# Amelioration of Salinity Stress: Recently Developed Strategies

A wide spectrum of reactive and proactive approaches has been experimented that can individually or in combination mitigate the salinity stress and improve growth and resistance in plants (glycophytes) under salty conditions (Ondrasek & Rengel, 2021). The classical genetic breeding and transgenic approaches enhance salinity tolerance in plants by improving their defense system via gene-modification. This involves the production and modification of compatible osmolytes, hormones, antioxidants, polyamines, transporter proteins, and regulator proteins and transcription and other splicing mechanisms. The genetic manipulation at hormone or protein level, cutting-edge techniques, and function of microRNAs as transcriptional players are key engineering practices that develop tolerance against salt in crop plants (Wani et al., 2020). Crassulacean acid metabolism, an evolved carbon fixation pathway in plant cells that help them strive in arid conditions, can also be triggered by salt stress, thus increasing water-use efficiency in plants. *Talinum triangulare* (Montero et al., 2018) and *Mesembryanthemum crystallinum L.* (Nosek et al., 2021) have shown salt-induced CAM, and consequently growth in naturally saline habitats. To understand the molecular mechanisms related to plants tolerance to abiotic stresses, especially salinity, clustered regularly interspaced short palindromic repeat/Cas9 (CRISPR/Cas9) has been the part of comprehensively opted genome-editing technologies of plant breeders for gene-modification (X. Li et al., 2022). Transcription activator-like effector nucleases (TALENs) is another powerful tool for gene editing (Sharma et al., 2023), used to improve abiotic stress tolerance in plants (X. Li et al., 2022). The genetic and breeding approaches, transgenic methods, molecular strategies, miRNAs mechanisms, CAM pathways, and CRISPR Cas have been successfully implemented for amelioration of salinity stress in plants, but their high dependency on technology, time constraints, predictability, and other limitations are under focus in present scenario (Ondrasek et al., 2022).

Gene modification and development of salt-tolerant plants is not a cost-effective approach to achieve sustainable agriculture goals and to fill the gaps, the plant microbiologists stepped in to study the microbial inoculation to alleviate salt stress in plants. Use of plant growth promoting microorganisms (PGPMs) in *Zea mays (L).* (Bano & Fatima, 2009), *Solanum lycopersicum L.* (Ali et al., 2014), *T. aestivum* (Barnawal et al., 2017), *Oryza sativa* (Kumar et al., 2021), *Medicago truncatula* (L. Li et al., 2017), *Lactuca sativa* (Fasciglione et al., 2015), and *Phaseolus vulgaris L.* (Talaat, 2019) and their mechanisms including phosphate solubilization, biological nitrogen fixation, production of 1-Aminocyclopropane-1-carboxylate deaminase (ACC), volatile organic compounds (VOCs) synthesis, siderophore synthesis, biofilm production inhibition, quorum sensing, systemic resistance, etc., have been literature. The potential of PGPMs towards stress resistance and sustainable agriculture offers an adaptive pathway towards the replacement of pesticides, artificial fertilizers, and other chemical supplements (Bhattacharyya & Jha, 2012).

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| **Sr.** | **Specie** | **Family** | **Role (or application) under salinity stress** | **Plant (Chosen for experiment)** | **Experiment Condition** | **Reference** |
| **1** | *Acinetobacter sp.* | Moraxellaceae | produce osmoprotectants i.e., exopolysaccharides, trehalose, etc. | *Saccharum sp.* (Sugarcane) | Greenhouse | (Patel et al., 2022) |
| **2** | *Actinobacteria* | Actinomycetaceae | produce IAA (Indole-3-acetic acid), suppress pathogens increase in soil, and improve nutrient uptake | *Solanum lycopersicum* (Tomato) | Culture media | (Rangseekaew et al., 2021) |
| **3** | *Alcaligenes faecalis* | Alcaligenaceae | produce IAA and solubilize phosphorus | *Triticum aestivum L.* (Wheat) | Field experiment | (Omer, 2017) |
| **4** | *Anabaena sp.* | Nostocaceae | reduce osmotic potention of soil (saline soil) | *Cupressus lusitanica* (cedar-of-Goa/Mexican cedar) | Pot experiment | (Brito et al., 2022) |
| **5** | *Arthrobacter ilicis* | Micrococcaceae | produce plant growth hormones and regulators and increase nutrient uptake | *Zea mays* (Maize) | Cuture media | (Vanissa et al., 2020) |
| **6** | *Arthrobacter mysorens* | Micrococcaceae | produce ACC (1-aminocyclopropane-1-carboxylate) deaminase | *Solanum lycopersicum* (Tomato) and *Zea mays* (Maize) | Culture media | (Oliva et al., 2023) |
| **7** | *Arthrobacter pokkalii* | Micrococcaceae | produce stress metabolites and modulate stress responsive genes | *Oryza sativa* (Pokkali Rice) | Culture media | (Krishnan et al., 2016) |
| **8** | *Azospirillum brasilense* | Rhodospirillaceae | produce plant growth hormones and regulators and modulate stress responsive genes | *Trifolium repens* (White Clover) | Pot experiment | (Khalid et al., 2017) |
| **9** | *Azotobacter chroococcum* | Azotobacteraceae | produce antioxidant enzymes, compatible solutes, and modulate stress responsive genes | *Brassica napus L.* (Canola/Rapseed) | Pot experiment | (Abdel Latef et al., 2021) |
| **10** | *Bacillus subtilis* | Bacillaceae | produce stress metabolites and enhance plant growth | Triticum aestivum L. (Wheat) | Pot experiment | (Gul et al., 2023) |
| **11** | *Brevibacterium oxydans* | Microbacteriaceae | produce IAA and improve nutrient uptake | Oryza sativa L. (Rice) | Pot experiment | (Chatterjee et al., 2018) |