



## **Emergence of Plant Growth-Promoting Rhizobacteria (PGPR) In Agriculture Field- A Review**

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### **ABSTRACT**

*Plant growth promoting rhizobacteria (PGPR) are rhizosphere microorganisms that can improve plant growth through a number of different mechanisms, including phosphate solubilization, siderophore production, biological nitrogen fixation, rhizosphere engineering, and production of 1-amino cyclopropane carboxylate deaminase (ACC), interferences with quorum sensing (QS) signaling PGPR offers a desirable alternative to the use of chemical fertilisers, pesticides, and other supplements, its potential in agriculture is rapidly growing. In addition to influencing a systemic resistance to elicit a defense response in host plants, plant growth promoting rhizobacteria (PGPR) are a variety of groups of plant associated microorganisms that can lessen the severity or incidence of disease through antagonism between bacteria and soil-borne pathogens. Signal interference and inhibition of biofilm formation, phyto hormone production, exhibiting antifungal activity, production of volatile organic compounds (VOCs), induction of systemic resistance, promoting beneficial plant-microbe symbioses, interference with pathogen toxin production etc. Growth promoting substances are likely to be produced in large quantities by these rhizosphere microorganisms that influence indirectly on the overall morphology of the plants. Lipopolysaccharides, lipopeptides, siderophores. Pyocyanin, antibiotic 2, 4 diacetyl photoglucinol, the volatile 2, 3 butanediol, N-alkylated benzylamine and non-regulated substances are the main determinants of PGPR mediated induced systemic resistance (ISR). A few of the strategies used by PGPR to colonise the rhizosphere include the ability to recognize chemical uses and nutrients from root exudates, antioxidant activity, Biofilm motility, effective immune system Evasion and repression. PGPR offers a desirable alternative to the use of chemical fertilisers, pesticides, and other supplements, its potential in agriculture is rapidly growing*  
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### **INTRODUCTION**

The twenty-first century has been witnessing rapid rise in human population along with critical issues in global agro-ecosystems, leading to decreased productivity and degeneration of sustainable agro-ecosystems. Food is a fundamental need of people that assumes a significant function in human well-being and social advancements. While feeding the geometrically progressing human population, required balanced value-added food to supplement a diet is significantly difficult. The ever-increasing population exhibits pressure on arable land to increase crop yield, leading to indiscriminate use of chemical fertilizers, insecticides, pesticides etc. by the farmers. Drought is a major limiting factor for crop production as it causes plant growth disturbances and crop [1], leading to huge economic losses and to the decline of food availability across the world. Water deficit may cause morphological, biochemical, and physiological injuries on plants affecting various important cellular processes. Among the most deleterious effects are damages on the photosynthetic apparatus and oxidative injuries on proteins, membrane lipids and other cellular component [2]. In addition, These negative effects are often associated with decreases in the microbial activity of the soil and in the amount of macro and micronutrients available to plants Maize (*Zea mays* L.) is one of the most produced food crops in the world (<http://faostat3.fao.org>), contributing to the survival of billions of people [3]. However, maize yield suffered a reduction up to 40% on a global scale due to drought, according to a meta-analysis performed by, based on published data between 1980 and 2015. Finding mitigation strategies to tackle the impact of water shortage on maize production is a priority. Indeed, the development of new stress-tolerant varieties through conventional

breeding and/or by plant genetic engineering [4], as well as the application of inorganic and organic chemicals, including osmoprotectants and plant hormones has been used to improve maize tolerance to drought. However, some drawbacks have been associated to these approaches, since they are time-consuming, cost and labor-intensive, and there is the risk of unwanted transfer of transgenic genes to the environment [5].

### BACTERIAL INOCULANTS

The rhizobacteria strains *Cupriavidus necator* sp. 1C2 (B1) and *Pseudomonas fluorescens* S3X (B2) were previously isolated from an environmental degraded area [6]. These bacterial strains were selected based on their plant growth promoting traits [6], comprising very good siderophore and indole acetic acid (IAA) production, and 1-aminocyclopropane-1-carboxylic acid (ACC)-deaminase activity, and on their proven ability to enhance maize growth under stressful conditions, such as metal pollution [7].



**Fig. 1:** Above-ground and below-ground symptoms from tomato in response to *Meloidogyne* sp. infections [7]

Plant-parasitic nematodes management strategies, including bio control methods, offer a safer and more practical option [8]. The term "biological control" (or bio control) refers to an ecologically sound and successful method for eliminating or suppressing plant-parasitic nematodes using naturally occurring species with pesticidal activity or manipulating the environment or introducing opponents [9]. Distribution of root-knot nematode in Egypt. Fig 1 shows *Meloidogyne* spp. cause important diseases affecting numerous plant crops in Egypt and hence has a significant economic impact. *Meloidogyne arenaria* Chitwood, *M. javanica* Chitwood, and *M. incognita* Chitwood are the most economically important species in Egypt [10]. They are particularly damaging in tropical, subtropical, and warm regions [10]. Root-knot nematodes are particularly significant disease-causing agents in Egypt, affecting numerous agricultural plants and food supplies due to their widespread distribution, broad host ranges, and association with disease-causing fungi and bacteria.

Classification of the extracted CDS of the eight rhizobacteria strains based on the Clusters of Orthologous Groups of proteins (COG) database demonstrated a close resemblance of the *Pseudomonas*-related strains with *Pantoea brenneri*, similarly to the phylogenetic analysis. The *Acinetobacter calcoaceticus* and the *Chryseobacterium* sp.-related strains were grouped together, on the basis of their low number of genes per functional classification. The COG functional classification of the CDS revealed 1,574 to 2,346 CDS associated with at least one function. Four main functional gene classes related to metabolism were identified in all genomes: (i) Amino acid transportation; (ii) Translation, ribosomal structure and biogenesis; (iii) Energy production and conversion; and (iv) Coenzyme transport and metabolism. In addition, the categories of inorganic ion transport, cell wall and envelope biogenesis, post-translational modification, as well as replication and repair were highly represented in all strains. The genome of the *Chryseobacterium* sp. (SAESo14) included only four potential CDS in the cell-motility category, whereas the other strains, each had > 36 potential genes in this category.

### INDUCED SYSTEMIC RESISTANCE (ISR)

Induced resistance refers to a plant's improved capacity to defend itself against a diverse variety of pests after being appropriately stimulated [11]. Systemic acquired resistance (SAR) refers to the enhanced defense response caused by an inducing substance following infection by a pathogen or pest [12]. Induced systemic resistance can be induced by PGPR, whereas SAR refers to the resistance generated by other microorganisms. Both generated resistances protect against a wide spectrum of diseases, including those caused by fungi, nematodes, bacteria, insects, and viruses [13]. Numerous defense enzymes are linked to systemic resistance, such as superoxide dismutase, polyphenol oxidase, peroxidase, catalase, lipoxygenase, chitinase, phenylalanine ammonia lyase,  $\beta$ -1, 3-glucanase ascorbate, peroxidase, and proteinase [14]. These enzymes initiate the resistance-inducing process by generating phenolic chemicals and phytoalexins [15]. Extensive research has demonstrated that PGPR reduce the population of plant-parasitic nematodes by increasing the plant's systemic resistance [16]. This induced tolerance is achieved

through cell wall intensification, callose sedimentation, phenolic compound accumulation, and up regulation of biochemical compounds such as jasmonic acid, pathogenesis-related (PR) proteins, lipopolysaccharides, phytoalexin, siderophores, chitinase, and salicylic acid [16]. Another study showed that *B. cereus* significantly decreased *M. incognita* and *M. javanica* populations in roots of *Arabidopsis* through the development of systemic resistance [17] found that *Agrobacterium radiobacter* (G12) plays an essential role in preventing *Globodera* spp. juveniles from penetrating potato (*S. tuberosum*) roots. Interestingly, tomato roots (*S. lycopersicum*) treated with *P. fluorescens*, Pf128 plus *Bacillus subtilis*, Bbv57, showed increased activity of enzymes and decreased *M. incognita* populations [18]. This demonstrates the possible function of PGPR in establishing systemic resistance to nematodes by animating and compiling defense enzymes such as polyphenol oxidase, peroxidase, and phenylalanine ammonia lyase. The overall mechanisms of action of PGPR as nematode biocontrol agents [19].

### CONCLUSION

The relationships between plants and the phytomicrobiome are ancient and represent the result of a very long coevolution. [20] Evolution is pragmatic, random and relentless, and we should expect to discover many additional and sometimes surprising relationships that are beneficial to crops, and therefore global food production. [21] It is clear that members of the phytomicrobiome offer huge potential in terms of new and more sustainable crop management practices, however, it is also clear that we understand only a tiny amount of this potential and a very great deal remains to be done.

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### CONFLICT OF INTEREST:

The authors declare that they have no conflict of interest

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