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Microbiomes of Wheat (*Triticum aestivum* L.) Endowed with Multifunctional Plant Growth Promoting Attributes

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The microbiomes of wheat (*Triticum aestivum* L.) can enhance plant growth, productivity, soil fertility and protect from plant pathogens. Microbiomes of wheat include, epiphytic, endophytic and rhizospheric microbes belonging to all three domain archaea, bacteria and fungi. The microbes associated with wheat have been shown to promote plant growth directly, e.g. by production of phytohormones such as auxin, cytokinin, and gibberellins; fixation of atmospheric nitrogen; production of siderophores (catecholates, hydroxamates and carboxylates); solubilization phosphorus, potassium and zinc; and in-directly by production of ammonia, hydrogen cyanides, Fe-chelating compounds, hydrolytic enzymes and bioactive compounds. Wheat (*Triticum aestivum* L.) is the world's most important cereal crop, contributing 45% of digestible energy and 30% of total protein in human diet, as well as a substantial contribution to feeding livestock [1]. Wheat is a major staple food crop for more than one third of the world population and is the main staple food of Asia [2].

The productivity of wheat crops may be increase using biofertilizers an eco-friendly technology for sustainable agriculture and environments. There are many reports of microbiomes of wheat as rhizospheric microbiomes belonging to genera *Azospirillum, Alcaligenes, Arthrobacter, Acinetobacter, Bacillus, Paenibacillus, Burkholderia, Enterobacter, Erwinia, Flavobacterium, Methylobacterium, Pseudomonas, Rhizobium* and *Serratia; Epiphytic microbiomes Agrobacterium, Methylobacterium, Pantoea* and *Pseudomonas*; and endophytic microbiomes such as *Achromobacter, Bacillus, Burkholderia, Microbiospora, Micromomospora*, *Nocardioides, Pantoea, Planomonospora, Pseudomonas, Streptomyces* and *Thermomonospora* [3-11]. There are many reports on microbiomes of wheat for plant growth and enhance yield promotion by bacteria *Achromobacter xylosoxidans, Aeromonas* sp., *Arthrobacter methylotrophus, Azospirillum brasilense, Azotobacter* sp., *Bacillus cereus, Bacillus cereus, Bacillus horikoshii, Bacillus mojavensis, Methylobacterium, Pantoea monteiiii, Pseudomonas putida, Psychrobacter fozii, Stenotrophomonas* sp., and as biocontrol agents *Bacillus amyloliquefaciens, Exiguobacterium acetylicum, Paenibacillus polymyxa* [12].

The microbiomes of wheat play important role in plant growth, crop yields, and soil health under the normal as well as abiotic stress conditions [13,14]. There are many reports on plant growth promotion of wheat under the abiotic stress conditions e.g. at low temperature by *Mycobacterium phlei* MbP18, *Mycobacterium* sp. 44, *Mycoplana bullata* MpB46, *Pantoea agglomerans* 050309 and *Pseudomonas fluorescens* PsIA12 [15], *Pseudomonas* sp. NARs9, *Pseudomonas fluorescens* PPRs4, *Pseudomonas jessani* PGRs1, *Pseudomonas koreensis* PBRs7, *Pseudomonas lurida* NPRs3 and *Pseudomonas putida* PGRs4 [16,17], *Bacillus cereus* AS4, *Bacillus megaterium* AS15, *Bacillus megaterium* AS8, *Cellulomonas turbata* AS1, *Enterobacter cloacae* AS6 and *Pseudomonas putida* AS3 [18], *Arthrobacter sulfonivorans* IARI-L-16 [19], *Arthrobacter methylotrophus* IARI-HHS1-25, *Bordetella bronchiseptica* IARI-HHS2-29, *Kocuria kristinae* IARI-HHS2-64, *Pseudomonas extremorientalis* IARI-HHS2-1, *Bacillus altitudinis* IARI-HHS2-2 [20-22]. There are many reports on microbiomes of wheat under the salinity for plant growth promotion by different groups of microbes such as *Pseudomonas fluorescens* 153, *Pseudomonas putida* 108 [23], *Aeromonas hydrophila* MAS-765, *Bacillus insolitus* MAS17, *Bacillus* sp. MAS617/620/820 [24], *Achromobacter xylosoxidans* 249, *Enterobacter* sp. 12, *Pseudomonas* sp. 33, *Serratia marcescens* 73 [25], *Pseudomonas aurantiaca* TSAU22, *Pseudomonas chlororaphis* TSAU13, *Pseudomonas extremorientalis* TSAU20, *Pseudomonas extremorientalis* TSAU6, *Pseudomonas putida* TSAU1 [26], *Aeromonas vaga* BAM-77 [27], *Klebsiella* sp. SBP-8 [28], *Bacillus licheniformis* HSW-16 [29], *Bacillus amyloliquefaciens* BNE12, *Bacillus methylotrophicus* BNE2, *Paenibacillus xylanexedens* BNE18 *Planomicrobium okeanokoites* BNE8 [21].

There are many reports on microbiomes of wheat under the drought and heat stress for plant growth promotion by different groups of microbes such as *Pseudomonas putida* AKMP7 [30], *Azospirillum brasilense* Sp245 [31], *Azospirillum lipoferum* AZ1, AZ9, AZ45 [32], *Bacillus safensis* W10, *Ochrobactrum pseudogregnonense* IP8 [33], *Pantoea theicola* NBRC 110557T, *Pantoea intestinalis* DSM 28113T [34], *Azospirillum brasilense* NO40 [35], *Bacillus amyloliquefaciens* 5113 [35], *Azospirillum brasilense* Sp245 [36], *Glomus mosseae* (AMF) [37], *Burkholderia phytofirmans* PsJN [38], *Achromobacter spanius* IARI-NIAW2-15, *Alcaligenes faecalis* IARI-NIAW1-6, *Delftia lacustris* IARI-NIAW1-34, *Duganella violaceus niger* IARI-IIWP-23, *Kocuria* sp. IARI-IHD-9, *Micrococcus* sp. IARI-IIWP-20, *Paenibacillus dendritiformis* IARI-IIWP-4, *Pseudomonas poae* IARI-NIAW2-1, *Psychrobacter fozii* IARI-IIWP-12, *Rhodobacter sphaeroides* IARI-NIAW1-7 [22], *Bacillus alcalophilus* BCZ14, *Bacillus altitudinis* BPZ4, *Bacillus aryabhattai* BCZ17, *Bacillus licheniformis* BPZ5, *Bacillus tequilensis* BCZ6, *Exiguobacterium acetylicum* BPZ8, *Paenibacillus amylolyticus* BPZ10, *Paenibacillus dendritiformis* BCZ2, *Paenibacillus tundrae* BCZ3, *Planococcus salinarum* BCZ23, *Achromobacter spanius* IARI-NIAW2-15, *Bacillus mojavensis* IARI-NIAW2-23, *Delftia acidovorans* IARI-NIAW1-20, *Methylobacterium mesophilicum* IARI-NIAW1-41, *Pseudomonas poae* IARI-NIAW2-1, *Rhodobacter sphaeroides* IARI-NIAW1-7 [21], and *Piriformospora indica* (Pi) [39]. The wheat in acidic/alkaline soil face a significant challenge of high levels of aluminum released in the acidic soils can stunt crop growth. There are many reports on plant growth promotion of wheat under the acidic or alkaline soil conditions such as *Micrococcus roseus* SW1 [40], *Aeromonas vaga* BAM-77 [27], *Bacillus nanhaiensis* IARI-THD-20, *Lysinibacillus fusiformis* IARI-THD-4, *Staphylococcus epidermidis* IARI-THW-28 [41], *Bacillus aerophilus* BSH15, *Bacillus altitudinis* BNW15, *Bacillus circulans* BSH11, *Bacillus endophyticus* BNW9, *Bacillus nanhaiensis* BSH7, *Lysinibacillus sphaericus* BNW22, *Lysinibacillus sphaericus* BSH6, *Paenibacillus xylanexedens* BNW24, *Planococcus salinarum* BNW25, *Planococcus salinarum* BSH13, *Planomicrobium* sp. BSH14, and *Staphylococcus arlettae* BNW27 [21,42].

On review of different research of microbial diversity associated with wheat plants, it may be concluded that the microbiomes of wheat distributed in rhizosphere, phyllosphere and endophytic may varies and their diversity and abundance differ each other e.g. *Bacillus amyloliquefaciens, Paenibacillus polymyxa, Pseudomonas aeruginosa, Pseudomonas chlororaphis, Pseudomonas fluorescens, Pseudomonas rhodesiae*, *Stenotrophomonas maltophilia, Bacillus megaterium, Bacillus sphaericus, Bacillus subtilis, Arthrobacter nicotianae* were most dominant and reported common from rhizosphere, phyllosphere and in inside tissue of wheat plant. Along with common pre-dominant bacteria, there were some niche specific bacteria reported as associated with wheat e.g. *Arthrobacter methylotrophus, Brevundimonas diminuta, Corynebacterium callunae, Methylobacterium phyllosphaerae, Microbacterium phyllosphaerae, Pseudomonas argentinensis, Pseudomonas fuscovaginae, Pseudomonas plecoglossicida*, and *Psychrobacter fozii* from phyllosphere; *Achromobacter piechaudii, Achromobacter spanius, Acinetobacter lwoffii, Delftia acidovorans, Gluconacetobacter xylinus, Ochrobactrum anthropi, Pantoea eucalypti, Pseudomonas monteilii, Variovorax dokdonensis, Variovorax paradoxus, Variovorax* soli as endophytic bacteria and *Arthrobacter nicotinovorans, Azotobacter tropicalis, Bacillus atrophaeus, Bacillus bronchiseptica, Bacillus methylotrophicus, Bacillus thuringiensis, Exiguobacterium acetylicum, Lysinibacillus fusiformis, Paenibacillus tundra, Planomicrobium okeanokoites, Pseudomonas stutzeri, Rhodobacter sphaeroides, Staphylococcus succinus* and *Stenotrophomonas rhizophila* as wheat rhizospheric microbiomes. Similarly to this there are also many reports of biodiversity of microbiomes as niche-specific or host specific e.g. Low temperatures [19,43-47], High temperatures [48-50], Hypersaline habitats [13,51,52] and Polyextremophiles [52,53].

Plant growth promoting (PGP) microbes are associated with plant roots, and either directly or indirectly stimulates plant growth. The application of PGP microbes is a promising agricultural approach that plays a vital role in crop protection, growth promotion or biological disease control and sustained soil fertility. In modern agriculture, the natural processes for replenishing nitrogen, phosphorus and potassium used up by crops are too slow to sustain the productivity needed. Major contributors of fixed N solubilized P and K in the soil are nitrogen fixing, P and K solubilizing microbes respectively. It is generally assumed that PGP microbial stimulation of plant growth requires the binding of the bacterium to the plant root. The successful use of either rhizobial or PGP microbial inoculants in agriculture depends upon the delivery of viable bacteria to the root zone which is most frequently accomplished by inoculating seeds with a preparation of dormant bacterial cells, by means of coated seed or bulk inoculants. Biofertilizers is defined as a substance which contains living microorganisms and when applied to seed, plant surfaces or soil, colonizes the rhizosphere or the interior of the plant and promotes growth by increasing the supply or availability of primary nutrients to the host plant. The studies on microbiomes of wheat may help to modern agriculture, which is mostly dependent on chemical fertilizers to meet the food demands of ever increasing population. Application of high doses of chemical fertilizers may temporarily help to increase crop production. However, this may turn into bitter and highly regrettable consequences where soil fertility will be depleted or become acidic and devoid of macro and micro nutrients for crops to grow and microorganisms to proliferate.

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Competing Interests

The authors declare no conflict of interest.

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