

## Beneficial role of extremophilic microbes for plant health and soil fertility

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### Perspective

The Plant microbiomes have capability of colonizing the rhizosphere, phyllosphere and internal tissues for different plant parts. The plant microbiomes (epiphytic, endophytic, and rhizospheric) have ability to produce phytohormones, solubilize nutrients, and antagonistic against pathogens. The plant associated microbes have been isolated from plant growing under the diverse abiotic stresses conditions and these extremophilic microbes help in plant growth promotion and adaptations under harsh environments of temperatures, salinity, pH and drought stresses. The microbes isolated from plant growing under different abiotic stresses are term as plant associated extremophilic microbes. The plant associated extremophiles have been reported from all three domain archaea, bacteria and eukarya of different phylum/groups e.g. Actinobacteria, Ascomycota, Bacteroidetes, Basidiomycota, Crenarchaeota, Euryarchaeota, Firmicutes and Proteobacteria ( $\alpha/\beta/\gamma/\delta$ ). The microbes possess the multifarious plant growth promoting attributes and these efficient and potential microbes may be applied as biofertilizers for crops improvements and soil health for sustainable agriculture. The microbes isolated from different plants growing under the abiotic stresses conditions of temperature, salinity, pH and water deficiency are said to be psychrophiles ( $-2^{\circ}\text{C}$  to  $20^{\circ}\text{C}$ ), thermophiles ( $60^{\circ}\text{C}$  to  $115^{\circ}\text{C}$ ), halophiles (2-5M), acidophiles (pH<4), alkaliphiles (pH>9) and xerophiles (water potential  $0.75\text{ kPa}$ ) [1]. Extreme habitats/niches represent unique ecosystems which harbour novel biodiversity with potential adaptations ability to diverse stresses. In order to survive under such extreme conditions, these organisms referred to as extremophiles, have developed adaptive features which permits them to grow optimally under one or more environmental extremes, while poly-extremophiles grow optimally under multiple conditions [2].

Today, it is a widely accepted fact that certain strains of rhizospheric bacteria, referred to as plant growth promoting bacteria (PGPB), stimulate plant growth and fitness. Thanks to the knowledge of communication signals between rhizosphere organisms, we are able to understand, at least partially, the PGP mechanisms of action. Microbial diversity associated with crops is considered important for maintaining for the sustainability of agriculture production systems. A microbe helps plant for growth, yield and adaptation. Microbes associated with crops could be classified into three groups, e.g. rhizospheric, phyllospheric and endophytic. The rhizosphere is the zone of soil influenced by roots through the release of substrates that affect microbial activity [3]. A number of microbial species have been reported associated with the plant rhizosphere belonging to genera *Azospirillum*, *Arthrobacter*, *Burkholderia*, *Bacillus*, *Paenibacillus*, *Burkholderia*,

*Enterobacter*, *Methylobacterium*, *Pseudomonas*, *Rhizobium* and *Serratia* [4-6]. The epiphytic microbes have been reported from different phyllospheric part of plants. The phyllosphere is common niches for synergism between different potential microbes and plant. The epiphytic microbes are most adaptive in nature as they tolerate high temperature ( $40^{\circ}\text{C}$ – $55^{\circ}\text{C}$ ) and UV radiation. The microbe related to different genera such *Agrobacterium*, *Methylobacterium*, *Pantoea* and *Pseudomonas* have been reported in the phyllosphere of different crops growing in normal as well as harsh environmental conditions [7-9]. The endophytic microbes are referred to those microbes, which colonizes in the interior of the plant parts, viz: root, stem or seeds without causing any harmful effect on host plant. These microbes have been isolated from a variety of plants including wheat [10]; Rice, Soybean, Pea, Common Bean, Chickpea and Pearl millet [11]. The endophytic microbial species belonging to different genera including *Achromobacter*, *Azoarcus*, *Burkholderia*, *Enterobacter*, *Gluconoacetobacter*, *Herbaspirillum*, *Klebsiella*, *Microbiospora*, *Micromonospora*, *Nocardioides*, *Pantoea*, *Planomonospora*, *Pseudomonas*, *Serratia*, *Streptomyces* and *Thermomonospora* have been sorted out from different host plants [6,12-14].

The microbes associated with plants can be enumerated using serial dilution techniques with help of different nutrient media combination in form of diverse selective and complex media e.g. nutrient agar for heterotrophic, trypticase soya agar for *Arthrobacter*, soil extract agar for soil-specific microbes, Jensen's agar for  $\text{N}_2$ -fixing bacteria, King's B agar for Pseudomonads, yeast extract mannitol agar for *Rhizobium*, Modified Dobereiner medium and Luria Bertani agar for endophytic microbes [3]. For identification of microbes, Genomic DNA can be isolated using Zymo Research Fungal/Bacterial DNA MicroPrep™ following the standard protocol prescribed by the manufacturer. Different primers can be used for amplification of 16S rRNA gene for archaea and bacteria while 18S rRNA gene for fungi. PCR amplified 16S/18S rRNA genes have to purified and sequenced [15]. The partial 16S or 18S rRNA gene sequences should be compared with sequences available in the NCBI database.

Biotechnology has opened up new possibilities concerning the application of beneficial microbes to the soil for the promotion of plant growth and the biological control of soil-borne pathogens. The nutritional and environmental requirements of these microbes are very diverse. The microbial inoculation has a much better stimulatory effect on plant growth in nutrient deficient soil than in nutrient rich soil. An understanding of microbial diversity perspectives in agricultural context is important and useful to arrive at measures that can act as indicators of soil quality and plant productivity. The different groups of microbes have been reported as plant associated such

as archaea, eubacteria and fungi, which included different phylum mainly: Acidobacteria, Actinobacteria, Ascomycota, Bacteroidetes, Basidiomycota, Deinococcus-Thermus, Euryarchaeota, Firmicutes and Proteobacteria. Overall the distribution of microbes varied in all bacterial phyla, Proteobacteria were most dominant followed by Actinobacteria. Least number of microbes was reported from phylum Deinococcus-Thermus and Acidobacteria followed by Bacteroidetes [16-20].

Soil salinity is an important limiting factor for agricultural crops especially in arid and semi-arid regions of the world. Although many technologies have been implicated in the improvement of salt tolerance, only PGP microbes-elicited plant tolerance against salt stress has been previously studied [7,21-23]. Microbes associated crops have a high potential for agriculture because they can improve plant growth, under limiting or stress conditions of temperatures. The microorganisms from extreme environments are of particular importance in global ecology since the majority of terrestrial and aquatic ecosystems of our planet are permanently or seasonally submitted to cold temperatures. Microorganisms capable of coping with low temperatures are widespread in these natural environments where they often represent the dominant flora and they should therefore be regarded as the most successful colonizers of our planet. In the past few years, the diversity of microorganisms inhabiting cold environments has been extensively investigated [24-27]. Drought stress limits the growth and productivity of crops, particularly in arid and semi-arid areas [6-7,28]. Alkaline/Acidic environments are also hot spot for microbial diversity with plant growth promoting attributes. Many acidotolerant bacterial genera have been reported from plant growing in acidic environments. The different groups of microbes have a potential role in different possess and applications e.g. Archaea for P-solubilization and mobilization [23], bacteria and cyanobacteria as probiotics [29,30], biodegradation at low temperature [31], cold adapted enzymes (lipase, amylase, protease, cellulase and xylanase) for industrial applications [24]; anti-freezing compounds production from psychrophilic and psychrotrophic microbes [25,32] and microbes with multifarious PGP attributes for plant growth and soil health for sustainable agriculture [33].

In conclusion, plants play an important role in selecting and enriching the types of bacteria by the constituents of their root exudates. Thus, depending on the nature and concentrations of organic constituents of exudates, and the corresponding ability of the microbes to utilize these as sources of energy, the microbial community develops in the interaction as epiphytic/endophytic/rhizospheric. Microbes associated with crops are of agriculturally important as they can enhance plant growth; improve plant nutrition through biological N<sub>2</sub>-fixation and other mechanisms. Microbes may increase crop yields, remove contaminants, inhibit pathogens, and produce fixed nitrogen or novel substances. The growth stimulation by microbes can be a consequence of biological N<sub>2</sub>-fixation, production of phytohormones, such as IAA and cytokines; biocontrol of phytopathogens through the production of antifungal or antibacterial agents, siderophores production, nutrient

competition and induction of acquired host resistance, or enhancing the bioavailability of minerals [11,34,35]. The need of today's world is high output yield and enhanced production of the crop as well as fertility of soil to get in an eco-friendly manner. Hence, the research has to be focused on the new concept of microbial engineering based on favorably partitioning of the exotic biomolecules, which create a unique setting for the interaction between plant and microbes. Future research in microbes will rely on the development of molecular and biotechnological approaches to increase our knowledge of microbes and to achieve an integrated management of microbial populations of endophytic, epiphytic and rhizospheric.

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