Halotolerant Plant Growth-Promoting Rhizobacteria in Mitigating Salinity Stress

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Soil salinity is one of the major abiotic constraints in agricultural ecosystems worldwide. High salinity levels have negative impacts on plant growth and yield, and affect soil physicochemical properties. Salinity also has adverse effects on the distribution and abundance of soil microorganisms. Halotolerant plant growth-promoting rhizobacteria (HT-PGPR) secrete secondary metabolites, including osmoprotectants, exopolysaccharides, and volatile organic compounds. The importance of these compounds in promoting plant growth and reducing adverse effects under salinity stress has been widely recognised. HT-PGPR are emerging as effective biological strategies for mitigating the harmful effects of high salinity; improving plant growth, development, and yield; and remediating degraded saline soils.

exopolysaccharides

osmoprotectants

growth hormones

soil microbes

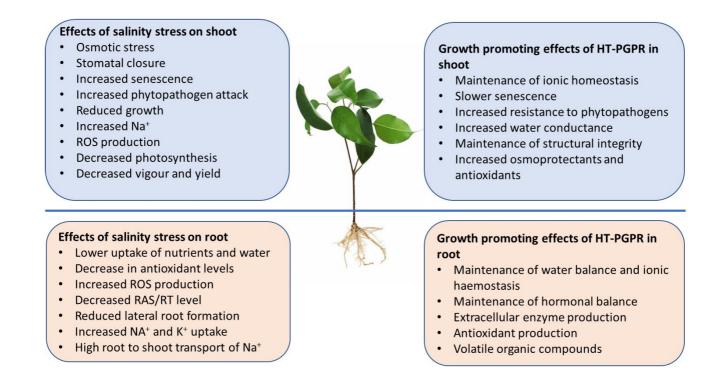
volatile organic compounds

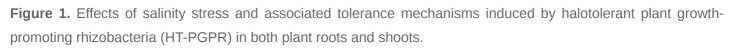
1. Introduction

Food insecurity is a growing problem globally, owing to population growth, changing climates, and declining agricultural land, which threaten sustainable agriculture ^{[1][2]}. By 2070, the world population is expected to rise from 8 billion to 10 billion people ^[3]. This will require more farmland to meet the increasing food demand, but environmental factors including rising temperatures, erratic rainfall patterns, drought and soil salinity already limit land suitable for agricultural production ^[4]. Soil salinization is a major contributor to the degradation of agricultural land and reductions in crop productivity, with salinity affecting over 800 million hectares of land or 6% of the total worldwide land area ^[5]. Crop growth is impeded by salinity due to the toxicity of certain ions, nutrient imbalances, and osmotic stress ^[6], and low levels of organic matter in the soil, all of which can amplify the unfavourable effects of salinization ^{[7][8]}. The replacement of the ions responsible for salinity, either chemically or through the addition of organic materials has been effective in the amelioration of saline soils ^[9]. The productivity of such saline soils can therefore be increased through the adoption of new sustainable approaches, such as the use of inorganic or organic soil amendments and salt-resistant crop varieties ^[10].

Based on their responses to saline conditions, plants can be separated into two categories, glycophytes and halophytes, with the majority of plant species being glycophytes, and therefore relatively intolerant to salinity ^{[11][12]}. Halophytes, salt tolerant species, have evolved specialised strategies for survival in these conditions, such as root

and shoot salt exclusion, ion compartmenting into various organs, and the synthesis of compatible solutes. The metabolic capacity of plants to respond to salt stress can also be enhanced by microbial interactions ^[13]. Research has shown many instances where microorganism-based plant biotechnology has proven to be more effective than traditional plant breeding or genetic modification techniques, and even soil amelioration approaches in alleviating soil constraints ^[14]. Microbes such as halotolerant plant growth-promoting rhizobacteria (HT-PGPR) can use a wide range of metabolic and genetic strategies to assist plants in mitigating the effects of salt stress and other abiotic stresses caused by harsh environmental conditions ^{[15][16]}. HT-PGPR are able to produce a wide range of secondary metabolites that aid in plant protection and assist in maintaining growth under saline environments, for both the symbiotic plant and bacteria species ^{[17][18]}. Most of these metabolites are only formed under abiotic stress conditions and enable the plant to survive in extreme climatic conditions, by acting on vital survival mechanisms including ion transport systems and uptake of osmoprotectants (**Figure 1**) ^[19]. Associated organic compounds have recently been shown to support plants in better adapting to saline conditions ^[20].





2. HT-PGPR: Diversity and Their Effect on Crop Production

The use of HT-PGPR has recently emerged as a viable solution to issues associated with increasing soil salinity in agricultural lands ^[21]. These halophilic and halotolerant microorganisms are already adapted to thrive in salty environments ^[22] and through symbiotic relationships with associated plant species, they can influence host plant survival, root development, and growth (**Figure 2**) ^[23]. HT-PGPR can not only recognise and react to signal molecules secreted by plant roots, but also secrete a diverse range of signalling molecules that influence plant behaviour. These microbes also synthesis beneficial molecules including siderophores, phytohormones, volatile

organic compounds (VOCs), exopolysaccharides (EPS), and other metabolites, along with solubilising nutrients such as phosphorus (P), zinc (Zn), and potassium (K) (**Figure 2**) ^{[14][15]}. These metabolites can assist plants through a wide range of biochemical, physiological, and molecular responses, including preserving ionic homeostasis through Na⁺/K⁺ transporters, enhancing water capacity, and activating *SOS* (*Salt-Overly Sensitive*) genes ^{[24][25]}, together with acting as osmoprotectants, antioxidants, and compatible solutes. This three-tiered interwoven action–cumulation association between HT-PGPR and plant salt stress responses includes the existence of the bacteria itself in hyperosmotic conditions, the induction of salt-resistance in crops, and the improvement of soil quality ^[26] (**Figure 1**). Crop salt stress has been found to be reduced by several HT-PGPR species, including *Azospirillum, Arhrobacter, Burkholderia, Alcaligenes, Bacillus, Enterobacter, Klebsiella, Microbacterium, Streptomyces, Pseudomonas, Pantoea*, and *Rhizobium* ^[27]. These species may occur naturally around crop species or can be isolated from native halophytic plants.

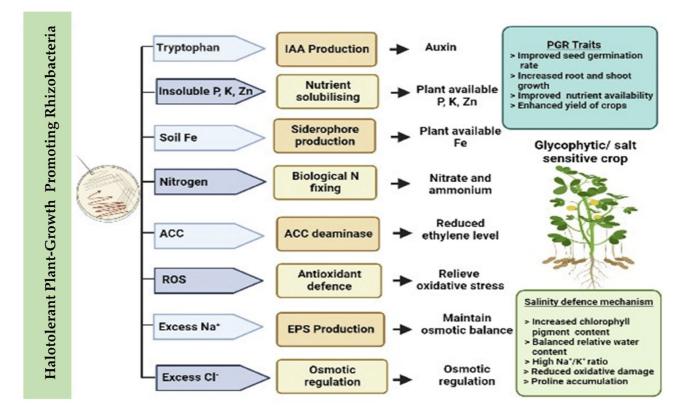


Figure 2. Effect of HT-PGPR on plant growth and salinity tolerance in glycophytic plants. The plate shown includes potential HT-PGPR isolated from native halophytes and consists of rhizobacteria and endophytes. Beneficial effects are shown in blue boxes, the underlying processes in orange boxes, and benefits plants in the last column.

Wheat inoculated with HT-PGPR *Enterobacter cloacae*, *Pseudomonas putida*, *Pseudomonas fluorescens*, and *Serratia ficaria*, then cultivated in naturally saline fields (ECe = 15 dSm^{-1}), had increased germination rates, percentage, and index by 51%, 43%, and 123%, respectively, in comparison to the nontreated controls, along with increased yield ^[28]. Another study found that the shoot and root fresh and dry biomass weights of *Brassica juncea*, cultivated in saline conditions (ECe = 12 dSm^{-1}), significantly increased after inoculation with salt-tolerant *Pseudomonas azotoformans* JMM15 and *Pseudomonas argentinensis* HMM57 strains ^[29]. Additionally, an F-11

halotolerant *Staphylococcus jettensis* F1 increased the dry biomass of *Zea mays* by a factor of three when plants were grown under 200 mM saline stress ^[30]. *Pseudomonas putida* performed best among strains tested under high salinity (15 dSm⁻¹), increasing plant height by 52%, root length by 60%, grain output by 76%, 100-grain weight by 19%, and straw yield by 67%, in wheat compared to the uninoculated crop ^[31]. Although it has been shown that HT-PGPR may improve crop production (in salt-affected soil) and reduce salinity stress, there is still much to learn about the interactions and processes that take place between plants and microorganisms under multidimensional stresses like salinity.

3. HT-PGPR and Their Effects in Mitigating Salt Stress in Crops

HT-PGPR provide plants with resistance to salt stress through several key processes. One such process is the regulation of the salt overly sensitive (*SOS*) pathway, which is involved in salt influx/efflux across membranes, through metabolites and associated gene expression patterns. It has been shown that the *SOS1* gene is directly regulated by metabolites such as EPS, VOCs, and suitable solutes (i.e., proline, glycine betaines, and trehalose) ^[25], which also direct stress regulation in *SOS* genes ^[3], *HKT1* transporter (high-affinity K) expression ^[32], and other genes implicated in the reduction in salt stress, i.e., ethylene biosynthesis and antioxidant protein encoding genes ^{[33][34]}. Examples of the beneficial effects of HT-PGPR, along with how they help plants cope with saline conditions in different plants, are reviewed and presented in **Table 1**.

Table 1. Effects of inoculating plant species with various halotolerant plant growth-promoting rhizobacteria (HT-PGPR) species. Table summarises genes involved, mechanisms to increase salt tolerance, and actual effects observed in different plants.

Plant Species	HT-PGPR Species	Gene/s Involved	Mechanism to Mitigate Stress	Effect Observed	References
Arabidopsis thaliana L.	Bacillus oryzicola YC7007	RD22, KIN1, RD29B, RD20, RD22, and ERD1	Stem and the root of the seedlings released stress- related genes	Enhanced plant tolerance to salt stress	[<u>35]</u>
	Pseudomonas putida PS01	APX2 and GLYI7	APX2 and GLYI7 genes were downregulated	ABA signalling, jasmonic acid production route, ROS scavenging, detoxification	[<u>36]</u>
	Pseudomonas knackmussii MLR6	NHX1, HKT1, SOS2, SOS3, SAG13, and PR1	Enhanced stomatal conductance, transpiration rate, chlorophyll, and carotenoid levels	Reduced electrolyte leakage and priming ROS accumulation increasing cell	[<u>37]</u>

Plant Species	HT-PGPR Species	Gene/s Involved	Mechanism to Mitigate Stress	Effect Observed	References
	Bacillus amyloliquefaciens SQR9	NHX1 and NHX7	Involved in reducing GSH biosynthesis	membrane stability Reduced ion toxicity by sequestering Na ⁺ into vacuoles and releasing Na ⁺ from the cell	[<u>38]</u>
	Burkholderia phytofirmans PsJN	Upregulation of <i>RD29A</i> and <i>GLYI7</i> , and downregulation of <i>LOX2</i>	Enhancement of proline and transcription of genes related to abscisic acid signalling and downregulated gene <i>Lipoxygenase</i> <i>2</i>	Abscisic acid signalling, ROS reduction, detoxifying, jasmonate synthesis, and ion transport	[<u>39]</u>
	Paenibacillus yonginensis DCY84 ^T	AtRSA1, AtVQ9 and AtWRKY8	Upregulated salt- stress genes	Promoted more resistance to salinity, drought, and aluminium stresses	[<u>40][41]</u>
	<i>Enterobacter</i> sp. EJ01	DREB2b, RD29A, RD29B, RAB18, P5CS1, P5CS2, MPK3, and MPK6	Upregulated salt- stress genes	Promoted more resistance to salinity and enhanced plant growth	[<u>42</u>]
	Bacillus subtilis GB03	HKT1	Down- and upregulates HKT1 in roots and shoots, respectively	Decreased total plant Na ⁺ accumulation	[<u>23</u>]
Bacopa monneri L.	Dietzia natronolimnaea STR1	SOS1, SOS4, TaST, TaNHX1, TaHAK, and TaHKT1	Reduction in ABA- signalling, upregulated <i>TaABARE</i> and <i>TaOPR1</i>	Abscisic acid signalling, ROS scavenging, antioxidant enzyme activity, enhanced ion transporter expression, high K ⁺ /Na ⁺ ratio	[<u>24]</u>

Plant Species	HT-PGPR Species	Gene/s Involved	Mechanism to Mitigate Stress	Effect Observed	References
	Bacillus pumilus STR2, Exiguobacterium oxidotolerens STR36	-	Mixture of plant growth-promoting traits under primary and secondary saline condition	Produced higher yield, high proline/lipid content peroxidation	[2]
Cicer arietinum L.	Planococcus rifietoensis (RT4) and Halomonas variabilis (HT1)	-	Biofilm and exopolysaccharides production	Improved crop growth, soil aggregation, and soil fertility	[<u>43</u>]
	Arthrobacter woluwensis AK1	-	Reduced endogenous ABA and controlled antioxidant activity	Mitigated salinity stress and increased plant growth	[44]
	Microbacterium oxydans, Arthrobacter woluwensis, Arthrobacter aurescens, Bacillus aryabhattai, and Bacillus megaterium	-	Increased production of IAA, GA, siderophores, and phosphate solubilisation	Increased antioxidant enzymes and K absorption; reduced Na ⁺ in plant tissue; phytohormone	[<u>45</u>]
Glycine max L.	Pseudomonas simiae AU	P5CS, PPO and HKT1	Downregulated HKT1, LOX, PPO, and P5CS genes	Increased chlorophyll, phosphate solubilisation, IAA, and siderophores; decreased root surface in saline	[<u>46]</u>
	Pseudomonas sp. strain AK-1	HTK1	Improve K ⁺ /Na ⁺ ratio and Exopolysaccharide production binds free Na ⁺ from soil	Increased shoot/root length and decreased Na ⁺ /K ⁺ ratio	[<u>33]</u>
	Pseudomonas simiae AU	VSP2	Increase vegetative storage protein (VSP), gamma- glutamyl hydrolase (GGH), and RuBisCo proteins	Reduced Na, increased K and P in soybean seedling roots, high proline and chlorophyll content	[<u>47]</u>

Plant Species	HT-PGPR Species	Gene/s Involved	Mechanism to Mitigate Stress	Effect Observed	References
Helianthus annuus L.	Pseudomonas libanensis TR1	-	ACC-deaminase and exopolysaccharide production	Ni and Na ⁺ accumulation potential increased along with plant growth.	[<u>48]</u>
	Pseudomonas spp.	-	Upregulating of ACC deaminase	Improved P and K contents, and K ⁺ /Na ⁺ ratio in shoot	[<u>49]</u>
	Bacillus mojavensis, B. pumilus and Pseudomonas fluorescens	S1 and S3	ACC deaminase, IAA, and proline production	Reduced plant Na concentration, stimulated root growth, improved water and nutrient absorption	[<u>50]</u>
	B. aryabhattai MS3	BZ8, SOS1, GIG, and NHX1	Increased salt stress resistance and accumulation	Adaptation of plant under saline condition	[<u>51</u>]
Hordeum vulgare L.	Bacillus amyloliquefaciens SN13	DHN	Upregulated salt stress-responsive genes and protein- related genes	Lipid peroxidation and electrolyte leakage reduced; increased rice biomass, water content, proline, and total soluble sugar	[52]
	Bacillus megaterium ST2-1	-	IAA production	Stimulated the growth of rice roots and dry biomass	[<u>53]</u>
	Pseudomonas pseudoalcaligenes ST1, Bacillus pumilus ST2	EU440977 and FJ840535	Accumulation of proline decrease with inoculation, antioxidative activity	Enhanced plant growth by ROS scavenging and higher accumulation of osmoprotectant	[<u>54]</u>
Puccinellia tenuiflora L.	Bacillus subtilis (GB03)	-	Upregulated <i>PtHKT1;5</i> and	Na homeostasis modulation,	[<u>55</u>]

Plant Species	HT-PGPR Species	Gene/s Involved	Mechanism to Mitigate Stress	Effect Observed	References
			PtSOS1 genes, downregulated PtHKT2;1	exclusive K+ absorption	
Solanum lycopersicum L.	Leclercia adecarboxylata MO1	-	ACC deaminase and IAA production	Increased soluble sugars: organic glucose, sucrose, fructose, malic, amino acid, and proline	[<u>56]</u>
	Sphingobacterium sp. BHU-AV3	-	Reduction in ROS concentration in plant	Enhanced antioxidant activities and energy metabolism	[<u>57</u>]
	<i>Enterobacter</i> sp. EJ01	DREB2b, RD29A, RD29B, and RAB18	Downregulated P5CS1 and P5CS2, and upregulated MPK3 and MPK6	Biosynthesis, defence pathway modulation, salt response	[<u>42</u>]
	Pseudomonas putida UW4	Toc GTPase	Toc GTPase genes were upregulated and reduction in ACC deaminase	Increased shoot length and chlorophyll concentration	[<u>58]</u>
Trifolium repens L.	<i>Bacillus subtilis</i> (GB03)	-	Reduced shoot and root Na ⁺ , improving K ⁺ /Na ⁺ ratio	Decreased Na ⁺ , increased chlorophyll, leaf osmotic potential, cell membrane integrity	[<u>59]</u>
Triticum aestivum L.	Pseudomonas aeruginosa GI-1, and Burkholderia gladioli GI-6	-	P solubilisation, catalase activity, IAA production, N assimilation, and siderophores production	Encouraged growth and yield and improve soil fertility	[<u>60][61]</u>
	Arthrobacter nitroguajacolicus	-	Upregulated 152 genes whereas 5 genes were downregulated	Amplified ACC, IAA, siderophore, and phosphate solubility. ROS	[<u>62</u>]

Plant Species	HT-PGPR Species	Gene/s Involved	Mechanism to Mitigate Stress	Effect Observed	References
				detoxification, Na ⁺ homeostasis, abiotic stress	
	Serratia marcescens CDP- 13	-	Increased salt tolerance in plant	ACC deaminase, phosphate solubilisation, siderophore, indole acetic acid, N fixation, and ammonia synthesis	[<u>63]</u>
	Pseodomonas sp and Enterobacter cloacae (R-10)	<i>B-22</i> and <i>S-49</i>	K and Zn solubilisation for identifying antifungal activity	Enhanced K ⁺ uptake, dry matter of wheat	[<u>64]</u>
	Hallobacillus sp. SL3 Bacillus halodenitrificans PU62	acdS	IAA production and siderophore production, phosphate solubilising, and siderophore production	Increased root elongation and dry weight	<u>[65]</u>
Zea mays L.	Serratia liquefaciens KM4	Upregulation of stress-related genes (APX, CAT, SOD, RBCS, RBCL, H ⁺ -PPase, HKT1, and NHX1)	Regulating redox potential and stress-related gene expression	Higher leaf gas exchange, osmoregulation, antioxidative defence mechanisms, and nutrient uptake boosted maize growth and biomass production	[<u>66</u>]
	Azospirillum lipoferum, Azospillum sp., Azotobacter chroococcum, Azotobacter sp., and Bacillus sp.	-	Exopolysaccharide inoculation in the soil	Increased root and shoot dry weights, chlorophyll and carotenoids, restricted Na and Cl uptake, and increased shoot N, P, and K	[<u>67]</u>

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Plant	HT-PGPR	Gene/s	Mechanism to	Effect	References ^{rcia}
Species	Species	Involved	Mitigate Stress	Observed	Effects
Abelmoschus esculentus L.	<i>Enterobacter</i> sp. UPMR18	X55749	ROS pathway upgradation and enhancement in antioxidant enzyme activities	Higher germination, growth, and chlorophyll improved salt tolerance	^[68] owth

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