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Impact of Salinity Stress on Major Cereal Crops and Integrated Management Strategies for Sustainable Production

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ABSTRACT

Abiotic stress factors, particularly salinity, pose a major threat to global agriculture by significantly reducing the growth and yield of major cereal crops such as wheat (*Triticum aestivum*), rice (*Oryza sativa*), and maize (*Zea mays*), which are fundamental to global food security. The increasing extent of salt-affected soils—driven by climate change, inappropriate irrigation practices, and natural soil processes—highlights the urgent need for sustainable and practical management strategies. Addressing salinity requires an integrated approach that combines improved agronomic practices, including gypsum application, efficient irrigation management, balanced fertilization, organic amendments, and the judicious use of plant growth regulators, with advanced breeding strategies. Recent progress in quantitative trait loci (QTL) mapping, marker-assisted selection, genetic engineering, and CRISPR-Cas9 genome editing has enhanced the precision and efficiency of developing salt-tolerant cultivars. In addition, beneficial microorganisms such as plant growth-promoting bacteria and arbuscular mycorrhizal fungi play a crucial role in enhancing hormonal balance and strengthening plant defense systems under saline conditions. Collectively, these integrated strategies provide a sustainable pathway to improve crop resilience, maintain cereal productivity, and ensure food security in salt-affected regions.

Keywords: Cereal crops, salinity stress, agronomic practices, breeding strategies, plant growth-promoting microbes, arbuscular mycorrhizal fungi.

INTRODUCTION

Abiotic stressors such as drought, salinity, cold, and extreme temperatures adversely affect plant growth, development, and yield. These stresses are estimated to reduce global crop production by approximately 50%. (Ray, 2025). Among them, salinity is considered one of the most detrimental factors affecting the plant life cycle. Salinity is defined as the accumulation of soluble salts, including as sodium (Na^+), chloride (Cl^-), calcium (Ca^{2+}), potassium (K^+), sulfates and magnesium (Mg^{2+}) deteriorate soil health, impair water quality and ultimately reduce agricultural productivity (Lekka *et al.*, 2024; Price *et al.*, 2022; Stavi *et al.*, 2021). Globally, approximately 20% of cultivated land and about 6% of irrigated land are affected by salinity (Silveria *et al.* 2025). Projections suggest that by 2050, nearly 50% of arable land may be impacted if appropriate mitigation strategies are not implemented. (Demo *et al.* 2025; Silveria *et al.* 2025).

Climate change further exacerbates soil salinity through rising temperatures, altered precipitation patterns, and increased evaporation rates. These factors accelerate salt accumulation in soils, while increased reliance on irrigation often with poor-quality water introduces additional salts into agricultural systems.

Cereal crops such as rice, wheat, and maize are staple foods for the majority of the world's population and contribute more than half of global caloric intake. To meet the demands of a growing population, global cereal production must increase significantly by 2050. However, salinity stress poses a serious constraint to achieving this target.

Salinity affects plants through osmotic stress, ion toxicity, and nutrient imbalance, leading to reduced germination, impaired photosynthesis, restricted growth, and ultimately yield loss. These effects vary depending on crop species, growth stage, and stress severity. This review aims to critically examine the impact of salinity on major cereal crops and evaluate integrated management strategies, including

agronomic practices, breeding approaches, and the role of beneficial microorganisms in enhancing salinity tolerance.

Major cereal crops and salinity's impact on them: Figure. 1: Many important field crops, including sorghum (*Sorghum bicolor* L.), cotton (*Gossypium hirsutum*), sugarcane (*Saccharum officinarum*), rice (*Oryza sativa* L.), maize (*Zea mays* L.), and wheat

(*Triticum aestivum* L.), respond negatively to salinity. Salinity threshold values, which are commonly defined as the highest salt concentration that plants can withstand in the root zone without impairing their growth, may, however, have no effect on plant growth or grain yield until salinity reaches a particular level (Table 1).

Table 1. Classification of major field crops according to their salinity levels.

Crop type	Tolerance based on	Threshold EC levels (dS m ⁻¹)	25% yield loss (dS m ⁻¹)	50% yield loss (dS m ⁻¹)	Zero yield (dS m ⁻¹)	Ranking	References
Wheat	Grain yield	6–8	6.3	10	16–24	MT	Asana and Kale, 1965; Bouafiane <i>et al.</i> 2025)
Rice	Grain yield	3	3.2	3.5–4	8–16	S	Venkateshwarlu <i>et al.</i> 1972: Reshna & Beena (2025)
Maize	Ear FW	1.8	2.5–6.8	8.6	15.3	MS	Maas <i>et al.</i> 1988: Atta <i>et al.</i> 2023)
Sorghum	Grain yield	6.8	7	10	30	MT	Maas and Hoffman, 1977: Seleiman <i>et al.</i> 2022)
Cotton	Seed cotton	7.7	8.37	17	16–24	T	Bernstein and Ford 1959: Atta <i>et al.</i> 2023)
Sugarcane	Shoot DW	1.7	3.9	13.3	16–24	MS	Dev and Bajwa, 1972: Pradhan <i>et al.</i> 2025)

EC = Electrical Conductivity, FW = Fresh Weight, DW = Dry Weight, S = Sensitive, MS = Moderately Sensitive, MT = Moderately Tolerant and T = Tolerant

For more than half of the world's population, paddy rice is a basic diet (Fu *et al.* 2023; Qian *et al.* 2023), represents more than 20% of all cereal harvested areas worldwide (FAO,2022; Prasad *et al.*2017). It is predominantly cultivated in Asia particularly in countries like China, India, and Indonesia, while paddy rice cultivation has also expanded to parts of sub-Saharan Africa (Chen *et al.* 2024), the Caribbean, and Latin America (Muthayya *et al.* 2014). Rice farming is highly resource-intensive, particularly in its demand for water (Pan *et al.* 2021) with an estimated 784 billion m³ consumed annually to sustain global rice production (Chapagain *et al.* 2011). However, Rice is sensitive to salt stress, with its tolerance varying across developmental stages, organ types, and varieties (Chinnusamy *et al.*, 2005; Lee *et al.*, 2003; Nam *et al.*, 2015). Among cereal crops, rice shows the greatest vulnerability to salt stress on a comparatively small concentration of sodium chloride (30 mmol L⁻¹). Paddy plants' growth and productivity are severely hampered by salinity (Kumar *et al.* 2022; Li *et al.*, 2023a). Young seedlings are generally more prone to salinity stress than plants at later vegetative stages, and roots are often the most sensitive organs (Nam *et al.*, 2015). Studies on Asian rice genotypes indicate that *Japonica* rice, with its higher amylopectin content, is typically much susceptible to salt as compared to *Indica* rice. Growth is restricted by salinity stress, which lowers biological yield, incomplete fertility, and reduced rice production (Radanielson *et al.*, 2018; Razzaq *et al.*, 2020; Tsai *et al.*, 2019). Although irrigation is essential for rice,

which is commonly grown under flooded conditions, excessive irrigation can exacerbate fluctuations in soil salinity levels (Asamoah *et al.*, 2012). In Ghana, irrigation techniques in rice fields have dramatically increased salty soil conditions from 318,000 hectares in 1989 to 790,000 hectares in 2000, confirming this issue with irrigation application (Asamoah *et al.*, 2013). According to a survey conducted among Ghanaian rice farmers, sixty percent of poor yields were caused by salt stress, and many have turned to irrigate their field by flooding method which have proved beneficial in coping with saline conditions (Bissah *et al.*, 2022).

Wheat (*Triticum aestivum* L.), one of the most widely grown and consumed crops, provides staple food for millions of people worldwide and holds immense importance in global agriculture and food security. Wheat production is significantly reduced under saline conditions. The crop begins to exhibit sensitivity against salt stress when the EC of soil touches approximately 6 dS m⁻¹. Wheat plants are subject to osmotic and ionic stresses as the soil becomes more salinized because the water potential in the soil decreases and in results the Na⁺ concentration in plant tissues increases. The Food and Agriculture Organization (FAO) estimates that salt stress severely affects around 397 m ha of wheat-growing land, posing a serious danger to world food security (World Health Organization, 2019). When salinity exceed the threshold level (6 dS m⁻¹) in wheat, several physiological functions are negatively affected.

Germination, photosynthesis, and transpiration rates decline, which ultimately reduces crop yield. Moreover, elevated salinity levels exacerbate the accumulation of sodium (Na^+) and chloride (Cl^-) ions within plant tissues, thereby interfering with essential metabolic functions (Hasanuzzaman *et al.*, 2017; Hussain *et al.*, 2021). Salt stress disturbs the enzymatic activities, photosynthesis, membrane structure,

hormonal balance, water, and nutrient uptake, and induces oxidative stress (Ibrahimova *et al.*, 2021). Salinity also affects the wheat plant's water-use efficiency (WUE), reactive oxygen species (ROS) formation, and antioxidant scavenging characteristics. Table 2 summarizes the different approaches that salt stress affects the wheat crop's photosynthetic and physiological characteristics

Table 2. Impact of increasing salinity on physiological processes and photosynthetic efficiency in wheat

Salinity Level	Effects	References
18 dS m^{-1}	Salt stress significantly reduced the photosynthetic rate, stomatal conductance, and K^+ concentration, while increasing electrolyte leakage and Na^+ accumulation.	Wahid <i>et al.</i> , (2007)
15 dS m^{-1}	Salinity stress led to a decline in chlorophyll content and relative water content, along with an increased accumulation of Na^+ ions.	Badawy <i>et al.</i> , (2021)
12.0 dS m^{-1}	Salt stress decreased leaf chlorophyll levels and caused notable alterations in leaf anatomical structure.	Nassar <i>et al.</i> , (2020)
10 dS m^{-1}	Leaf water potential, relative water content, chlorophyll content, and K^+ levels decreased, whereas Na^+ accumulation increased.	Soni <i>et al.</i> , (2021)
8 dS m^{-1}	Salinity reduced relative water and chlorophyll contents and resulted in membrane damage.	Yadav <i>et al.</i> , (2020)
6.25 dS m^{-1}	Salinity stress inhibited root and shoot growth and promoted the accumulation of H_2O_2 , lipid peroxidation, as well as increased levels of proline and amino acids.	Sadak, (2019)

Maize ranks among the foremost cereal crops cultivated and consumed worldwide. In practical terms, maize, rice, and wheat are the three major grains that make up nearly 42% of the world's caloric consumption (Erenstein *et al.* 2022; World Health Organization, 2021). According to the FAO statistics, the amount of maize produced worldwide in 2022 was 1.16 billion tons, up from 1.21 metric tons in 2021. The United States of America accounted for 49.6% of the regional share of maize output, followed by Asia (33.5%), Europe (8.8%), Africa (8.0%), and Oceania (0.1%) (<https://www.fao.org/faostat/en/#data>). In terms of usage, 56% of the maize produced is primarily used as feed, 13% is used for food, and one-fifth is utilized for purposes other than food (Erenstein *et al.* 2022; Szeles *et al.* 2019). Maize (*Zea mays*), a C_4 cereal crop belonging to the family Poaceae, is typically regarded as having a modest sensitivity to salinity. Nonetheless, there is a significant amount of genetic variation among maize varieties, providing potential for improving salt tolerance through breeding. When salinity levels exceed this limit, plant growth and development become restricted, often resulting in reduced vigor and significant physiological damage (Chinnusamy *et al.*, 2005; Menezes-Benavente *et al.*, 2004). Wakeel *et al.* (2011) noticed that shoot growth is dramatically decreases during osmotic stress in maize under saline conditions. Salinity has a negative effect on seed germination in several ways. First, the presence of salts in the soil lowers the soil's osmotic potential, making it more difficult for seeds to absorb the water they need to start germinating. Second, high concentrations of ions such as Na^+ and Cl^- can be toxic to the developing embryo inside the seed. As a result, the combined effects of osmotic stress and ion toxicity under saline conditions often slow down the germination process or

reduce the overall germination rate (Farsiani and Ghobadi, 2009). Salinity significantly restricts maize growth by affecting several key developmental processes. Under saline conditions, the formation and expansion of leaves are reduced, internode growth is suppressed, and leaf shedding tends to increase. These changes ultimately weaken overall plant development. In addition, salinity negatively affects grain formation by decreasing both the number and weight of kernels, which results in lower maize yields. This reduction is mainly associated with limited assimilate supply to the developing grains (sink limitation) and decreased activity of acid invertase enzymes in the growing kernels, leading to poor kernel development and fewer grains. Figure 1

Managing salinity in cereal crops requires an integrated approach that combines breeding innovations with effective agronomic practices. Screening of salt-tolerant genotypes (Chattha *et al.*, 2020), conventional breeding, marker-assisted breeding, and molecular breeding are important strategies to enhance crop resilience under saline conditions. Greater emphasis must be placed on agronomic practices. The application of gypsum on saline soils improves soil structure and promotes sodium leaching, thereby reducing sodicity. Seed priming, nutrient management, and hormone application have shown promising results in mitigating salinity stress (Erdal *et al.*, 2011; Hasanuzzaman *et al.*, 2017). Organic amendments such as animal manure and compost improve soil organic carbon, stimulate microbial activity, enhance soil structure, and increase water-holding capacity, ultimately reducing salinization risks (Naveed *et al.*, 2014; Saha *et al.*, 2024). Water management is equally critical. Micro-irrigation improves salt leaching near emitters and

helps maintain lower salinity levels compared to conventional irrigation systems (Yang *et al.*, 2023). Furthermore, the presence of growth-promoting

bacteria adapted to saline environments can improve plant productivity in salt-affected soils (Orhan, 2016).

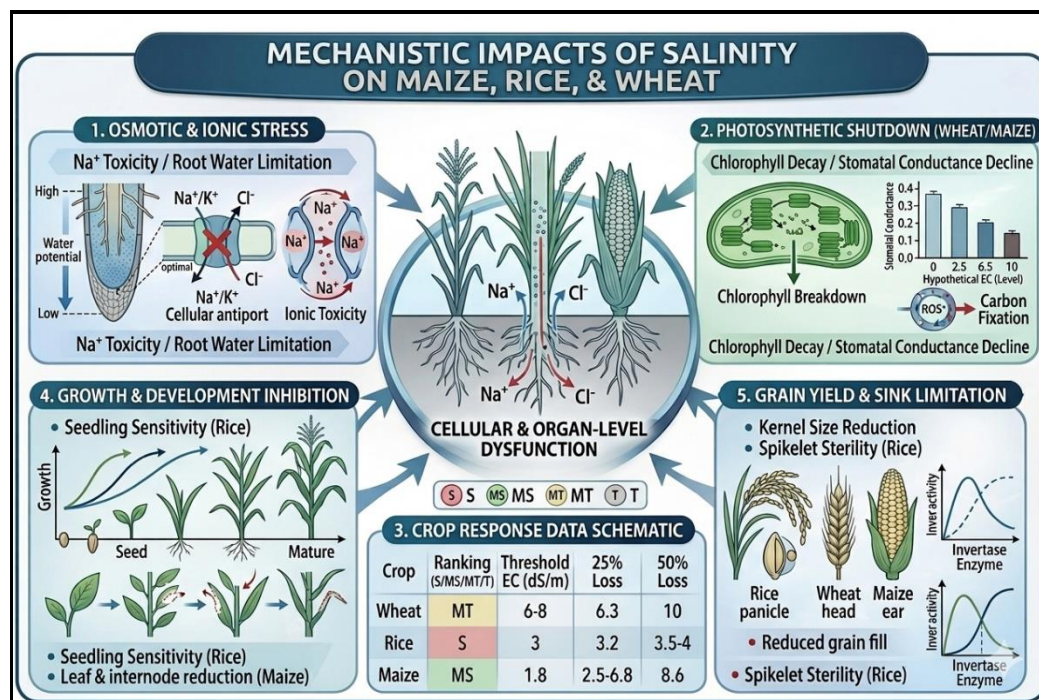


Fig 1: Mechanistic impacts of salinity on maize, rice and wheat and crop response data in hypothetical diagram.

Agronomic practices to deal with salinity

Importance of gypsum in saline Soils: Application of calcium prevents soil surface crusting by displacing sodium from the exchange sites. Gypsum (calcium sulfate $\text{CaSO}_4 \cdot 2\text{H}_2\text{O}$) is one of the most often used calcium sources for remediating sodium-contaminated soil. It is mixed with the soil, and irrigation water free from salt is used (Gashi *et al.*, 2025; Sonon *et al.*, 2015). The application of gypsum demonstrated optimal efficacy in soil reclamation across varying textures, with treatment levels tailored to specific soil types. For loamy-sand soils, the incorporation of gypsum at a 25% rate (designated as G25) proved most effective, whereas sandy loam soils exhibited maximum improvement with a 50% gypsum application (G50). In clay loam textures, the most favorable outcomes were observed at the highest tested rate of 75% gypsum (G75). These treatment regimens not only offer a cost-effective strategy for ameliorating salt-affected soils but also substantially reduced both the Sodium Adsorption Ratio (SAR) and Electrical Conductivity (EC). Specifically, SAR values were diminished to levels below $5.92 \text{ (mmol L}^{-1}\text{)}$, while EC was lowered to less than 0.97 dS m^{-1} , indicating a significant mitigation of soil sodicity and salinity hazards (Ahmad *et al.*, 2012). According to Ahmad *et al.* (2001), applying gypsum and CaCl_2 enhanced the

yield of rice and wheat varieties when compared to the control. Ahmad *et al.*, (2012) investigated the use of various soil amendment strategies to cultivate rice in salt-affected soils. The study included three treatments: T₁ served as the control, T₂ had a 100%, and T₃ had a 50% gypsum requirement (GR). The T₂ treatment (100% GR) yielded the maximum performance, with 14.60 t ha^{-1} of rice biomass and 3.50 t ha^{-1} of rice grains. Under control situations, rice biomass and grain yield were 7.22 t ha^{-1} and 1.62 t ha^{-1} , respectively (Gashi *et al.* 2025; Shen *et al.* 2025)

Zaka *et al.* (2009) evaluated different gypsum-based amendments, including 100% gypsum requirement (GR) alone, gypsum at 25 t ha^{-1} combined with organic manure (FYM) and soil chiseling, and integration of all these treatments. The findings indicated applying gypsum alone resulted in maximum wheat and rice grain production, confirming it as the most effective single treatment. Gypsum combined with FYM also performed well, while the combination of gypsum with chiseling was less effective. However, integrating farmyard manure, gypsum, soil chiseling improved the total conditions of experimental soil. The table 3 summarizes the particular gypsum needs for replenishing exchangeable sodium in the soil (Gashi *et al.* 2025; Shen *et al.* 2025; Sonon *et al.*, 2015)

Table 3. Gypsum requirement for replacing exchangeable sodium in soil. Gypsum used: $\text{CaSO}_4 \cdot 2\text{H}_2\text{O}$. 1 acre-foot of soil $\approx$ 4,000,000 lb; 1 acre–6 inches of soil $\approx$ 2,000,000 lb. Gypsum amounts are rounded to the nearest 0.1 ton.

Soil exchangeable sodium (lbs/acre)	Gypsum required (tons/acre-foot)	Gypsum required (tons/acre-6 inches)	Gypsum required (lbs/1000 ft ² -1 foot)	Gypsum required (lbs/1000 ft ² -6 inches)
460	1.70	0.90	80	40
920	3.40	1.70	160	80
1380	5.20	2.60	240	120
1840	6.90	3.40	320	160
2300	8.60	4.30	400	200
2760	10.30	5.20	480	240

Role of Seed Priming Techniques under Salt Stress conditions:

Seed priming is a simple and low-cost approach that has demonstrated good results in enhancing crop's production against saline soils (Al-hakimi *et al.* 2001; Janah *et al.* 2025). This method enhances sprouting of seeds and promotes better young planation in cereals including wheat (Kaya *et al.* 2006; Seleiman *et al.* 2021). The positive outcomes attributed to seed priming largely stem from enhanced metabolic processes within the seed. These include heightened levels of adenosine triphosphate (ATP), the stimulation of key enzymatic reactions, and the biosynthesis of essential compounds which collectively facilitate and accelerate germination (Hussain *et al.* 2021). Moreover, this technique is also considered an authentic, low-cost, and a minimal risk containing approach that can easily be adopted by farmers (Hameed *et al.* 2025; Iqbal *et al.* 2005; Tavili *et al.* 2011). Different priming methods have been developed to enhance germination rate, seedling growth, and overall crop performance, including hydration priming in water, osmotic conditioning with nutrient solutions, and saline preconditioning using various salt concentrations (Jisha *et al.* 2013).

Seed priming has proven to be an effective technique for improving germination and seedlings in cereals grown at tropical as well as subtropical regions, particularly under saline conditions (Yari *et al.*, 2011). By enhancing germination rate and early seedling establishment, primed seeds often show greater tolerance to salt stress and ultimately produce higher crop yields (Tavili *et al.*, 2011). For example, tolerance against salinity in wheat was improved by applying hydration priming technique against a salt level of 15 dS m⁻¹ (Afzal *et al.*, 2008). Similarly, osmo-priming with ascorbic acid (AsA) increased ascorbic acid levels and catalase (CAT) activity inside the plants, which ultimately enhanced wheat's tolerance (Al-Hakimi *et al.*, 2001). Halo-priming with calcium chloride (CaCl_2) has also been shown to lower Na^+ accumulation while increasing K^+ uptake, helping maintain ionic balance and improve salt tolerance (Janah *et al.*, 2025). In addition, seed priming with indole-3-acetic acid (IAA) stimulates amylase activity, promoting germination and reducing the inhibitory effects of salinity. Likewise, priming with salicylic acid (SA) at 100 mg

L⁻¹ has been reported to enhance photosynthetic pigments (chlorophyll a and b) and improve osmotic adjustment in wheat under salt stress (Hameed *et al.*, 2025; Janah *et al.*, 2025).

Water Management in Saline Soils: The growth of cereal crops can be reduced by applying irrigation water that contain high rates of EC, SAR, RSC and pH values (Murtaza *et al.*, 2006). Ensuring the use of good-quality irrigation water is therefore critical, as proper water management plays a key role in supporting crop survival and maximizing yield under challenging conditions. Draining or leaching the soluble salts from the root zone with high-quality water is an effective way to improve soil management and plant development (Ezeaku *et al.*, 2015). When it comes to irrigating cereals, water coming from canals is a viable substitute for brackish subterranean water. If canal water is unavailable, gypsum mixed with brackish underground water is the best option under salinity situations. It boosted rice productivity by 25–294% and wheat production by 182% (Zaka *et al.*, 2009). A superior ameliorative effect was observed when canal water was applied in conjunction with a complete gypsum amendment, significantly reducing electrical conductivity (EC), pH, and sodium adsorption ratio (SAR) in the surface soil layer (0–30 cm) compared to saline water irrigated plots receiving the same gypsum treatment (Mehdi *et al.*, 2013). When good-quality water is limited, applying 25% gypsum along with lower-quality irrigation water can be an effective alternative. It is important to avoid mixing poor-quality surface water with unsuitable underground or tube well water, and to follow proper irrigation schedules to optimize crop growth (Zaka *et al.*, 2009).

Nutrient and Fertilizer Management: Salinity stress can be effectively managed through proper nutrient management, particularly by supplying calcium (Ca^{2+}) through gypsum ($\text{CaSO}_4 \cdot 2\text{H}_2\text{O}$). Gypsum improves soil structure, enhances water infiltration, and supports better plant growth under saline conditions. Studies have shown that applying gypsum alone or in combination with amendments such as farmyard manure (FYM), sulfuric acid (H_2SO_4), pyrite, humic acid (HA), and chiseling improves soil properties, increases plant biomass, and enhances yields in crops like rice, wheat, maize, and sorghum (Ezeaku *et al.*,

2015; Manzoor *et al.*, 2014). Applying nitrogen, phosphorus, potassium, sulfur, zinc, boron and manganese alone as well as in various combinations boosted total rice's biological and grain production against saline stressed conditions (Dash *et al.*, 2015; Pandey *et al.*, 2013). Humic acid plays an important role in improving nutrient availability by chelating essential elements such as P, K, Ca, Fe, Zn, and Cu that are otherwise unavailable to plants. It also helps to maintain the pH of soil and increases the activity of microbes, enzymes, and physiological processes, which collectively assist plant development in saline situations (Manzoor *et al.*, 2014; Khattak *et al.*, 2013). Furthermore, in rice, integrating gypsum and humic acid has been found to be more effective than humic acid alone in reducing soil salinity indicators such as EC and SAR, mainly due to its chelating ability that improves nutrient availability under saline stress (Shaaban *et al.*, 2013). Sesbania as a cover crop, green manure, poultry manure, and sugarcane by-product (press-mud) are all excellent choices for amending soil to lessen the impact of salt due to the presence of various essential elements (Ismail, 2009). Several other agronomic practices can also help reduce the harmful effects of salt stress on plants. These include the periodic use of fresh water to dilute and leach salts, as well as soil management practices such as subsoiling, deep tillage, and use of sand to improve soil structure and drainage. In addition, the application of both organic and inorganic fertilizers enhances soil fertility and plant nutrition. Adopting appropriate crop rotation systems further supports soil health and helps crops better cope with saline conditions (Ezeaku *et al.*, 2015).

Application of Hormonal Regulators to Mitigate Salinity Stress: Salinity stress often interrupts with the hormonal balance in plants, which negatively affects plant's growing conditions as well as development. To overcome this problem, various plant growth regulators are used to regulate hormonal activity and improve plant tolerance to salt stress. For instance, compounds such as 1-methylcyclopropane (1-MCP), ethephone and aminoethoxyvinylglycine (AVG) are used to regulate ethylene activity under saline conditions. These regulators help improve plant development, including better boll formation in cotton and enhanced spikelet development in rice (Hussain *et al.*, 2019).

Similarly, the external application of hormones such as brassinosteroids (BRs), Absciscic Acid (ABA) and their synthetic equivalents such as D-31 and D-100 has proved to be beneficial against saline conditions as well as in improving crop's overall performance. These substances help plants maintain physiological balance and support growth against various salt conditions (Ashraf *et al.*, 2010; Singh *et al.*, 1987).

Breeding strategies to develop salt tolerance in plants

Screening against Salt Stress: Plants behave differently and are sensitive at various growth stages against salinity stress which is one of the main factors

affecting salinity tolerance phenotypes. Cereal crop (Rice, wheat and maize) shows high sensitivity at seedling stages when plants are young but show low sensitivity at reproductive stage (Lutts *et al.*, 1995). A good and proper technique for screening is necessary to assess the reaction of any germplasm. Two salt sensitive phases are important in the screening process Figure 2. Screening at the time of young seedling plants (vegetative stage) is very simple and quick method and it can be performed at either field or lab conditions but screening at field conditions is quite difficult then lab conditions (Ali *et al.*, 2021) because of some other factors affecting crop like soil heterogeneity and other abiotic stresses. So, screening under lab conditions is easy and perfect then field conditions.

Crop plants are affected in three ways such as physiological, biochemical and molecular levels by a variety of abiotic stress. First of all, agronomic characters were kept as basics in the screening process of salinity tolerance but experiments were then conducted on developing salt tolerant genotypes which were based upon conventional breeding techniques and selection (Mittova *et al.*, 2002). In which screening at the morphological levels of plants was done which was based upon different agronomic and physiological characters. Parameters defining effectiveness of salinity like the lengths of plants above (shoot) and below ground (root) parts, total biomass of the plant, sodium and potassium ratio in shoot were checked while performing screening process at morphological way (Zeng *et al.*, 2007). The morphological screening starts after 10 days of applying screening solution to rice crop seedlings for a healthy screening process in sorting out tolerant genotypes from susceptible ones (Gregorio, 1997). Because of the effect of environment conditions, the screening based upon agronomical characters are less successful and less productive. The research by many scientists have proved that the screening of genotypes at biochemical level can be much better defined when understanding the salinity tolerance mechanism and assessment of the rice (Sarkar *et al.*, 2013). It tells and gives an idea about potential indicators of salinity tolerance of the whole plant and its tissue (cellular) level. The mechanism of crop plants to withstand under salinity stress and the identification of those metabolic sites of the plants which are infected by salt stress are also being well understood. Molecular way of screening salt tolerance genotypes/lines relies on the recent approaches for understanding how rice crop respond to salt stress and also knocking out those alleles which are causes of this stress (Kanawapee *et al.*, 2011). Thomson *et al.*, 2010 identified *saltol* QTLs has expanded the opportunities for further work and a development in genetic approach in mitigating salt stress (Soda *et al.*, 2013).

QTL mapping and Marker-assisted breeding for salinity tolerance: The selection of superior genotypes against salinity stress direct from the field conditions is prohibited due to the effects of other environmental factors affecting crop (Richards 1996). It has been

proved by many researches that resistance against salinity is a complex trait which is involved in the functions of many genes (Foolad, 2004). Salt tolerance in plants is not static it changes throughout their growth cycle. The capacity to withstand saline conditions during one developmental phase doesn't automatically predict how well the plant will cope during another. These tolerances often operate independently of each other (Foolad, 2004). Salt tolerance in various crops such as corn, tomato, wheat, barley and rice increases with the age of the plant. Salt tolerant QTLs seen at the seed germination in tomato (Foolad, 2004), Arabidopsis (Quesada *et al.*, 2002) and barley (Mano and Takeda, 1997) were quite different than those QTLs which were seen at the early growth stages of the crops. The plants which showed their higher tolerance against salinity at germination level did not showed similar results at vegetative or reproductive growth stages. As molecular biology tools have improved, so has our ability to create DNA markers that identify QTLs. The two have gone hand in hand better techniques mean better markers. The efficiency of selection has been improved and become simple by the use of QTLs especially for those traits which are governed by many genes and are also sensitive against environmental factors (Flowers, 2004). Marker-assisted selection using QTLs beats out traditional phenotypic screening in a couple of key ways. Since most marker detection methods rely on PCR, they tend to be faster and less vulnerable to environmental interference. Researchers have put together quite a bit of evidence showing that salt tolerance isn't controlled by just one gene it's actually a mix of multiple QTLs working together. Some of these traits get passed down through additive effects, while others depend on dominance, so it's a bit of both (Flowers, 2004; Foolad, 2004). These days, scientists are stacking or "pyramiding" different traits to really push for better salinity tolerance. And that's become a lot easier with high-density DNA maps that pull together markers like microsatellites, RFLP, and AFLP, plus all the recent upgrades in marker-assisted selection (Ali *et al.*, 2021).

Breeders should use marker-assisted selection (MAS) and genetic engineering to accelerate crop genetic development by using genes and their molecular pathways for salt tolerance for agriculture crops (Guo *et al.* 2022). Among the greatest accomplishments of biotechnology is the discovery of molecular markers. They are widely used to investigate DNA polymorphisms in the plant system and are very helpful to plant researchers and breeders in identifying a specific attribute associated with molecular markers in early plant stages without the need for phenotyping screening experiments (Singh *et al.* 2023). Developing elite crop lines with improved salinity tolerance largely depends on identifying new quantitative trait loci (QTLs). The genetic basis of salt tolerance is inherently complex, involving numerous genes that are organized into distinct QTLs. These QTLs collectively influence how a plant perceives and responds to saline

conditions, with different regions potentially controlling different aspects of tolerance. The expression and effectiveness of these QTLs are also strongly influenced by environmental conditions, making their identification and characterization essential for breeding salt-tolerant varieties. Nguyen *et al.* (2022) identified a QTL using conventional breeding methods in rice. That QTL shows a great tolerance ability towards salinity stress by regulating the ratio of sodium ion into potassium ion in aerial parts of plants at seedling stage. Maintaining a balanced Na^+/K^+ ratio is an important trait related to improved tolerance against salinity in major cereal crops. Marker-assisted backcrossing stands out as an effective conventional breeding tool because it offers a reliable way to introduce beneficial alleles into high-performing cultivars. The method allows breeders to target only the specific genes that they want to improve without disrupting the rest of the genetic makeup (Singh *et al.* 2023).

However, conventional breeding approaches often face limitations when dealing with complex traits such as salinity tolerance in crops like wheat, because these traits are controlled by multiple QTLs and are strongly influenced by environmental conditions. In contrast, molecular markers are largely independent of environmental effects and have been widely used for QTL analysis in different mapping populations. Molecular breeding techniques involve several steps that ultimately enable researchers to identify and track specific genes or QTLs linked to desirable traits, thereby improving the efficiency of crop improvement programs (Gupta *et al.* 2022).

Genetic modifications: Genetic modification allows scientists to introduce useful characters into plants which were not naturally found in their genome before. This is usually done using techniques such as Agrobacterium-mediated transformation or gene gun methods to insert desired genes into plant cells. After gene insertion, the transformed cells are regenerated into whole plants and carefully evaluated to confirm the successful expression of the introduced traits. Through these methods, several genetically modified crops—including rice, maize, soybean, and tomato—have been developed with improved tolerance to environmental stresses such as salinity, drought, and osmotic stress (Kim *et al.*, 2020; Ma *et al.*, 2018; Thirumalaikumar *et al.*, 2018; Zhang *et al.*, 2015). Genetic transformation has been a valuable tool in improving rice's tolerance against biotic threats like insects and fungi or coping with abiotic stresses such as heat, salt, and water scarcity. For instance, the development of Bt rice has significantly enhanced resistance to insect pests (Li *et al.*, 2023b). Beyond pest resistance, similar techniques have been used to improve the nutritional quality of rice (Zafar and Jianlong, 2023). Transgenic rice carrying *AtRPM1(D505V)* gene in overexpressed lines handled drought and salinity far better than conventional varieties (Li *et al.*, 2023). Transcriptional analysis

indicated that multiple stress-responsive genes *OsDREB2A*, *OsDREB2B*, *OsRD22*, and *OsRD29A* were significantly upregulated in the transgenic plants, offering a mechanistic explanation for their enhanced tolerance to drought and salinity. The increased activity of antioxidant enzymes also highlighted the potential of genetic transformation for developing stress-resilient rice varieties.

Recent advances in genetic transformation have shown great promise for developing new salt-tolerant crop varieties. A notable example involves the *ZmPDI* gene from *Zoysia matrella*, which is naturally induced under saline conditions. When constitutively expressed in rice, this gene conferred significantly enhanced tolerance to salt stress (Wang *et al.*, 2024). This improvement was achieved by regulating key stress-related genes, including *Laccase-6*, *Zingipain-2*, *FKBP65*, *Pho1*, *AKR4C10*, *WIP3*, *GBSSII*, and *TRXf1*, and by increasing proline levels, malondialdehyde content, and peroxidase activity. Conversely, knocking out the homologous rice gene (*OsPDI*) using CRISPR/Cas9 reduced salt tolerance, highlighting the important role of *ZmPDI* and its potential for breeding salt-resilient rice varieties (Wang *et al.*, 2024).

Genome editing and CRISPR-Cas9 system: Genome editing platforms such as CRISPR-Cas9, TALENs, and ZFNs allow for precise modifications at targeted loci within plant genomes. These tools can be deployed to knock out genes, insert desirable sequences, or introduce point mutations with a level of accuracy which was not possible with earlier methods. Unlike traditional genetic modification, genome editing often does not involve adding foreign genes, making it more widely accepted. CRISPR-Cas9, for instance, has proven effective in developing rice cultivars with enhanced tolerance to abiotic and biotic stresses including salinity alongside with producing aroma-based rice lines. These genetically edited traits are stably inherited across generations, highlighting a clear advantage over the outcomes typically achieved through conventional breeding (Aziz and Masmoudi, 2025). Globally, genome editing has been used extensively used to target particular genes linked to salt tolerance in order to increase rice's ability to respond to salinity. Knocking out the *OsRR22* gene via CRISPR-Cas9 yielded rice lines with markedly improved performance under saline conditions (Zhang *et al.*, 2019). Meanwhile, the technology has also driven progress in other areas of rice breeding, such as haploid induction, demonstrating its versatility beyond straightforward trait improvement. Developing doubled haploid populations has been greatly facilitated via genetic knockout of specific genes, including *OsPLA1*, in *indica* rice, which enhances efficiency for achieving homozygosity (Liu *et al.*, 2024). This approach holds particular significance for breeding initiatives focused on recalcitrant genotypes, a context in which traditional methods frequently prove inadequate. Nevertheless, while mutations in *OsPLA1* proved effective, the same study showed that edits in

OsDMP3 or *OsDMP6* did not result in haploid induction. This discrepancy highlights both the specificity and the current limitations of the approach. Ultimately, these findings validate *OsPLA1* as a key target for developing novel breeding strategies, yet they also serve as a crucial reminder that optimizing CRISPR/Cas9 protocols depends on the meticulous selection of genes. Beside the formation of haploids, editing gene has significantly improved the ability of rice to withstand abiotic stress and biofortification of various minerals and nutrition elements. These developments open the door to more accurate and effective breeding methods by demonstrating the wider applicability of genome editing tools for bolstering rice resilience and also enriching its nutritional composition (Gajardo *et al.*, 2023; Kumar *et al.*, 2022).

The advent of CRISPR-Cas9 has fundamentally reshaped modern agriculture, offering the capability to introduce targeted genetic modifications with remarkable precision in diverse crops. This technology enables the creation of diverse germplasm, which is vital for the research being conducted in plant breeding, it also helps scientists analyze the functions of genes to identify that improve important crop traits. Its application has also accelerated the production of hybrid seeds in crops like rice, maize, wheat, foxtail millet, and soybean, resulting in cultivars with greater vigor and increased agronomic performance. One of its major advantages is the ability to overcome trade-offs between traits, allowing multiple desirable characteristics to be improved simultaneously without compromising any, resulting in high-yielding and resilient crops (Mohamed *et al.*, 2024). Because salt tolerance is controlled by multiple genes, strategies like gene pyramiding and multiplex editing are particularly effective, enabling several salt-tolerance genes to be targeted across different developmental stages for stronger and more consistent stress resistance. Beyond improving stress tolerance, CRISPR-Cas9 also supports asexual reproduction in rice, ensuring uniform and reliable crop production, and facilitates the *de novo* domestication of wild species, such as rice and tomato, by introducing key domestication traits into otherwise undomesticated relatives.

Role of microorganisms in mitigating salinity stress

Plant growth promoting microbes: Plant growth-promoting bacteria, rhizobia, and arbuscular mycorrhizal fungi are all included in the large category of helpful microorganisms known as plant growth-promoting microorganisms (PGPMs). They live in the endosphere (internal tissues), rhizosphere (soil surrounding roots), or rhizoplane (root surface) of the plants. PGPMs support plant growth through several mechanisms, such as producing indole-3-acetic acid (IAA), solubilizing phosphate to make it available for the uptake by plants, fixing N₂ and producing useful enzymes that lessen oxidative stress, such as catalase (CAT). They also produce ACC deaminase, which lowers ethylene (ET) levels and promotes root growth, and siderophores that chelate iron, making it more

accessible to plants (Mohanty *et al.*, 2021; Singh *et al.* 2025). Previous studies have shown a number of PGPM–plant interactions during salt stress (Hoque *et al.*, 2023; Kaushal, 2020; Kumar *et al.*, 2020; Kumawat *et al.*, 2024; Liu *et al.*, 2022; Mishra *et al.*, 2021; Mishra *et al.*, 2023; Shrivastava and Kumar, 2015). Here, we categorize the fundamental mechanisms underlying PGPM-mediated mitigation of salinity stress in plants.

Role of PGPMs in the uptake and utilization of different mineral elements: Essential nutrients are fundamental for proper plant growth and achieving higher crop yields. In saline soils, the availability of these nutrients is often limited, but potassium-solubilizing bacteria (KSB) can help overcome this problem by increasing nutrient accessibility to plants. Bacterial species such as *Pseudomonas* and *Bacillus* are known to release potassium from silicate minerals, making it more available for plant uptake (Jaiswal *et al.*, 2016; Vasanthi *et al.*, 2018). Research indicates that *Burkholderia cepacia* SE4, a plant growth-promoting rhizobacterium, possesses the capacity to solubilize potassium in the soil, consequently improving its accessibility for cucumber (*Cucumis sativus*) cultivation (Kang *et al.*, 2014). In wheat, the introduction of halotolerant rhizobacteria like *Bacillus aquimaris* has been shown to sustain and even enhance the uptake of essential nutrients, including potassium, phosphorus, and nitrogen, under saline conditions (Singh *et al.*, 2025; Upadhyay and Singh, 2015). In maize, inoculation with *Azospirillum lipoferum* or *Azotobacter chroococcum* has also been found to increase potassium accumulation and improve tolerance against salt conditions (Abdel Latef *et al.*, 2020). Aside from potassium, plant growth-promoting microorganisms also help improve the availability of other important nutrients such as Fe, Zn, and S, thereby supporting better plant development against challenging environmental circumstances (Mishra *et al.*, 2023) Figure. 2.

a. Contribution of PGPMs in the production of antioxidants Plants rely on several antioxidant enzymes—such as ascorbate peroxidase (APX), catalase (CAT), glutathione reductase (GR), peroxidase (POX), and superoxide dismutase (SOD)—to protect their cells from oxidative damage, especially under stress conditions (Upadhyay and Singh, 2015). PGPMs can boost the activity of these antioxidant systems, helping plants better cope with salinity stress. For example, when maize was inoculated with *Azospirillum lipoferum* or *Azotobacter chroococcum*, antioxidant enzymes like catalase and peroxidase became much more active, increasing the plant's resistance against saline environment (Abdel Latef *et al.*, 2020). In a similar vein, rice cultivated in saline circumstances showed increased CAT and SOD activity when *Curtobacterium albidum* strain SRV4 was applied, as opposed to non-inoculated plants, which ultimately enhanced the ability of plants against salinity stress (Singh *et al.* 2025; Vimal *et al.*, 2019).

b. PGPM's contribution towards phytohormone synthesis and their regulation: The growth, development and all the physiological functions of plants are governed by various phytohormones (Acharya *et al.*, 2013; Acharya *et al.*, 2017; Miransari and Smith, 2014). Under salinity stress, hormones such as auxins, cytokinins (CK), ethylene (ET), and gibberellins (GAs) play key roles in helping plants adjust and survive in stressful conditions (Acharya *et al.*, 2022; Kaundal *et al.*, 2021). Many plant growth-promoting microorganisms (PGPMs) are capable of producing and releasing these hormones, which can be absorbed by plant roots. This interaction not only stimulates plant growth but also helps maintain hormonal balance, thereby improving the reactions of plants against salinity (Backer *et al.*, 2018).

For example, it has been demonstrated that the halotolerant PGPM strain *Glutamicibacter* sp. YD01, which contains ACC deaminase activity, improves salt tolerance in rice seedlings by lowering ethylene levels in saline environments (Ji *et al.*, 2020). In addition, PGPMs can synthesize several phytohormones—including auxins, cytokinins, ethylene, gibberellins, and salicylic acid (SA) that regulate plant physiological processes through various molecular mechanisms (Orozco-Mosqueda *et al.*, 2023; Singh *et al.*, 2025). Moreover, these microorganisms produce a variety of organic compounds that influence plant physiological activities, highlighting their vital part in promoting the growth of plants, health, and resilience under stress conditions.

Role of Arbuscular mycorrhizal fungi (AMF) against salinity stress: Figure 2: Both hypertonic and hyperosmotic conditions that cause plant mortality are experienced by plants in salt-stressed settings. Because of their persistent nature in the soil, arbuscular mycorrhizal fungi (AMF) are important for enhancing soil health (Navarro *et al.*, 2014), and increases plant growth during salinity (Seleiman and Hardan, 2021). AMF are considered crucial in helping plants tolerate salt stress in improving the absorption of water essential mineral nutrients. Their association with plant roots also enhances photosynthetic efficiency and promotes the accumulation of osmolytes that help plants cope with salinity stress (Hajiboland *et al.*, 2010; Sheng *et al.*, 2008). Under high salinity, plants often produce excessive malondialdehyde (MDA). This accelerates lipid peroxidation and compromises membrane stability (Alqarawi *et al.*, 2014; Hashem *et al.*, 2016). However, plants inoculated with AMF tend to produce lower levels of MDA while showing increased activity of antioxidant enzymes, which helps protect cells from oxidative damage (Hashem *et al.*, 2015).

Several studies have also reported that antioxidant enzyme activity is higher in AMF-colonized plants compared with non-inoculated plants, leading to better tolerance under salt stress (Hashem *et al.*, 2014; Latef and Chaoping, 2011). In addition, AMF-inoculated plants often maintain higher chlorophyll content during

salinity stress, which enhances photosynthesis and supports carbohydrate production (Aroca *et al.*, 2013; Hajiboland *et al.*, 2010). Improved availability and uptake of essential mineral nutrients further help plants reduce the negative effects of salinity (Al-Karaki, 2000; Kohler *et al.*, 2009). AMF colonized plants absorb plenty of minerals (Asghari *et al.*, 2005) facilitating a high water uptake (Ruiz-Lozano and Azcon, 1995) and boosting plant's performance in saline soils (Jahromi *et al.*, 2008). Plant hormones such as auxins (IAA, ABA) and gibberellins (GA) play important roles in regulating plant growth and development. Under salt stress, the levels of these growth regulators usually decline, which negatively affects plant growth. However, arbuscular mycorrhizal

fungus-inoculated plants frequently exhibit significantly higher concentrations of these hormones under saline conditions, helping to improve plant growth and tolerance to salinity (Hashem *et al.*, 2015; Latef and Chaoxing, 2011; Waqas *et al.*, 2012).

Grain yield, water absorption ratio and uptake of various nutrients was enhanced when PGPR and AMF were used together (Najafi *et al.*, 2012; Shirmardi *et al.*, 2010). Their combined action helps plant to adapt to a range of biotic and abiotic stressors. Other research is required to identify the most effective combinations of PGPR and AMF in order to maximize plant productivity under both biotic and abiotic stress conditions

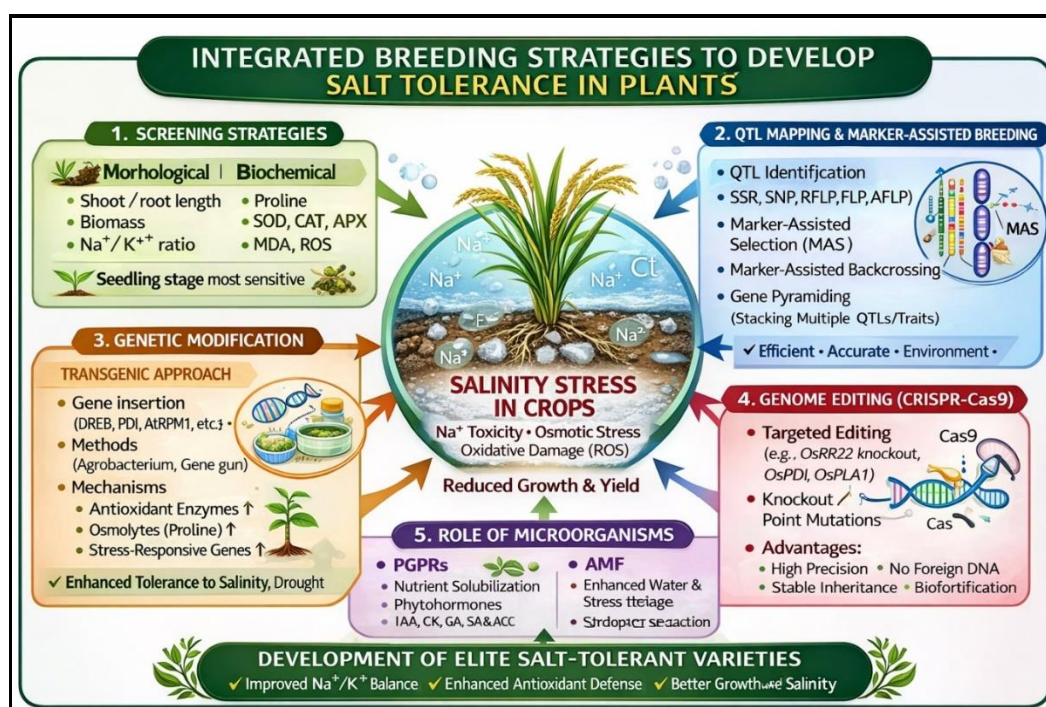


Figure 2: Integrated schematic of breeding and biotechnological approaches for improving salinity tolerance in crops, including screening, QTL mapping, genetic modification, CRISPR/Cas9, and microbial interventions. These integrated strategies mitigate ionic, osmotic, and oxidative stress, leading to enhanced growth, resilience, and yield under saline conditions.

CONCLUSION

Salinity is a "silent" but accelerating threat to global food systems that demands immediate and multi-dimensional action. This review demonstrates that no single strategy be it chemical, biological, or genetic—is sufficient to address the problem in isolation. While agronomic practices such as gypsum application, seed priming, water, nutrient and fertilizer management and applications of growth hormones provide immediate, cost-effective relief at the field level. Conventional Breeding strategies such as screening the genotypes against salt stress, Marker-Assisted Breeding and molecular approaches provide the long-term genetic foundation necessary for inherent crop resilience. Furthermore, the emerging role of Plant Growth-Promoting Microbes (PGPMs) and

Arbuscular mycorrhizal fungi (AMF) acts as a vital bridge, enhancing the plant's innate physiological defenses through improved nutrient uptake and antioxidant regulation. To meet the 2050 food production targets and sustain the world's growing population, a synergistic approach that integrates all management strategies for sustainable cereal production are not just recommended, but essential for future agricultural stability.

Research gaps and limitations

1. Despite extensive research on salinity stress management in cereal crops, several critical gaps persist that limit the development of robust and scalable solutions.

2. Current studies are largely reductionist and fragmented, focusing on single interventions such as genetic improvement, chemical amendments, or microbial applications under controlled environments. There is a notable lack of integrated, field-based investigations that evaluate the synergistic effects of these approaches under heterogeneous agro-ecological conditions.

3. Although salt-tolerant genotypes have been identified, their performance stability across diverse environments is poorly characterized due to limited multi-location and long-term studies.

4. At the molecular level, while significant progress has been made in identifying stress responsive genes, the complex polygenic nature of salinity tolerance is not fully resolved. Functional validation of candidate genes and their regulatory networks under field conditions remains limited, constraining their effective utilization in breeding programs.

5. Similarly, the application of plant growth-promoting microorganisms (PGPMs) and arbuscular mycorrhizal fungi (AMF) shows promising results in controlled settings; however, their field-level consistency, survival, and ecological adaptability under saline stress are not well established.

6. In addition, there is a lack of emphasis on long-term soil health and system sustainability. Most current management strategies address short-term stress alleviation rather than the underlying processes of soil salinization and degradation.

7. Finally, the integration of emerging technologies, including precision agriculture, remote sensing, and digital soil mapping, remains underexplored in salinity research, particularly in terms of their practical applicability and accessibility for farmers in developing regions.

Future Perspectives: Looking ahead, the development of integrated, climate-resilient management frameworks will be essential to effectively address salinity stress in cereal production systems. Such frameworks should synergistically combine advances in plant breeding, soil science, microbiology, and digital agriculture, moving beyond disciplinary boundaries toward a more unified approach. Emphasis should also be placed on translational research, ensuring that scientific innovations are scalable, economically viable, and adaptable to diverse farming systems. Strengthening linkages between researchers, extension services, and policymakers will be critical for facilitating the adoption of improved practices at the field level.

Furthermore, future strategies must prioritize farmer-centric solutions, recognizing the socio-economic realities that influence technology uptake. Incorporating indigenous knowledge, participatory

research approaches, and locally adapted practices will enhance the relevance and sustainability of proposed interventions. Ultimately, bridging the gap between experimental research and real-world application will determine the success of salinity management strategies. A shift toward systems-based, interdisciplinary, and impact-oriented research is imperative to ensure long-term productivity and resilience in salt-affected agroecosystems.

AUTHORS CONFLICT OF INTEREST

The authors declare that they have no competing interests.

AUTHOR CONTRIBUTIONS

All authors made equal contributions to this work and have read and approved the final manuscript.

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