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Role Of Halophilic Microorganisms in the Bioremediation of Salt-Affected Soils

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ABSTRACT

The biology that supports and restores higher creatures is influenced by the bacteria that live in the soil. Many different halophilic and halotolerant microorganisms, spanning numerous evolutionary groupings, predominate in the salt-affected soil types. When plants are stressed by salt, these bacteria may be able to promote plant development and release enzymes. Since plant growth is inhibited in high salinity soils, halophiles have the potential to improve plant growth and yield in salinity-affected soils. Recent study has highlighted the value of this environmentally benign method of using halophiles to bioremediate salt-affected soils and maximize crop yields under stress.

Key words: *Halophilic microorganisms, saline soils, bio-remediation, halo tolerance*

1. INTRODUCTION

Life can be found in all types of natural habitats, including freshwater settings, hypersaline lakes and oceans, and other areas where sodium chloride is present in high concentrations, such as saline and saline-alkali soils. Often, the characteristics of the soil serve as the most definitive indicator of the boundaries within which the ecosystem may function, and the soil is invariably the element of the ecosystem that is most adaptable to changes. The impact of the elevated salt concentrations obscures additional soil formation mechanisms, soil characteristics, and environmental factors, frequently modifying them.

Salt-affected soil is defined as having an excess of salts that reduces its production (Figure 1) (Chhabra, 1996). Saline soil, which has a high concentration of soluble salts such as Ca2+, Mg2+, K+, and Na+; sodic soil, which is dominated by Na+ salt; and saline-sodic soil, which has a high concentration of soluble salts such as Ca2+, Mg2+, K+, and Na+. An estimated 952.2 million hectares of land worldwide are thought to have salt-affected soils, making up around 7% of all land and roughly 33% of all land that could be arable. Salt-affected soils make up 6.727 million hectares (2.1%) of India's total land area.

Increases in the amounts of exchangeable cations, soil response, physical characteristics, and the impacts of osmotic and specific ion toxicity are just a few of the ways that an accumulation of soluble salts in the soil can affect farm production. It is not cost-effective to recover them by physical or chemical means, and there are issues with gypsum and other chemical amendment supply. By directly promoting vegetation development and hence indirectly raising agricultural yields in salinized soils, halophilic bacteria are applied to restore salinized soils. In order to remove sodium ions from the inside of the cell, all halophilic bacteria have strong transport systems, which are often based on Na+/H+ antiporters (Oren, 2002).

Auxins are produced by certain halophiles, which encourage the growth of roots, and some of them exhibit ACC deaminase activity, which eliminates stress and ethylene from the rhizosphere. Salt is also extracted from saline soils by halophilic microorganisms (Bhuva et al., 2013). According to studies (Ravikumar et al., 2007; Chakraborty et al., 2011), potentially salt-tolerant bacteria that have been isolated from soil or plant tissues and possess a plant growth promotion trait help to reduce salt stress by encouraging seedling growth and increasing the biomass of crop plants grown under salinity stress.

The production of phytohormones, the biocontrol of host plant diseases, and the enhancement of plant nutritional status have all been linked to endophytic salt-tolerant bacteria living within plant tissues, either directly or indirectly promoting plant growth (Pandey et al., 2008; Rosenblueth and Romero, 2006; Arora et al., 2014). Furthermore, according to Hung and Annapurna (2004) and Son et al. (2006), they have the ability to solubilize phosphates. A more effective technique for reclaiming soils impacted by salinity is plant-microbe interaction, which is a mutually beneficial relationship between plants and microbes. When using this technique, bacteria are the most often utilized microorganism. Still, other potentially useful microorganisms include actinomycetes, fungus, and archaea, which can be found in high salinity conditions.

Halophilic microorganisms have a significant potential for use in bio-remediation applications for salt-affected soils

Halophilic microorganisms

Salt-affected habitats are specialized ecotones because many organisms are severely limited by the presence of high osmotic pressure, ion toxicity, unfavorable soil physical conditions, and/or soil floods. Many of the endemisms that were discovered there had evolved defense mechanisms to withstand such unfavorable conditions. Known as "salt-loving" or halophilic microorganisms, they thrive in high-salinity settings that would be lethal to most other microorganisms. Microorganisms that are both halophilic and halotolerant can flourish in hypersaline conditions, although only halophiles in particular need at least 0.2 molar (M) of salt to develop. Microbes that are halotolerant are limited to medium that have less than 0.2 milligrams of salt in it. Based on how much salt they require and can tolerate, distinct types of halophilic bacteria can be distinguished.

Microbes that respond to salt fall into five categories, under Kushner's (1993) classification:

1. A non-halophilic salt with a concentration of less than 0.2 M (~1%).

2. 0.2–0.5 M (~1-3%) salt, mild halophiles

3. Mildly halophilic salts, 0.5–2.5 M (~3–15%)

4. Extremely close to the border halophiles, 1.5–4.0 M (~9–23%) of salt

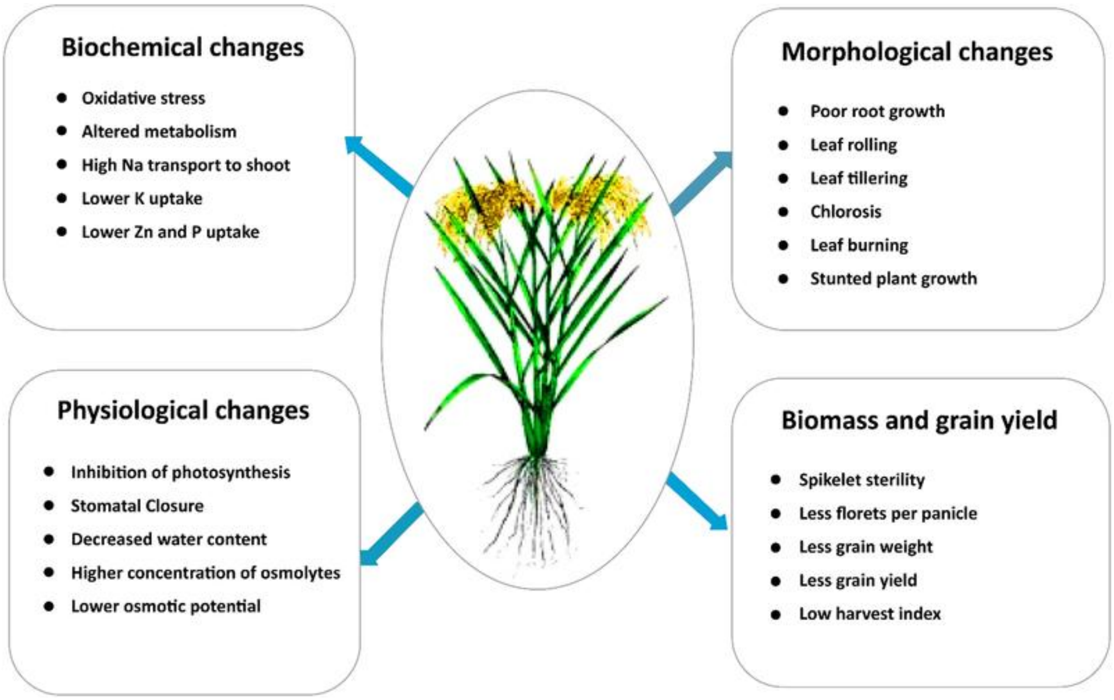
5. Severe halophiles, 2.5–5.2 M (~15–32%) of salt.

In medium with less than 0.2 M (~1%) salt, the halotolerant grows most readily. High salt concentrations are also tolerated by it. Many papers make frequent reference to this definition (Ventosa et al., 1998; Yoon et al., 2003; Arahal and Ventosa, 2002).

Diversity of soil microbes

The distribution of the microbial community in the soil is not random. The host plant and various other factors, including soil composition, organic matter, pH, water and oxygen availability, are important in determining which natural plants are selected (Ross et al., 2000). The soil becomes more significant, particularly in agricultural soils that are salinized due to irrigation techniques and chemical fertilizer application. This effect is always more noticeable in the rhizosphere because of the plants' higher transpiration-induced water intake. Therefore, according to Tripathi et al. (1998), a category of the most adapted microorganisms is the rhizobacteria. Numerous Grampositive organisms have been found in saline or hypersaline soils, and they have been taxonomically described.

Microbial strains available as biofertilizers for different crops do not perform effectively under salt stress and their activity decreases when used in salt-affected soils due to osmolysis. Halophilic plant growth-promoting microbes have potential to ameliorate salt-affected soils by directly supporting the growth of vegetation and thus indirectly increasing crop yields under salt stress (Arora et al., 2021).



Source:- Razzaq et al., (2019).

The microbiota found in hypersaline soils is not as similar to that found in hypersaline waters as it is to that found in nonsaline soils. According to Quesada et al. (1983), this indicates that environmental characteristics as a whole have a greater influence on the microbiota within a certain habitat than do individual parameters like high salinity. Plant species (Marshner et al., 2001; Miethling et al., 2000) and soil properties (Degens et al., 2000) are the primary determinants of rhizosphere microbial communities, and the structure and function of plant root systems contribute to the establishment of the rhizosphere microbial population (Russell, 1977). Compared to the surrounding soil environment, the microbial community in the rhizosphere—the area around plant roots—is typically substantially larger (Nihorimbere et al., 2011).

In comparison to the bulk soil, it indicates that the rhizosphere supports higher microbial growth rates and activity. The greater availability of soluble organic molecules as a result of plant root exudation is one of the primary causes of these faster development rates. Although the volume and quality of root exudates vary depending on plant species and abiotic factors like temperature and water content, they usually consist of carbohydrates, amino acids, and sugars. Bacteria, archaea, fungi, viruses, actinomycetes, and vesicular arbuscular mycorrhiza (VAM) are the most often observed organisms in habitats with high concentrations of salt. Halophilic bacteria are a source of new enzymes with highly desirable features that are useful for industrial biocatalysis.

The inherent durability of halotolerant and halophilic microorganisms at high salt concentrations has led to the description of several enzymes from these microorganisms over the years, opening up new opportunities for industrial operations. These enzymes may find application in demanding industrial procedures like washing, biosynthetic processes, and food processing (Ventosa et al., 2005). At high salt concentrations, hemophilic enzymes remain active and stable due to unique molecular characteristics that enable them to withstand osmotic stress. These enzymes have a limited amount of hydrophobic residues at their surface and an excess of acidic residues over basic residues, as demonstrated by Mevarech et al. (2000).

The low molecular weight organic substances known as compatible solutes, which are accumulated intracellularly by halophilic and halotolerant bacteria to attain osmotic equilibrium, include polyols, amino acids, sugars, and betaines. In contrast, halophilic bacteria that are heavy metal resistant may be employed in saline-polluted settings as bioassay indicator organisms. Numerous bacteria that are halophilic and halotolerant that were isolated from hypersaline soils may withstand high concentrations of various metals, including Co, Ni, Cd, or Cr (Nieto et al., 1989; Rios et al., 1998). Because of the extremely salty circumstances in the biological therapy, the commonly used microorganisms only exhibit weak degradative activity.

Innovative research is promised by the potential of halophilic organisms in the treatment of wastewater. Apart from that, halophilic acid is also utilized to restore saline soil by directly promoting vegetation development, which in turn raises crop yields in saline soil indirectly.

DIVERSITY OF HALOPHILIC SOIL MICROORGANISMS

Halophilic soil bacteria

For bacteria, the soil is a vital home. Soil bacteria exist in two forms: as individual cells or as microcolonies embedded in a polysaccharide matrix. Soil-dwelling bacteria contribute to the preservation and rehabilitation of higher creatures' biology. Many different kinds of halophilic and halotolerant microorganisms spanning numerous evolutionary groupings are found in the domain bacteria (Ventosa et al., 1998). Proteobacteria are divided into several branches, each of which has halophilic members and frequently near nonhalophilic cousins. Halophiles are also present in actinomycetes, cyanobacteria, spirochetes, and the Flavobacterium-Cytophaga branch (Oren, 2002). Halophiles are present in both the anaerobic and aerobic branches of the lineages of Gram-positive bacteria (Firmicutes), including *Bacillus* and related organisms.

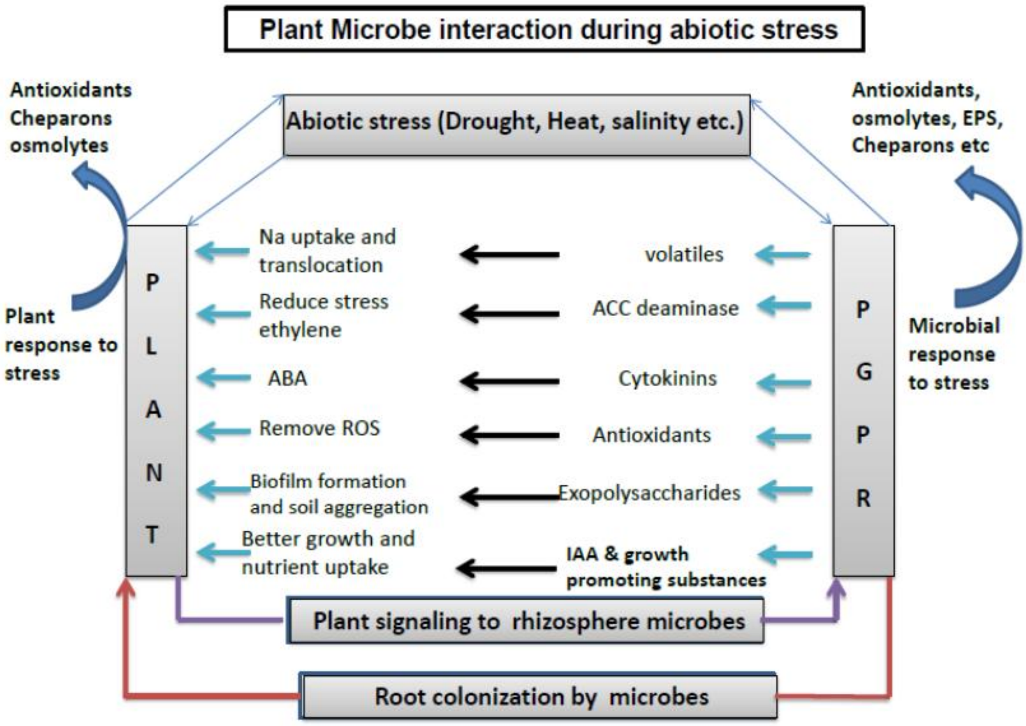
In general, it may be said that moderate halophiles predominate over extreme halophiles among the bacteria in the domain (Table 1). Still, a few species have salt tolerance and needs similar to those of the Archaeal halophiles of the Halobacteriaceae family.

Saline soil has a large amount of halophilic bacteria, according to Rodriguez-Valera (1988), and the most common species found there are from the genera Alcaligenes, Bacillus, Micrococcus, and Pseudomonas. In saline soils and saltern sediments found in various parts of Spain, Garabito et al. (1998) identified and examined 71 halotolerant Gram-positive endospore-forming rods.

S/N	Species	Gram's nature	Isolation Source	Reference
1	*Bacillus krulwichiae*	P	Soil from Tsukuba, Ibaraki,Japan	Yumoto et al. (2003)
2	*Bacillus haloalkaliphilus*	P	Showa, Saitama	Akinobu Echigo et al. (2005)
3	*Bacillus oshimensis*	P	Soil from Oshymanbe, Oshima, Hokkaido, Japan	Yumoto et al. (2003)
4	*Bacillus patagoniensis*	P	Rhizosphere of the perennial shrub Atriplex lampa in north-eastern Patagonia, Argentina	Olivera et al. (2005)
5	*Gracilibacillus halotolerans*	P	Shiki, Saitama	Akinobu Echigo et al. (2005)
6	*Halobacillus halophilus*	P	Salt marsh and saline soils	Spring et al. (1996)
7	*Halobacillus karajensis*	P	Saline soil of the Karaj region, Iran	Amoozegar et al. (2003)
8	*Halomonas anticariensis*	N	Soil from Fuente de Piedra. Málaga, Spain	Martínez-Cánovas et al. (2004)
9	*Halomonas boliviensis*	N	Soil around the lake Laguna Colorada, Bolivia	Quillaguaman et al. (2004)
10	*Halomonas maura*	N	Soil from a solar saltern at Asilah, Morocco	Bouchotroch et al. (2001)
11	*Halomonas organivorans*	N	Saline soil from Isla Cristina, Huelva, Spain	Garcia et al. (2004)

As highly halotolerant microorganisms, most of these isolates were categorized as belonging to the genus Bacillus and could grow in up to 20 or 25% of salts.

Halophilic traits were observed in several alkaliphilic Bacillus species that were isolated from soil samples. Straight and rod-shaped, with peritrichous flagella that yield ellipsoidal spores, Bacillus krulwichiae is a facultatively anaerobic (Yumoto et al., 2003) bacteria that was identified in Tsukuba, Japan. The only carbon source that they may use is benzoate or mhydroxybenzoate. The rhizosphere of the perennial shrub Atriplex lampa in northeastern Patagonia was the source of Bacillus patagoniensis (Olivera et al., 2005). As stated by Yumoto et al. (2005), Bacillus oshimensis is another. This species is facultatively alkaliphilic, halophilic, and nonmotile. The genus Virgibacillus is another illustration. This genus contains eight species, two of which, Virgibacillus salexigens (Heyrman et al., 2003) and the recently identified Virgibacillus koreensis (Lee et al., 2006), are moderately halophilic and have been isolated from soil samples. Other somewhat halophilic, endospore-forming, aerobic or facultatively anaerobic Gram-positive bacteria have been categorized under taxa related to Bacillus. Among the genera that contain halophilic species that have been isolated from soil samples are Filobacillus, Tenuibacillus, Lentibacillus, and Thalassobacillus. The genera Filobacillus, Thalassobacillus, and Tenuibacillus have species that are somewhat halophile.



(Source: Sanjay Arora 2021- Unpublished data)

Based on the type of peptidoglycan present in its cell walls, the genus Halobacillus can be distinguished from other closely similar genera. Two halophilic species within these genera have been identified from soils: Halobacillus halophilus (Spring et al., 1996) and Halobacillus karajensis (Amoozegar et al., 2003). Two halophilic soil species have been found in the genus Lentibacillus. A Lentibacillus salarius from a saline sediment in China (Jeon et al., 2005) and a Lentibacillus salicampi recovered from a salt field in Korea (Yoon et al., 2002). Three genera are included in the family Nocardiopsaceae: Streptomonospora (Cui et al., 2001), Thermobifida (Zhang et al., 1998), and Nocardiopsis (Meyer, 1976).

According to Li et al. (2006), a few species of the genus Nocardiopsis that have been isolated from soil samples and are somewhat halophilic are Nocardiopsis gilva, Nocardiopsis rosea, Nocardiopsis rhodophaea, Nocardiopsis chromatogenes, and Nocardiopsis baichengensis. Each of these was isolated from salty sediment found in China's Xinjiang Province. Gram negative, moderately halophilic bacteria, such as Natranobacterium sp-1, were found in salt pans in Kovalam, Kanyakumari district, Kerala, India, during a study of diversity over time (Saju et al., 2011).

The family Halomonadaceae currently includes a large number of Gram-negative, highly halophilic, or halotolerant species. Three genera—Halomonas, Chromohalobacter, and Cobetia—have halophilic species within this family. Halomonas is one of the genera that makes up this family; it has around 40 species with a wide range of characteristics. Species that were isolated from soil samples include: As a result of their ability to thrive in media with pH values between 8 and 9, Halomonas organivorans and Halomonas boliviensis (Quillaguaman et al., 2004)—species of bacteria that originated from saline soil samples in Spain—were characterized as alkaliphilic and alkalitolerant, moderately halophilic, respectively.

The species Marinobacter hydrocarbonoclasticus belongs to the genus Marinobacter, which was established in 1992 to accommodate Gram-negative, moderately halophilic, anaerobic Gammaproteobacteria that use a range of hydrocarbons as their only source of carbon and energy (Gauthier et al., 1992). Additionally, Marinococcus halophilus and Marinococcus albus, which are somewhat halophilic, can be accommodated (Hao et al., 1984). A third species, Marinococcus halotolerans, was reported by Li et al. (2005) to be incredibly halophilic. They grow as motile cocci up to 20% NaCl and in a broad range of salt concentrations.

The 13 species in the genus include the moderately halophilic Marinobacter lipolyticus (Martin et al., 2003), Marinobacter excellens (Gorshkova et al., 2003), Marinobacter sediminum (Romanenko et al., 2005), and the recently identified Marinobacter koreensis (Kim et al., 2006). They were isolated from soil samples.

Fungal diversity in saline environment

It was not until the last ten years that the significance of halophilic fungi—which are essential components of hypersaline ecosystems—became apparent. An review of the biology of the most common and halophilic/halotolerant yeasts and fungi was provided by Gunde-Cimerman (2009) in Ljubljana, Slovenia. These include Aureobasidium pullulans, which grows up to 3 M NaCl, Wallemia ichthyophaga, a true halophile that needs at least 1.5 M NaCl to grow to saturation, and the black yeast Hortaea werneckii, which grows up to 5 M NaCl. GundeCimerman et al. (2009) state that the most recent definition of halophilic fungus is those species that are frequently isolated on selected saline media from habitats with salinities above 10% and that can thrive in vitro on media with at least 17% NaCl. All of these are frequently found in hypersaline lakes as well as a wide range of other, frequently surprising, settings, such as polar ice, home dishwashers, and maybe even spider webs in desert caves (Gunde-Cimerman et al., 2009). A low osmotic potential causes morphological alterations and altered gene expression in fungus, leading to the development of thick-walled spores (Juniper and Abbott, 2006; Liang et al., 2007). It also reduces hyphae growth and spore germination. It has been shown that fungi are more susceptible than bacteria to osmotic stress. In soils salinized with varying sodium chloride concentrations, the overall fungus count significantly decreases.

Low salt concentrations are retained in the cytoplasm of halophilic and halotolerant fungi, which use polyols including glycerol, erythritol, arabitol, and mannitol as osmotic solutes. Plemenitas et al. (2014) (Ljubljana, Slovenia) reported molecular investigations on the osmotic adaptation of Hortaea werneckii and Wallemia ichthyophaga. The study conducted by Vaupotic et al. (2007) revealed the identification and structural characteristics of Na+-sensitive 3-phosphoadenosine5-phosphatase HwHal2, which is a potential factor in halotolerance in H. werneckii and a possible transgenic for enhancing halotolerance in crops.

Some chemoheterotrophic cell-walled eukaryotes, such as yeasts and other fungi, are highly suited to survive in hypersaline conditions. They thrive in anaerobic environments on carbohydrates in a pH range of acidic to neutral at moderate temperatures. Isolated from seawater, Debaromyceshansenii is a halotolerant yeast that can grow aerobically in salinities as high as 4.5 mol/L NaCl. During the logarithmic phase, it yields glycerol, a compatible solute, and during the stationary phase, arabitol. In the Great Salt Lake, it was discovered that Cladosporium glycolum, a saprophytic hyphomycete, was growing on submerged wood panels at a salinity higher than 4.5 mol/L NaCl NaCl. From salted fish, halophilic fungi such as Polypaecilum pisce and Basipetospora halophila have also been isolated (DasSarma and Arora, 2001).

Vesicular arbuscular mycorrhiza

In saline environments, VA-mycorrhizal fungi naturally occur (Khan and Belik, 1994). A number of scientists looked into the connection between the salinity of the soil and the presence of mycorrhizae on halophytes. They observed that when the concentration of salt varied, so did the quantity of VAM spores or the infectivity of VAM fungi (Juniper and Abbott, 1993). Saline soil stressors can affect the growth of fungi, plants, or both. Glomus spp. are the VA-mycorrhizal fungi that are most frequently found in salty soils (Juniper and Abbott, 1993). This suggests that the fungus may be suited to grow in saline circumstances, but ecological specificity has not been proven. Research suggests that elevated salinity significantly alters the distribution of VAM species (Stahl and Williams, 1986). Glomus intraradices, G. versiform, and G. etunicatum were the most common species of arbuscular mycorrhizal fungus (AMF) in the extremely salinized soils of the Tabriz plains, according to Aliasgharzadeh et al. (2001). The scientists also discovered that the quantity of AMF spores was not considerably impacted by the salinity of the soil, and they noted a comparatively high spore number (mean of 100 per 10 g soil). The increased density of fungal spores in salty soils could be attributed to the stimulation of sporulation by salt stress (Tressner and Hayes, 1971). This implies that under extreme saline circumstances, AMF could generate spores at low levels of root colonization (Aliasgharzadeh et al., 2001).

Few studies have shown that mycorrhizal fungi can promote the growth of plants that are found in saline environments (Ojala et al., 1983; Pond et al., 1984). Although the exact process is unknown, VA-mycorrhizal fungus may be able to shield plants from salt stress. According to the scant information that is currently available, fungus may be able to promote plant development by improving nutrient uptake. The effectiveness of three AMF species—*Glomus mosseae, Glomus intraradices*, and *Glomusclaroideum*—to reduce salt stress in olive trees grown in nurseries was recently investigated by Porras-Soriano et al. (2009).

Mechanisms for halotolerance

The ability of living things to withstand high salinity is known as halotolerance. As water is lost to the external medium until osmotic equilibrium is reached, high osmolarity in hypersaline conditions can be harmful to cells. A lot of microbes build up osmotica in their cytosol in response to an increase in osmolarity, which shields them against cytoplasmic dehydration (Yancey et al., 1982). Since biological membranes are water-permeable, all microorganisms need to maintain their cytoplasm at least isoosmotic with their surroundings to avoid losing cellular water; if turgor pressure is to be maintained, the cytoplasm should even be slightly hyperosmotic. There is an evolutionary relevance to adaptation to high salinity environments.

The concentration of brines throughout prebiotic evolution points to the early evolutionary stages of haloadaptation (Dundas, 1998). Osmophily is associated with the osmotic characteristics of living in high salinity environments, particularly desiccation, turgor pressure, and cellular dehydration. The ionic needs for life at high concentrations of salt are referred to as halophily. The two ways that halophilic bacteria typically employ to survive in saline environments are the "salt-in" strategy and the "compatible solute" strategy (Ventosa et al., 1998).

Cell volume is preserved once an isoosmotic balance with the medium is reached. Most moderately halophilic and halotolerant bacteria, as well as certain yeasts, algae, and fungi, use a compatible solute strategy. By balancing their osmotic potential through the synthesis or uptake of organic compatible solutes and minimizing the exclusion of salts from their cytoplasm, cells employ this technique to maintain low concentrations of salt in their cytoplasm. The small organic molecules known as suitable solutes, or osmolytes, are soluble in water to molar concentrations and build up in halophiles. They are utilized in all three domains of life and are widely available.

The chemicals are divided into two groups: (1) amino acids and their derivatives, which include proline, glutamine, glutamate, glycine betaine, ectoine, and N-acetyl-β-lysine; and (2) polyols, which include glycine betaine, ectoine, sucrose, trehalose, and glycerol, and do not interfere with metabolic processes or have a net charge at physiological pH. According to Shivanand and Mugeraya (2011), there are two ways to achieve accumulation: absorption from the medium or de novo synthesis.

The first known chloride-dependent bacterium is Halobacillus, which is essential for the activation of solute accumulation among other cellular processes. By producing several suitable solutes, Halobacillus adjusts its osmolyte strategy based on the salinity of its surroundings. Proline and ectoine predominate at high salinities, but glutamine and glutamate dominate at intermediate salinities. Glutamate synthetase is activated and its expression is stimulated by chloride. Next, by stimulating the expression of the genes responsible for proline biosynthesis, the product glutamate initiates the manufacture of proline (Saum et al., 2012).

Applications of halophilic bacteria

The activities of halophilic bacteria in natural environments, such as their involvement in the biogeochemical processes of C, N, S, and P, the formation and dissolution of carbonates, the immobilization of phosphate, and the production of growth factors and nutrients, as well as their simple nutritional requirements, make them highly promising for use in biotechnological applications (Rodriguez-Valera, 1993). Most of them are able to get their only carbon and energy from a wide variety of substances. The majority can thrive in environments with high salt concentrations, reducing the possibility of contamination. It also appears possible to manipulate the halophiles' genetic makeup because a number of genetic tools created for nonhalophilic bacteria can also be used for halophiles (Ventosa et al., 1998).

Compatible solutes produced by halophilic bacteria are helpful for the biotechnological synthesis of osmolytes. As well as stabilizing enzymes, nucleic acids, membranes, and entire cells, certain suitable solutes, particularly glycine, betaines, and ectoines, can be employed as stress protectants against desiccation, freezing, high salinity, and heat denaturation. These substances have the most promising industrial uses in enzyme technology. The greatest effectiveness of lactate dehydrogenase protection against freeze-thaw treatment and heat stress was demonstrated by the other suitable solutes, such as trehalose, glycerol, proline, ectoines, sugars, and hydroxyectoine from halophilic bacteria.

Moreover, some extra- and intracellular enzymes as well as antibacterial substances of current commercial importance are produced by halophilic bacteria (Kamekura and Seno, 1990). Strong industrial processes benefit from the ability of halophilic bacteria to produce enzymes with maximum activity at high salinities. Halophilic bacteria can be used in environmental biotechnology to:

(1) recover salty soil;

(2) decontaminate industrial effluent that is either saline or alkaline; and

(3) break down harmful substances in hypersaline situations.

The theory behind using halophilic bacteria to restore saline soils is that microbial activity in the soil may encourage plant development in salt-stressed environments. By using these bacteria as bio-indicators in saline wells, the second theory is supported. Depending on how well they thrive at various salt concentrations, indicator microorganisms can be chosen. Based on these organisms, it may be possible to reduce soil desertification by using well water to produce low salinity contamination of plants or soils (Ramos- Cormenzana, 1993). The last theory proposes the use of genetic manipulation to apply the DNA of halophilic bacteria to wild type plants in order to help them adapt to thrive in saline soil by providing necessary enzymes that are taken from halophiles.

2. CONCLUSIONS

Our present understanding of the physiology, ecology, taxonomy, and evolutionary relationships of halophilic bacteria from salty soils has expanded as a result of numerous investigations. Few hypersaline settings have been thoroughly investigated with molecular techniques. According to recent research on metabolic activity of bacteria and archaea, these settings could support a variety of consortia of microorganisms that are difficult to cultivate. The peaks of hypersaline conditions, could produce very intriguing taxa. There are several difficulties with explaining the behavior of microorganisms in saline soil environments that persist as unsolved. The research described earlier indicates that VA mycorrhizal endobiont fungi and flood-tolerant plants coexist, and that the fungi may be able to lessen the stress that flooding causes on plants in aquatic environments. According to certain recent research, rice grown in wetlands and highlands will both benefit from VA mycorrhizal endobiont. However, there are numerous biological concepts that require explanation, including infection strategy and food intake in hypersaline environments. In addition, halophiles have a significant biotechnological potential as a source of suitable solutes, enzymes, and other substances of commercial relevance, similar to other extremophilic microbes. Moreover, their industrial uses are more promising in a number of disciplines. The biotechnological use of halophiles or genes produced from them may therefore eventually encompass a far larger range of bacteria from this incredibly diverse group. Potential fields of application could include developing lucrative substances, cleaning up contaminated soils and rivers, and eventually finding answers to the world's issues. In terms of biotechnology, halophiles probably present a lot of options. Hypersaline habitats are becoming more common due to both natural and human-caused worldwide changes. Moreover, the concentration of sea water in arid settings can readily produce hypersaline habitats. It appears from these data and the discovery of new, stable macromolecules in halophiles that these organisms will become even more valuable in the future

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