Amino acids containing thiol and sulfur groups are highly susceptible to ROS attack. Free radicals, including $^1O_2$ and $OH^{\cdot}$, can reduce the amount of thiol groups that are attached to proteins.

One of the primary mechanisms affecting the activity of numerous enzymes and translation factors in plants is salt-induced disulfide bond formation. Enzyme activity and shape are influenced by the formation of sulfenic acid generated by hydrogen peroxide, which creates a disulfide bond between two cysteine molecules. This leads to altered enzyme activity. Tryptophan hydroperoxides are a highly unstable form of tryptophan that is rapidly converted to kynurenine and N-formylkynurenine by ROS, which regulates photosynthesis and induce photoinhibition in plants. During salinity stress, superoxide radicals are released, leading to oxidative stress that permanently suppressed iron sulfur-containing enzymes and oxidisze amino acids like Arg (R), Thr (T), Pro (P), His (H) and Lys (K). Enzymes like glycine decarboxylase, pyruvate dehydrogenase and acotinase can be inhibited by the oxidation and carboxylation; this results in an inhibition of Tricarboxylic acid cycle (TCA) or weakening of the cell's energy status (Camejo et al., 2015).

ROS attack the genetic material of plants' nucleus and organelles. Oxidative stress due to salinity generates a large amount of ROS, which oxidize sugar residues, modify nucleotide bases, break DNA strands, cross-link DNA and proteins, etc. The hydroxyl radicals, in particular, are responsible for segregating sugar hydrogen atoms from DNA molecules to create deoxyribose radicals, which then disrupt the DNA backbones and cause mutation.

8. EFFECT OF SALINITY IN PLANT WATER RELATIONS:

Plant cells' osmotic potential is negatively affected by salinity, which creates outward gradient that draws water out from the cell and reduced turgor pressure (Betzen et al., 2019). The relative water content, water absorption, and evaporation rate of plants in *Corchorus olitorius* were found to decrease when short-term salt stress was applied. The extent of depletion of leaf water potential and osmotic potential in plant cells is determined by the root mediums' osmotic potential and mode of salinity stress. Maintenance of a stable turgor pressure is achieved in plants by reducing their osmotic potential relative to total water potential under progressive salinity stress. The hydrostatic pressure gradient regulates the apoplastic pathway that water follows from the soil to the root xylem in transpiring conditions. Water travels across membranes through the cell-to-cell pathway when salinity restricts evaporation (Mirfattahi et al., 2017).

9. EFFECT ON YEILD:

During the reproductive phase, a family of class I high-affinity K^+ transporters (HKT) remove Na^+ from leaf blades, which affects sodium ion homeostasis under salinity stress (Suzuki et al., 2016). Changes in water conditions, evaporation, nutrient imbalances, stomatal conductance and oxidative damage caused by salt stress all contribute to reduced yields. By altering morpho-physiological and biochemical processes, salinity reduces agricultural yields and production. The reduction of photosynthetic activity, biomass accumulation, and source-sink activity results in negative effects on yield response variables and accelerated aging of reproductive organs (Khataar et al., 2018).

Changes in water potential lead to reductions in flag leaf and vascular tissue thickness, mesophyll cell size, cell elongation and epidermal cell size, affect leaf area, flag leaf, assimilate synthesis, and ultimately yield potential. For example, salinity reduces grain production by 39.1, 24.3 and 13.4% in different stages of wheat such as anthesis, almost initiation and medium grain filling (Sabagh et al., 2021). The salinity level had a negative impact on wheat yield, nutritional content (gluten content, fiber, fats, moisture, and moisture), and mineral content (Mg, P, Ca, Zn, K and Fe) (Nadeem et al., 2020). At 8 dSm^{-1}, *Brassica oleracea* var. *capitata* may fall to 62% (Parvin et al., 2017).

Many studies have been conducted to study the effect to salinity on yield of plant viz., moong bean, *B. oleracea* var. *capitata* (Parvin et al., 2017), tomato (Parvin et al., 2015) and *B. oleracea* var. *italica* (Parvin and Haque, 2017).

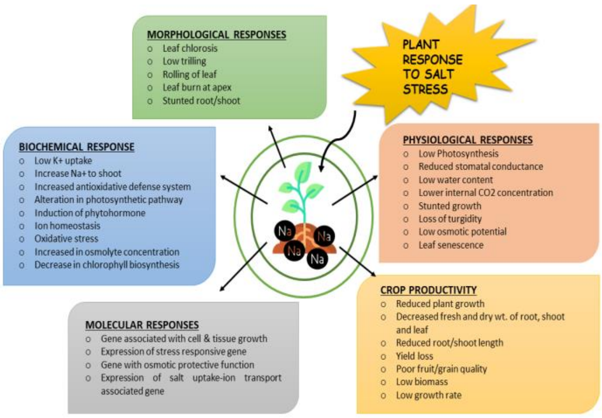

Figure 3: Various responses in plant due to salinity stress

IV. PLANT TOLERANCE MECHANISM TO SALINITY STRESS:

1. Osmotic adjustment by carbohydrate:

Plants are able to tolerate salt stress due to the presence of soluble sugars such as glucose, sucrose, and trehalose. The presence of more soluble sugars in the system shields dissolved enzymes from the impact of higher intracellular inorganic ion concentrations under salt stress (Singh et al., 2022). Salt-stressed plants also store sugars such as glucose, fructose, and trehalose. The carbohydrates are beneficial in promoting tension, osmotic protection, and neutralizing reactive oxygen species. A significant number of plant species exhibit salinity stresses, leading to an increase in the proportion of reducing and non-reducing sugars (sucrose and fructose). Pilling up of trehalose serves as a carbohydrate reserve and bolsters against various stresses, including salinity. The sucrose content in tomatoes (*Solanum lycopersicum*) decreased with salinity due to the increased activity of saccharophosphate synthase.

When treated with NaCl, plants overexpressing the TaSST salt-related wheat gene were found to have higher soluble sugar content than wild-type Arabidopsis plants (Liang et al., 2018). Despite the involvement of soluble sugars, polyols also act as compatible ROS scavengers and scavengers. For example, mannitol, an acyclic polyol, plays an important role in osmotic regulation and improves salt tolerance in higher plants.

2. Ion homeostasis and compartmentalization:

Insufficient ion balance due to salinity stress is detrimental to the growth and development of many plants. Ion homeostasis refers to a fundamental dynamic process in plants that involves an energetically expensive gradient for assimilation of necessary ions and elimination of toxic ions. Glycophytes and halophytes exhibit an inclination towards higher levels of Na^+ in the cytoplasm. The primary site of sodium uptake in plants is the root-soil interface, which may be facilitated by non-selective cation channels like cyclic nucleotide-gated channels (CNGCs) and glutamate receptors (GLRs).

Plants Na^+ uptake is facilitated by the use of aquaporins and high-affinity potassium transporters (HAK) (Byrt et al., 2017). Plants have the ability to remove excess salt ions from the cytosol by primary and secondary transport to maintain a balance between the cytosolic concentrations of Na^+ and K^+ ions, which keeps the concentration of Na^+ ions low in the cytosol because they are very much harmful to cells when present at higher levels (Farooq et al., 2015). These ions are dispersed in the cell vacuole by transporters such as plasma membrane H^+-ATPase, Vacuolar H^+-ATPase, H^+-pyrophosphate, and Ca^{2+} ATPase.

3. Salt- overly sensitive (SOS) gene:

Arabidopsis thaliana exhibits salt-sensitive (SOS) signaling, which involves three genes: SOS1, SOS2, and finally SOS3, ultimately indicating the exportation of Na^+ to the external environment or apoplast. An antiporter Na^+/H^+ binds to SOS1 and regulates both the local transfer of Na^+ at the cell level as well as long-distance transport of these Na^+ ions from the roots to the shoot, thus increasing plant adaptation to salinity. Salt tolerance in plants is greatly influenced by SOS2, which encodes a serine/threonine kinase, and SOS3, whose myristoylation site contain protein.

4. High-affinity potassium transporter (HKTS):

High-affinity potassium transporters (HKTs) are essential for the absorption of potassium by plants. In the Trk/ Ktr/ HKT superfamily, HKT transporters are commonly referred to as monovalent cation transporter groups. HKTs can be used as Na^+ /K^+ sensors by mediating Na^+ import, and some members of HKTs are capable of mediating Mg^{2+} /Ca^{2+} permeation across the plasma membrane of plant cells. Four MPM repeats are present in the structure of HKT'S, with "P" representing the "pore loop region" and ("M") representing each individual transmembrane segment. The $M1_A$-P_A-$M2_A$-$M1_D$-P_D-$M2_D$ repeat and the $P_A$configuration of the structural determinant located in the first P region define two classes of HKT: HKT1 type and HKT-2 type. In HKT2-type proteins, the MPAM motif contains a Gly residue that determines Na^+ or K^+ permeability and thus functions as a Na^+/K^+ symporter. HKT transporters have Na^+-specific permeability and are in the HK1-like group when Gly is replaced by Ser, inhibiting Na^+ transport and accumulation in shoots by extracting excess Na^+ from the sap and holding it within the xylem parenchymal cells, this process prevents salt from entering shoot (Almeida et al., 2017).

5. Proton pumps:

By either sequestering excess Na^+ in the vacuole or exporting it from the cytosol, glycophytic and halophytic plants can maintain a non-toxic cellular Na^+ concentration at levels that are believed to be non-toxic due to salinity. The regulation of Na^+ accumulation and K^+ uptake is a crucial factor in salt tolerance, and it is often interpreted as important because of the cytosolic K^+ /Na^+ ratio. As a result, membrane proton pumps, ion transporters and channels become part of plant salt stress tolerance mechanisms. Primary plant proton pumps or "workhorses" include plasma membrane H^+-ATPase (P-type H^+-ATPase), vacuolar H^+-ATPase, and vacuolar H^+-pyrophosphatase (H^+-PPase).In the plasma membrane, P-type H^+-ATPase is a homodimerized form of its own monomeric polypeptide. Although all plant tissues contain varying amounts of multiple P-type H^+-ATPase isoforms, some isoforms have a more specific spatial expression.

P-type H^+-ATPase plays a role in mediating turgor pressure, cell wall expansion, and intracellular pH by playing an important role. The vacuolar H^+-ATPase is a complex bilateral structure that has been combined into two major subcomplexes: the integral membrane complex V_O and the peripheral V_1complex, which represents the proton transporter and gated ATPase. The proton pump's significance under salt stress has been accurately characterized as an ecoenzyme. Vacuolar H^+-pyrophosphatase is a homodimer of the single polypeptide, which has subunit sizes of 80 K. Inorganic pyrophosphate (Mg_2PP_i) is utilized by the electrogenic proton pump to generate a gradient of protons and transport them up from the cytosol to the vacuole. Only one H^+ -PPase, also known as type-1 H^+-PPase (AtVHP1 or AVP1), is targeted to the vacuolar membrane. Vacuolar H^+-PPases play an important role in maintaining cytosolic PP homeostasis and produce an electrochemical proton gradient across the vacuole, which is responsible for the creation of the proton motive force (PMF) Proton-coupled Na^+ and K^+ antiporters use PMF to actively sequester excess toxic ions from the cytosolic vacuole under salinity stress conditions as secondary transporters.

6. Na+/H+ antiporter (NHX):

Vacuolar NHXs exchange H^+ with Na^+ by exchanging it for the latter. This is true in both cases. Based on their subcellular location, the Arabidopsis monovalent ion exchangers are classified into an eight-member NHX family. AtNHX7/SOS1 and AtNHX8 are located at the plasma membrane and AtNHX1-4 are located at the vacuole membrane, while the other members AtNHX5 and AtNHX6 are located at the inner membrane Golgi membrane AtNHX5 also helps transport Na^+ to the vacuole.Overexpression of AtNHX1 results in elevation of salt-tolerance in many plant species such as Arabidopsis (Pehlivan et al., 2016), rice, cotton (Long et al., 2020), and tomato. Apoplastic barriers and Na^+ immobilization are effective methods for reducing Na^+ accumulation. Casparian bands and suberin lamellae act as extracellular hydrophobic apoplastic barriers located in the endodermal cell wall and play an important role in limiting the free diffusion of solutes. The casparian band in endodermal root cells prevents the transfer of ions from the root to the shoot. This translocation pathway allows plants to partially exclude harmful ions by limiting their movement into the xylem. Suberin laminae have a relatively minor effect on reducing the amount of Na^+ leakage into endodermal cells, which reduces plant energy needs.

7. Polyamines:

Cationic, aliphatic polyamines (PAs) are low molecular weight and they have roles in normal growth and development such as cell proliferation, metamorphogenesis, flowering, and fruit development. Plants are more resistant to stress when polyamine concentration increase. Under salinity stress, polyamines promote cellular responses by modulating ROS homeostasis. The alleviation of salinity stress through the use of polyamines has been suggested (Rathinapriya et al., 2020), as well as the limitation of plant resistance by its catabolism products (e.g. H_2O_2) over time (Saha et al., 2015).

8. Nitric oxide:

Numerous essential plant processes, such as root development and respiration, stomatal closure, flowering, cell death prevention or stress responses are all dependent on the small volatile compound, nitric oxide. The interaction between lipid radicals and NO prevent the oxidation of fatty acids through the breakdown of superoxide compounds, leading to the formation of peroxynitrite that can be neutralized by other cell processes. In addition, it activates antioxidant enzymes (SOD, CAT, GPX, APX and GR). NO can alleviate stress through exogenous application, but its concentration dependent. NO has been shown to mediate salt stress tolerance in plants by suppressing germination inhibition, growth inhibition (Ageeva-Kieferle et al., 2019) and its role in ion homeostasis.

9. Phytohormones:

Abscisic acid (ABA), salicylic acid (SA), jasmonic acids (JA) and ethylene (ET) are examples of plant hormones that have been well-documented as stress response hormone (Verma et al., 2016). Osmotic stress and water scarcity lead to an increase in salt stress, resulting in the production of ABA in vascular tissues and its distribution throughout roots and shoots. The positive correlation between ABA accumulation and salinity tolerance is believed to be due to the presence of potassium, calcium, and compatible solutes in root vacuoles that prevent Na^+ and Cl^- uptake. In rice seedlings, endogenous salicylic acid levels increased under salinity stress. Plants are able to overcome salt-induced osmotic stress by activating the synthetic ABA genes, including adenovirus (ABA)-aldehyde oxidase, epoxycarotenoid dioxygenases, zeaxanthin oxidase, and Mo containing sulfurase that accumulate enzymatically in the plant.

Brassinosteroids have been shown to decrease salinity. By using brassinosteroids, the concentration of SOD, POX, APX and GPX antioxidant enzymes increased, while non-enzymatic antioxidant compounds like tocopherol, ascorbate, and reduced glutathione were also observed.

Plant hormones, cytokinins that are typically present at the root tips, are transported through the xylem to the upper parts of plants and play a role in various developmental processes that enhance their ability to survive in high salinity conditions. Pospisilova (2005) elucidated that the plant's stomata closes and leaves senescence as a result of cytokinins under salt stress.

Akbari et al., (2007) suggested that the application of indoleacetic acid (IAA) to wheat seeds aids the plant in coping with salt stress. The accumulation of endogenous jasmonic acid in salt-tolerant crops is higher than that in sensitive ones, indicating that higher levels can help alleviate salt problems in plants. The plant's growth is regulated by gibberellic acid, which is an important hormone due to the increased protein abundance of DELLA during salt stress. These proteins are directly involved in the modulation of growth, flowering, and plant hormone signalling pathways that improve salt stress tolerance in plants. Plants can become more tolerant to salt stress, increase their germination rate, and other processes can be enhanced by overexpressing EIN3 through the use of ethylene signalling. Moreover, numerous signalling pathways through ethylene mediate plant growth. Phytohormone and their effects in various plants are summerized in Table: 2.

Table 2: Effects of phytohormone on plant against salinity stress

TYPES OF PLANT	DOSE AND APPLICATION METHOD OF PHYTOHORMONE	SALINITY LEVEL	EFFECTS ON PLANT	REFERENCES
Cereal crops:				
Wheat (*Triticum aestivum* L.)	Tryptophan, 4.89 mol L^{-1}	150mM NaCl	Rise in net CO_2 assimilation rate.	Iqbal and Ashraf 2013
	Methyl Jasmonate, 0.1 µM	2% NaCl	Rise in level of cytokinin.	Avalbaev et al. 2016
	ABA, 10 µM	300mM NaCl	Increased Proline content.	Kaur and Asthir 2020
Rice (*Orzya sativa* L.)	GA3, 10 µM, Seedling treatment	100mM NaCl	Increase in lipid biosynthesis.	Liu et al. 2018
	Salicylic acid, 0.5 and 1 mM	100mM NaCl	Lowering in Na^+, lipid peroxidation, electrolyte leak age, CAT, SOD and APX content.	Kim et al. 2018
	ABA, 100 µM, Spraying.	0.5% NaCl	Up-regulation of Proline, OsP5CS1 and OsP5CR gene expression.	Sripinyowanich et al. 2013
	Ethylene, 10 µL L^{-1}, Gaseous form using a syringe	200mM NaCl	Down regulation of MHZ6/OsEIL1 and OsEIL2 in roots and coleoptiles.	Yang et al. 2015
	24-Epibrassinolide, 10^{-7} M, Seed priming	125mM NaCl	Rise in antioxidant activity and lowering of MDA content.	Sharma et al. 2013
	Melatonin, 20 µM	25 mg L^{-1} NaF	Amplification of GA, ABA, Proline, CAT, GPOX, GPX activity and depletion of IAA, MAD, Protein carbonylation, methylglyoxal, Fluoride bioaccumulation.	Banerjee and Roychoudhury 2019
	Polyamine (Putrescine), 1 and 2 mM	200mM NaCl	Boost in GPX, GR activity.	Ghosh et al. 2012
Maize (*Zea mays* L.)	Auxin (IAA), 2 mM	100mM NaCl	Rise in photosynthetic pigment concentration and leaf Na^+/K^+ ratio, and lowering of Membrane permeability.	Kaya et al. 2013
Sorghum (*Sorghum*	GA_3, 288 µM	50mM NaCl	Accelerates seed germination and water absorption.	Zhu et al. 2019

TYPES OF PLANT	DOSE AND APPLICATION METHOD OF PHYTOHORMONE	SALINITY LEVEL	EFFECTS ON PLANT	REFERENCES
bicolour (L.) Moench)				
Barley (*Hordeum vulgare* L.)	GA_3, 100 µM	100mM NaCl	Enhanced shoot length and the dry shoot weight.	Abdel-hamid 2016
	Salicylic acid, 0.5, 1.0, 1.5 and 2.0 mM, Foliar application	12 dS m^{-1}NaCl	Boost in proline, phenolics, soluble carbohydrates, phenylalanine ammonia lyase in roots and leaves and antioxidant enzyme (POX, CAT and polyphenol oxidase).	Ardebili et al. 2019
Fruits:				
Cucumber (*Cucumis sativus* L.)	Salicylic acid, 0.3 mM, Nutrient solution	50mM NaCl	Rise in RGR, leaf photosynthetic and RSA, negative regulation of GL2 and RHD2 gene.	Miao et al. 2020
	Melatonin, 1 µM	150mM NaCl	Enhanced SOD, CAT, POD, GA activity and low ABA concentration.	Zhang et al. 2014a
	Calcium carbide, 30 mg, Powder form	150mM NaCl	Amplification of amylase, SOD, CAT activity, soluble sugars, free amino acids and protein contents, lowering of H_2O_2 and MDA content.	Shakar et al. 2016
	Melatonin, 100 µM	200mM NaCl	Increase in SOD, peroxidase, CAT, APX activity and ascorbic acid, glutathione content.	Wang et al. 2016
Strawberry (*Fragaria ananassa* L.)	Salicylic acid, 100 µM, Foliar application	100mM NaCl	Increase in Root length, leaf weight, PS II activity, and lowering of MDA content.	Samadi et al. 2019
Grapes (*Vitis vinifera* L.)	Melatonin, 50 µM	200mM NaCl	Incresase in ethylene content.	Xu et al. 2019
Leafy vegetable:				
Lettuce (*Lactuca sativa* L.)	GA_3, 10^{-6} M, Nutrient solution	20mM NaCl	Boost in biomass accumulation, leaf expansion, stomatal conductance, water and nitrogen use efficiency.	Vetrano et al. 2020

TYPES OF PLANT	DOSE AND APPLICATION METHOD OF PHYTOHORMONE	SALINITY LEVEL	EFFECTS ON PLANT	REFERENCES
Vegetable:				
Pea (*Pisum sativum* L.)	GA_3, 0.5 mM, Seed priming	100, 200, 300 mM NaCl	Up-regulation of Na^+/H^+ antiporters, antioxidant system, proline production, total phenol and flavonoid content.	Ahmad et al. 2021
Common bean (*Phaseolus vulgaris* L.)	Ascorbic acid, 1 mM GA_3, 0.05 mM	200mM NaCl	Amplification of protein content, GPOX and decreased H_2O_2, MDA content.	Saeidi-Sar et al. 2013
Brinjal (*Solanum melongena* L.)	6-benzyladenine, 10 µM, Nutrient solution	90mM NaCl	Enhanced SOD, POX, ascorbate activity and downfall of O^{2-}, MAD, GSH.	Wu et al. 2014
	24-Epibrassinolide (EBR), 100 nM, Rooting media	90mM NaCl	Rise in chlorophyll content, net photosynthetic rate, stomatal conductance and intercellularCO_2 content, reduction of non-photochemical quenching (NPQ).	Xue-Xia Wu 2012
Ladyfinger (*Abelmoschus esculentus* L.)	GA_3, 0.1 mM, Foliage spray Ascorbic acid (AsA), 0.1 mM, Foliage spray	100mM NaCl	Amplification of chlorophyll, carotenoids, stimulating activities of antioxidant enzymes content, lowering of electrolyte leakage, H_2O_2 content and lipid peroxidation.	Wang et al. 2019
Oil-yeilding plants:				
Soybean (*Glycine max* L.)	Salicylic acid, 0.5 mM, Foliar application	100mM NaCl	Enhanced proline, phenolics, soluble carbohydrates, phenylalanine ammonia lyase in roots and leaves and antioxidant enzyme (POX, CAT and polyphenol oxidase).	Ardebili et al. 2019
	ABA, 200 µM	200mM NaCl	Up-regulation of RAV gene.	Zhao et al. 2017
	24-Epibrassinolide, 100 M, Seed priming	100mM NaCl	Enhanced antioxidant activity and osmolyte accumulation.	Soliman et al. 2020
Safflower	Salicylic acid, 1 mM,	100 and	Rise in Glycine betaine, total	Shaki et al. 2018

TYPES OF PLANT	DOSE AND APPLICATION METHOD OF PHYTOHORMONE	SALINITY LEVEL	EFFECTS ON PLANT	REFERENCES
(*Carthamus tinctorius* L.)	Nutrient solution	200mM NaCl	soluble protein, carbohydrates, chlorophylls, carotenoids, flavonoid and anthocyanin contents.	
Cotton (*Gossypium hirsutum* L.)	ABA, 100 µM Mannitol, 200 mM	200mM NaCl	Positive-regulation of GhMPK17 gene.	Zhang et al. 2014b
Model plant:				
Mouse-ear cress (*Arabidopsis thaliana* L.)	Ethephon, 30 µM	NaCl, 50, 100 mM	Retained K^+ in shoots.	Yang et al. 2013
Sea lavender (*Limonium bicolour* L.)	Salicylic acid, 0.08 mM, Nutrient solution	200mM NaCl	Positive-regulation of gibberellic acid and alpha amylase activity, decrease ABA content	Liu et al. 2019
Ryegrass (*Lolium perenne* L.)	6-benzylaminopurine, 25 µM, Foliar spray	250mM NaCl	Boost in SOD, CAT, APX, MDAR, GR activity.	Ma et al. 2016

RSA Root system architecture, RGR Relative growth rate (Source: Mangal et al., 2022).

10. Antioxidant defence system:

By utilizing their antioxidant defense system, plants can effectively scavenge for ROS-superoxide radicals, hydroxyl radical and singlet oxygen and hydrogen peroxide. It is made up of enzymes found in various compartments of the cell and purifies salt stress by removing toxic free radicals.

a) ENZYMATIC-ANTIOXIDANT DEFENCE:

Enzymes play crucial role in defending plants from stress. These enzymes which scavenge plant from ROS include Catalase (CAT); Superoxide dismutase (SOD); Ascorbate peroxidase (APX); Glutathione reductase (GR); Monodehydroascorbate reductase (MDHR) and Guaiacol peroxidase (GPX). Antioxidative enzyme and their functions are summerized in Table: 3.

i. Catalase (CAT):

The first enzyme to be found to have a role in preventing damage from oxidative stress, is CAT. CAT's specificity lies in its ability to convert H_2O_2 into both H_2O and O_2. The production of hydrogen peroxide radicals is mainly carried out in peroxisomes, but some recent studies have revealed that this enzyme can also be found in chloroplasts as well as mitochondrion and cytosol (Mhamdi et al., 2010).

Peroxisomes undergo β-oxidation and photorespiration, which involve the expulsion of H_2O_2. The absence of a reducing agent is exemplified by this enzyme. There are three CAT genes present in the studied angiosperms, which are namely CAT1, CAT2, and CAT3 is effective in mitigating ROS produced during photorespiration, and plants that lack peroxisomal CAT are considered crucial for studying hydrogen dioxide signaling under different stress conditions (Kerchev et al., 2016). Kibria et al,. (2017) discovered that salt stress on rice plants leads to a significant rise in CAT activity, which results in the plant's ability to tolerate salt. Sobahan et al., (2018) observed similar results in rice seedlings under salt stress.

ii. Superoxide Dismutase (SOD):

The superoxide radical ($O_2^{\cdot -}$) is broken down into oxygen and hydrogen peroxidation by SOD. It is believed that this enzyme is the first line of defense against oxidative damage. Based on the metal ions used, SOD is divided into three isozymes, namely Fe-SOD in the chloroplast, Mn-SOD found mitochondria, and Cu/Zn-SOD in the cytosol, chloroplast and peroxisomes.

The increase in SOD activity during stress conditions confirms that plants can withstand environmental stresses more effectively. It was observed that rice cultivars had leaves with higher SOD activity and were more tolerant to salinity than other plants. Elgawad et al., (2016) also found that SOD activity increases the salt tolerance of maize seedlings under salt stress. In *Cicer arietinum*, the plant's response to salt stress was enhanced by an increase in SOD activity.

iii. Ascorbate Peroxidase (APX):

Both CAT and the APX in plant cell, functions in the same way in both their chloroplast and cytosol. It plays an important part in the ascorbate-glutathione (ASC-GSH) cycle. APX is different from CAT in that it uses ascorbic acid (AA) as a reducing agent to remove hydrogen peroxide. The amino acid sequence of higher plants indicates the existence of five different types of isozymes, which can be found in mitochondria, thylakoids, and stroma, as well as several other plant cells. Its highest affinity for hydrogen peroxide radicals makes it a proficient H_2O_2 scavenger in plants under stressful environments and prevents cell damage. Taibi et al., (2016), research revealed that salinity enhanced APX activity in *Phaseolus vulgaris* and enabled plants to tolerate H_2O_2 under different saline conditions.

iv. Glutathione reductase (GR):

GR is a member of the disulfide-containing flavoenzymes. GR is an NAD(P)H-dependent enzyme that reduces glutathione disulfide (GSSG) to GSH and balances the cellular GSH/GSSG ratio. The enzyme is predominantly located in chloroplasts, with a smaller amount in mitochondria. GSH reacts with ROS such as hydroxyl radicals and superoxide radicals using nicotinamide adenine dinucleotide phosphate hydrogen (NADPH), which prevents oxidative damage to the cell. The increase of GR activity in plants leads to the accumulation of GSH and ultimately gives plants stress tolerance.

Activity of GR was found to be increased by researchers in various plant like cowpea, French bean (*Phaseolus vulgaris*), and *Reaumuriasoongorica*(Pall.).

v. Monodehydroascorbate Reductase (MDHR):

MDHAR, a FAD enzyme, utilizes NADPH as an electron donor to convert MDHA radicals back into ascorbic acid. Phenoxyl radicals are reduced by this enzyme, which is the only known one that uses MDA as a substrate. It has different isozyme forms in different organelles e.g. chloroplast, mitochondrion, cytosol and peroxisomes where it absorbs H_2O_2. In the context of transgenic tobacco, it was observed that MDHAR overexpression led to increased tolerance to salt stress by scavenging harmful ROS.

vi. Guaiacol Peroxidase (GPX):

GR, which is a type of enzyme that contains heme, can eliminate excess hydrogen peroxide radicals from plant cells under stress and normal conditions. Catalysis utilizes guaiachicol and pyrogallol as electron donors. The enzyme GPX is purportedly an anti-stress agent that can eliminate peroxy and other oxygen radical forms.

b) NON-ENZYMATIC ANTIOXIDANT DEFENCE:

The use of non-enzymatic antioxidants is crucial for plant growth and development, as they protect against environmental stress conditions by interacting with different cellular components and metabolic processes.

I. Proline, Pro (P):

When exposed to salinity stress, cysteine, arginine, and methionine (which make up roughly 55% of the free amino acids) reduced while proline concentration increased. Proline is a typical osmolyte found in plants and increases in concentration as reactivity to environmental stresses. As a plant growth regulator, this amino acid has multiple functions and influences various signaling pathways. Under salt stress, plants increase their endogenous proportion of proline to counteract the adverse effects of ROS. The presence of proline in plant cells can help mitigate the negative impact of salinity by reducing the concentration of Na^+ and Cl^- in the cell. By scavenging for hydroxyl radicals (OH^-) and superoxide radical ($^1O_2$), Proline inhibits lipid peroxidation, and serves as a pH buffering agent for subcellular structures. At moderate and high salinity levels two pistachios cultivar exhibited a significant surge in the free proline concentration in their leaves and roots, which is necessary to protect plants from salt stress (Rahneshan et al., 2017).

II. Glycine Betaine:

An amino acid that is amphoteric, electrically neutral, and highly soluble is Glycine betaine. This non-toxic cellular osmolyte enhances the osseous density of plant cells when exposed to stress and reduces detrimental salt stress effects. The substance helps stabilize cell proteins, prevents oxidative damage to photosynthetic pigments, and decreases ROS production, while also maintaining cellular osmotic regulation by evenly dispensing sodium and chloride ions in the cell vacuole and cytoplasm. Enhanced levels of glycine betaine balance out redox imbalance and improve salinity tolerance by maintaining membrane integrity, enzymatic activity, and scavenging harmful ROS (Kurepin et al., 2015).

III. Ascorbate:

One of the most crucial low molecular weight antioxidants in plant cytoplasm is ascorbate. Plants under salt stress increase endogenous ascorbate levels, accelerate plant growth, increase carbohydrate, mineral and phenolic content, and play an important role in various physiological processes such as metabolism, differentiation and growth by donating electrons to several non-enzymatic reactions and to reactions carried out by enzymes. Ascorbate safeguards the membrane's reaction with superoxide and hydrogen peroxide radicals, rejuvenating α-tocopherol, and maintaining the activity of enzymes that contain prosthetic transition metal ions. It was found that exogenous application of ascorbate alleviates the adverse effects of salinity stress on various plants such as cherry tomato (Abdelgawad et al., 2019), sugarcane and promotes recovery from salt stress.

IV. Tocopherols:

Lipophilic antioxidants are classified into four groups, namely, α, β, γ and δ. In salt stress conditions, tocopherols are responsible for protecting the basic structure and essential functions of photosystem II B by scavenging harmful oxygen free radicals, lipid peroxidation, and singlet oxygen from chloroplasts. Of all four types of tocopherols, α-tocopherol, which has three methyl groups attached to its phenolic ring, has the highest antioxidant activity. Tocopherols are potent free radical scavengers as they hinder the progression of the autoxidation chain in lipids. Accumulation of tocopherols particularly α-tocopherol has been shown to induce salinity tolerance in several plant species such as *Medicago sativa.*

V. Carotenoids:

Lipophilic antioxidants, known as carotenoids in plants and microorganisms play a crucial role in scavenging various types of ROS in plant tissue. By scavenging singlet oxygen and suppressing the production of triplet-(Chl*), carotenoids prevent the formation of singlet oxygen thereby protecting important photosynthetic apparatus. Sugarcane plants exhibit better salt tolerance due to an increase in carotenoids.

Table 3: Enzymatic and non-enzymatic antioxidants in ROS scavenging

ANTIOXIDANT SYSTEM	LOCATION	CHARACTERSTIC FEATURE	REFERENCES
Enzymatic-antioxidant:			
Superoxide dismutase (SOD)	Mitochondria and Peroxisomes	Breakdown of H_2O_2 to H_2O and O_2.	Quintero et al., 2011
Catalase (CAT)	Mitochondria, Peroxisomes, Chloroplast and Cytosol	Scavenging of $O^{\cdot -}$ by converting it to H_2O and O_2.	Mallick et al., 2000
Ascorbate Peroxidase (APX)	Mitochondria, Peroxisomes, Chloroplast and Cytosol	Reduces H_2O_2 into H_2O and DHA using (AA) as reducing agent.	Scandalios et al., 1990
Guaiacol Peroxidase(GPX)	Mitochondria, Chloroplast, Endoplasmic reticulum and Cytoplasm	Quenches O_2 and peroxy radicals.	Chen et al., 2006
Monodehydroascorbate Reductase (MDHR)	Mitochondria, Chloroplast and Cytoplasm	Regenerstion of AA from MDHA by use of NADPH as reducant.	Wang et al., 1999
Glutathione reductase (GR)	Mitochondria, Chloroplast and Cytoplasm	Main enzyme of ASC-GSH cycle catalyzes the formation of a disulfide bond in glutathione disulfide to maintain a high cellular GSH/GSSG ratio and detoxifies H_2O_2 generated by Mehler reaction in chloroplast.	Ushimaru et al., 1997
Dehydroascorbate reductase	Mitochondria, Chloroplast and Cytoplasm	Reduces DHA to AsA by using GSH as substrate.	Yoshida et al., 2006
Non-Enzymatic-antioxidant:			
Proline (Pro, P)	Mitochondria, Chloroplast and Cytosol	Catalysis of $OH^{\cdot}$ and $^1O_2$and prevent negative effect of LPO.	Van et al., 1994
AA	Mitochondria, Peroxisomes, Chloroplast, Vacuole, Apoplast and Cytosol	Protect metal-binding enzyme and membrane oxidative damage.	Fini et al., 2011
Flavonoids	Vacuoles	Scavenges $OH^{\cdot}$, $^1O_2$ and H_2O_2.	Yildiz et al., 2013
α -Tocopherol	Green tissue only	Prevents chain propagation in lipid	Li et al., 2008

ANTIOXIDANT SYSTEM	LOCATION	CHARACTERSTIC FEATURE	REFERENCES
		autooxidation, quenches excess energy, maintains PSII structurally and functionally.	
Carotenoids	Green and non-green parts	Quenching of excess energy from PSI and PSII, inhibits lipid peroxidation, scavenges $^1O_2$ and triplet Chlorophyll (3Chl*) molecules.	Roychoudhury et al., 2012
Reduced Glutathione (GSH)	Mitochondria, Endoplasmic reticulum, Peroxisomes, Chloroplast, Vacuole, Apoplast and Cytosol	Scavenges $OH^{\cdot}$, $^1O_2$, H_2O_2 and $O^{\cdot -}$, also plays role in regeneration of ascorbic acid to produce GSSG, helps in chelation of heavy metal ions in plants.	Barnes et al., 2002

(Source: Mushtaq et al., 2020)

V. EPIGENETIC REGULATION OF SALINITY STRESS:

Epigenetics is the process of controlling gene expression through heritable covalent changes in chromatin architecture that enable access to genes by the transcription machinery.DNA methylation, histone modifications, and histone variants, as well as certain non-coding RNAs (ncRNA) are all crucial components of epigenetic processes, including gene expression and genome stability.DNA methylation is a well-studied epigenetic modification that involves the addition of methyl group to the 5' position of cytosine in DNA sequence contexts like CG, CHG, and CHH (H stands for A, T, or C). A significant decrease in the methylation level of the promoter of TaFLS1, a wheat flavonol synthesis gene that responds to salt stress was observed in this cultivar that tolerant to it, suggesting an important role for DNA methylation in salt tolerance. Acetylation, methylation, ubiquitination, phosphorylation and sumoylation are among the covalent modifications that occur in the tails of histone or at N' termini of histone proteins, with DNA methylation.The regulation of genes under salt stress is influenced by specific histone modification enzymes that determine these modifications. In 2022, the discovery of GsMYST1 by Feng et al., is protein that is homologous to histone acetyltransferase, in wild soybean, found that GsSnRK1 kinase coordinated phosphorylation of Glycosythomin-1 (GsMYST1) and then acetylation of histone H4 at target genes increased stress-responsive gene expression, leading to an increase in salt tolerance.

$H_3K_4me_3$ and $H_2K_{27}me_3$ methylation, which are present in castor bean, play a role in regulating the transcription of RSM1(encoding the RADIALIS LIKE SANT-an MYBrelated transcription factor), an essential transcriptional factor that participates in salt stress signaling via ABA (Han et al., 2020). According to studies by Nguyenetal., 2019 the brm-3 mutant displayed elevated levels of ABA-related PP2C genes (ABI1, ABI2, and HAI1) on the transcript level after being treated with NaCl (Nguyen et al., 2019).These genes may be repressed by BRM, which is the chromatin-remodeling enzyme BRAHMA.Salt stress caused the chromatin associated with PP2C genes to shift from a repressor-mediated state to an activator-transcription state.

VI. GENES INVOLVED IN MITIGATING SALINITY STRESS:

The expression of quantitative markers is influenced by genes located in genomic regions, which are known as quantitative trait loci (QTL). Reports suggest that biparental QTL mapping can provide valuable information for the subsequent use of map-based cloning methods to produce salt tolerance genes and MAS in economically significant crops like rice, maize, pearl millet etc. (Luo et al., 2017). Salinity tolerance research is hindered by the polygenic inheritance pattern and the significant impact of genotype-environment interactions, which are the primary barriers to progress. Recent years have seen noteworthy progress in mapping salinity tolerance using plant-specific traits, including cultivar growth stage importance in screening and stress-related markers. (Table: 4).

a. Rice (Orzya sativa):

The reproductive stage is deemed more significant than the seedling stage because it has a direct impact on grain yield, and QTL reports are typically restricted to the initial stage to prevent laborious phenotyping (Singh et al., 2021). Saltol is a widely known QTL in rice planting stage that has been reported by several research groups. Population mapping of Indica recombinant inbred lines (RILs) identified six QTLs at the seedling stage distributed on chromosomes1 and 4 (Dahanayaka et al., 2017), using a set of introgressed lines (IL) from donor parent Nona Bokra and identified 18 QTLs for salt tolerance indices (Puram et al., 2018). This study suggestedNa^+exclusion, Na^+; K^+ homeostasis and Na^+ compartmentalization as probable mechanisms of salt tolerance in "Nona Bokras".Another QTL mapping study performed on the F2 population at their reproductive stage identified sixteen QTLs associated with salinity stress in four linkage groups (Hossain et al., 2015).

b. Maize (Zea mays):

Among the 209 double haploid (QTL) lines studied, 41 out of 61 QTL were found to have salt tolerance for biomass-related trait. Chromosomes 1, 3, 7, and 9 were grouped with salt tolerance specific QTLs, and the 13 QTL effects on chromosome 1 caused the most significant differences in phenotypic variation (Luo et al., 2019). The population of 240 individuals demonstrated a significant QTL for plant height on chromosome 1 when salinity is present (Luo et al., 2017).For QTL analysis, 161 $F_{2:5}$ RILs were used in a field and hydroponic experiment(Cui et al., 2015). A total of 29 QTLs clustered on chromosomes 1, 3 and 5 were identified of these, 14 showed significant QTL treatment (Q × T) interaction effects.

c. Sorghum (Sorghum bicolour):

Three traits in the germination stage and nine traits were identified in seedling stage in mapping population of 181 RILs from each parent, resulting in 12 QTL (PVE region 5.4-6%) and 29 QLT (PV region 5.3-21.9%), respectively.The detection of 53 QTL for six characters indicating whole plant growth stages was observed under salt and control conditions of which six QTLs were identified as the most crucial (Wang et al., 2020). A high-density genetic map of 10 sorghum chromosomes with 1991 markers was created using 177 $F_{3:5}$ interspecific RIL populations in a recent study. 10 QTLs that are specific to salt stress were identified on the gene map as being related to plant growth and plant health. Four QTLs that are located on chromosome 4 had an effect on plant height, total biomass, and root biomass.The salt-sensitive QTLs contained genes that are associated with tolerance to the osmotic and ion environments, as well as several aquaporins (Hostetler et al., 2021).

d. Medicago truncatula:

In a model study of *Medicago truncatula* legume, 133 RIL lines (Jemalong A17 (JA17) × F83005.5 (F83)) were screened for salt tolerance. The development of dry biomass and the presence of Na^+ and K^+ ions in roots, stems, and leaves were taken into account by plant phenotyping. Among the eight linkage groups, there were 13 QTLs mapping out 6 in the control group, 2 for salt and 5 for the salt sensitivity index.

Most QTLswere found clustered on Chr-1, but no QTLs were found on Chr-5 and 6.

e. Cotton (Gossypiumsp.):

In the F2-derived F3 population, a study using SNP-based QTL mapping revealed 66 QTRs, which were identified using the tolerant cotton line CCRI35 and the susceptible Nan Dan (NH)(Diouf et al., 2017). At the time of seedling, plants were screened for morpho-physiological parameters at three different salinity levels. Of all theQTLs identified, only 14 (10 from male parents and four from female parents) showed correspondence between the three saline environments for the six traits, accounting for 2.72–9.87% of the PVE.

f. Zoysia grass (Zoysia japonica):

Guo et al., (2014), found that 120 descendants of a salt-tolerant *Zoysia japonica* (Z105) and the salt sensitive accession (Z061) from whose offspring were selected for their F1 mapping population on chromosome 4, two QTLs were identified, and their impact on leaf appearance was significant.Another important QTL for shoot dry weight reduction was identified on chromosome- 5.

g. Soybean (Glycine max):

174 individuals from an F9 generation RIL population (salt-sensitive cultivar, Cheongja 3 × salt-tolerant landrace, IT162669) were tested for salt tolerance at the vegetative stage (Cho et al., 2021).After 2 weeks of salt stress, important physiological markers such as vegetative damage and Na^+-K^+ ion concentrations were detected through phenotypic data. Two new major QTLon chromosomes 6 and 10 were identified as related to ionic stressand other important physiological parameters under salinity, respectively. By exploring 132 F2:3 populations, including moderately susceptible Williams 82 and tolerant Fiskeby III (PI 438471), Do et al. (2018) found that major chromosomal loci associated with salt stress were present.After being exposed to salt stress for two weeks, the plants were phenotypedaccording to their vegetative parameters and ion concentrations.QTL produced by Fiskeby III located onChr-3 had a significant correlation with leaf browning, chlorophyll content ratio, and sodium/chloride ion concentrations. In addition,another allele associated with leaf sodium concentration was identified andmapped to Chr-13.

h. Chickpea (Cicer arietinum):

A study of 200 RILs from a cross between two *Cicer arietinum* cultivars Rupali and Genesis836 under greenhouse and field conditions revealed that 42 QTLs had different effects on growth parameters.Among the six QTLs found on the fourth, fifth, and sixth chromosomes, salt tolerance was the most significant factor. Significant QTLs that are associated with yield and yield-related components were identified in CaLG03 and CaCG06, which deal with salinity stress.Histidine kinase, Ca-dependent protein proteins, antiporter genes, and transcription factors like WRKY and MYB were among the candidate genes for salt tolerance (Soren et al., 2020).

i. Wheat (Triticum asetivum):

The discoveryof 61 major QTLs across 15 chromosomes during germination and earlyseedling stages was made in a study of over 186 F10 RILs by two major QTLs for primary leaf fresh weight andcoleoptile fresh weight were identified on chromosomes 5 and 2, respectively (Rezaei et al., 2021). The study by Asif et al., (2020), determined six QTL for salt tolerance traits, namely sodium accumulation, chloride accumulation and K^+-Na^+ ratio as well as the ability of the shoot to maintain salinity under stress from Excalibur Kukri mating in a RIL wheat population.

Table 4: Major QTLs detected in different crop plants.

TYPES OF CROP	CROP STAGE	TYPE OF MP	QTLs FOUND	CHROMOSOME	PVE (%)	REFERENCES
Rice (*Orzya sativa* L.)	Seedling	100 RILs (At354 × Bg352)	*qSSI1*, *qSL1*, *qSNK1*, *qSL4*, *qSNK4*, *qSSI4*	1, 1, 1, 4, 4	10.8, 10, 8.9, 15, 11,16	Dahanayakaet al. (2017)
	Seedling	112 ILs (Cheniere × Nona -Bokra)	*qK3.1*, *qNaK3.1*, *qSHL8.1*, *qDWT8.1*, *qSRI-K9.1*, *qSRI-NaK9.1*	3, 3, 8, 8, 9, 9	14.8, 14.6, 14.2, 17.6	Puram et al.(2018)
Maize (*Zea mays* L.)	Seedling	209 DH lines (hybrid Xianyu 335)	*qRLS1*, *qFLS1-2*, *qRLR1*, *qFLS1-2*	1,1,1,1	63.19, 55.21, 58.35, 55.21	Luo et al.(2019a)
	Matured	240 DH lines (PH6WC × PH4CV)	*qSPH1*, *qPHI1*	1,1,1	31.2, 25.94	Luo et al.(2017)
Sorghum (*Sorghum bicolour* L.)	Whole-plant growth	181 RILs (Shihong137 × L- Tian)	*qTB6, qSFW9, qJW9, qBrix2, qBrix10*, *qSTI-Brix9*	6,9,9,2,10,9	11.15, 17.7, 14.4, 12.83, 11.58, 15.45	Wang et al.(2020)
	45 DAT	177 RILs (*S. propinquum*× *S. bicolor*)	*qHT45_4.STI, qTB45_4.STI, qTB45_4.S, qRB45_4.ST*	4,4,4,4	9, 13.4, 10.37, 11.4	Hostetler et al.(2021)
*Medicago truncatula*L.	Vegetative	133 RILs (F_8) (JA17 × F83)	*LeaKCsi.1, LeaNaKCsl.1, RoNaKCct.1, LeaNaTQct.1*	1,1,1,1	11.7, 9.8, 10, 10.8	Arraouadi et al.(2012)
Cotton (Gossypium sp.)	seedling	277 $F_{2:3}$ (CCRI35 × NH)	*qEC_A12_110.2, qSLW_A06_110, qFW_D03_110.2*	A12, A06, D03	8.29, 7.91, 9.87	Diouf et al.(2017)
Zoysiagrass (*Zoysia japonica*L.)	30 DAT	120 F_1s (*Z. japonica* Z105 × Z061	*qLF-1*, *qLF-2*, *qSCW-1*	4,4,5	13.1, 29.7, 65.6	Guo et al.(2014)
Soybean	Vegetative	174 RILs (F_9)	*qST10* *(STR,*	10,6	20.07-	Cho et

TYPES OF CROP	CROP STAGE	TYPE OF MP	QTLs FOUND	CHROMOSOME	PVE (%)	REFERENCES
(*Glycine max* L.)		(Cheongja-3 × IT162669)	*SPAD, FW, DW), qST6 (Na$^+$, K$^+$:Na$^+$)*		24, 14.07-24.38	al.(2021)
	Vegetative	132 F$_{2:3}$ (Williams-82 × Fiskeby III)	*qLSS, qCCR, qLSC, qLCC, qLSC*	3,3,3,3,13	48.2, 31.3, 20.6, 58.9, 11.5	Do et al. (2018)
Chickpea (*Cicer arietinum* L.)	Reproductive	201 RILs (F$_8$) (ICCV 10 × DCP 92-3)	*qSSIYP6.1, SSI_YP, qSSIYP3.1, and qSSI100SW3.1*	6,3	12.2-28.3, 10, 10.1	Soren et al.(2020)
	Reproductive	200 RILs (Rupali × Genesis836)	*salSYqtl.2, saltolSYqtl.1, saltolSNqtl.2*	4,5,4	22, 17.9, 28.5	Atieno et al.(2021)
Wheat (*Triticum asetivum*)	Germination and early seedling	184 RILs	*QPfw-5B2, QCl-2B1*	5,2	43.99, 20.38	Rezaei et al.(2021)
	Whole-plant growth	350 RILs (ZM175 ×XY60	*QPh-4B, QHi-4B*	4,4	32.43, 22.02	Luo et al.(2021b)
	Seedling	254 RILs (ZM175 × XY60)	*QRl-2B.1, QsK-4B, QTrad-2B, QTrsa- 2B, QMrl-2B*	2,4,2,2,2	46.43, 12.87, 23.05, 15.14, 15.2	Luo et al.(2021a)

MP, Mapping Population; DAT, Days After Treatment; PVE, Phenotypic Variance Explained (with respect to mentioned QTL). (Source: Atta et al., 2023)

VII. EASEMENT OF SALINITY STRESS

1) PHYSICAL METHODS:

a. Scrapping:

In soil improvement, the process of "scraping" involves breaking down the salt layer on top of the ground using a mechanical device and using the lower saltier layer for organic cultivation. This technique has had limited success because the ground level below water causes the water table salt to re-appear and accumulate. Thus, it again aggravates the problem. Due to high expenses, this approach is not frequently utilized.

b. Flushing:

Desalination can also be achieved by removing water from the soil.In this technique, the salt that has been built up on the surface is swept away by water due to its high salt content and low permeability.This technique has minimal practical value and is highly effective initially, but it gradually diminishes when the saline concentration drops.

c. Leaching:

In this method, excess salt can be removed by sprinkling water on the soil the soluble salt dissolves and moves through the soil and is thus removed from the root zone by drainage.The amount of liquid required for this process varies depending on the soil's properties. Effective leaching is influenced by the quality of dissolved salt per unit volume of water used, as well as collection methods, surface water distribution consistency, and drainage practices. Factors such as initial salinity, soil salinity after leaching, and root zone depth become important in estimating the quality of water needed for leaching.

Continuous ponding and intermitted ponding are two ways in which salts from the soil can be progressively leached.The conventional approach to removing irrigated salts from the soil involves continuous ponding. In this method, water flows in macropores and salts in micropores to diffuse into the moving water.The method is commonly used for faster processing even when time constraints are a concern. Intermittent ponding is the most effective flushing when water is the limiting factor.Whileintermittent ponding requires 35% less water than continuous ponding, the main drawback of this technique is that it runs much slower.

2) CHEMICAL METHOD:

a. Gypsum:

Due to its greater availability and supply capacity of Ca^{2+}, gypsum is the most suitable adjuvant for sodic soil restoration. Ca^{2+} replaces Na^+ from soil colloids and leaches $NaSO_4$ deeper into the soil profile (Singh et al., 2018).The use of gypsum and langbeinite, which has high levels of Mg^{2+} and K^+, led to a decrease in theNa^+/SAR (sodium adsorption ratio)and an improvement in its soil saturated water conductivity.

Phosphogypsum can contain hazardous elements like Cd and may result in lower solubility compared to gypsum.During the Flue gas desulphurization (FGD) process, sulfur gases are removed from coal-fired power plants and excreted as FGD gypsum, which is also a valuable source of Ca^{2+} that can replace Na^+ with Ca^{2+} of soil exchange sites.

b. Organic Amendments:

Various organic additives have been utilized for sodic soil recovery, including biochar, municipal solid waste compost, and inorganic additive with high calcium content (such as fly ash, gypsum, phosphogypsum, etc.) and zeolites (Mishra et al., 2019). The utilization of the forementioned remedial agents enhances soil bulk density, aggregate stability, water conductivity and lowers pH, EC, ESP in salt-emitting environments(Sundha et al., 2020).Moreover, soil biological properties, such as enzyme activity, microbial population and N and P concentrations of biomass microbes were improved by beneficial amendments. Amount of some common amendments for sodic soil reclamation are given in Table 5.

Table 5: Equivalent quantities of some common amendments for sodic soil reclamation

Amendment	**Relative quantity**
Gypsum ($CaSO_4$ $2H_2O$)	1.00
Calcium chloride ($CaCl_2.2H_2O$)	0.85
Sulphuric acid (H_2SO_4)	0.57
Iron sulfate ($FeSO_4.7H_2O$)	1.62
Aluminumsulfate [$Al_2(SO_4)_3.18H_2O$]	1.29
Sulfur (S*)	0.19
Pyrite (FeS_2*) (30% S)	0.63
Pressmud (Lime sulfur, 9% Ca, 24% S)	0.77

*Based on assumption of 100% oxidation of materials like sulfur or pyrite in order to be as effective as soluble calcium compounds. Since in practice this assumption is not fulfilled, their effectiveness is much lower than gypsum. (Source: Choudhary and Kharche, 2015).

c. Zeolites:

Zeolites, which are hydrated crystalline alkali and alkaline earth metals can be used to clean up contaminated soils.The use of zeolites, including clinoptilolite, erionite, and heulandites, enhances soil quality and increases the availability of nutrients (Manjaiah et al., 2019).The use of clinoptilolite, which is rich in Ca, has been shown to significantly increase the yield and improve the quality of saline soil by adsorbing Na into mineral cavitie. In the same way, adding 5% zeolite to saline soil resulted in an increase of 19 and 10% in the concentrations of Ca^{2+}, Fe^{2+} and Mn^{2+} trace elements respectively.Ion exchange, adsorption, and salt storage are the primary methods used by zeolites to carry out desalination(Wen et al., 2018).

d. Compost:

Soil salinity can be boosted initially by green waste compost, green manure compost and municipal solid waste compost, but it is reduced significantly at a later stage.The restoration of saline soil by Halima et al.,(2019) involved the use of green waste compost(mixture of melon rind and olive pomace), sugar cane compost and gypsum. They stated that the application of an organic additive (green waste compost) and gypsum. A rise in soil EC, which was initially 3.8 mg/g, over 100 days during this period, was caused by dissolved salts in compost and limited flushing. However, EC decreased from 2.80to 16.65 dS/m after 120 days due to exchange of Na^+ by Ca^{2+}soil exchanges and solute leaching.

Byutilizing 100% of the recommended nitrogen dose (RDN) and composting, vermicompost has been effective in decreasing soil density, pH, EC, ESP, as well as Na^+ concentration and solubilityof soil in degraded marsh sol by 2.0, 4.2, 26.5, 42.8 and 56.6% respectively and increased soil organic carbon (SOC) concentrationby 34.6% compared to the control (Singh et al., 2019).

e. Biochar:

Soil carbon layers are often treated with biochar, while also being used to improve soil health and as a salt remediation agent in challenging environments.Biochar may contain significant amounts of N, P, K and trace elements, which vary depending on the raw material and production conditions (Purakayastha et al., 2019). High biochar application rates can increase N volatile losses due to the high pH of biochar applied to the soil (Sun et al., 2017).

P availability in saline soils can be improved by lowering the pH by 0.3 units, blocking clay adsorption sites with dissolved organic carbon, and releasing organic acids to mobilize P into the soil. Wood-based biochar, which was pyrolyzed at 450ºC and made from hardwood raw materials, had an acidic pH level 5.6 that can be used for saline soil remediation (Shaheen et al., 2018). Acid wood biochar of pH = 3.25 can be used to decrease pH of saline soil by using pyrolysis at a temperature of 650ºC (Qi et al., 2018).

Depending on the type of soil and biochar used, biochar increased K availability by 44% in saline soil, according to report by (Lin et al., 2015). Therefore, biochar feedstock selection and pyrolysis temperature are important factors to consider before applying this amendment to salt-stressed soils.

In (2016) by Amini et al., it was observed that biochar (acidic versus basic) has significant impacts on soil physical traits, including saturated hydraulic conductivity and aggregate stability in a saline-clay soil.The incorporation of polyvalent cations and clay particles in biochar improved particle aggregation in dissolved salts by the presence of organic molecules. Soil structure and SOC content were found to be improved in saline soil with biochar application while reducing ESP (Amini et al., 2016). Consequently, the combined application of poultry manure and biochar resulted in a 42% reduction in soil EC_e.

3) BIOLOGICAL METHOD:

a. Phytoremediation:

By growing trees, shrubs, and grasses that are resistant to salt, the soil can be restored to its original state at a low cost with minimal harmful chemicals. Plants remove excess salts from the soil by root absorptionand store them in their biomass. This process is called phyto-accumulation or phyto-extraction. This reduces the concentration of exchangeable sodium and soluble salt in the soil.Approximately 4 Pg of carbon in aboveground and belowground C biomass can be retained by replacing 75 million hectares of degraded land with suitable trees and plants through reforestation. Afforestation and agroforestry have been extensively documented for their use in recovering sodic and saline soils(Dagar and Minhas, 2016). Some promising species for improving sodic soils are *Prosopis juliflora*, *Acacia nilotica*, *Casuarina equisetifolia*, *Tamarixarticulata*,*Eucalyptustereticornis*and *Leptochloafusca*(Dagar et al., 2016),and for saline waterlogged soils are*Prosopisjuliflora, Tamarix articulata, Casuarina glauca, Acacia farnesiana, Acacia nilotica, Acacia tortilis*, and *Parkinsonia aculeate*. *Eucalyptus tereticornis*, *Populus deltoises*, and *Tectona grandis* are all capable of rejuvenating saline soils. The use of a raised-sunken bed technology allowed for the successful planting of trees such as pomegranate (Fruit tree) and *Salvadora persica* (Non-edible oil tree) in rejuvenating sodic soils.

Several species of grasses that are suitable for saline soil have been discovered, but not all the varieties found in fields are effective because they absorb and store sodium and other poisonous substances in their leaves, so they are not used as fodder. Paragrass (*Brachiariamutica*), rose grass (*Chloris gayana*), matricaria (*Matricariarecutila*), carnal (*Leptochloafusca*) were found to be the most promising herb suitable for alkaline soil. *Aeluropuslagopoides, Chloris barbata, Echinocloacolonum, Dicanthiumannulatum, Sporobolus helvolus*, *Phragmites* spp. and *Sida* spp. are other herbs that have the potential to heal saline soil. Medicinal and aromatic plants such as isabgol (*Plantago ovata*), aloe (*Aloe barbadensis*), kalmeg(*Andrographis paniculata*), *Matricaria chamomilla*, *Vetiveriazizanioides*, *Cymbopogon martini* and *Cymbopogon flexuosus*have been observed to produce high biomass under saline irrigated conditions.

Compared to the alluvial clay soils of the Indo-Gangetic plains, salt affected vertisol (such as black cotton soil) are difficult and laborious in restoring. The high clay contentofthese soils make them vulnerable to even low salt and exchangeable sodiumconcentrations. A large patch (about 1.21 million hectares) of saltaffecting black cotton soil (Vertisol) in Gujarat.These lands are also present in significant quantities in Karnataka, Maharashtra, and Rajasthan as well.Plants that are tolerant to salt, such as *Salvadora persica*, dill(*Anethum graveolens*), *Euphorbia*, Mulethi(*Glycyrrhiza glabra*), castor, and sunflower can be grown for commercial purposes and are proven useful in rehabilitating these soils and are mostly used by farmers.

In biodrainage, wood species that reduce water content by means of evaporation are utilized for treatment, with a focus on areas with waterlogged structures.To date *Eucalyptus* has been effective in lowering groundwater levels within canal control areas(Dagar et al., 2016). It has been suggested thattrees that require a lot of water such as eucalyptus (*E. tereticornis*), populous (*Populusdeltoides*) and panicum (*Panicum maximi*) and leptochloa (*Leptochloafusca*) can mitigate waterlogged saline soil.

b. Bioremediation:

The use of various microorganisms or a consortium of microbes is involved in bioremediation, which involves cleaning soil with salt.Soil microbes, such as rhizobacteria (PGPR), bacteria, mycorrhiza organisms and cyanobacteria, can heal salt-contaminated soil by producing hormones or other beneficial substances that enhance plant growth and improve soil quality.

I. Plant growth promoting rhizobacteria (PGPR):

It has been shown through multiple PGPR studies that the saline soil healing by improving plant growth.ACC (1-aminocyclopropane-1-carboxylate) deaminase, IAA (indole acetic acid), and exopolysaccharides are the primary mechanisms that promote crop growth (Singh, 2015). Plant growth promoting rhizobacteria and their mechanisms on agricultural crops in salt-affected soils are summerizrd in Table 6.

Table 6: Working mechanism of PGPR in different plants under salinity stress.

TYPES OF PLANTS	PLANT GROWTH PROMOTING RHIZOBACTERIA (PGPR)	WORK MECHANISM OF PGPR	REFERENCES
Wheat (*Triticum asetivum*L.)	*Pseudomonas* sp.	ACC deaminase	Nadeem et al., 2013
	Enterobacter sp.	ACC deaminase	Sarkar et al., 2018
	Pseudomonas fluorescens and *Azospirillumbrasilense*	Phopshate solubilisation, auxin production	Kadmiri et al., 2018
Maize (*Zea mays* L.)	*Azotobacter* sp.	IAA, N-fixation	Rojas-Tapias st al., 2012
	Pseudomonas fluorescens	IAA	Zerroul et al., 2016
Oats (*Avena sativa* L.)	*Klebsiella* sp.	IAA, organic acids	Sapre et al., 2018
Rice (*Orzya sativa* L.)	*Alcaligenes* sp. and *Bacillus* sp.	ACC deaminase	Bal et al., 2013
	Bacillales	ACC deaminase, siderophore production	Zhang et al., 2018
Black gram (*Vigna mugo*L.)	*Pseudomonas fluorescens*	IAA, siderophore	Yasin et al., 2018
Canola (*Brassica napus* L.)	*Pseudomonas fluorescens* and *pseudomonas putida*	ACC deaminase	Jalili et al., 2009
	Enterobacter cloacae	IAA, ACC deaminase	Li et al., 2017
Soybean (*Glycine max* L.)	*Bacillus amyloliquefaciens*	Gibberalic acid, abcisic acid	Kim et al., 2017
Tomato (*Solanum lycopersicum* L.)	*Pseudomonas* sp.	ACC deaminase	Win et al., 2018
Ladyfinger (*Abelmoschus esculentus* L.)	*Enterobacter* sp.	ACC deaminase	Habib et al., 2016
Alfalfa (*Medicago sativa* L.)	*Enterobacter aerogenes* and*Pseudomonas aeruginosa*	ACC deaminase	Liu et al., 2018

(Source: Mukhopadhyay et al., 2020)

II. Salt-tolerant bacteria:

Salt-tolerant bacteria typically need a significant amount of salt and thrive in extremely high saline environment to manage the high osmotic pressure.*Ammoniphilus, Arthrobacter, Azospirillum, Bacillus*, *Brevibacillus,* and *Brevibacterium* are genera that produce IAA, gibberellic acid, and other organic acids that can transform nutrients into nutrient-soluble compounds in the soil. Some salt-tolerant endophytes have been reported to have mechanisms similar to PGPR in salt tolerance.It was discovered that both *Bacillus foraminis* and *Bacillus gibsonii* have the capacity to withstand up to 7.5% doses of NaCl.

III. Mycorrhiza:

Mycorrhiza is a symbiotic relationship between the roots of higherplants and fungi.The solubility of nutrients in saline environments can be maintained by mycorrhizae. There are reports by Chang et al., (2018) about beneficialeffects of mycorrhiza, such as improved mobility andavailability of nutrients (Zn^{2+},

Cu^{2+}, P) in the soil.Vesicular arbuscular mycorrhizae (VAM) normally help solubilize the supply of phosphate and P to plant roots in saline soils,because phosphate remains in precipitated formdue to Ca^{2+} and Mg^{2+}-based carbonate salts (Zhu et al., 2016).Moreover, the retention of a high K^+/Na^+ ratio by VAM fungi demonstrated the mechanism behind their ability to tolerate salt in saline soil. Another mechanism involved in mycorrhizal effects on salt tolerance is the control of abscisic acid (ABA) accumulation under osmotic stress (Auge et al., 2015).

IV. Cynobacteria:

Gram-negative, prokaryotic, autotrophic, and blue-green bacteria are known as cyanobacteria.In extreme salt environment; they can thrive and improve the soil's nutrient content (Rossi et al., 2017). Blue-green algae have been mainly used as biofertilizer.Although it is challenging to remove salts from soil with blue-green algae quantitatively, incorporating them into tolerant plants of salt helps to increase the amount of salinity (Jesus et al., 2015). The main mechanisms used by cyanobacteria are N-fixation, production of high biomassand production of extracellular polymeric substances (EPS)which help microorganisms to survive under salt stress conditions.

Cyanobacterial genera used in various pot and field studiesincluding Nostoc *Anabaena, Calothrix* and *Spirulina* (Li et al., 2019). In the context of Indian saline soil, *Nostoc ellipsosporum* and *Nostoriumpunctiforme* HH-206 were used to increase both soil fertility and enzyme activities (Nisha et al., 2018) while decreasing soil pH and EC (Singh and Singh, 2015) *Anabaena laxa* RPAN8, showed 21-fold higher acetylene-reducing activity under salt stress, suggesting N fixation (Babu et al., 2015). The intracellular concentration of trehalose in *Anabaena fertilissima* increased significantly under 250 mmol NaCl concentrations (Swapnil and Rai, 2018). The *Nostoc carneum* TUBT04 and *Nostoc commune* TUBT05 were discovered to have IAA concentrations of 20 and 27 g/ml, respectively under 250 mmol NaCl (Chittapun et al., 2018).

c. Nanoparticals mediated mitigation of saline soil:

The utilization of nanotechnology-based solutions is on the rise in various fields of human activity, including agroecosystems. For example, applications of certain nanomaterials (e.g. single/multi-wall C-based nanotubes, poly-chitosan, graphene, fullerol, fullerene), nanoparticles (nano-fertilizers, nano-pesticides) and nano-based technologies and approaches (nanofiltration) in brackish water reservoirs for irrigation, transport and accumulation of trace elements into crop tissues have been shown to be usefuland secondary strategies for mitigating nutrient deficiencies and increasing crop food production under various abiotic conditions, including excess salinity and induced salinity deficiency (Ditta et al., 2016). Furthermore, the presence of TiO_2 NPs can promote the growth promotion through photosterilization and photogeneration of reactive oxygen radicals, which enhances stress resistance and facilitates the absorption of H_2O and O_2 necessary for rapid germination. (Figure: 4).

Inrecent work by Pandey et al., (2018) demonstrated that adding two C-based nanomaterials - multi-walled C–nanotubes and graphene NPs to an added growth medium significantly increased seed germination and total biomass in grass and sorghum plants.Graphene- or C-based nanotubes were added to a NaCl–exposed (100 mM) growth medium, which confirmed the reduction of salt stress symptoms in test plants during the same study. This result is explained by - (i) the effect of C-based NPs on plant transcriptional capacity (e.g., increased expression of aquaporins) and (ii) the physical interaction of C-based NPs with toxic ions (i.e., removal of toxic Na^+ ions from the salt solution).

Aquaporins, which are water channels, are essential for water absorption/transport in stress conditions. The wheat TaNIP aquaporin gene was overexpressed in transgenic *Arabidopsis* and showed increased salt tolerance than wild-type, while the wheat TaAQP8 aquaporin genes were found to improved salt tolerance in transgenic tobacco.Utilizing both an inhibitor-test and a genetic approach, Zhao et al., (2019), demonstrated that multi-walled C-nanotubes improved salt tolerance in canola seedlings exposed to NaCl stress.Despite the need for restoration of redox and other-ion homeostasis, they demonstrated how endogenous NO, which is an essential signaling molecule that may improve salt tolerance in some plants, can still act downstream of multi-walled C-nanotubes to signal salt exposure to NaCl stress.

Nano-based phytonutrients have been shown to be more effective than conventional fertilizer salts due to their unique mechanisms of action, such as increased active surface area, improved application efficiency, slow release, reduced nutritional losses, and reduced deterioration of the environment, considering their lower application doses (Rossi et al., 2019). Furthermore, most plant nutrients can be incorporated into the nanostructures of naturally occurring zeolites, i.e., Si-Al minerals, which have a huge active surface area and 10x higher cation exchange capacity than soil (Ditta et al., 2016). The effects of metal NPs (such as Al, Alumina, multi-walled C-nanotubes, Zn, and ZnO) on six test plants and discovered that only Zn-NPs and ZnO-NPs were clearly effective in suppressing seed germination and root growth this showed that the suppressed effect also varied significantly depending on the concentration, plant, or metal NPs used. Also, more recent studies have found that ZnO NPs were more beneficial for coffee plant growth and physiological activity than zinc sulfate (Rossi et al., 2019), and Fe_2O_3 nanoparticles could replace traditional Fe fertilizers in cultivation of groundnut plants in sandy pedosphere (Rui et al., 2016).

Evidence suggests that the inclusion of Si-NPs (1 mM SiO2) improved early seedling growth and germination of lentil genotypes after exposure to 100 mmM NaCl, as well as stimulated immune mechanisms against salt toxicity (Sabaghnia et al., 2015).Moreover, the application of ZnO-NPs rather than use of the traditional ZnO form resulted in an increase in chlorophyll content and quantum yield as well as biomass production in NaCl-stress sunflowers (Torabian et al., 2016); further research by Alharby et al., (2016) revealed that this approach could partially alleviate salt stress effects on different tomato species, mainly, by increasing the activity of superoxide dismutase and glutathione peroxidases. In a study by Morales et al., (2019), noted that Se-NPs could improve some beneficial biocompounds like lycopene, carotenoids, flavonoids, phenols in tomato fruits and have a positive impact on salt-stressed tomato plants, particularly in terms of excessively high photosynthetic pigments and improved photosynthesis. By adding N:P:K to chitosan nanoparticle (NP) fertilizers which is cationic, biodegradable, and bacterial polymers may be obtained with different compositional characteristics and greater colloidal suspension stability. In Table 7 has shown some recent work showing the effect of various NPs in different plant.

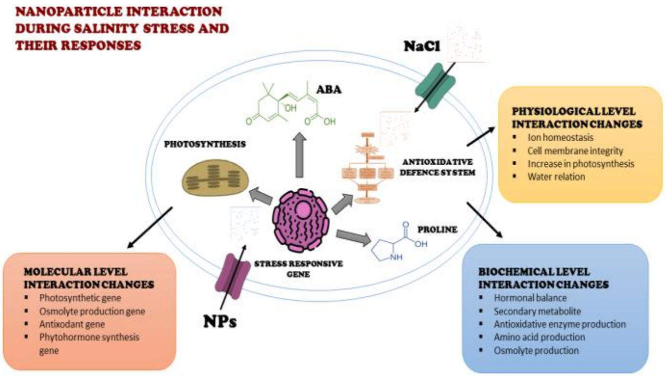

Figure 4: Nanoparticle interaction during salinity stress and their responses.

Table 7: Effect of nanoparticles (NPs) in mitigation of salinity stress

NANOPA-RTICLES (NPs)	PLANTS USED	SALT DOSE	NPs DOSEAND APPLICATION	MAJOR EFFECTS	REFER-ENCES
Au NPs (Phytofabri-cated)	*Spinacia oleracea* L.	50mM	150µM	Enhanced chlorophyll, sugar content, improved relative water content and stomatal conductance, increased in proline and flavonoid content, reduction in ABAcontent, ROS production and LPO.	Ansari et al., 2024
Ag NPs	*Eustoma grandiflorum*L.	2, 4, and 6 gL^{-1}	5, 10, and 20 mg L^{-1}; Priming	Boost in SOD and CAT activity and lowering of POD activity.	Youssef et al. (2020)
	Satureja hortensis L.	0, 40, 60, and 80 mg L^{-1}	0, 30, 60, 90, and 120 mM ; Priming	Enhanced germination average; plants shoot length and plants resistance to salinity.	Nejatzadeh(2021)
Carbon NPs	*Ocimum basilicum*L.	50 and 100 mM	25, 50 and 100 mg L^{-1}; Nutrient solution	Rise in chlorophyll and enzymatic and non-enzymatic antioxidant such as CAT, APX, GP and phenolic content.	Gohari et al. (2020b)
	*Sophora alopecuroides*L.	100mM	50 mg L^{-1}; Foliar spraying	Enhanced PSII activity, total protein contents of leaves and roots, leaf soluble sugar content and Cu content in the	Wan et al. (2020)

NANOPA-RTICLES (NPs)	PLANTS USED	SALT DOSE	NPs DOSEAND APPLICATION	MAJOR EFFECTS	REFER-ENCES
				leaves, reprogrammed carbon/nitrogen metabolism and aid glycolysis and TCA cycle to generate energy and boosts up the levels of unsaturated fatty acids to maintain membrane integrity under salt stress.	
	*Lactuca sativa*L.	0.3%;	Priming	Aids lateral root growth and accumulation of chlorophyll content of seedlings and obstructs the elongation of primary roots.	Baz et al. (2020)
Chitosan NPs	*Vigna radiata* L.		0,4 and 8 dS m^{-1}; Priming	Enhanced chlorophyll content and metabolism by lowering in H_2O_2 and MDA contents leads to better growth.	Sen et al. (2020)
Fe NPs	*Lycopersicon esculentum*L.	150mM	10, 50 and 100 mg L^{-1}; Foliar spraying	Better morphological traits, photosynthesis and increased in activity of some enzymes like CAT	Faizan et al. (2021)

NANOPA-RTICLES (NPs)	PLANTS USED	SALT DOSE	NPs DOSEAND APPLICATION	MAJOR EFFECTS	REFER-ENCES
				and SOD.	
	*Trachyspermumammi*L.	4, 8, and 12 dS m^{-1}	3 mM; Foliar spraying	ImpeovedK$^+$uptake, K^+/Na^+ ratio, Fe content, endogenous levels of SA, and activities of antioxidant enzymes.	Abdoli et al. (2020)
	*Pistacia vera*L.	0, 100, and 200 mM solution	2.9 mg L^{-1}; Nutrient	Reduction in plasma membrane damage and chlorophyll degradation.	Karimi et al. (2020)
Mn NPs	*Capsicum annuum*L.	100mM	0.1, 0.5, and 1 mg L^{-1}; Priming	Better morphological traits such as root development.	Ye et al. (2020b)
Si NPs	*Lycopersicon esculentum*L.	50mM	250 and 500 mgL^{-1}; Growing medium	Preserved concentration of chlorophylls, GSH, vitamin C, and PAL activity.	Pinedo-Guerrero et al. (2020)
	*Musa acuminate*L.	-	0, 200, 400 and 600 mgL^{-1}; Foliar spraying	Enhanced photosynthesis, and increased K^+ and K^+/Na^+ percent. Shoot growth, and chlorophyll content.	Mahmoud et al. (2020a)
Si, Se and Cu NPs	*Capsicum annuum*L.	25 and 50 mM	10 and 50 mgL^{-1} Se-NPs, 200 and 1000 mgL^{-1} Si- NPs, and 100 and 500 mgL^{-1} Cu NPs;	Enhanced chlorophylls, lycopene and glutathione peroxidase activity in the leaves and	Gonz´alez-García et al. (2021)

NANOPARTICLES (NPs)	PLANTS USED	SALT DOSE	NPs DOSEAND APPLICATION	MAJOR EFFECTS	REFER-ENCES
			Nutrient solution	riseAXO, POD, CAT and phenylalanine ammonia lyase activity, and also phenols, flavonoids, glutathione, β-carotene, and yellow carotenoids in fruits.	
TiO_2 NPs	*Zea mays* L.	200mM	40, 60 and 80 mg L^{-1}; Priming	Ameliorate morphological traits, K concentration, activity of enzymatic antioxidant, proline, and phenolic content.	Shah et al. (2021)
	*Dracocephalummoldavica*L.	0, 50 and 100 mM	0, 50, 100, and 200 mg L^{-1}; Nutrient solution	Rise in antioxidant enzyme activity and essential oil.	Gohari et al. (2020a)
ZnO NPs	*Trigonella foenumgraecum*L.	0, 75, 150, and 225 mM	1000 and 3000 mg L^{-1}; Foliar spraying	Rise in trigonelline content.	Noohpisheh et al. (2021)
	*Abelmoschus esculentus*L.	0%, 10%, 25%, 50%, 75% and 100% sea water	10 mg L^{-1}; Foliar spraying	Enhanced chlorophyll and antioxidant enzyme activity such as SOD and CAT and reduced proline and sugars content.	Alabdallah and Alzahrani (2020)

NANOPA-RTICLES (NPs)	PLANTS USED	SALT DOSE	NPs DOSEAND APPLICATIO N	MAJOR EFFECTS	REFER-ENCES
	*Teriticumaestivum*L.	200mM	50 mg L^{-1}; Priming	Escalate trapped energy flux and electron transport flux, sucrose biosynthesis AND activated the antioxidant system.	Wan et al. (2020)
Zn, B, Si and Zeolite NPs	*Solanum tuberosum* L.	4.2 dS m^{-1}	20 mg L^{-1} Zn NPs, 1 mg L^{-1} B NPs, 15 mg L^{-1} Si, and 1.3 L ha^{-1} zeolite; soil	Ameliorate morphological traits, enhanced concentration of nutrients (N, P, K, Ca, Zn, and B), GA3, carbohydrates, and antioxidant enzymes (e.g., PPO and POD).	Mahmoud et al. (2020c)

(Source: Etesami et al., 2021)

d. Omics approach in salinity mitigation:

Omics is a biological domain that encompasses data on the variations in cellular, DNA, protein, and metabolite levels.The objective of genomics, transcriptomics, proteomics and metabolomics is to map genomes and identify the biological processes, variation, and functional roles in plants through descriptive genomic studies.Multi-omics offers the molecular knowledge needed for stress tolerance in plant breeding.

I. Genome-wide association studies (GWAS):

The use of genome-wide association studies (GWAS) is a powerful tool for uncovering genomic regions that exhibit natural variation, particularly due to genetic markers and biotic or abiotic stress. Exact mapping of QTLs involved in the plant's response to abiotic stress, including salinity stress at different stages is essential.The GWAS method was employed to identify crucial QTLs and salinity stress resistance genes in cotton from a significant multi-parental Advanced Generation Inter-cross (MAGIC) population. The results described 23 QTLs for salt tolerance, pH and SDW, of which 9 QTLs were common under drought stress. In cotton, (NHX2, NHX4, NHX6, and NHX7) were identified as sodium transporters in a salt stress-based GWAS study (Akram et al., 2020).

Almost 25 NHX genes have been identified with GbNHX7 interacting with the CBL-CIPK protein involved in the salt-responsive pathway.GWAS analysis of HKT15 genes against salt stress in barley was conducted to identify molecular mechanisms of salt tolerance using 2671 barely lines.Through GWAS, the mapping results revealed that HKT1 gene that facilitates Na^+ evacuation from the xylem and its distribution and transport to other parts of the body is responsible for this process.

11 QTL for various wheat traits in a large population under two different salt treatments were estimated by using GWAS study. The biparental population was responsible for the increase in salt tolerance in wheat, with three major salt exposure loci being identified. The alfalfa was found to have 27 SNP markers that were associated with salt tolerance and potentially candidate genes in GWAS research (Medina et al., 2020).Additionally, the GS models were optimized for improved alfalfa reproduction and salt tolerance.The identification of 19 novel marker-trait associations (MTAs) near candidate genes linked to transcription factors, membrane transporters, and signal transducers that affect salt tolerance was discovered in rice by GWAS study.During the reproductive phase, the genomic regions and functions of candidate genes were identified through measurements of fruit production, salt damage, and physiological parameters under salt stress (Warraich et al., 2020).

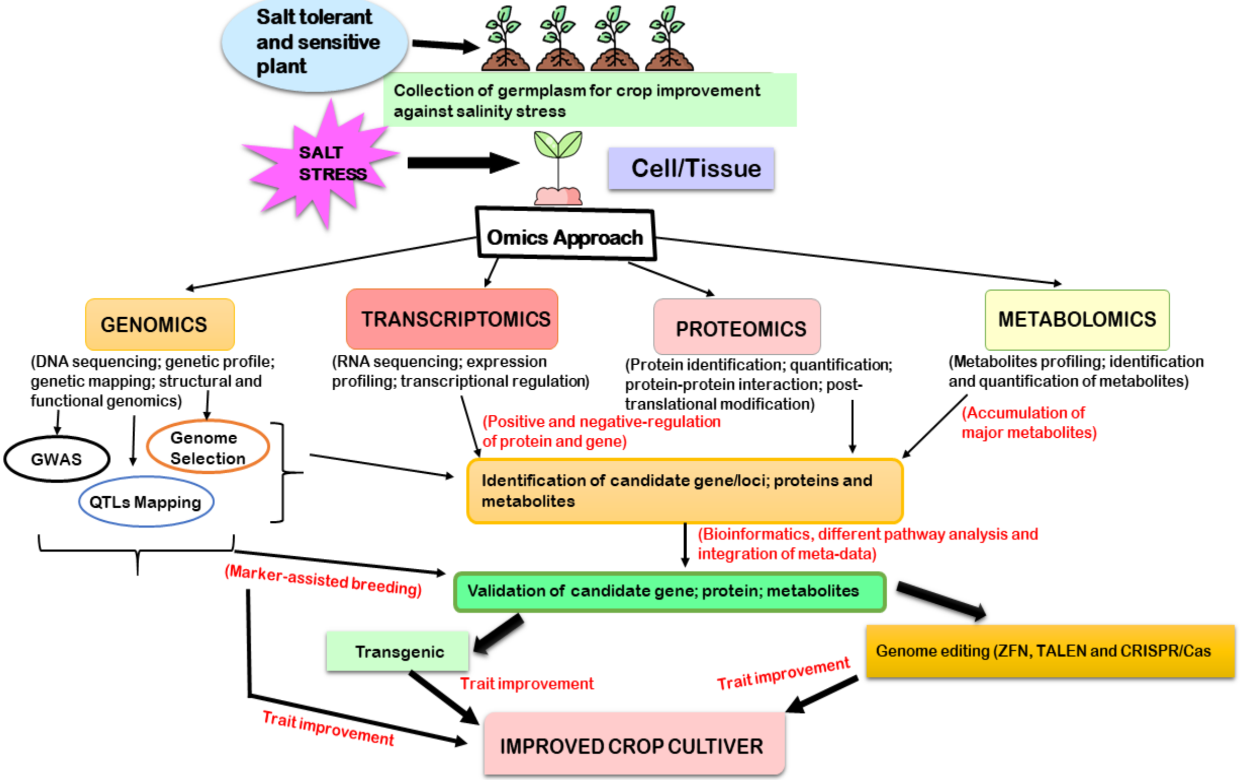

Figure 5: An overview of omics approaches for crop improvement under salinity stress.

II. Transcriptomics:

The field of transcriptomics deals with the working sequence and abundance of transcriptional units in a living organism, as well as their post-translational modifications (Rich-Griffin et al., 2020). Plant transcriptome studies can be performed using a variety of techniques, such as RNA sequencing (RNA-seq), microarray, and other sequencing methods.A mutant line (M4-7330) and a wild-type cultivar (WT-Zarjou) were studied using RNA sequencing to identify genes that regulate salinity by modulating ion transporters. These genes are known as SOS1/SUS3/SO2 and TPK1,/KCO1, HAK and HKT Ca^{2+} -, Na^+ and K^+transportwhich helps to increase the salinability of barley salts (Yousefirad et al., 2020).Salinity-responsive transcription factors (TFs) such as WRKY, AP2/ERF, NAC, CTR/DRE, MAD, HSF, and bZIP were identified using RNA-seqdata.In mutant lines, photosynthesis and respiration rates were significantly reduced while protecting tissues from the damaging effects of salinity which also consumed energy and carbon.

In response to salinity stress, RNA-seq analysis revealed the presence of approximately 70,401 genes in bread wheat (Ma Q et al., 2020). The identified genes were engaged in ROS scavenging, chaperone and carbohydrate metabolism, and several early and late stress response genes were also identified. Enrichment analysis showed that carbohydrate metabolism, secondary metabolites and pentose phosphate pathways were highly enriched in salinity (Ma Q et al., 2020). Additionally, another recent report investigating mechanisms of adaptation to salt tolerance in the legume *Medicago truncatula* model through global transcriptomic profiling using microarray analysis of the salt-sensitive cultivar TN6-18 found decreased expression of several stress signaling genes not previously associated with salinity and corresponds to the TIR-NBS-LRR gene class (Filippou et al., 2021).

Another study used RNA-seq analysis of wheat genotypes to identify those that are tolerant and susceptible in the osmotic (Zentos-tolerant, Syn86-sensitive) and ionic (Altay2000-resistant and Bobur-responsive) phases. In response to salt-related osmotic stress, upregulation of Ca^{2+} binding and cell wall synthesis genes was observed in the tolerant genotype and was considered to be a key player in improving salt tolerance.An improved photosynthetic reserve during the osmotic phase is linked to higher expression of photosynthesis-related and Ca^{2+}-binding genes and increased levels of oxidative stress in the sensitive genotype. The precise upregulation of some ABC transporters and Na^{+}/Ca^{2+} transporters in the tolerant genotype during the ion phase determines their contribution to Na elimination and ion homeostasis (Duarte-Delgado et al., 2020).

III. Proteomics:

Proteomics encompasses the examination of functional proteins, encompassing their function and organization in stress-related scenarios or their interdependence with other proteins.Proteomics enables us to examine post-transcriptional changes and protein levels in greater depth. A recent study described the proteome of rice plants exposed to salinity. Two rice varieties namely Vytilla-4 (high salt tolerance) and Jhelum (salt sensitive) were used.Various protein expressions and responses to salt stress were detected in rice plants during the study. In particular, proteins involved in photosynthesis, such as Chl a-b binding protein, carboxylase small chain and ferredoxin, are triggered by salinity stress in Vytilla. Conversely, PS-II CP47 was suppressed in Jhelum.Vytilla showed significant increase in activity of other carbon-fixing proteins, including cytochrome c oxidase subunit 5C, peroxisomal (S)-2-hydroxyacid oxidase GLO1, and peroxysomal (S)-2-hydroxy-acid oxidase GLO5. This clearly indicates that these proteins can be potential biomarkers that regulate plant responses to salinity without harming growth (Frukh et al., 2020).

Hormone-related proteins in hulled barley were measured while under salinity stress.The salinity stress test was conducted on two cultivars, namely salt-sensitive landrace lk621 and salt tolerance lk573 cultivar germinated well under saline conditions compared to the slow sporulation rate of lk621.The salt-tolerant cultivar exhibited 171 differentially expressed proteins (DEPs) after 4 h of salt stress, proteins involved in nitrogen metabolism, ascorbate and aldarate metabolisms, ABC transporters, and other terpenoid quinone biosynthesis were observed to express.As previously noted, the ABC transporter and terpenoid quinone hormones are closely monitored. On the other hand, in lk621, most of the expressed proteins were related to terpenoid backbone biosynthesis and fatty acid biosynthesis.This implies that barley seed germination is controlled by DEPs and plant hormones when exposed to salinity stress (Lai et al., 2020).

Sorghum (*Sorghum bicolor* L.) is a naturally stress-resistant and highly adaptable crop that thrives in harsh environments (Chakrabarti et al., 2020).Two sorghum genotypes (G-46 and CSV 44F) underwent proteomic analysis to examine the potential stress-responsive proteins.G-46 and CSV 44F are two genotypes that can tolerate salt and produce significant proteins associated with salt stress (Punia et al., 2020).As anticipated, the majority of α, β, γ-kafirin were found and expressed in both genotypes.By examining these proteins in detail, it is possible to identify regulatory networks in stressed sorghum and use them in breeding programs to create stress-tolerant and high-yielding sorghum genotypes.

In soil enriched with 300 mM of NaCl, two nearly isogenic lines were grown for barley: salt-tolerant (T46 and T66) and salt sensitive (N33 and N5Through proteomic analysis, a group of proteins was identified that both tolerant and susceptible lines could be mapped to activities related to photosynthesis, ROS scavenging, and ATP biosynthesis were predominantly carried out by proteins that are primarily expressed in tolerant lines (Zhu et al., 2020).

IV. Metabolomics:

Stress can lead to modifications in plants' transcripts, proteins, and biochemical levels. Often, the plant responds to stress only at the biochemical level, without changing its transcription and protein expression.Molecular biology involves the study of metabolites, which are also known as'metabolomics' (Raza et al., 2022).

In harsh environmental conditions, foxtail millet is the preferred crop for its ability to thrive.Young seedlings of foxtail millet was subjected to salinity to investigate the impact of salt stress on their metabolism. Two cultivars, Yugu2 and An04, were used in this study and both have different levels of tolerance. Using a metabolomics approach, different metabolites were identified in cultivar Yugu2. Prominent metabolites associated with stress resistance, i.e., MDA, glutathione, and ascorbate, were increased under salt stress during initial growth phase. Other stress-responsive metabolites such as cinnamoyl-CoA reductase (CCR), cinnamyl-alcohol dehydrogenase (CAD) and 3-ketoacyl-CoA synthase (KCS) are essential lignin biosynthesis metabolites that showed induced accumulation after salinity stress (Pan et al., 2020).

Maize is prone to salt stress and has a relatively high salt sensitivity during this stage of reproduction. The metabolomics technique was used to detect the response of corn plants to salt stress.Two salt tolerant genotypes, PH6WC and the other salt sensitive genotyping, were subjected to 100 mM NaCl.A set of metabolites, including sugars, amino acids, spray and organic acids (as well as alkaloids), were found to induce more than twice the PH6WC genotype in comparison to the control treatment (Yue et al., 2020).

In a study by Abdel-Farid et al., (2020) tomato (*Solanum lycopersicum* L.) and cucumber (*Cucumis sativus* L.) were exposed to different degrees of salt stress (25, 50, 100 and 200 mM NaCl). Cucumber and tomato are highly susceptible to salinity stress and can produce essential metabolites that aid in breeding programs. A study was conducted to investigate the metabolic response of cucumber and tomato to salt stress. When exposed to 200 mM NaCl salt stress, cucumber and tomato plants showed a significant increase in flavonoid concentrations. Compared to their control treatments, cucumber and tomato showed an increase of 2 and 30%, respectively. Phenolic compounds were strongly accumulated only in tomatoes, no changes were observed in cucumber. Similarly, saponin content was downregulated in cucumber under salt stress (200 mM), which conversely increased significantly in tomato. It can be assumed that cucumber and tomato plants react differently to salinity at the metabolic level.

Table- 8: Some recently conducted transcriptomics, proteomics, and metabolomics studies under salinity stress in different crop plants.

Plant species	**Stress condition**	**tissue**	**Approch**	**Key finding**	**References**
Transriptomics					
Barley (*Hordeum vulgare*)	300mM NaCl; 6hrs.	Roots and shoots	RNA-seq	7116DEGs Salinity stress-responsive different TFs were identified from WRKY, ERF, AP2/EREBP, NAC, CTR/DRE, AP2/ERF, MAD, MIKC, HSF, and bZIP. As a key mechanism, photosynthesis and respiration were reduced in the mutant and maintained the plants' tissues under salinity by consuming stored energy and carbon. The expression of ion transporters and channels-related genes were up-regulated to maintain the ion homeostasis	(Yousefirad et al., 2020)
Tomato (*Solanum chilense*)	500mM NaCl; 21dys	Leaf	RNA-seq	265 158DEGs 134 566 DEGs up-regulated and 130592 DEGs down-regulated. Several DEGs	(Kashyap et al., 2020)

Plant species	Stress condition	tissue	Approch	Key finding	References
				were involved in Ca^{2+}, auxin, and ethylene-mediated signalling networks and were identified as key genes against salinity. Genes encoding proline and arginine metabolism, ROS scavenging systems, transporters, osmotic regulation, defense, and stress response, and homeostasis were significantly induced and up-regulated under salinity.	
Wheat (*Triticum aestivum)*	150mM NaCl; 24hrs	Root and shoot	RNA-seq	8DEGs Most of the identified genes were involved in ROS scavenging, chaperons, and carbohydrate metabolism. Early stress-responsive genes (LOXs, BGLU, OPR2, CAD, UDPG, RPs, GLUD, and PAL). Late stress-	(Ma et al.., 2020)

Plant species	**Stress condition**	**tissue**	**Approach**	**Key finding**	**References**
				responsive genes (6-PGDH, CPODs, GSTs, BGLUs, SAM, PODs, and OXO). Carbohydrate metabolism, secondary metabolites, and pentose phosphate pathways are highlighted as enriched under salt stress.	
Zoysia macrostachya	30mM NaCl; 24h	Leaf	RNA-seq	8703 DEGs 4903 DEGs up-regulated and 3800 DEGs down-regulated. Identified genes were involved in the hormone signal transduction, ion homeostasis, and ROS scavenging.	(Wang et al., 2020)
Oats *(Avena sativa)*	150 and 300mM NaCl; 24h	Roots	RNA-seq	3915/13 492, 16 076/23 707, 4898/3414, and 34 040/14 757 DEGs in BY2/ BY5 genotypes. The expression of several Na^+/K^+ transporter genes was up-regulated under both NaCl level. Identified DEGs	(Xu et al., 2021)

Plant species	**Stress condition**	**tissue**	**Approach**	**Key finding**	**References**
				were enriched in starch and sucrose metabolism, galactose metabolism, and glycolysis/ gluconeogenesis pathways.	
Cucumber *(Cucumis sativus)*	100mM NaCl; 72h	Seeds	RNA-seq	1420 DEGs Common enriched pathways were porphyrin and chlorophyll metabolism, photosynthesis, linoleic acid metabolism, glyoxylate and dicarboxylate metabolism, fatty acid degradation, carbon metabolism, carbon fixation in photosynthetic organisms, biosynthesis of unsaturated fatty acids, biosynthesis of secondary metabolites, and alpha-linolenic acid metabolism Identified genes were involved in signal transduction of plant hormone, photosynthesis,	(Du et al., 2021)

Plant species	Stress condition	tissue	Approach	Key finding	References
				and argine and proline metabolism.	
Proteomics					
Wheat (*Triticum aestivum*)	150mM NaCl; 24h	Roots and shoots	iTRAQ	180 DEPs. Identified DEPs were involved in ethylene dependent salt response. The majority of the proteins are enriched in ribosome of the translation process, pyrimidine metabolism, purinemetabolism, pentose phosphate pathway, cyanoamino acid metabolism, and pyruvate metabolism. Mainly, nucleoside diphosphate kinases, trans aldolases, beta-glucosidases, phosphoenl pyruvate carboxylases, and SODs were significantly up-regulated under salt stress.	(Ma et al.., 2020)
Barley (*Hordeum vulgare*)	300mM NaCl;2,4	Leaves and		53 and 51 DEPs in leaves and roots.	(Zhu et al., 2020)

Plant species	**Stress condition**	**tissue**	**Approach**	**Key finding**	**References**		
	, and 6d	roots		Identified DEPs related to photosynthesis, ROS scavenging, and ATP synthase were significantly up-regulated.			
Alfalfa (*Medicago sativa*)	50,100,200 and 400mM NaCl; 14d	Leaf	LC-MS/MS	226 DEPs 118 DEPs were involved in glutathione metabolism and oxidation-reduction pathways, and these antioxidant-related metabolisms were pointedly up-regulated. TCA and CBB cycle, and ROS metabolism were found to be key pathways for improving salinity tolerance.	(Li et al., 2020)		
Beet (*Beta vulgaris*)	300mM NaCl; 3weeks	Leaves	Nano LC–MS/MS	82 DEPs 54 DEPs up-regulatedand 28 down-regulated. Identified DEPs were involved in lipid metabolism, cell wall modification,	(Rasouli et al., 2020)	MALD TOF-TOF	53 and51 DEPs in leaves and roots. Identified DEPs related to photosynthesis, ROS scavenging, and ATP synthase

Plant species	**Stress condition**	**tissue**	**Approach**	**Key finding**	**References**		
				ATP biosynthesis, and signalling. Several stress-related proteins, such as lipid transfer protein, chaperone proteins, heat shock proteins, and inorganic pyrophosphatase 2 were significantly up-regulated under salt stress			were significantly up-regulated.
Cucumber (*Cucumis sativus*)	200mM NaCl; 7d	Leaves	MALDI-TOF/TOF-MS	61DEPs Identified DEPs associated with plant pathogen interaction, sulfur-containing metabolism, cell defense, and signal transduction pathways. Key proteins were cysteine synthase1, glutathione S-	(Jiang et al., 2020)	LC-MS/MS	226DEPs 118DEPs were involved in glutathione metabolism and oxidation-reduction pathways, and these antioxidant-related metabolisms were pointedly up-regulated.

Plant species	**Stress condition**	**tissue**	**Approach**	**Key finding**	**References**	
				transferase U25-like, protein disulfide-isomerase, and peroxidase2.		TCA and CBB cycle, and ROS metabolism were found to be key pathways for improving salinity tolerance.
Wheat (*Triticum aestivum*)	200mM NaCl; 24, 48, 72 and 96h	Leaves	MALDI-TOF/TOF MS	194 DEPs Identified DEPs were involved in thelight dependent reaction. Several DEPs were significantly up-regulated that relate to the Calvin cycle, transcription and translation, amino acid, carbon, and nitrogen metabolisms. Further, DEPs associated with plastoglobule development, protein folding and proteolysis, hormone, and vitamin synthesis, were also significantly up-regulated under salinity.	(Zhu et al., 2021)	
Metabolomics						

Plant species	**Stress condition**	**tissue**	**Approch**	**Key finding**	**References**
Bean (*Phaseolus vulgaris*)	125mM NaCl; 3d	Roots and leaf	GC-CMS	79 DAMs Mainly, lysine, valine, and isoleucine metabolites were strongly induced by salinity stress. Salinity stress boosted amino acids and carbohydrate metabolisms.	(Niron et al., 2020)
Tomato (*Solanum lycopersicon*)	60mM NaCl; 45d	Pericarp	GC-TOF-MS	114 DAMs Identified DAMs including alkyl amines, amino acids, carbohydrates, fatty acids, organic acids, and nucleotides metabolites were significantly accumulated. Mainly, L-tryptophan, L-valine, L-aspartic acid, trehalose, D-galactose, chlorogenic acid, alpha-tocopherol, and glycolic acid were induced by salt stress. Identified metabolites were involved in alanine, aspartate, and glutamate	(Tang et al., 2020)

Plant species	Stress condition	tissue	Approch	Key finding	References
				metabolism, pentose and glucuronate interconversions, arginine biosynthesis, TCA cycle, ascorbate and aldarate metabolism, and beta-alanine metabolisms	
Barley (*Hordeum vulgare*)	150mM NaCl; 14 d	Seeds	GC-MS	14 DAMs Under salinity, amino acids, sugars, sugar alcohols, sugar acids, and other derivatives acted as osmolytes. Identified DAMs were involved in amino acids metabolism, sugar metabolism, and TCA cycle pathways.	(Derakhshani et al., 2020)
Rimth Saltbush (*Haloxylonsalicornicum*)	400mM NaCl; 21 d	Shoots	GC-QTOF –MS and HPLC-DAD	47 DAMs Most of the DAMs are belongs to amino acids, organic acids, amines, sugar alcohols, sugars, fatty acids, alkaloids, and phytohormones. In response to salinity, several amino acids were	(Panda et al., 2021)

Plant species	Stress condition	tissue	Approach	Key finding	References
				down-regulated and carbohydrates were up-regulated. Enrichment analysis showed that amino sugar and nucleotide sugar metabolism, TCA cycle, starch, and sucrose metabolism, phenylalanine metabolism, cysteine, methionine, glycine, serine, and threonine metabolism, etc. were significantly enriched by salinity stress.	
Oats (*Avena sativa*)	150 and 300mM NaCl; 24h	Roots	GC-TOF MS	201 DAMs Several vital DAMs were accumulated under salt stress, i.e., sucrose, sophorose, isomaltose, melibiose, and 3, 6-Anhydro D-galactose. Identified DAMs were involved in amino acids, carbohydrates, and organic acids metabolisms and were also	(Xu et al., 2021)

Plant species	Stress condition	tissue	Approch	Key finding	References
				significantly accumulated.	
Potato (*Solanum tuberosum*)	20mM LiCl; 45 d	Shoots	GC-MS	50 DAMs Mainly, sugars, terpenes, alkanes, fatty acids, amines, and organic acids were induced by salt stress.	(Hamooh et al., 2021)

DEGs: differentially expressed genes; DEPs: differentially expressed proteins; DAMs: differentially accumulated metabolites; ROS: reactive oxygen species; TCA cycle: the citric acid cycle (Source: Raza et al., 2022).

VIII. CONCLUSION AND FUTURE PROSPECTIVE:

Soil salinization is a gradual process that can be caused by improper fertilization, irrigation with reclaimed water and soil degradation in agricultural land. Globally, salinity is one of the primary abiotic stress factors that results in significant yield loss for agricultural crops. The increasing problem of salinity stress has led to the adoption of different approaches to decrease yield loss. Salinity-causing salt sources can be remedied by a range of mitigation techniques, including amendments (biochar, zeolites, and compost), salt-tolerant genotypes and underwater drainage water bodies in salt deposits, micro-irrigation techniques such as the drip system, cultivation techniques or agriculture and forestry methods. Now-a-days, nanotechnology and gene editing is one of the advance technologies to mitigate the saline soil. Globally, the utilization of these technologies can lead to alterations in both physicochemistry (pH, EC, bulk density, available soil nutrients) and biological properties (enzyme activity, MBC), which could improve soil health and crop productivity. Further, more research is needed in different ways of using nanoparticle in save way to control the salinity and the use of green nanoparticle instead of chemically synthesised can be more efficient and eco-friendly. There is also research needed to use salt-tolerant gene and produce genetically modified organism, GMOs that can tolerate salinity there are many biotechnological tools can be used to perform gene editing like CRISPER/CAS system, ZFN, TALEN these tools are most emerging and promising in genetic engineering of stress tolerant genes for future prospects.

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Priya Kushwaha did the resources, writing the original draft of the paper and performing writing the review article. Amit Kumar Singh and Pallavi Dixit supervised the paper. Rahul Verma did the editing and correction of the paper. Priya Kushwaha and did the process of investigation and conceptualization. Priya Kushwaha wrote and prepared the original draft. Amit Kumar Singhand Pallavi Dixit had close supervision in the process of preparing the paper. All authors have read and agreed to the published version of the manuscript.

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