Microbe-Mediated Tolerance in Plants Against Biotic and Abiotic Stresses

7

Syed Sarfraz Hussain

7.1 Introduction: A Glimpse of Plant Productivity Under Environmental Stresses

A plethora of data suggested that significant climatic changes have welcomed the twenty-first century (Kumar and Verma 2018). Many research reports have pointed that environmental stresses constitute significant threat to future food security around the globe (Battisti and Naylor 2009) with the ever-increasing world population which would be at least nine billion by 2050 (Singh et al. 2011; Hussain et al. 2012, 2014). Current estimates have revealed that over 800 million people are experiencing food shortage and malnutrition worldwide. Agricultural sustainability is threatened by a multitude of factors including unpredictable climate variation, population and reduction in soil health (Cushman and Bohnert 2000). Global food production is limited by several reasons, primarily by extreme climatic stresses which cause 20–30% yield losses globally (Savary et al. 2012; Dikilitas et al. 2018). Similarly, diseases can significantly affect virtually all crop plants with the potential to reduce both yield and quality, and an estimated 20–40% global harvest is lost to diseases alone (Savary et al. 2012; Dikilitas et al. 2018). Indiscriminate and widespread use of pesticides and weedicides for disease eradication has negatively impacted the environment; therefore, development of resistant/tolerant crop plant is human friendly and an effective strategy to enhance productivity (Hussain et al. 2011), which causes major loss of beneficial microbial diversity from the soil (Kumar and Verma 2018). However, benefits of green revolution are now over

---

S. S. Hussain (✉)
Department of Biological Sciences, Forman Christian College (A Chartered University),
Lahore, Pakistan

School of Agriculture, Food & Wine, Waite Campus, University of Adelaide,
Adelaide, SA, Australia
e-mail: sarfrazhussain@fccollege.edu.pk

D. P. Singh et al. (eds.), *Microbial Interventions in Agriculture and Environment*,
https://doi.org/10.1007/978-981-13-8391-5_7

mainly due to uncontrolled world population, narrow range of germplasm resources, lengthy breeding process and extreme climatic stresses (Hussain et al. 2012).

Therefore, it is well conceived that conventional breeding alone cannot keep pace with future food needs of the world population. Selective breeding and genetic modifications have played a promising role for the improvement of all major crop plants in order to meet the human food requirements (Capell et al. 2004; Bartels and Hussain 2008; Hussain et al. 2012). Combining general breeding schemes and current molecular strategies have been wisely utilized to develop crop plant with enhanced stress tolerance (Capell et al. 2004; Hussain et al. 2012). Plants overexpressing several different genes have shown improved tolerance to different environmental stresses and promotion of plant health and yield (Roy et al. 2014; Hussain et al. 2016) under both laboratory and greenhouse conditions. Currently, plant engineering approaches have been designed to transfer important genes playing significant role (synthesis of osmolytes, antioxidants and stress-related proteins such as Lea, HSP) in biochemical pathways (Wang et al. 2003; Vinocur and Altman 2005; Valliyodan and Nyugen 2006; Sreenivasulu et al. 2007; Kathuria et al. 2007; Bartels and Hussain 2008; Hussain et al. 2012, 2014; Marasco et al. 2016; Thao and Tran 2016). However, identification and isolation of key genes and acceptance of transgenic products at community level pose the main bottleneck of this strategy. Similarly, several research reports have revealed that crop health, adaptation and tolerance to various stresses are not only linked to the genome of the plant but evidence suggest that these might also be intricately influenced by multiple environmental factors (Munns and Gilliham 2015; Tiwari et al. 2017). Potentially, plant-associated microbes represent possible strategies to decrease the negative effects of chemical fertilizers, pesticides, herbicides and abiotic stresses.

There is now overwhelming research evidence that plant microbiome including symbiotic associations through numerous mechanisms help (Vandenkoornhuyse et al. 2015) significantly to sustainable plant yield management strategies (Berendsen et al. 2012; Mendes et al. 2013; Wagg et al. 2014; Mueller and Sachs 2015; Gouda et al. 2018). Emerging plant-associated microbiome-based technologies have received attention which offer potential increase in plant growth and development, nutrient acquisition, health, enhanced biotic/abiotic stress tolerance and host immune regulation leading to enhanced crop yields (Mayak et al. 2004; Glick et al. 2007; Marulanda et al. 2009; Yang et al. 2009; Berendsen et al. 2012; Bakker et al. 2013; Mendes et al. 2013; Turner et al. 2013; Berg et al. 2014; Lakshmanan et al. 2014; Ngumbi and Kloepper 2016). Several researchers have reported the beneficial impact of integration and utilization of mycorrhizal fungi (Rodriguez and Redman 2008; Bonfante and Anca 2009; Singh et al. 2011; Aroca and Ruiz-Lozan 2012; Azcon et al. 2013), bacteria for atmospheric nitrogen fixation (Lugtenberg and Kamilova 2009) and PGPR (Kloepper et al. 2004; Mayak et al. 2004; Glick et al. 2007; Kim et al. 2009; Glick 2012; Pineda et al. 2013; Chauhan et al. 2015) on crop plants for enhanced tolerance to various biotic and abiotic stresses (Timmusk and Wagner 1999; Mayak et al. 2004; Dimpka et al. 2009; Sandhya et al. 2009; Grover et al. 2011; Kasim et al. 2013; Coleman-Derr and Tringe 2014; Nadeem et al. 2014; Hussain et al. 2018). However, this should be noted that this is a vast but still largely an untrapped area which calls for more systematic and intensive research efforts for completely realizing its potential in increasing yields in a changing climate (Hussain et al. 2018).

Similarly, very little is known of how plants strategically prioritize their requirements, such as investing energy resources into defence at the expense of other vital functions, to modify the internal system to enhance tolerance to different environmental stresses (Schenk et al. 2012a, b). With the availability of high-throughput molecular tools, several diverse and unexpected research discoveries have revealed the underlying responses of plant adaptation to stress tolerance using plant-related microbiome (Mendes et al. 2011; Bulgarelli et al. 2012; Lundberg et al. 2012; Berg et al. 2016; Timmusk et al. 2017; White et al. 2017; Hussain et al. 2018). Although several different PGPRs have helped plants in mitigating various stresses, the mechanisms involved remain mostly unexplored. Meanwhile, several plant-associated microbes have been characterized for improved growth, development and stress management which significantly contributed to our understanding to design strategies for the use of these PGPRs (Hayat et al. 2010; Lakshmanan et al. 2012; Mapelli et al. 2013; Vejan et al. 2016). Integration and exploitation of plant-associated microbes hold great promise which can play important roles in improving plant health, growth and development (Rolli et al. 2015; Wallenstein 2017), by managing plant tolerance to various environmental stresses (Mapelli et al. 2013; Vejan et al. 2016) and enhancing plant productivity for food security (Lugtenberg and Kamilova 2009; Celebi et al. 2010; Mengual et al. 2014; Rolli et al. 2015; Berg et al. 2016; Marasco et al. 2016). Overall, sustainable agriculture challenged by abiotic stresses needs nonconventional strategies like the use of plant-related microbiomes (Schaeppi and Bulgarelli 2015; Bulgarelli et al. 2015). Taken together, the identification, characterization and use of microbes which enhance plant abiotic stress tolerance by diverse mechanisms would help to sustain agriculture in the future (Jorquera et al. 2012; Bhardwaj et al. 2014; Nadeem et al. 2014).

Innumerable reviews have highlighted several plant traits which are used by microbes for developing stress tolerance (Rosenblueth and Martinez-Romero 2006; Hardoim et al. 2008; Lugtenberg and Kamilova 2009; Rodriguez et al. 2009; Yang et al. 2009; Grover et al. 2011; Friesen et al. 2011; Singh et al. 2011; de Zelicourt et al. 2013; Bulgarelli et al. 2013; Nadeem et al. 2014; Qiu et al. 2014; Wellenstein 2017). It is the need of the time to join hands for exploring microbial traits beneficial to both plants and the environment because this strategy has a huge potential for sustainable agriculture in the future (Lally et al. 2017). This chapter highlights the advantages of the plant-related microbial community approach, especially increasing plant tolerance to various environmental stresses which constitute a serious threat to food security around the globe.

7.2 Plants and Their Microbial Environment: Exploring Plant Microbiome Diversity

It is well established that virtually the whole plant is populated by an uncountable number of microorganisms (Quiza et al. 2015) and has been classified mainly on the basis of plant part they colonized such as endophyte (present inside the plant part), epiphyte (aerial plant part like leaves and twigs) and rhizosphere (on the roots under the soil) (Ali et al. 2012; Penuelas and Terradas 2014; Bai et al. 2015; Santoyo et al. 2016). Under natural conditions, plants establish multiple mutually beneficial interactions with these microbes (Schenk et al. 2012a, b) for improvement of plant characters such as seed germination and vigour, growth and development, plant health (environmental stress tolerance) and crop productivity (Mendes et al. 2013; Quiza et al. 2015).

Despite their potential utility for plant productivity and other traits, progress in identification, characterization and utilization of these extremely complex microbial communities has been hampered mainly due to technological limitations (Hussain et al. 2018). Historic documents that report the use of microbes in agriculture date back to 1800, and rhizobium bacteria were first recommended for use in legume crops to enhance growth, development and uptake of nutrients from the soil (Jones et al. 2014). Initial efforts to use microbes have focused on exploring the functional roles of few members of plant-associated microbial groups which met with limited success largely because of the fact that most microbes are not culturable (Amann et al. 1995; Andreote et al. 2009; Schenk et al. 2012a, b; Balbontin et al. 2014; Larimer et al. 2014; van der Heijden et al. 2015). However, several individual microbes helping in improving plant health, growth and development, such as atmospheric nitrogen-fixing microbes (Olivares et al. 2013; de Bruijin 2015) and mycorrhizal fungi (Smith and Read 2008; Chagnon et al. 2013; van der Heijden et al. 2015), have been successfully characterized. On the other hand, concerted efforts to study microbial system recognize the utility of saprophytic or symbiotic interactions with plants ranging from beneficial to pathogenic (Mendes et al. 2013; Quiza et al. 2015). It is further noticed that pathogenic microbes despite their detrimental effects may use plant-derived organic substances for growth, hence may indirectly play a functional role in nutrient cycling and modifying plant environment (Schenk et al. 2012a, b), while beneficial microbes promote plant growth by improving nutrient acquisition (Mishra et al. 2012; Santoyo et al. 2012; Bulgarelli et al. 2013; Santoyo et al. 2016; Calvo et al. 2017), synthesizing growth regulators (Glick 2012) and suppressing different stresses by biosynthesis of pathogen-inhibiting compounds (Glick 2012; Santoyo et al. 2012; Martinez-Absalon et al. 2014; Hernandez-Leon et al. 2015) and other mechanisms (Smith and Read 2008; Berg 2009; Schenk et al. 2012a, b; Chagnon et al., 2013; Olivares et al., 2013; de Bruijin 2015; van der Heijden et al. 2015; Orozco-Mosqueda et al. 2018).

Lederberg and McCray (2001) used for the first time plant microbiome representing microbes occupying plants with beneficial outcomes such as plant health and plant productivity. Technically speaking, the term microbiome has been broadly applied to microbial community composition and their interaction (Beneficial or pathogenic) with specific hosts or environment (Mendes et al. 2011; Lakshmanan et al. 2012; Boon et al. 2014; Ofek et al. 2014; Panke-Buisse et al. 2015; Lareen et al. 2016). The current focus of plant-microbe interaction research involves three aspects. These include microbes involved in nutrient acquisition by symbiosis between plants and arbuscular mycorrhizal fungi (AMF) (Smith and Smith 2011; Sessitsch and Mitter 2014) and atmospheric nitrogen-fixing rhizobia (Oldroyd et al. 2011; Lundberg et al. 2012), microbes improving plant tolerance to various stresses (Doornbos et al. 2011; Ferrara et al. 2012; Marasco et al. 2012; Kavamura et al. 2013; Zolla et al. 2013) and disease-causing microbes (Kachroo and Robin 2013; Mendes et al. 2011, 2013; Wirthmueller et al. 2013; Quecine et al. 2014). Previous research efforts considered the plant-microbe association initially in relation to plant diseases (Mendes et al. 2013). However, advanced research in this field demonstrated that a huge amount of microbes are involved in beneficial functions to plants (Mendes et al., 2013; Bhardwaj et al. 2014; Santoyo et al. 2016, 2017). However, apart from well-known mutualistic interactions among plant and microbes, other characterized or uncharacterized useful microbes often are not included in field-based plant production strategies.

7.3 Shaping Plant Microbiome: Technical Progress

Extensive research efforts have attributed several functions to plant-associated microbes. However, these microbial communities, comprising of several diverse microbial strains, represent an extremely complex and dynamic fraction of plant microbiome (Farrar et al. 2014; Mueller and Sachs 2015). Therefore, research studies have partitioned plant microbiome and targeted different fractions separately. A plant environment has been divided into three major components such as rhizosphere, endosphere and phyllosphere based on the microbial presence where these can live and develop (Hardoim et al. 2008; Hirsch and Mauchline 2012; Haney and Ausubel 2015; Haney et al. 2015; Nelson 2018; Orozco-Mosqueda et al. 2018). In fact, new developments and technical advances resulted in enhanced research in this unexplored field (Porras-Alfaro and Bayman 2011; Berendsen et al. 2012; Bakker et al. 2013; Bulgarelli et al. 2013; Philippot et al. 2013; Schlaeppi et al. 2013; Turner et al. 2013; Guttman et al. 2014; Berg et al. 2014; Knief 2014; Lebeis 2014; Schaeppi and Bulgarelli 2015; Santoyo et al. 2017). Keeping in view the plant nutrition, it is important to characterize microbes that are involved in nutrient recycling and uptake for plants under various extreme soil situations (Leveau et al. 2010; Mapelli et al. 2012; Tajini et al. 2012; Krey et al. 2013; Lally et al. 2017). The scientific literature provides several examples of well-characterized microbes like bacteria (PGPR) and fungi (PGPF) with both antagonistic and synergistic interactions which contribute to enrich plant growth (Verma et al. 2010; Murray 2011; Rout and Callaway 2012; Bhardwaj et al. 2014). Furthermore, these microbes produce different phytohormones like auxin and siderophores (Khalid et al. 2004; Cassan et al. 2009; Abbasi et al. 2011; Filippi et al. 2011; Yu et al. 2011) which play critical roles in host nutrition, growth and health and provide protection to plants from biotic and abiotic stresses (Berendsen et al., 2012; Bakker et al. 2013; Bulgarelli et al. 2013; Mendes et al. 2013; Rastogi et al. 2013; Berg et al. 2014; Lakshmanan et al. 2014; Prashar et al. 2014; Bell et al. 2014; Mueller and Sachs 2015; Wallenstein 2017; Hussain et al. 2018).

Well-explored systems for mutualistic interactions include *Rhizobia* spp. and arbuscular mycorrhizae (AM) that exchange plant carbohydrates and important amino acids (Moe 2013) for fixing atmospheric nitrogen and insoluble phosphate bioavailability (Spaink 2000, Luvizotto et al. 2010; Leite et al. 2014) for plants. Microbes inhabiting in rhizosphere also help plants by providing many trace elements such as iron (Zhang et al. 2009; Marschner et al. 2011; Shirley et al. 2011) and calcium (Lee et al. 2010). Likewise, plant microbiome also plays essential functions in degrading non-bioavailable organic compounds required not only for microbes own survival but also for plant's vital functions like growth and development in nutrient-poor and nutrient-contaminated soils (Leveau et al. 2010; Mapelli et al. 2012; Turner et al. 2013; Bhattacharyya et al. 2015). Taken together, shaping and strengthening plant microbiome will have a significant and positive effect on sustainable agriculture in the future (Mitter et al. 2017).

Many reports have designated microbiome as the second genome, while some other researchers treated microbiome as a holobiont to demonstrate the critical roles played by microbial communities associated with plants (Zilber-Rosenberg and Rosenberg 2008; Grice and Segre 2012; Agler et al. 2016; Clavel et al. 2016; Paredes and Lebeis 2016; Zmora et al. 2016). Currently, an effort to explore plant microbiome comprising of several different microbial communities is largely hindered due to several factors, mainly because of methodological constraints (Bulgarelli et al. 2013). Therefore, development and validation of protocols is essential for exploring the whole plant microbiome diversity (Calvo et al. 2017; Hussain et al. 2018). With the advent of next-generation sequencing, selection under artificial ecosystem and other molecular techniques like florescent tagging especially for studying unculturable species (endophytes) are now a gradually routine in research (Swenson et al. 2000; Bulgarelli et al. 2012; Hernández-Salmerón et al. 2016). A huge body of data are accumulated as a result of these technological advancements in the field (Martinez-Absalon et al. 2014; Hernandez-Leon et al. 2015; Hernández-Salmerón et al. 2016; Orozco-Mosqueda et al. 2018). On the other hand, integration of different computational models is also essential for dissection of this complex and dynamic hidden treasure (Farrar et al. 2014; Mendes and Raaijmakers 2015) with the aim of searching for new beneficial microbes and effectively manipulating plant microbiome for increasing plant productivity (Hussain et al. 2018).

Taken together, investment in research aimed at exploring microbial traits that are beneficial to plants and environment constitutes an ideal approach towards next-generation sustainable plant productivity (Schaeppi and Bulgarelli 2015; Goswami et al. 2016; Khan et al. 2016; Compant et al. 2016). Despite the above-mentioned facts, assessing and accessing the microbiome of important local plants and native habitats represents a yet unexplored field to exploit synergism between microbes and plant traits in modern agriculture. However, understanding microbe-microbe dynamics is critical to identify key factors that help to shape and establish microbial communities. Therefore, information extracted from the indigenous plant-associated microbiome constitutes an integral part for designing/engineering a microbiome to be used for sustaining agriculture in the future.

7.4 Reinstating a Functional Plant Microbiome: Smart Solution to a Complex Problem

Researchers are suffering from information gap which is negatively affecting the ability to manage and manipulate the rhizosphere microbiome (rhizobiome) while the strategy to use microbes for increasing plant productivity is not new. Current data reveal the potential of engineering rhizosphere microbiome which offers a unique opportunity to achieve maximum benefits in plant production despite different challenges (Bakker et al. 2012; Berendsen et al. 2012; Bainard et al. 2013; Qiu et al. 2014; Bulgarelli et al. 2015; Yadav et al. 2015). It is noteworthy that rhizosphere represents an extremely competitive environment for microbes, while these microbes play a critical role in plant growth and productivity (Berendsen et al. 2012; Ziegler et al. 2013; Chaparro et al. 2014). Therefore, plenty of progress has been achieved in engineering sustainable plant productivity through engaging microbial communities (Bakker et al. 2012; Lebeis et al. 2012; Bulgarelli et al. 2013; Su et al. 2015).

Huge research endeavours have resulted in isolation, identification and characterization of hundreds of bacterial/fungal strains with known beneficial effects and are currently being utilized in developing microbial consortia (Patel and Sinha 2011; Kim and Timmusk 2013; Dong and Zhang 2014). Several researches have demonstrated the importance of microbial consortia approach which has contributed significantly towards increased agricultural production with less chemical inputs, reduced emission of greenhouse gases and high tolerance to different stresses (Barka et al. 2006; Adesemoye et al. 2009; Yang et al. 2009; Singh et al. 2010; Bakker et al. 2012; Jha et al. 2012; Jorquera et al. 2012; Adesemoye and Egamberdieva 2013; Berg et al. 2013; Turner et al. 2013; Egamberdieva et al. 2017). This is crucial for keeping pace with the rapidly growing world population (Zolla et al. 2013; Nadeem et al. 2014). Another way to extract maximum benefits out of this approach is to exploit knowledge from microbes with publically available genome sequences and synthetically develop a microbiome that can help to improve plant traits as reported for a few important plants including wheat, rice, *Arabidopsis*, maize, *Brassica rapa*, potato, barley, sugarcane and rice (Rasche et al. 2006; Bulgarelli et al. 2013, 2015; Lundberg et al. 2012; Peiffer et al. 2013; Lebeis et al. 2015; Panke-Buisse et al. 2015; Raajimakers 2015; Yeoh et al. 2016). Furthermore, it is expected that microbes in their natural habitats have the potential to contribute significantly in the improvement of crop productivity under environmental challenges.

Consequently, research reports have demonstrated the potential of these microbes which have positively impacted many plant traits including growth, development and productivity under various environmental stresses (Bhattacharya and Jha 2012; Goh et al. 2013; Coleman-Derr and Tringe 2014; Schlaeppi et al. 2014; Tkacz et al. 2015;

Lebeis et al. 2015; Yeoh et al. 2016). It is extremely vital to understand thoroughly both way interactions (microbe-microbe and plant-microbe) for the successful engineering of beneficial soil microbiome (rhizosphere). Similarly, available data have revealed the genetic and molecular basis of these interactions (Bloemberg and Lugtenberg 2001; Wang et al. 2005; Lim and Kim 2013; Timmusk et al. 2014; Vargas et al. 2014; Kim et al. 2015; Busby et al. 2017; Lally et al. 2017; Iannucci et al. 2017), and this information can be used for genetically modifying either partner using genetic engineering protocols for enhanced plant productivity. However, it is worthy to note that microbiome interactions are dynamic and complex depending on several factors including soil biochemistry, plant genotypes and external environment which heavily influence the composition and colonization of several bacterial communities with plant roots. Additionally, these factors involved are in crucial functions such as triggering plant-genotype-specific physiological responses, resulting in different exudation patterns in roots (Hamel et al. 2005; Bais et al. 2006; Hartmann et al. 2009; Dumbrell et al. 2010; Oburger et al. 2013). As a result of increased interest in this research, these factors (different soil types, different native plant species and microbial communication) have been extensively reviewed on the rhizomicrobiome (Tarkka et al. 2008; Berg and Smalla 2009; De-la-Pena et al. 2012; Philippot et al. 2013; Bulgarelli et al. 2013, 2015; Lareen et al. 2016). A broader picture of these interactions revealed that these factors played significant roles in the selective enrichment of microbial communities in rhizosphere microbiome (Berendsen et al. 2012; Miller and Oldroyd 2012; Schenk et al. 2012a, b; Sugiyama and Yazaki 2012; Morel and Castro-Sowinski 2013; Oldroyd 2013), by coordinating the establishment and recruitment of diverse bacterial communities for engineering a specific rhizobiome with positive impact on plant productivity (Bulgarelli et al. 2013, 2015; Peiffer et al. 2013; Philippot et al. 2013; Schlaeppi et al. 2014; Su et al. 2015; Tkacz et al. 2015; Lebeis et al. 2015; Yadav et al. 2015; Yeoh et al. 2016).

Multiple studies have reported positive interaction between specific plants and belowground soil-dwelling microbial communities (Micallef et al. 2009; Inceoglu et al. 2013). This clearly highlighted the fact that plant root exudates play critical roles in identification and recruitment of specific microbes which result in changes in composition and diversity of microbes in the rhizosphere (Haichar et al. 2008; Badri et al. 2009, 2013; Moe 2013; Weston and Mathesius 2013). Based on the above discussion, some useful approaches have been devised to reinstate the root-associated microbiome and re-route microbial activity by enhancing root exudates through more systematic breeding efforts (Bakker et al. 2012; Huang et al. 2014a, b; Reyes-Darias et al. 2015; Yuan et al. 2015; Corral-Lugo et al. 2016; Webb et al. 2016). Root exudates not only serve as food for root-associated microbes but also act as a signal molecule for the initiation of diverse physical and chemical interactions around plant roots (Berendsen et al. 2012; Hawes et al. 2012; Baetz and Martinoia 2013; Chaparro et al. 2013; Vacheron et al. 2013; Huang et al. 2014a, b; Reyes-Darias et al. 2015; Yuan et al. 2015; Corral-Lugo et al. 2016; Webb et al. 2016). Significant growing evidence suggested that progress has been made towards the development of PGPR and/or PGPF consortia using knowledge derived from plant ecosystem for mimicking or partially reconstructing the plant microbiome/

rhizobiome (Adesemoye et al. 2009; Atieno et al. 2012; Masciarelli et al. 2014; Mengual et al. 2014). It is worthy to note that the success of a tailored design of a plant microbiome depends on several factors including identification of the genetic components of the microbiome control and smart integration of critical players in the system. Similarly, it is speculated that changes in root system architecture (RSA) through breeding techniques may help in the recruitment of beneficial plant-specific rhizobiome. However, more systematic and detailed investigations will be required to study these interactions.

7.5 Plant Microbiome and Biotic Stress

Pathogen-free plants present the important and most ignored trait of the plant-associated microbes. Different pathogens especially viruses, bacteria and fungi are responsible for biotic stresses, and crop productivity is significantly reduced (≥15%) by these stresses worldwide (Strange and Scott 2005; Haggag et al. 2015). Stress (both biotic and abiotic) is a major challenge to agricultural yield, and huge economic losses urgently require the development of resistant crop plants. Gusain et al. (2015) have revealed adverse impacts of biotic stress on plants in detail. Several microorganisms belonging to different genera (*Burkholderia*, *Pseudomonas*, *Bacillus*, *Azotobacter* and *Azospirillum*) are the major group of PGPR that are involved in eliciting induced systemic resistance (ISR) response in plants (Alstrom 1991; Van Peer et al. 1991; Wei et al. 1991; Riggs et al. 2001; Shaharoona et al. 2006; Lebeis 2015; Tiwari et al. 2017; Hussain et al. 2018). Similarly, some microbial species belonging to a symbiotic group of rhizobacteria are also involved directly or indirectly with different PGPRs and can evoke ISR in plants (Elbadry et al. 2006). Inoculation of plants or their parts with PGPR which exhibits resistance to different pathogens of biotic stress (Ngumbi and Kloepper 2016). Zamioudis et al. (2013) demonstrated that *P. fluorescens* WCS417 is able to promote important plant traits in *A. thaliana*. This report further revealed that the improvement of different traits occurs via an auxin-dependent and JA-independent mechanism resulting in ISR (Zamioudis et al., 2013). Thus, PGPR/PGPF interactions with their host plant revealed the power to unravel mechanisms which act as the prime barrier of plant defence (Badri et al. 2009; De-la-Pena et al. 2012; Dangl et al. 2013). In fact, PGPR and PGPF are also involved in induction of immune "priming", by secreting signalling compounds which do not result in direct immune activation, but just activate and govern the immune responses against different pathogens (Conrath 2006; Badri et al. 2009; De-la-Pena et al. 2012; Dangl et al. 2013), even in distal tissues.

The defensive capacity of plants represents a physiological condition which is evoked by different signalling molecules known as elicitors. Thus, elicitors are molecules that induce different plant immune responses. Several reports have described two mechanisms which constitute plant immune responses include induced systemic resistance (ISR) and systemic acquired resistance (SAR). Thus, rhizobacteria infection triggers induced systemic resistance (ISR; Ortiz-Castro et al. 2008), while arbuscular mycorrhizae (AM) can produce mycorrhizal-induced resistance (MIR; Pozo and Azcon-Aguilar, 2007; Zamioudis and Pieterse, 2012) suggesting that microbial exploitation is common which gives strength to plants to face pathogen attacks. PGPR-mediated ISR requires interaction between bacteria and plant root which renders plants resistance to some pathogenic microorganisms by the activation of plant natural defences (Raaijmakers et al. 1995; Lugtenberg and Kamilova 2009; Prathap and Ranjitha 2015). ISR is triggered by the interaction of usually non-pathogenic microorganisms in roots and further extending to shoots (Ramos-Solano et al. 2008). Activation of ISR primes the plants to respond faster and stronger against the attack of several pathogenic species including bacteria, protists, nematodes, virus, fungi, viroids and insects (Verhagen et al. 2004; Conrath 2006; Berendsen et al. 2012; Walters et al. 2013).

Therefore, it is known that ISR is a non-specific defence reaction, but it provides strength to the plants to fight different plant diseases (Kamal et al. 2014). Several reports have shown that root inoculation with several different PGPRs rendered the entire plant tolerant to lethal pathogens (Schuhegger et al. 2006; Choudhary et al. 2007; Tarkka et al. 2008). Hence, research has proved ISR as one of the PGPR-mediated mechanisms which reduce plant disease by bringing about critical changes in the host plants at physical and biochemical levels (Pieterse et al. 2002). Since then, the PGPR-elicited ISR is regarded as vital biocontrol mechanism and is under intensive research in plants such as maize, bean, *Arabidopsis*, wheat, tomato, rice, tobacco, radish, soybean, cucumber and carnation (Bevivino et al. 1998; van Loon et al. 1998; Ruy et al. 2004; Compant et al. 2005; Han et al. 2005; Landa et al. 2006; Rashedul et al. 2009; Senthilkumar et al. 2009; Filippi et al. 2011; Neeraj 2011; Pereira et al. 2011; Mavrodi et al. 2012; Martins et al. 2013). However, understanding the metabolic pathway participating in this method is not yet complete (Ramos Solano et al. 2008), which necessitates multidisciplinary intensive research efforts.

On the other hand, it is established that phytohormones such as ethylene and jasmonic acid behave as a signalling agent in ISR, and plant defence response is dependent on these molecules (van Loon 2007). In contrast to the above-mentioned two phytohormones, salicylic acid (SA) acts as a key determinant in SAR. However, a study has shown some overlap between ISR and SAR in some cases (Lopez-Baena et al. 2009). In fact, well-known biotic elicitors are cell wall polysaccharides, along with some others including different phytohormones and signalling molecules (Shuhegge et al. 2006; van Loon 2007; Ramos Solano et al. 2008; Berg 2009; Fouzia et al. 2015; Kanchiswamy et al. 2015; Ulloa-Ogaz et al. 2015; Wang et al. 2015; Meena et al. 2016; Goswami et al. 2016; Islam et al. 2016; Ramadan et al. 2016; Raza et al. 2016a, b; Santoro et al. 2016; Sharifi and Ryu 2016; Gouda et al. 2018).

7.6 Microbiome for Abiotic Stress Alleviation in Crop Plants

Virtually, stress is defined as any factor which negatively affects plant health, growth, and productivity (Foyer et al. 2016). Due to climate change, plants are frequently subjected to various environmental stresses (Hussain et al. 2018). Because expanding the agricultural land is near impossible, increasing demands for food place a serious threat to current crop production systems. Hence, a scientifically improved farming method is required for keeping pace with unprecedented demands and maintaining the soil fertility under intense farming. Currently, sustainable agriculture is based on several improved agricultural techniques (Kumar 2016; Mus et al. 2016; Passari et al. 2016; Perez et al. 2016; Shrestha 2016; Suhag 2016; Ubertino et al. 2016). On the other hand, heavy investment in stress-related research has increased our understanding of the molecular mechanisms implicated in environmental stress tolerance (Tripathi et al. 2015, 2016, 2017; Pontigo et al. 2017; Singh et al. 2017). Therefore, in the development of stress tolerance coupled with better nutritional value, crop plants significantly contributed towards sustainable agricultural development. Engaging beneficial microbes is one possible way to address stress tolerance in plants (Vejan et al. 2016). Following this, recent research has shown that a strain of *Bacillus amyloliquefaciens* living in rice rhizosphere is able to reduce various abiotic stresses via cross-talk with pathways regulating stresses and phytohormones (Tiwari et al. 2017). Similarly, it is known that several soil-inhibiting microbes such as *Paecilomyces formosus* can help reduce plant stress caused by different factors especially heavy metals such as nickel (Bilal et al. 2017). The advantages of using root-associated microbes include their capacity to alleviate negative effects of different abiotic stresses in a wide range of crop plants (Timmusk and Wagner 1999; Mayak et al., 2004; Sandhya et al. 2010; Kasim et al. 2013; Tkacz and Poole 2015) and also their capability to simultaneously tackle several biotic and/or abiotic stresses (Ramegowda et al. 2013; Sharma and Ghosh 2017). Consequently, these beneficial microorganisms are under intensive research as one of the most climate-friendly agents for safe crop management practices.

Currently, plant rhizobiome has attracted extreme attention for tackling plant stresses and enhancing plant yields by several mechanisms to fuel new innovations in sustainable crop production as part of the next green revolution (Marulanda et al. 2009; Yang et al. 2009; Mendes et al. 2011; Bulgarelli et al. 2012; Lau and Lennon 2012; Lundberg et al. 2012; Marasco et al. 2012, 2013; Bainard et al. 2013; Sugiyama et al. 2013; Berg et al. 2014; Bonilla et al. 2015; Panke-Buisse et al. 2015; Prosser 2015; Rolli et al. 2015; Jez et al. 2016; Premachandra et al. 2016; Fierer 2017; Goodrich et al. 2017; Hussain et al. 2018). In fact, isolation and characterization of microbes constitute an integral part to identify beneficial microbes. Extensively researched microbial communities include the symbiotic bacteria (Spaink 2000; Lugtenberg and Kamilova 2009; Luvizotto et al. 2010; Leite et al. 2014), mycorrhizal fungi (Khan et al. 2008; Ruiz-Lozano et al. 2011; Sheng et al. 2011; Singh et al. 2011; Aroca and Ruíz-Lozan 2012; Bashan et al. 2012; Azcon et al. 2013) and PGP rhizobacteria (Kloepper et al. 2004; Glick 2012; Rout and Callaway 2012; Bhardwaj et al. 2014; Gabriela et al. 2015). PGPR contains a huge range of well-studied rhizosphere bacteria (Gupta et al. 2015) which are able to produce several different enzymes and metabolites that play critical roles in host nutrition, growth and health and protect plants from environmental stresses (Dimpka et al. 2009; Kim et al. 2009; Yang et al. 2009; Grover et al. 2011; Timmusk and Nevo 2011; Berendsen et al. 2012; Bulgarelli et al. 2013; Mendes et al. 2013; Berg et al. 2014; Prashar et al. 2014; Rastogi et al. 2013; Ding et al. 2013; Kim et al. 2013; Pineda et al. 2013; Timmusk et al. 2014; Chauhan et al. 2015; Lidbury et al. 2016; Ofaim et al. 2017; Sanchez-Canizares et al. 2017; Syed Ab Rahman et al. 2018). Currently, efforts have been directed at exploring and utilizing naturally occurring, soil-inhibiting microbes for enhanced plant yield under changing climate (Yang et al. 2009; Nadeem et al. 2014; Bhattacharyya et al. 2016; Bashiardes et al. 2018; Jansson and Hofmockel 2018; Yuan et al. 2018). Convincing evidence has witnessed beneficial effects of plant-associated microbes, and this partnership has significantly contributed to establishing smart solutions under nutrient deficiency and mitigating other stresses using diverse mechanisms (Hayat et al. 2010; Mapelli et al. 2013; Vejan et al. 2016).

7.7 Drought Stress

Drought is one of the serious agricultural problems worldwide resulting in reduced growth, development and plant yield (Vinocur and Altman 2005; Hussain et al. 2012, 2014; Naveed et al. 2014a, b; Tiwari et al. 2016). It is also noteworthy that the frequency and intensity of water deficit are expected to increase in the future due to rapid environmental deterioration. Recent investigation revealed that different microbes have the power to support vital plant traits such as plant growth and development through interaction with plant root system under drought stress (Hussain et al. 2012; Huang et al. 2014a, b) to ensure tolerance to environmental stresses (Mendes et al. 2011; Ngumbi 2011; Lakshmanan et al. 2012; Marasco et al. 2012, 2013; Bainard et al. 2013; Sugiyama et al. 2013; Berg et al. 2014; Edwards et al. 2015; Rolli et al. 2015; Panke-Buisse et al. 2015; Hussain et al. 2018). Several approaches have been chalked out and applied to address the drought-associated negative impact on crop productivity. However, use of plant-associated microbes offers a sustainable solution to abiotic stresses by diverse mechanisms (Farooq et al. 2009; Budak et al. 2013; Cooper et al. 2014; Hussain et al. 2014; Porcel et al. 2014). Kang et al. (2014) reported that inoculated soybean with *Pseudomonas putida* H-2-3 mitigated drought impact by decreasing antioxidant activity, producing different osmolytes, enhancing chlorophyll contents, improving shoot length and productivity. Similarly, two maize cultivars inoculated with *Burkholderia phytofirmans* strain PsJN showed 70% and 58% increase in root biomass and with *Enterobacter* sp. strain FD, 47% and 40%, respectively, under water deficit (Naveed et al. 2014a, b). Similarly, several other researchers reported a positive impact of these microbes on roots in different plants like maize and wheat (Yasmin et al. 2013; Timmusk et al. 2013, 2014). Inoculated plants showed promising results compared to non-inoculated control plants under low water condition which led to the conclusion that an increase in root biomass resulted in enhanced water uptake by plants under water deficit stress. Timmusk et al. (2014) have also demonstrated the positive effects on shoot biomass in corn and wheat under drought when inoculated with PGPR.

Crop plants treated with PGPR demonstrated several adjustments at molecular, biochemical and physiological levels for improving several traits such as growth and development, nutrient and water use efficiency, high chlorophyll content for increased photosynthesis, biocontrol activity and ultimately enhanced crop yield by bringing about alterations in root and shoot, phytohormonal activity, high relative water content, EPS production, osmotic adjustment due to osmolyte accumulation, ACC deaminase activity and antioxidant defence (Bano et al. 2013; Kasim et al. 2013; Marasco et al. 2013; Huang et al. 2014a, b; Naveed et al. 2014a, b; Naseem and Bano 2014; Sarma and Saikia 2014; Timmusk et al. 2014; Cohen et al. 2015; Fasciglione et al. 2015; Ortiz et al. 2015; Rolli et al. 2015; Ma et al. 2016a, b; Tiwari et al. 2016; Yang et al. 2016a). PGPR treatment has improved the growth of important crops like rice, wheat, sorghum, maize, sunflower, soybean, pea, tomato, lettuce and pepper under water deficit (Alami et al. 2000; Creus et al. 2004; Mayak et al. 2004; Dodd et al. 2005; Cho et al. 2006; Marquez et al. 2007; Figueiredo et al. 2008; Arshad et al. 2008; Kohler et al. 2008; Sandhya et al. 2010; Castillo et al. 2013; Kasim et al. 2013; Kim et al. 2013; Lim and Kim 2013; Perez-Montano et al. 2014; Naseem and Bano 2014; Sarma and Saikia 2014; Timmusk et al. 2014, 2017; Marasco et al. 2016).

7.8 Salinity Stress

Salinity is a major environmental stress and globally challenging plant growth and productivity (Wicke et al. 2011; Hussain et al. 2014). Researchers have adopted several approaches for tackling salinity problem including agronomic practices, physiological adjustments and molecular (genetic) engineering. However, despite appreciated utility, these practices are not environmentally friendly and practically sustainable due to the incomplete understanding of stress tolerance mechanism and rapidly deteriorating climate. On the other hand, a growing evidence highlighted that different microbial communities improved plant health with enhanced productivity by altering the selectivity of Na^+, K^+ and Ca^{2+} and sustaining a higher K^+/Na^+ ratio in roots under high salinity stress (Barassi et al. 2006; Berendsen et al. 2012; Damodaran et al. 2013; Zuppinger-Dingley et al. 2014; Fasciglione et al. 2015; Sloan and Lebeis 2015; Bacilio et al. 2016; Bharti et al. 2016; Kasim et al. 2016; Mahmood et al. 2016; Sharma et al. 2016; Khan et al. 2017; Shahzad et al. 2017; Timmusk et al. 2017; de la Torre-Gonzalez et al. 2017). Consequently, engaging both PGPR and PGPF has demonstrated a promising success under salinity stress (Upadhyay et al. 2011; Shukla et al. 2012; Bharti et al. 2016; Yang et al. 2016b). Crop plants growing on salty soil which are inoculated with PGPR/PGPF performed better with optimal yield (Tiwari et al. 2011; Shabala et al. 2013; Paul and Lade 2014; Qin et al. 2014; Ruiz et al. 2015). Similarly, multiple reports have demonstrated practical utility of microbial communities where plants like rice, barley, wheat, canola, tomato, mung bean, maize, oat, lettuce and peanuts have developed significantly higher biomass in high salt condition (Mayak et al. 2004; Upadhyay et al. 2009; Ahmad et al. 2011; Jha et al. 2012; Shukla et al. 2012; Nautiyal et al. 2013; Ali et al. 2014; Chang et al. 2014; Jha and Subramanian 2014; Leite et al. 2014; Timmusk et al. 2014; Fasciglione et al. 2015; Suarez et al. 2015; Bharti et al. 2016; Mahmood et al. 2016; Sharma et al. 2016; Zhao et al. 2016).

It is well documented that microbes living in harsh environments modify their physiology accordingly and serve as potential candidates for enhancing plant growth and productivity under stress conditions (Rodriguez et al. 2008; Timmusk et al. 2014). Several researchers isolated bacterial strains from plant roots challenged with high salt stress. Researchers isolated 130 rhizobacterial strains from wheat roots facing salinity stress, and 24 out of 130 isolates showed good growth in culture at 8% of NaCl stress (Upadhyay et al. 2009; Siddikee et al. 2010; Upadhyay et al. 2011; Arora et al. 2014). Different PGPR strains mitigate stress using various mechanisms. For example, Korean halotolerant strain inoculation resulted in enhanced growth because bacterial ACC deaminase activity negatively affected ethylene production under stress (Siddikee et al. 2010). Wheat inoculated with EPS-producing PGPR demonstrated high biomass by binding with cations and zero negative effect on plants under salinity stress (Upadhyay et al. 2011; Vardharajula et al. 2011). A plethora of research has used several PGPR strains including *Hartmannibactor diazotrophicus* E19, *Pseudomonas alcaligenes* PsA15, *Bacillus polymyxa* BcP26, *Mycobacterium phlei* MbP18, *P. fluorescens*, *P. aeruginosa*, *P. stutzeri* and *B. amyloliquefaciens* that have been successfully utilized in different plant species for mitigating salinity stress (Egamberdiyeva 2007; Bano and Fatima 2009; Tank and Saraf 2010; Bal et al. 2013; Nautiyal et al. 2013; Suarez et al. 2015).

Plants inoculated with PGPF showed significant tolerance to high salinity condition (Giri and Mukerji 2004; Grover et al. 2011; Velazquez-Hernandez et al. 2011) due to diverse mechanisms like osmotic adjustment, root growth, increased phosphate and decreased Na^+ concentration in shoots, improved photosystem II efficiency and antioxidant systems and reduced ROS compared to un-inoculated controls (Shukla et al. 2012; Navarro et al. 2014; Ruiz-Lozano et al. 2016). Therefore, maize, rice, cucumber, mung bean, clover, citrus and tomato have shown improved salt tolerance after PGPF treatment which could serve as potential tool for alleviating salt stress especially in stress-sensitive crop plants (Jindal et al. 1993; Al-Karaki et al. 2001; Feng et al. 2002; Ben Khaled et al. 2003; Yang et al. 2009; Grover et al. 2011; Velazquez-Hernandez et al. 2011; Shukla et al. 2012; Navarro et al. 2014; Ruiz-Lozano et al. 2016).

7.9 Heavy Metal Stress

Researchers have shown that industrialization leads to heavy metal accumulation with a huge impact on plant and human health (Qin et al., 2015; Wu et al., 2015). However, the heavy metal problem has received research priority around the globe in recent years due to non-degradable nature of these contaminants (Duruibe et al. 2007; Kidd et al. 2009; Ma et al. 2011; Rajkumar et al. 2012; Ma et al. 2016a, b). Apart from heavy metals, some metalloids such as antimony (Sb) and arsenic (As) are also contributing a huge toxicity (Duruibe et al. 2007; Park 2010; Wuana and Okieimen 2011; Pandey 2012). Heavy metals also constitute significant threat to agricultural productivity and soil health. Many biophysiochemical approaches adopted to reclaim contaminated soils have failed because these were environmentally unsafe, deleterious to soil structure, and unacceptable to the community (Boopathy 2000; Vidali 2001; Doble and Kumar 2005; Glick 2010). Phytoremediation strategy uses different plants supported by microbial communities to clean up heavy metal contaminants in soil and is believed to be a sustainable and cost-effective technology with no negative impact on environment and accepted by the communities (Broos et al. 2004; Hadi and Bano 2010; Afzal et al. 2011; Beskoski et al. 2011; Chen et al. 2014; Fester et al. 2014; Arslan et al. 2017; Hussain et al. 2018). The only limitation of phytoremediation is that plants used for soil reclamation (heavy metals) suffer from negative effects on plant growth due to nutrient shortage and heavy metal-based oxidative stress (Gerhardt et al. 2009; Hu et al. 2016). However, microbe-assisted phytoremediation represents a novel and working alternative (Jamil et al. 2014), whereby microbial activities increase soil reclamation using several unique mechanisms such as efflux, volatilization, metal complexation and enzymatic detoxification (Rajkumar et al. 2010; Ma et al. 2011; Aafi et al. 2012; Yang et al. 2012; Fatnassi et al. 2015; Ghosh et al. 2015; Zhang et al. 2015; Kumar and Verma 2018). It is an established fact that microbes promote plant growth and development by restricting ethylene production and production of plant growth substances such as IAA, cytokinins and gibberellins, siderophores, EPS and ACC deaminase under different stresses including heavy metal stress (Ahmad et al. 2011; Babu and Reddy 2011; Luo et al. 2011, 2012; Wang et al. 2011; Verma et al. 2013; Bisht et al. 2014; Kukla et al. 2014; Waqas et al. 2015; Ijaz et al. 2016; Santoyo et al. 2016; Deng and Cao 2017).

Waqas et al. (2015) have mentioned a few PGPR genera among rhizosphere microbes which demand more intensive research because these can be actively involved in phytoremediation process. These microbes are able to enhance process efficiency by bringing changes in soil pH and other allied oxidation/reduction processes (Khan et al. 2009; Kidd et al. 2009; Uroz et al. 2009; Wenzel 2009; Rajkumar et al. 2010; Ma et al. 2011). Recently, it has been demonstrated that soybean inoculation with *Paecilomyces formosus* exhibited significantly improved growth in soils with Ni accumulation (Bilal et al. 2017).

Similarly, Jamil et al. (2014) reported the positive impact of *Bacillus licheniformis* strain NCCP-59 inoculation with rice, whereby rice seeds exhibited improved germination in Ni-accumulated soil compared to control plants, indicating the ability of *Bacillus licheniformis* strain NCCP-59 to confer protection against Ni toxicity. Recently, a huge data have demonstrated that common heavy metals that include mercury (Hg), manganese (Mn), chromium (Cr), arsenic (As), cadmium (Cd), lead (Pb), chromium (Cr), zinc (Zn), nickel (Ni), aluminium (Al) and copper (Cu) can be efficiently removed by microbes using a plethora of mechanisms in different crop plants such as rice, *Brassica*, maize, lettuce and others (Sheng et al. 2008; Hadi and Bano 2010; Mani et al. 2016; Jing et al. 2014; Adediran et al. 2015; Hristozkova et al. 2016; Mani et al. 2016; Stella et al. 2017; Hussain et al. 2018). A wide diversity of PGPRs including *Bacillus* sp., *Rhizobia*, *Serratia*, *Azospirillum*, *Enterobacter*, *Klebsiella*, *Burkholderia* sp. and *Agrobacterium* have efficiently improved the phytoremediation efficiency by enhancing biomass in heavily contaminated soils (Wani et al. 2008; Kumar et al. 2009; Mastretta et al. 2009; Luo et al. 2012; Nonnoi et al. 2012; Afzal et al. 2014; Glick 2014, 2015; Ghosh et al. 2015; Hardoim et al. 2015; Jha et al. 2015; Deng et al. 2016; Ijaz et al. 2016; Singh et al. 2016; Zheng et al. 2016; Feng et al. 2017).

7.10 Nutrient Deficiency Stress

Despite continuous depletion of soil fertility, soil microbes are playing a vital role in enhancing crop productivity in conventional agricultural production systems (Berendsen et al. 2012). Exploring and utilizing plant microbiome is one of the nonconventional solutions required for maintaining the sustainability of crop plants which are facing nutrient deficiency (Schaeppi and Bulgarelli 2015). The main challenge is the efficient monitoring of processes mediated by these microbes because global attention has been diverted towards their role in plant nutrition only recently (Lebeis et al. 2012; Bulgarelli et al. 2013; Turner et al. 2013; Wei et al. 2016). Plant symbiosis with microbes (rhizobia, bradyrhizobia and AMF) represents one of the widely researched plant-microbe interactions (Hawkins et al. 2000; Jefferies and Barea 2001; Richardson et al. 2009; Miransari 2011; Wu et al. 2016), where these microbes participate in crucial functions for maintaining adequate plant nutrient and high productivity by developing nitrogen-fixing nodules and mycorrhizal arbuscules, respectively (Adesemoye et al. 2009; Miao et al. 2011; Adesemoye and Egamberdieva 2013; Adhya et al. 2015).

Generally, rhizobial symbiosis only occurs in leguminous plants, while AMF-based symbiosis is widespread, and over 80% of land plants experience this symbiosis (Guimaraes et al. 2012; Oldroyd 2013; Hussain et al. 2018). It has been observed that apart from *Rhizobium* and *Bradyrhizobium*, several other bacterial endophytes establish symbiosis or symbiosis-like relationship with plants for bioavailable nitrogen fixation in unspecialized host tissues using nodule-less system (Zehr et al. 2003; Gaby and Buckley 2011; Guimaraes et al. 2012; Santi et al. 2013). *Cyanobacteria*, for example, establish symbiotic relationship with several plants and develop heterocysts instead of nodules which are suitable for BNF using nitrogenase (Berman-Frank et al. 2003; Santi et al. 2013). Leite et al. (2014) reported that sugarcane root-associated bacteria are helpful in fixing nitrogen and solubilizing phosphorus, respectively. Apart from the above reports, some algal genera such as *Anabaena*, *Aphanocapra* and *Phormidium* are also actively involved in fixing nitrogen in field-grown rice by some unknown mechanisms (Shridhar 2012; Hasan 2013).

Similarly, a recent work reported the benefits of mycorrhizal fungi-based symbiosis for making available nutrients and minerals such as phosphorous and essential minor elements (Hartmann et al. 2009; Gianinazzi et al. 2010; Tian et al. 2010; Adeleke et al. 2012; Jin et al. 2012; Carvalhais et al. 2013; Johnson and Graham 2013; Lareen et al. 2016; Salvioli et al. 2016) to many crop plants for meeting their nutritional requirements (Johnson et al. 2012; Philippot et al. 2013; Salvioli and Bonfante 2013; Schlaeppi et al. 2014). Furthermore, research reports also highlighted the significant role of AMF in improving soil structure and establishing beneficial microbes (Bulgarelli et al. 2012; Peiffer et al. 2013; Dell Fabbro and Prati 2014; Tkacz et al. 2015; Wu et al. 2016). Recently, Symanczik et al. (2017) demonstrated that naranjilla (*Solanum quitoense*) inoculated with AMF showed improved plant growth and enhanced nutrition and soil water retention due to the successful establishment of AMF symbiosis which led to the high acquisition of phosphorous (up to 104%) compared to control plants. Furthermore, this study proved that highly diverse belowground systems like AMF play a significant role in maintaining soil structure and aggregation by hyphae and exudates which is essential for sustainable soil productivity (Van der Heijden et al. 2008; De Vries et al. 2013; Wagg et al. 2014). On the other hand, there are published reports revealing many non-AMF involved in AMF like symbiotic benefits to plants (Cai et al. 2014; Ghanem et al. 2014; Pandey et al. 2016).

Keeping the importance of nutrients in plant life, it would be logical to identify bacterial and AMF strains that effectively increase macro- and micronutrient uptake in plants under nutrient deficiency stress (Leveau et al. 2010; Mapelli et al. 2012; Pankaj et al. 2016; Wang et al. 2017). As a matter of fact, rhizospheric microbes can also help in the uptake of many trace elements such as iron and calcium (Zhang et al. 2009; Lee et al. 2010; Marschner et al. 2011; Shirley et al. 2011) from the soil with improved plant root system (Cummings and Orr 2010; Qiang et al. 2016). Taken together, it is safe to conclude that microbes residing in the rhizosphere are especially playing a vital role in degrading insoluble organic compounds which are not only required for their own life but also needed for proper plant growth under nutrient deficiency stress (Leveau et al. 2010; Mapelli et al. 2012; Turner et al. 2013; Bhattacharyya et al. 2015; Pankaj et al. 2016; Wang et al. 2017).

7.11 Extreme Temperature Stress

Rapid climate changes have increased the frequency of global temperature fluctuations. As a result of these changes, extreme temperatures (hot and cold) have now been treated as significant abiotic stress (Hussain et al. 2018; Kumar and Verma 2018). Reports have predicted that global temperatures will increase by 1.8–3.6 °C by the end of this century due to extreme changes (International Panel on Climate Change (IPCC 2007)). High temperatures are not only considered a major obstacle in crop growth and productivity but also negatively impact microbial colonization (Carson et al. 2010). Both plants and microbes respond to high temperature by producing heat shock proteins (HSPs) which help to avoid major cellular damage such as protein degradation and aggregation (Rodell et al. 2009; Alam et al. 2017). Stress adaptation in microbes constitutes a complex regulatory mechanism that may comprise of many gene expressions (Srivastava et al. 2008), helping microbes in developing strategies to mitigate the stress (Kumar and Verma 2018; Yang et al. 2016a).

As have been mentioned, high soil temperature significantly affects the performance of plant-associated microbes. However, several microbes have been isolated from hot environments, and these microbes performed significantly under heat stress. And based on observation, these microbes may be suitable candidates to use with crop plants under high temperature. In a study, wheat cultivars Olivin and Sids1 were treated with *Bacillus amyloliquefaciens* UCMB5113 or *Azospirillum brasilense* NO40, and young seedlings were tested for effect of short-term heat stress (Abd El-Daim et al. 2014). Few stress-associated genes also showed raised transcripts in leaves of control plants. However, such genes exhibited much lower expression in plants inoculated with microbes compared to control plants (Abd El-Daim et al. 2014). Similarly, low reactive oxygen species production was observed with non-significant changes in metabolome in wheat seedling treated with bacteria under high temperature. Certain microbes mitigate heat stress by exopolysaccharide (EPS) synthesis. EPS has the ability to hold water and has cementing characteristics which lead to confer stress tolerance mainly by biofilm synthesis traits (Hussain et al. 2018). *Pseudomonas putida* strain NBR10987 was isolated from chickpea rhizosphere under drought. Inoculated chickpea plants exhibited thermotolerance. Detailed investigations showed that thermotolerance in chickpea was due to stress sigma factor (δs) overexpression as well as thick biofilm synthesis (Srivastava et al. 2008). Similarly, inoculation of sorghum seedlings with two *Pseudomonas* strains AKM-P6 and NBR10987 improved thermotolerance manifested by better physiological and metabolic performance through diverse mechanisms (Redman et al. 2002; Ali et al. 2009; Grover et al. 2011). McLellan et al. (2007) noticed induction of small heat shock HSP101 and HSP70 proteins and enhanced heat tolerance in *Arabidopsis* when inoculated with fungus *Paraphaeosphaeria quadriseptata*.

Plants primed with microbes adapted for low temperature show high growth and development under cold stress. Therefore, researchers used microbes to mitigate negative effects of low temperature stress. Various bacterial strains have been used to enhance cold stress tolerance in plants (Selvakumar et al. 2008a, b, 2009, 2010a, b). Several low temperature-adapted bacterial strains such as *Brevundimonas terrae*, *Pseudomonas cedrina*, and *Arthrobacter nicotianae* have demonstrated multifunctional plant growth-promoting attributes (Yadav et al. 2014). Similarly, *B. phytofirmans* PsJN conferred not only high stress tolerance to low non-freezing temperatures but also grapevine plants showed resistance to grey mold (Meena et al. 2015). Barka et al. (2006) used *Burkholderia phytofirmans* PsJN to inoculate grapevine roots and concluded that inoculated plants physiologically performed better as manifested by their fast root growth and high plant biomass at low temperature (4 °C). Theocharis et al. (2012) showed positive priming effect of endophyte on plant at low temperature mainly due to high accumulation of several stress proteins. It is known that soybean symbiotic activities are inhibited by low temperature but soybean seedlings inoculated with both *Bradyrhizobium japonicum* and *Serratia proteamaculans* responded to symbiosis at low temperature (15 °C) and showed higher growth (Zhang et al. 1995, 1996). Mishra et al. (2009) noted that wheat seedlings primed with *Pseudomonas* sp. strain PPERs23 exhibited higher root/shoot ratio with increased dry root/shoot biomass, and other physiological traits such as increased iron, anthocyanins, proline, protein and relative water contents and reduced Na^+/K^+ ratio and electrolyte leakage also contributed to enhanced cold tolerance (Mishra et al. 2009). The above-mentioned studies clearly highlighted the importance of cold-adapted microbes like *Burkholderia phytofirmans* PsJN inoculated in plant species such as grapevines, maize, soybean, sorghum, wheat and switch grass that seems to be promising agents for low-temperature stress tolerance (Kim et al. 2012).

7.12 Future Perspective

Feeding the growing population requires high and stable yields using smart crop production technologies. The current agriculture in developing countries apparently relied on the cultivation of high-yield, moderately stress-tolerant varieties further fuelled by agrochemicals. It is not surprising that abiotic stresses, especially high temperature, drought and salinity, are considered by researchers as the most significant threats to agriculture (Trabelsi and Mhamdi 2013; Busby et al. 2017). Given this, we have to either develop stress-tolerant crop plants or look for alternative and more realistic agricultural practices (Bulgarelli et al. 2012; Mengual et al. 2014). Developing more sustainable solutions to agricultural problems seems logical under rapidly changing global climate and uncontrolled human growth (Hussain et al. 2014). Opportunities for exploiting the plant-associated microbes for raising successful crops are uncountable and diverse which can play a promising role for effectively tackling stresses in sustainable next-generation agriculture (Vandenkoornhuyse et al. 2015; Hussain et al. 2018).

The development and integration of smart agricultural tools and practices will depend on the successful use of all players in the system. Moderate success has been achieved towards the development of model host-microbiome systems for poplar, rice, sorghum, maize, miscanthus, tomato and *Medicago truncatula* (Johnston-Monje and Raizada 2011; Sessitsch et al. 2011; Knief et al. 2012; Peiffer et al. 2013; Ramond et al. 2013; Spence et al. 2014; Edwards et al. 2015; Hacquard and Schadt 2015; Lakshmanan 2015; Tian et al. 2015; Li et al. 2016; Hussain et al. 2018). However, great variation and success depend on many factors including the individual plant species, genotype, native soil microbiota, microbiome and interplay between these players with their specific traits that interact with each other under given climatic conditions. Under such circumstances, it is recommended that established microbiomes are most likely suitable candidates for generating diverse but functionally variable associations to select on a trial basis (Mueller and Sachs 2015). Hence, novel methods to utilize the plant-associated microbiome in next-generation agriculture could be helpful in enhancing crop productivity under different stresses (Bakker et al. 2012; Marasco et al. 2012; Prudent et al. 2015; Celebi et al. 2010; Mengual et al. 2014; Nadeem et al. 2014; Rolli et al. 2015). Novel versions of the most recent and advanced technologies especially omics approaches, methods and techniques are also offering its open-ended services for generation and interpretation of data from the field level to assess the real impacts of the inoculants on crop plants (Baetz and Martinoia 2013; White et al. 2017).

7.13 Conclusion

Several reports have shown promising results of significant stress tolerance in crop plants primed with plant growth-promoting microbes (PGPM) under field conditions with some negative findings as well. Application of microbial consortium represents one promising strategy for beneficial outcome in field-based agriculture to collectively respond to specific environmental stresses with no apparent impact on plant growth and productivity. Development and application of multispecies consortia have the potential to address inconsistency in performance (Hernández-Salmerón et al. 2016). Therefore, the mechanisms by which microbes confer stress tolerance to their hosts need further exploration to develop ideal microbial consortia for use under different stresses. Recent strategies like the use of omics approaches in this field provide powerful insights to understand how different players interact with each other and establish the functional relationship among microbe-microbe and plant-microbe under stress.

References

Aafi NE, Brhada F, Dary M, Maltouf AF, Pajuelo E (2012) Rhizostabilization of metals in soils using *Lupinus luteus* inoculated with the metal resistant rhizobacterium *Serratia* sp. MSMC 541. Int J Phytoremediation 14:26174

Abbasi MK, Sharif S, Kazmi M, Sultan T, Aslam M (2011) Isolation of plant growth promoting rhizobacteria from wheat rhizosphere and their effect on improving growth, yield and nutrient uptake of plants. Plant Biosyst 145:159–168

Abd El-Daim IA, Bejai S, Meijer J (2014) Improved heat stress tolerance of wheat seedling by bacterial seed treatment. Plant Soil 379:337–350

Adediran GA, Ngwenya BT, Mosselmans JF, Heal KV, Harvie BA (2015) Mechanisms behind bacteria induced plant growth promotion and Zn accumulation in *Brassica juncea*. J Hazard Mater 283:490–499

Adeleke RA, Cloete TE, Bertrand A, Khasa DP (2012) Iron ore weathering potentials of ectomycorrhizal plants. Mycorrhiza 22:535–544

Adesemoye AO, Egamberdieva D (2013) Beneficial effects of plant growth-promoting rhizobacteria on improved crop production: prospects for developing economies. In: Maheshwari DK, Saraf M, Aeron A (eds) Bacteria in agrobiology: crop productivity. Springer-Berlin, Berlin, pp 45–63

Adesemoye AO, Torbert HA, Kloepper JW (2009) Plant growth promoting rhizobacteria allow reduced application rates of chemical fertilizers. Microb Ecol 58:921–929

Adhya TK, Kumar N, Reddy G, Podile AR, Bee H, Bindiya S (2015) Microbial mobilization of soil phosphorus and sustainable P management in agricultural soils. Curr Sci 108:1280–1287

Afzal M, Yousaf S, Reichenauer TG, Kuffner M, Sessitsch A (2011) Soil type affects plant colonization, activity and catabolic gene expression of inoculated bacterial strains during phytoremediation of diesel. J Hazard Mater 186:1568–1575

Afzal M, Khan QM, Sessitsch A (2014) Endophytic bacteria: prospects and applications for the phytoremediation of organic pollutants. Chemosphere 117:232–242

Agler MT, Ruhe J, Kroll S, Morhenn C, Kim ST, Weigel D, Kemen EM (2016) Microbial hub taxa link host and abiotic factors to plant microbiome variation. PLoS Biol 14:e1002352

Ahmad M, Zahir ZA, Asghar HN, Asghar M (2011) Inducing salt tolerance in mung bean through co-inoculation with rhizobia and plant-growth-promoting rhizobacteria containing 1-aminocyc lopropane-1-carboxylate deaminase. Can J Microbiol 57:578–589

Alam MA, Seetharam KM, Zaidi PH, Dinesh A, Vinayan MT, Nath UK (2017) Dissecting heat stress tolerance in tropical maize (*Zea mays* L.). Field Crop Res 204:110–119

Alami Y, Achouak W, Marol C, Heulin T (2000) Rhizosphere soil aggregation and plant growth promotion of sunflowers by exopolysaccharide producing *Rhizobium* sp. strain isolated from sunflower roots. Appl Environ Microbiol 66:3393–3398

Ali SKZ, Sandhya V, Grover M, Kishore N, Rao LV, Venkateswarlu B (2009) *Pseudomonas* sp. strain AKM-P6 enhances tolerance of sorghum seedlings to elevated temperatures. Biol Fert Soil 46:45–55

Ali S, Charles TC, Glick BR (2012) Delay of flower senescence by bacterial endophytes expressing 1-aminocyclopropane-1-carboxylate deaminase. J Appl Microbiol 113:1139–1144

Ali S, Duan J, Charles TC, Glick BR (2014) A bioinformatics approach to the determination of genes involved in endophytic behavior in *Burkholderia* sp. J Theor Biol 343:193–198

Al-Karaki GN, Ammad R, Rusan M (2001) Response of two tomato cultivars differing in salt tolerance to inoculation with mycorrhizal fungi under salt stress. Mycorrhiza 11:43–47

Alström S (1991) Induction of disease resistance in common bean susceptible to halo blight bacterial pathogen after seed bacterization with rhizosphere pseudomonads. J Gen Appl Microbiol 37:495–501

Amann RI, Ludwing W, Schleifer KH (1995) Phylogenetic identification and in situ detection of individual microbial cells without cultivation. Microbiol Rev 59:143–169

Andreote FD, Azevedo JL, Araújo WL (2009) Assessing the diversity of bacterial communities associated with plants. Braz J Microbiol 40:417–432

Aroca R, Ruíz-Lozan JM (2012) Regulation of root water uptake under drought stress conditions. In: Aroca R (ed) Plant responses to drought stress. Springer, Berlin-Germany, pp 113–128

Arora S, Patel PN, Vanza MJ, Rao GG (2014) Isolation and characterization of endophytic bacteria colonizing halophyte and other salt tolerant plant species from coastal Gujarat. Afr J Microbiol Res 8:1779–1788

Arshad M, Sharoona B, Mahmood T (2008) Inoculation with Pseudomonas spp. containing ACC deaminase partially eliminate the effects of drought stress on growth, yield and ripening of pea (*Pisum sativum* L.). Pedosphere 18:611–620

Arslan M, Imran A, Khan QM, Afzal M (2017) Plant–bacteria partnerships for the remediation of persistent organic pollutants. Environ Sci Pollut Res 24:4322–4336

Atieno M, Herrmann L, Okalebo R, Lesueur D (2012) Efficiency of different formulations of *Bradyrhizobium japonicum* and effect of co-inoculation of *Bacillus subtilis* with two different strains of *Bradyrhizobium japonicum*. World J Microbol Biotechnol 28:2541–2550

Azcon R, Medina A, Aroca R, Ruiz-Lozano JM (2013) Abiotic stress remediation by the arbuscular mycorrhizal symbiosis and rhizosphere bacteria/yeast interactions. In: de Bruijin FJ (ed) Molecular microbial ecology of the rhizosphere. Wiley Blackwell, Hoboken, pp 991–1002

Babu AG, Reddy S (2011) Dual inoculation of arbuscular mycorrhizal and phosphate solubilizing fungi contributes in sustainable maintenance of plant health in fly ash ponds. Water Air Soil Pollut 219:3–10

Bacilio M, Moreno M, Bashan Y (2016) Mitigation of negative effects of progressive soil salinity gradients by application of humic acids and inoculation with *Pseudomonas stutzeri* in a salt-tolerant and a salt-susceptible pepper. Appl Soil Ecol 107:394–404

Badri DV, Weir TL, Van Der Lelie D, Vivanco JM (2009) Rhizosphere chemical dialogues: plant-microbe interactions. Curr Opin Biotechnol 20:642–650

Badri DV, Chaparro JM, Zhang R, Shen Q, Vivanco JM (2013) Application of natural blends of phytochemicals derived from the root exudates of arabidopsis to the soil reveal that phenolic related compounds predominantly modulate the soil microbiome. J Biol Chem 288:4502–4512

Baetz U, Martinoia E (2013) Root exudates: the hidden part of plant defense. Trends Plant Sci 19:90–97

Bai Y, muller DB, Srinivas G, Garrido-Oter R, Potthoff E, Rott M, Huttel B (2015) Functional overlap of the Arabidopsis leaf and root microbiota. Nature 528:364

Bainard LD, Koch AM, Gordon AM, Klironomos JN (2013) Growth response of crops to soil microbial communities from conventional monocropping and tree-based intercropping systems. Plant Soil 363:345–356

Bais HP, Weir TL, Perry LG, Gilroy S, Vivanco JM (2006) The role of root exudates in rhizosphere interactions with plants and other organisms. Annu Rev Plant Biol 57:233–266

Bakker MG, Manter DK, Sheflin AM, Weir TL, Vivanco JM (2012) Harnessing the rhizosphere microbiome through plant breeding and agricultural management. Plant Soil 360:1–13

Bakker PA, Berendsen RL, Doornbos RF, Wintermans PC, Pieterse CM (2013) The rhizosphere is revisited: root microbiomics. Front Plant Sci 4:165

Bal HB, Nayak L, Das S, Adhya TK (2013) Isolation of ACC deaminase producing PGPR from rice rhizosphere and evaluating their plant growth promoting activity under salt stress. Plant Soil 366:93–105

Balbontin R, Vlamakis H, Kolter R (2014) Mutualistic interaction between *Salmonella enteric* and *Aspergillus niger* and its effects on *Zea mays* colonization. Microb Biotechnol 7:589–600

Bano A, Fatima M (2009) Salt tolerance in *Zea mays* (L.) following inoculation with rhizobium and Pseudomonas. Biol Fert Soil 45:405–413

Bano Q, Ilyas N, Bano A, Zafar N, Akram A, Hassan F (2013) Effect of Azospirillum inoculation on maize (*Zea mays* L.) under drought stress. Pak J Bot 45:13–20

Barassi CA, Ayrault G, Creus CM, Sueldo RJ, Sobrero MT (2006) Seed inoculation with Azospirillum mitigates NaCl effects on lettuce. Sci Hort 109:8–14

Barka EA, Nowak J, Clement C (2006) Enhancement of chilling resistance of inoculated grapevine plantlets with a plant growth-promoting rhizobacterium, *Burkholderia phytofirmans* strain PsJN. Appl Environ Microbiol 72:7246–7252

Bartels D, Hussain SS (2008) Current status and implications of engineering drought tolerance in plants using transgenic approaches. CAB Rev Persp Agric Vet Sci Nutri Nat Sci 3:020

Bashan Y, Salazar BG, Moreno M, Lopez BR, Lindermann RG (2012) Restoration of eroded soil in the sonorant desert with native leguminous trees using plant growth promoting microorganisms and limited amounts of compost and water. J Environ Manag 102:26–36

Bashiardes S, Godneva A, Elinav E, Segal E (2018) Towards utilization of the human genome and microbiome for personalized nutrition. Curr Opin Biotechnol 51:57–63

Battisti DS, Naylor RL (2009) Historical warnings of future food insecurity with unprecedented seasonal heat. Science 323:240–244

Bell TH, Joly S, Pitre FE, Yergeau E (2014) Increasing phytoremediation efficiency and reliability using novel omics approaches. Trends Biotechnol 32:271–180

Ben Khaled L, Gomez AM, Ourraqi EM, Oihabi A (2003) Physiological and biochemical responses to salt stress of mycorrhized and/or nodulated clover seedlings (*Trifolium alexandrinum* L.). Agronomie 23:571–580

Berendsen RL, Pieterse CMJ, Bakker P (2012) The rhizosphere microbiome and plant health. Trends Plant Sci 17:478–486

Berg G (2009) Plant-microbe interactions promoting plant growth and health: perspectives for controlled use of microorganisms in agriculture. Appl Microbial Biotechnol 84:11–18

Berg G, Smalla K (2009) Plant species and soil type cooperatively shape the structure and function of microbial communities in the rhizosphere. FEMS Microbiol Ecol 68:1–13

Berg G, Zachow C, Müller H, Philipps J, Tilcher R (2013) Next-generation bio-products sowing the seeds of success for sustainable agriculture. Agronomy 3:648–656

Berg G, Grube M, Schloter M, Small K (2014) Unraveling the plant microbe: looking back and future prospective. Front Microbiol 5:148

Berg G, Rybakova D, Grube M, Koberl M (2016) The plant microbioe explored: implications for experimental botany. J Exp Bot 67:995–1002

Berman-Frank I, Lundgren P, Falkowski P (2003) Nitrogen fixation and photosynthetic oxygen evolution in *Cyanobacteria*. Res Microbiol 154:157–164

Beskoski VP, Gojgic-Cvijovic G, Milic J, Ilic M, Miletic S, Solevic T, Vrvic MM (2011) Ex-situ bioremediation of a soil contaminated by mazut (heavy residual fuel oil), a field experiment. Chemosphere 83:34–40

Bevivino A, Sarrocco S, Dalmastri S, Tabacchioni S, Cantale C, Chiarini L (1998) Characterization of a free-living maize rhizosphere population of *Burkholderia cepacia*: effect of seed treatment on disease suppression and growth promotion of maize. FEMS Microbiol Ecol 27:225–237

Bhardwaj D, Ansari MW, Sshoo RK, Tuteja N (2014) Biofertilizers function as key player in sustainable agriculture by improving soil fertility, plant tolerance and crop productivity. Microbial Cell Fact 13:1–10

Bharti N, Pandey SS, Barnawal D, Patel VK, Kalra A (2016) Plant growth promoting rhizobacteria *Dietzia natronolimnaea* modulates the expression of stress responsive genes providing protection of wheat from salinity stress. Sci Rep 6:34768

Bhattacharya PN, Jha DK (2012) Plant growth-promoting rhizobacteria (PGPR): emergence in agriculture. World J Microbial Biotechnol 28:1327–1350

Bhattacharyya PN, Sarmah SR, Dutta P, Tanti AJ (2015) Emergence in mapping microbial diversity in tea (*Camellia sinensis* L.) soil of Assam, North-East India: a novel approach. Eur J Biotechnol Biosci 3:20–25

Bhattacharyya PN, Goswani MP, Bhattacharyya LH (2016) Perspective of beneficial microbes in agriculture under changing climatic scenario: a review. J Phytology 8:26–41

Bilal S, Khan AL, Shahzad R, Asaf S, Kang SM, Lee IJ (2017) Endophytic *Paecilomyces formosus* LHL10 augments *Glycine max* L. adaptation to Ni-contaimination through affecting endogenous phytohormones and oxidative stress. Front. Plant Sci 8:870

Bisht S, Pandey P, Kaur G, Aggarwal H, Sood A, Sharma S, Kumar V, Bisht NS (2014) Utilization of endophytic strain Bacillus sp. SBER3 for biodegradation of polyaromatic hydrocarbons (PAH) in soil model system. Eur J Soil Biol 60:67–76

Bloemberg GV, Lugtenberg BJJ (2001) Molecular basis of plant growth promotion and biocontrol by rhizobacteria. Curr Opin Plant Biol 4:343–350

Bonfante P, Anca IA (2009) Plant, mycorrhizal fungi and bacteria: a network of interactions. Annu Rev Microbiol 63:363–383

Bonilla N, Vida C, Martínez-Alonso M, Landa BB, Gaju N, Cazorla FM, de Vicente A (2015) Organic amendments to avocado crops induce suppressiveness and influence the composition and activity of soil microbial communities. Appl Environ Microbiol 81:3405–3418

Boon E, Meehan CJ, Whidden C, Wong DHJ, Langille MGI, Beiko RG (2014) Interactions in the microbiome: communities of organisms and communities of genes. FEMS Microbiol Rev 38:90–118

Boopathy R (2000) Factors limiting bioremediation technologies. Bioresour Technol 74:63–67

Broos K, Uyttebroek M, Mertens J, Smolders E (2004) A survey of symbiotic nitrogen fixation by white clover grown on metal contaminated soils. Soil Biol Biochem 36:633–640

Budak H, Kantar M, Yucebilgili Kurtoglu K (2013) Drought tolerance in modern and wild wheat. Sci World J 2013:548246

Bulgarelli D, Rott M, Schlaeppi K, Loren Ver van Themaat E, Ahmadinejad N, Assenza F, Rauf P, Huettel B, Reinhardt R, Schmelzer E, Peplies J, Gloeckner FO, Amann R, Eickhorst T, Schulze-Lefert P (2012) Revealing structure and assembly cues for *Arabidopsis* root-inhabiting bacterial microbiota. Nature 488:91–95

Bulgarelli D, Schlaeppi K, Spaepen S, Ver Loren van Themaat E, Schulze-Lefert P (2013) Structure and functions of the bacterial microbiota of plants. Annu Rev Plant Biol 64:807–838

Bulgarelli D, Garrido-Oter R, Munch PC, Weiman A, Droge J, Pan Y, McHardy AC, Schulze-Lefert P (2015) Structure and function of the bacterial root microbiota in wild and domesticated barley. Cell Host Microbe 17:392–403

Busby PE, Soman C, Wagner MR, Friesen ML, Kremer J, Bennett A, Morsy M, Eisen JA, Leach JE, Dangl JL (2017) Research priorities for harnessing plant microbiomes in sustainable agriculture. PLoS Biol 15:e2001793

Cai F, Chen W, Wei Z, Pang G, Li R, Ran W, Shen Q (2014) Colonization of *Trichoderma harzianum* strain SQR-T037 on tomato roots and its relationship to plant growth, nutrient availability and soil microflora. Plant Sci 388:337–350

Calvo P, Watts DB, Kloepper JW, Torbert HA (2017) Effect of microbial-based inoculants on nutrient concentrations and early root morphology of corn (*Zea mays*). J Plant Nutr Soil Sci 180:56–70

Capell T, Bassie L, Christou P (2004) Modulation of the polyamine biosynthetic pathway in transgenic rice confers tolerance to drought stress. Proc Natl Acad Sci U S A 101:9909–9914

Carson JK, Gonzalez-Quinones V, Murphy DV, Hinz MC, Shaw JA, Gleeson DB (2010) Low pore connectivity increases bacterial diversity in soil. Appl Environ Microbiol 76:3936–3942

Carvalhais LC, Dennis PG, Fan B, Fedoseyenko D, Kierul K, Becker A, von Wiren N, Borriss R (2013) Linking plant nutritional status to plant-microbe interactions. PLoS One 8:e68555

Cassán F, Perrig D, Sgroy V, Masciarelli O, Penna C, Luna V (2009) *Azospirillum brasilense* Az39 and *Bradyrhizobium japonicum* E109, inoculated singly or in combination, promote seed germination and early seedling growth in corn (*Zea mays* L.) and soybean (*Glycine max* L.). Eur J Soil Biol 45:28–35

Castillo P, Escalante M, Gallardo M, Alemano S, Abdala G (2013) Effects of bacterial single inoculation and co-inoculation on growth and phytohormone production of sunflower seedlings under water stress. Acta Physiol Plant 35:2299–2309

Celebi SZ, Demir S, Celebi R, Durak ED, Yilmaz IH (2010) The effect of arbuscular mycorrhizal fungi (AMF) applications on the silage maize (*Zea mays* L.) yield in different irrigation regimes. Eur J Soil Biol 46:302–305

Chagnon PL, Bradley RL, Maherali H, Klironomos JN (2013) A trait-based framework to understand life history of mycorrhizal fungi. Trends Plant Sci 18:484–491

Chang P, Gerhardt KE, Huang XD, Yu XM, Glick BR, Gerwing PD, Greenberg BM (2014) Plant growth-promoting bacteria facilitate the growth of barley and oats in salt-impacted soil: implications for phytoremediation of saline soils. Int J Phytoremedation 16:1133–1147

Chaparro JM, Badri DV, Vivanco JM (2013) Rhizosphere microbiome assemblage is affected by plant development. ISME J 8:790–803

Chaparro JM, Badri DV, Vivanco JM (2014) Rhizosphere microbiome assemblage is affected by plant development. ISMI J 8:790–803

Chauhan H, Bagyaraj DJ, Selvakumar G, Sundaram SP (2015) Novel plant growth promoting rhizobacteria prospects. Appl Soil Ecol 95:38–53

Chen L, Luo S, Li X, Wan Y, Chen J, Liu C (2014) Interaction of Cd-hyperaccumulator *Solanum nigrum* L. and functional endophyte Pseudomonas sp. Lk9 on soil heavy metals uptake. Soil Biol Biochem 68:300–308

Cho K, Toler H, Lee J, Ownley B, Stutz JC, Moore JL, Auge RM (2006) Mycorrhizal symbiosis and response of sorghum plants to combined drought and salinity stresses. J Plant Physiol 163:517–528

Choudhary DK, Prakash A, Johri BN (2007) Induced systemic resistance (ISR) in plants: mechanism of action. Indian J Microbiol 47:289–297

Clavel T, Lagkouvardos I, Blaut M, Stecher B (2016) The mouse gut microbiome revisited: from complex diversity to model ecosystems. Int J Med Microbiol 306:316–327

Cohen AC, Bottini R, Pontin M, Berli FJ, Moreno D, Boccanlandro H, Travaglia CN, Piccoli PN (2015) *Azospirillum brasilense* ameliorates the response of *Arabidopsis thaliana* to drought mainly via enhancement of ABA levels. Physiol Plant 153:79–90

Coleman-Derr D, Tringe SG (2014) Building the crops of tomorrow: advantages of symbiont-based approaches to improving abiotic stress tolerance. Front Microbiol 5:283

Compant S, Duffy B, Nowak J, Clément C, Barka EA (2005) Use of plant growth-promoting bacteria for biocontrol of plant diseases: principles, mechanisms of action, and future prospects. Appl Environ Microbiol 71:4951–4959

Compant S, Saikkonen K, Mitter B, Campisano A, Blanco JM (2016) Soil, plants and endophytes. Plant Soil 405:1–11

Conrath U (2006) Systemic acquired resistance. Plant Signal Behav 4:179–184

Cooper M, Gho C, Leafgren R, Tang T, Messina C (2014) Breeding drought-tolerant maize hybrids for the US corn-belt: discovery to product. J Exp Bot 65:6191–6204

Corral-Lugo A, De la Torre J, Matilla MA, Fernández M, Morel B, Espinosa-Urgel M, Krell T (2016) Assessment of the contribution of chemoreceptor-based signalling to biofilm formation. Environ Microbiol 18:3355–3372

Creus CM, Sueldo RJ, Barassi CA (2004) Water relations and yield in *Azospirillum*-inoculated wheat exposed to drought in the field. Can J Bot 82:273–281

Cummings SP, Orr C (2010) The role of plant growth promoting rhizobacteria in sustainable and low graminaceous crop production. In: Maheshwari DK (ed) Plant growth and health promoting bacteria. Springer, Berlin

Cushman JC, Bohnert HJ (2000) Genomic approaches to plant stress tolerance. Curr Opin Plant Biol 3:117–124

Damodaran T, Sah V, Rai RB, Sharma DK, Mishra VK, Jha SK, Kannan R (2013) Isolation of salt tolerant endophytic and rhizospheric bacteria by natural selection and screening for promising plant growth-promoting rhizobacteria (PGPR) and growth vigour in tomato under sodic environment. Afr J Microbiol Res 7:5082–5089

Dangl JL, Horvath DM, Staskawicz BJ (2013) Pivoting the plant immune system from dissection to deployment. Science 341:746–751

De Bruijin FJ (2015) Biological nitrogen fixation. In: Lugtenberg B (ed) Principles of plant-microbe interactions. Springer International Publishing Switzerland, Heidelberg, pp 215–224

de la Torre-González A, Navarro-Leon E, Albacete A, Blasco B, Ruiz JM (2017) Study of Phytohormone profile and oxidative metabolism as key process to identification of salinity response in tomato commercial genotypes. J Plant Physiol 216:164–173

De Vries FT, Thebault E, Liiri M, Birkhofer K, Tsiafouli MA, Bjornlund L, Jorgensen HB, Brady MV, Christensen S, de Ruiter PC, Hertefeldt T, Frouz J, Hedlund K, Hemerik L, Gera Hol WH, Hotes S, Mortimer SR, Setala H, Sgardelis SP, Uteseny K, der Putten WH, Wolters V, Bardgett RD (2013) Soil food web properties explain ecosystem sevices across European land use systems. Proc Natl Acad Sci U S A 110:14296–14301

de Zelicourt A, Al-Yousif M, Hirt H (2013) Rhizosphere microbes as essential partners for plant stress tolerance. Mol Plant 6:242–245

De-la-Peña C, Badri D, Loyola-Vargas V (2012) Plant root secretions and their interactions with neighbors. In: Vivanco JM, Baluška F (eds) Secretions and exudates in biological systems. Springer, Berlin, pp 1–26

Dell Fabbro C, Prati D (2014) Early responses of wild plant seedlings to arbuscular mycorrhizal fungi and pathogens. Basic Aggl Ecol 15:534–542

Deng Z, Cao L (2017) Fungal endophytes and their interactions with plants in phytoremediation: a review. Chemosphere 168:1100–1106

Deng B, Yang K, Zhang Y, Li Z (2016) Can heavy metal pollution defend seed germination against heat stress? Effect of heavy metals (Cu2C, Cd2C and Hg2C) on maize seed germination under high temperature. Environ Pollut 216:46–52

Dikilitas M, Karakas S, Ahmad P (2018) Predisposition of crop plants to stress is directly related to their DNA health. In: Egamberdieva D, Ahmad P (eds) Plant microbiome: stress response. Springer Nature, Singapore, pp 233–254

Dimpka C, Weinard T, Asch F (2009) Plant-rhizobacteria interactions alleviate abiotic stress conditions. Plant Cell Environ 32:1682–1694

Ding GC, Piceno YM, Heuer H, Weinert N, Dohrmann AB, Carrillo A, Andersen GL, Castellanos T, Tebbe CC, Small K (2013) Changes of soil bacterial diversity as a consequence of agricultural land use in a semi-arid ecosystem. PLoS One 8:e59497

Doble M, Kumar A (2005) Biotreatment of industrial effluents. Elsvier, Butterworth-Heinemann, Amsterdam/Boston, pp 1–5

Dodd IC, Belimov AA, Sobeih WY, Safronova VI, Grierson D, Davies WJ (2005) Will modifying plant ethylene status improve plant productivity in water-limited environments? 4th international crop science congress. http://www.cropscience.org.au/icsc2004/poster/1/3/4/510_doddicref.htm. Accessed 21 Aug 2017

Dong HN, Zhang DW (2014) Current development in genetic engineering strategies of *Bacillus* species. Microb Cell Factories 13:63

Doornbos RF, van Loon LC, Bakker PHM (2011) Impact of root exudates and plant defense signaling on bacterial communities in the rhizosphere: a review. Agron Sustain Dev 32:227–243

Dumbrell AJ, Nelson M, Helgason T, Dytham C, Fitter AH (2010) Relative roles of niche and neutral processes in structuring a soil microbial community. ISME J 4:337–345

Duruibe JO, Ogwuegbu MOC, Egwurugwu JN (2007) Heavy metal pollution and human biotoxic effects. Int J Phys Sci 2:112–118

Edwards J, Johnson C, Santos-Medellín C, Lurie E, Podishetty NK, Bhatnagar S, Eisen JA, Sundaresan V (2015) Structure, variation, and assembly of the root-associated microbiomes of rice. Proc Natl Acad Sci U S A 112:E911–EE20

Egamberdieva D, Wirth SJ, Alqarawi AA, Abd-Allah EF, Hashem A (2017) Phytohormones and beneficial microbes: essential components for plant to balance stress and fitness. Front Microbiol 8:2104

Egamberdiyeva D (2007) The effect of plant growth promoting bacteria on growth and nutrient uptake of maize in two different soils. Appl Soil Ecol 36:184–189

Elbadry M, Taha RM, Eldougdoug KA, Gamal-Eldin H (2006) Induction of systemic resis-tance in faba bean (*Vicia faba* L.) to bean yellow mosaic potyvirus (BYMV) via seed bacterization with plant growth promoting rhizobacteria. J Plant Dis Prot 113:247–251

Farooq M, Wahid A, Kobayashi N, Fujita D, Basra SMA (2009) Plant drought stress: effects, mechanisms, and management. Sustainable agriculture. Springer, Netherlands, pp 153–188

Farrar K, Bryant D, Cope-Selby N (2014) Understanding and engineering beneficial plant-microbe interactions: plant growth promotion in energy crops. Plant Biotechnol J 12:1193–1206

Fasciglione G, Casanovas EM, Quillehauquy V, Yommi AK, Goni MG, Roura SI, Barassi CA (2015) Azospirillum inoculation effects on growth, product quality and storage life of lettuce plants grown under salt stress. Sci Hortic 195:154–162

Fatnassi IC, Chiboub M, Saadani O, Jebara M, Jebara CA (2015) The impact of dual inoculation with Rhizobium and PGPR on growth and antioxidant status of *Vicia faba* L. under copper stress. Crit Rew Biol 338:241–254

Feng G, Zhang FS, Li XL, Tian CY, Tang C, Renegal Z (2002) Improved tolerance of maize plants to salt stress by *arbuscular mycorrhiza* is related to higher accumulation of leaf P-concentration of soluble sugars in roots. Mycorrhiza 12:185–190

Feng NX, Yu J, Zhao HM, Cheng YT, Mo CH, Cai QY, Li YW, Li H, Wng MH (2017) Efficient phytoremediation of organic contaminants in soils using plant-endophyte partnerships. Sci Total Environ 583:352–368

Ferrara FIS, Oliveira ZM, Gonzales HHS, Floh EIS, Barbosa HR (2012) Endophytic and rhizospheric enterobacteria isolated from sugar cane have different potentials for producing plant growth-promoting substances. Plant Soil 353:409–417

Fester T, Giebler J, Wick LY, Schlosser D, Kästner M (2014) Plant–microbe interactions as drivers of ecosystem functions relevant for the biodegradation of organic contaminants. Curr Opin Biotechnol 27:168–175

Fierer N (2017) Embracing the unknown: disentangling the complexities of the soil microbiome. Nat Rev Microbiol 15:579–590

Figueiredo MVB, Burity HA, Martinez CR, Chanway CP (2008) Alleviation of drought stress in common bean (*Phaseolus vulgaris* L.) by co-inoculation with *Paenibacillus polymyxa* and *Rhizobium tropici*. Appl Soil Ecol 40:182–188

Filippi MCC, da Silva GB, Silva-Lobo VL, Côrtes MVCB, Moraes AJG, Prabhu AS (2011) Leaf blast (*Magnaporthe oryzae*) suppression and growth promotion by rhizobacteria on aerobic rice in Brazil. Biol Control 58:160–166

Fouzia A, Allaoua S, Hafsa C, Mostefa G (2015) Plant growth promoting and antagonistic traits of indigenous fluorescent Pseudomonas spp. isolated from wheat rhizosphere and a thalamus endosphere. Eur Sci J 11:129–148

Foyer CH, Rasool B, Davey JW, Hancock RD (2016) Cross-tolerance to biotic and abiotic stresses in plants: a focus on resistance to aphid infestation. J Exp Bot 7:2025–2037

Friesen M, Porter S, Stark SC, von Wettberg EJ, Sachs JL, Martinez-Romero E (2011) Microbially mediated plant functional traits. Annu Rev Ecol Evol Syst 42:23–46

Gabriela F, Casanovas EM, Quillehauquy V, Yommi AK, Goni MG, Roura SI, Barassi CA (2015) Azospirillum inoculation effects on growth, product quality and storage life of lettuce plants grown under salt stress. Sci Hortic 195:154–162

Gaby JC, Buckley DH (2011) A global census of nitrogenase diversity. Environ Microbiol 13:1790–1799

Gerhardt KE, Huang XD, Glick BR, Greenberg BM (2009) Phytoremediation and rhizoremediation of organic soil contaminants: potential and challenges. Plant Sci 176:20–30

Ghanem G, Ewald A, Henning F (2014) Effect of root colonization with *Piriformospora indica* and phosphate availability on the growth and reproductive biology of a *Cyclamen persicum* cultivar. Sci Hortic 172:233–241

Ghosh P, Rathinasabapathi B, Ma LQ (2015) Phosphorus solubilization and plant growth enhancement by arsenic-resistant bacteria. Chemosphere 134:1–6

Gianinazzi S, Gollotte A, Binet MN, van Tuinen D, Redecker D, Wipf D (2010) Agroecology: the key role of *arbuscular mycorrhizae* in ecosystem services. Mycorrhiza 20:519–530

Giri B, Mukerji KG (2004) Mycorrhizal inoculant alleviate salt stress in *Sesbania aegyptiaca* and *Sesbania grandiflora* under field conditions: evidence for reduced sodium and improved magnesium uptake. Mycorrhiza 14:307–312

Glick BR (2010) Using soil bacteria to facilitate phytoremediation. Biotechnol Adv 28:367–374

Glick BR (2012) Plant growth-promoting bacteria: mechanisms and applications. Scientifica 2012:1–15

Glick BR (2014) Bacteria with ACC deaminase can promote plant growth and help to feed the world. Microbiol Res 169:30–39

Glick BR (2015) Phytoremediation: beneficial plant-bacterial interactions. Springer International Publishing, Cham, pp 191–221

Glick BR, Cheng Z, Czarny J, Duan J (2007) Promotion of plant growth by ACC deaminase-producing soil bacteria. Eur J Plant Pathol 119:329–339

Goh CH, Valiz Vallejos DF, Nicotra AB, Mathesius U (2013) The impact of beneficial plant-associated microbes on plant phenotypic plasticity. J Chem Ecol 39:826–839

Goodrich JK, Davenport ER, Clark AG, Ley RE (2017) The relationship between the human genome and microbiome comes into view. Annu Rev Genet 51:413–433

Goswami D, Thakker JN, Dhandhukia PC (2016) Portraying mechanics of plant growth-promoting rhizobacteria (PGPR): a review. Cogent Food Agric 2:1–19

Gouda S, Kerry RG, Das G, Paramithiotis S, Shin H-S, Patra JK (2018) Revitalization of plant growth promoting rhizobacteria for sustainable development in agriculture. Microbiol Res 206:131–140

Grice EA, Segre JA (2012) The human microbiome: our second genome. Annu Rev Genomics Hum Genet 13:151–170

Grover M, Ali Sk Z, Sandhya V, Rasul A, Venkateswarlu B (2011) Role of microorganisms in adaptation of agriculture crop to abiotic stresses. World J Bicrobiol Biotechnol 27:1231–1240

Guimaraes AA, Jaramillo PMD, Nobrega RSA, Florentino LA, Silva KB, de Souza Moreira FM (2012) Genetic and symbiotic diversity of nitrogen-fixing bacteria isolated from agricultural soils in the western Amazon by using cowpea as the trap plant. Appl Environ Microbiol 78:6726–6733

Gupta G, Parihar SS, Ahirwar NK, Snehi SK, Singh V (2015) Plant growth promoting rhizobacteria (PGPR): current and future prospects for development of sustainable agriculture. J Microbiol Biochem 7:96–102

Gusain YS, Singh US, Sharma AK (2015) Bacterial mediated amelioration of drought stress in drought tolerant and susceptible cultivars of rice (*Oryza sativa* L.). Afr J Biotechnol 14:764–773

Guttman D, McHardy AC, Schulze-Lefert P (2014) Microbial genome-enabled insights into plant-microorganism interactions. Nat Rev Genet 15:797–813

Hacquard S, Schadt CW (2015) Towards a holistic understanding of the beneficial interactions across the Populus microbiome. New Phytol 205:1424–1430

Hadi F, Bano A (2010) Effect of diazotrophs (*Rhizobium* and *Azotobacter*) on growth of maize (*Zea mays* L.) and accumulation of Lead (Pb) in different plant parts. Pak J Bot 42:4363–4370

Haggag WM, Abouziena HF, Abd-El-Kreem F, Habbasha S (2015) Agriculture biotechnology for management of multiple biotic and abiotic environmental stress in crops. J Chem Pharm 7:882–889

Haichar FZ, Marol C, Berge O, Rangel-Castro JI, Prosser JI, Balesdent J, Heutin T, Achouak W (2008) Plant host habitat and root exudates shape soil bacterial community structure. ISME J 2:1221–1230

Hamel C, Vujanovic V, Jeannotte R, Nakano-Hylander A, St-Arnaud M (2005) Negative feedback on perennial crop: fusarium crown and root rot of asparagus is related to changes in soil microbial community structure. Plant Soil 268:75–87

Han J, Sun L, Dong X, Cai Z, Sun X, Yang H, Wang Y, Song W (2005) Characterization of a novel plant growth-promoting bacteria strain *Delftia tsuruhatensis* HR4 both as a diazotroph and a potential biocontrol agent against various plant pathogens. Syst Appl Microbiol 28:66–76

Haney CH, Ausubel FM (2015) Plant microbiome blueprints. Science 349:788–789

Haney CH, Samuel BS, Bush J, Ausubel FM (2015) Associations with rhizosphere bacteria can confer an adaptive advantage to plants. Nat Plants 1:15051

Hardoim PR, van Overbeek L, van Elsas J (2008) Properties of bacterial endophytes and their proposed role in plant growth. Trends Microbiol 16:463–471

Hardoim PR, van Overbeek LS, Berg G, Pirtilla AM, Compant S, Campisano A, Doring M, Sessitsch A (2015) The hidden world within plants: ecological and evolutionary considerations for defining functioning of microbial endophytes. Microbiol Mol Biol Rev 79:293–320

Hartmann A, Schmid M, van Tuinen D, Berg G (2009) Plant-driven selection of microbes. Plant Sci 268:75–87

Hasan MA (2013) Investigation on the nitrogen fixing *Cyanobacteria* (BGA) in rice fields of North-West region of Bangladesh. J Environ Sci Nat Resour 6:253–259

Hawes MC, Curlango-Rivera G, Xiong Z, Kessler JO (2012) Roles of root border cells in plant defense and regulation of rhizosphere microbial population by extracellular DNA "trapping". Plant Soil 355:1–16

Hawkins HJ, Johansen A, George E (2000) Uptake and transport of organic and inorganic nitrogen by arbuscular mycorrhizal fungi. Plant Soil 226:275–285

Hayat R, Ali S, Amara U, Khalid R, Ahmed I (2010) Soil beneficial bacteria and their role in plant growth promotion: a review. Ann Microbiol 60:579–598

Hernandez-Leon R, Rojas-Solfs D, Contreras-Perez M, Orozco-Mosqueda M, Macias-Rodriguez L, Reyes-delaCruz H, Valencia-Cantero E, Santoyo G (2015) Characterization of antifungal and plant growth-promoting effects of diffusible and volatile organic compounds produced by *Pseudomonas fluorescens* strains. Biol Control 81:83–92

Hernández-Salmerón J, Hernández-León R, del Orozco-Mosqueda MAC, Moreno-Hagelsieb G, Valencia-Cantero E, Santoyo G (2016) Draft genome sequence of the biocontrol and plant growth-promoting rhizobacterium *Pseudomonas fluorescens* UM270. Stand Genom Sci 11:5

Hirsch PR, Mauchline TH (2012) Who's who in the plant root microbiome? Nat Biotechnol 30:961–962

Hristozkova M, Geneva M, Stanchova I, Boychinova M, Djonova E (2016) The contribution of arbuscular mycorrhizal fungi in attenuation of heavy metal impact on *Calendula officinalis* development. Appl Soil Ecol 101:57–63

Hu S, Gu H, Cui C, Ji R (2016) Toxicity of combined chromium (VI) and phenanthrene pollution on the seed germination, stem lengths, and fresh weights of higher plants. Environ Sci Pollut Res 23:15227–15235

Huang B, DaCosta M, Jiang Y (2014a) Research advances in mechanisms of turfgrass tolerance to abiotic stresses: from physiology to molecular biology. Crit Rev Plant Sci 33:141–189

Huang X-F, Chaparro JM, Reardon KF, Zhang R, Shen Q, Vivanco JM (2014b) Rhizosphere interactions: root exudates, microbes, and microbial communities. Botany 92:267–275

Hussain SS, Iqbal MT, Arif MA, Amjad M (2011) Beyond osmolytes and transcription factors: drought tolerance in plants via protective proteins and aquaporins. Biol Plant 55:401–413

Hussain SS, Raza H, Afzal I, Kayani MA (2012) Transgenic plants for abiotic stress tolerance: current status. Arch Agron Soil Sci 58:693–721

Hussain SS, Siddique KHM, Lopato S (2014) Towards integration of bacterial genomics in plants for enhanced abiotic stress tolerance: clues from transgenics. Adv Environ Res 33:65–122

Hussain SS, Asif MA, Sornaraj P, Ali M, Shi BJ (2016) Towards integration of system based approach for understanding drought stress in plants. In: Ahmad P, Rasool S (eds) Water stress and crop plants: a sustainable approach. Elsevier, Atlanta, pp 227–247

Hussain SS, Mehnaz S, Siddique KM (2018) Harnessing the plant microbiome for improved abiotic stress tolerance. In: Ahmad P, Egamberdieva D (eds) Microbiome: stress response and microbes for sustainable agriculture. Springer, Singapore, pp 21–43

Iannucci A, Fragasso M, Beleggic R, Nigo F, Papa R (2017) Evolution of crop rhizosphere: impact of domestication on root exudates in tetraploid wheat (*Triticum turgidum* L.). Front Plant Sci 8:2124

Ijaz A, Imran A, ul Haq MA, Khan QM, Afzal M (2016) Phytoremediation: recent advances in plant-endophytic synergistic interactions. Plant Soil 405:179–195

Inceoglu O, Overbeek LS, Salles JF, Elsas JD (2013) Normal operating range of bacterial communities in soil used for potato cropping. Appl Environ Microbiol 79:1160–1170

IPCC (2007) The physical science basis. Contribution of working group I to the fourth assessment report of the intergovernmental panel on climate change. Cambridge University Press, Cambridge

Islam S, Akanda AM, Prova A, Islam MT, Hossain M (2016) Isolation and identification of plant growth promoting rhizobacteria from cucumber rhizosphere and their effect on plant growth promotion and disease suppression. Front Microbiol 6:1–12

Jamil M, Zeb S, Anees M, Roohi A, Ahmed I, Rehman SU, Rha ES (2014) Role of *Bacillus licheniformis* in phytoremediation of nickel contaminated soil cultivated with rice. Int J Phytoremediation 16:554–571

Jansson JK, Hofmockel KS (2018) The soil microbiome: from metagenomics to metaphenomics. Curr Opin Microbiol 43:162–168

Jefferies P, Barea JM (2001) *Arbuscular mycorrhiza*: a key component of sustainable plant-soil ecosystems. In: Hock B (ed) The mycota (Vol. IX: fungal associations). Springer, Berlin

Jez JM, Lee SG, Sherp AM (2016) The next green movement: plant biology for the environment and sustainability. Science 353:1241–1244

Jha Y, Subramanian RB (2014) PGPR regulate caspase-like activity, programmed cell death, and antioxidant enzyme activity in paddy under salinity. Physiol Mol Biol Plant 20:201–207

Jha B, Gontia I, Hartmann A (2012) The roots of the halophyte *Salicornia brachiata* are a source of new halotolerant diazotrophic bacteria with plant growth-promoting potential. Plant Soil 356:265–277

Jha P, Panwar J, Jha PN (2015) Secondary plant metabolites and root exudates: guiding tools for polychlorinated biphenyl biodegradation. Int J Environ Sci Technol 12:789–802

Jin H, Liu J, Liu J, Huang X (2012) Forms of nitrogen uptake, translocation and transfer via arbuscular mycorrhizal fungi: a review. Sci China Life Sci 55:474–482

Jindal V, Atwal A, Sekhon BS, Rattan S, Singh R (1993) Effect of vesicular-arbuscular mycorrhiza on metabolism of moong plants under salinity. Plant Physiol Biochem 31:475–481

Jing YX, Yan YJ, He HD, Yang DJ, Xiao L, Zhong T, Yuan M, Cai XD, Li SB (2014) Characterization of bacteria in the rhizosphere soils of *Polygonum pubescens* and their potential in promoting growth and Cd, Pb, Zn uptake by *Brassica napus*. Int J Phytoremediation 16:321–333

Johnson NC, Graham JH (2013) The continuum concept remains a useful framework for studying mycorrhizal functioning. Plant Soil 363:411–419

Johnson D, Martin F, Cairney JWG, Anderson IC (2012) The importance of individuals: intraspecific diversity of mycorrhizal plants and fungi in ecosystems. New Phytol 194:614–628

Johnston-Monje D, Raizada MN (2011) Conservation and diversity of seed associated endophytes in zea across boundaries of evolution, ethnography and ecology. PLoS One 6:e20396

Jones MB, Finnan J, Hodkinson TR (2014) Morphological and physiological traits for higher biomass production in perennial rhizomatous grasses grown on marginal land. Glob Change Biol Bioenergy 7:375–385

Jorquera MA, Shaharoona B, Nadeem SM, de la Luz MM, Crowley DE (2012) Plant growth-promoting rhizobacteria associated with ancient clones of creosote bush (*Larrea tridentata*). Microb Ecol 64:1008–1017

Kachroo A, Robin GP (2013) Systemic signaling during plant defense. Curr Opin Plant Biol 16:527–533

Kamal R, Gusain YS, Kumar V (2014) Interaction and symbiosis of fungi, actinomycetes and plant growth promoting rhizobacteria with plants: strategies for the improvement of plants health and defense system. Int J Curr Microbial Appl Sci 3:564–585

Kanchiswamy CN, Malnoy M, Maffei ME (2015) Chemical diversity of microbial volatiles and their potential for plant growth and productivity. Front Plant Sci 6:151

Kang SM, Radhakrishnan R, Khan AL, Kim MJ, Park JM, Kim BR, Shim DH, Lee IJ (2014) Gibberellin secreting rhizobacterium, Pseudomonas putida H-2-3 modulates the hormonal and stress physiology of soybean to improve the plant growth under saline and drought conditions. Plant Physiol Biochem 84:115–124

Kasim W, Osman M, Omar M, Abd El-Daim I, Bejai S, Meijer J (2013) Control of drought stress in wheat using plant-growth promoting rhizobacteria. J Plant Growth Regul 32:122–130

Kasim WA, Gaafar RM, Abou-Ali RM, Omar MN, Hewait HM (2016) Effect of biofilm forming plant growth promoting rhizobacteria on salinity tolerance in barley. Ann Agric Sci 61:217–227

Kathuria H, Giri J, Tyagi H, Tyagi AK (2007) Advances in transgenic rice biotechnology. Crit Rev Plant Sci 26:65–103

Kavamura VN, Santos SN, Silva JL, Parma MM, Avila LA, Visconti A, Zucchi TD, Taketani RG, Andreote FD, Melo IS (2013) Screening of Brazilian cacti rhizobacteria for plant growth promotion under drought. Microbiol Res 168:183–191

Khalid A, Tahir S, Arshad M, Zahir ZA (2004) Relative efficiency of rhizobacteria for auxin biosynthesis in rhizosphere and non-rhizosphere soils. Aust J Soil Res 42:921–926

Khan IA, Ayub N, Mirza SN, Nizami SN, Azam M (2008) Yield and water use efficiency (WUE) of *Cenchrus ciliaris* as influenced by vesicular arbuscular mycorrhizae (VAM). Pak J Bot 40:931–937

Khan A, Jilani G, Akhtar MS, Naqvi SMS, Rasheed M (2009) Phosphorus solubilizing bacteria: occurrence, mechanisms and their role in crop production. J Agric Biol Sci 1:48–58

Khan Z, Rho H, Firrincieli A, Hung H, Luna V, Masciarelli O, Kim SH, Doty SL (2016) Growth enhancement and drought tolerance of hybrid poplar upon inoculation with endophyte consortia. Curr Plant Biol 6:38–47

Khan AL, Waqas M, Asaf S, Kamran M, Shahzad R, Bilal S, Khan MA, Kang SM, Kim YH, Yun BW, Al-Rwahi A, Al-Harassi A, Lee IJ (2017) Plant growth-promoting endophyte Sphingomonas sp.: LK11 alleviates salinity stress in *Solanum pimpinellifolium*. Environ Exp Bot 133:58–69

Kidd P, Barcelo J, Bernal MP, Navari-Izzo F, Poschenrieder C, Shilev S, Clemente R, Monterroso C (2009) Trace element behavior at the root-soil interface: implications in phytoremediation. Environ Exp Bot 67:243–259

Kim SB, Timmusk S (2013) A simplified method for gene knockout and direct screening of recombinant clones for application in *Paenibacillus polymyxa*. PLoS One 8:e68092

Kim YC, Glick BR, Bashan Y, Ryu CM (2009) Enhancement of plant drought tolerance by microbes. In: Aroca R (ed) Plant responses to drought stress. Springer, Berlin, pp 383–412

Kim S, Lowman S, Hou G, Nowak J, Flinn B, Mei C (2012) Growth promotion and colonization of switchgrass (*Panicum virgatum*) cv. Alamo by bacterial endophyte *Burkholderia phytofirmans* strain PsJN. Biotechnol Bioguels 5:37

Kim YC, Glick B, Bashan Y, Ryu CM (2013) Enhancement of plant drought tolerance by microbes. In: Aroca R (ed) Plant responses to drought stress. Springer, Berlin

Kim JS, Lee J, Seo SG, Lee C, Woo SY, Kim SH (2015) Gene expression profile affected by volatiles of new plant growth promoting rhizobacteria, *Bacillus subtilis* strain JS, in tobacco. Genes Genom 37:387–397

Kloepper JW, Ryu CM, Zhang S (2004) Induced systemic resistance and promotion of plant growth by Bacillus spp. Phytopathology 94:1259–1266

Knief C (2014) Analysis of plant microbe interactions in the era of next generation sequencing technologies. Front Plant Sci 5:216

Knief C, Delmotte N, Chaffron S, Stark M, Innerebner G, Wassmann R, von Mering C, Vorholt JA (2012) Metaproteogenomic analysis of microbial communities in the phyllosphere and rhizosphere of rice. ISME J 6:1378–1390

Kohler J, Hernandez JA, Caravaca F, Rolden A (2008) Plant growth promoting rhizobacteria and arbuscular mycorrhizal fungi modify alleviation biochemical mechanisms in water stressed plants. Funct Plant Biol 35:141–151

Krey T, Vassilev N, Baum C, Eichler-Löbermann B (2013) Effects of long-term phosphorus application and plant-growth promoting rhizobacteria on maize phosphorus nutrition under field conditions. Eur J Soil Biol 55:124–130

Kukla M, Płociniczak T, Piotrowska-Seget Z (2014) Diversity of endophytic bacteria in *Lolium perenne* and their potential to degrade petroleum hydrocarbons and promote plant growth. Chemosphere 117:40–46

Kumar A (2016) Phosphate solubilizing bacteria in agriculture biotechnology: diversity, mechanism and their role in plant growth and crop yield. Int J Adv Res 4:116–124

Kumar A, Verma JP (2018) Does plant-microbe interaction confer stress tolerance in plants: a review? Microbiol Res 207:41–52

Kumar KV, Srivastava S, Singh N, Behl HM (2009) Role of metal resistant plant growth promoting bacteria in ameliorating fly ash to the growth of *Brassica juncea*. J Hazard Mater 170:51–57

Lakshmanan V (2015) Root microbiome assemblage is modulated by plant host factors. In: Bais H, Sherrier J (eds) Plant microbe interactions. Advances in botanical research, 75. Academic, Amsterdam, pp 57–79

Lakshmanan V, Kitto SL, Caplan JL, Hsueh YH, Kearns DB, Wu YS, Bais HP (2012) Microbe-associated molecular patterns-triggered root responses mediate beneficial rhizobacterial recruitment in Arabidopsis. Plant Physiol 160:1642–1661

Lakshmanan V, Selvaraj G, Bais HP (2014) Functional soil microbiome: below ground solution to an above ground problem. Plant Physiol 166:689–700

Lally RD, Galbally P, Moreira AS, Spink J, Ryan D, Germaine KJ, Dowling DN (2017) Application of endophytic *Pseudomonas fluorescens* and a bacterial consortium to *Brassica napus* can increase plant height and biomass undergreenhouse and field conditions. Front Plant Sci 8:2193

Landa BB, Mavrodi OV, Schroeder KL, Allende-Molar R, Weller DM (2006) Enrichmentand genotypic diversity of phlD-containing fluorescent Pseudomonas spp. in two soils after a century of wheat and flax monoculture. FEMS Microbiol Ecol 55:351–368

Lareen A, Burton F, Schäfer P (2016) Plant root-microbe communication in shaping root microbiomes. Plant Mol Biol 90:575–587

Larimer AL, Clay K, Becer JD (2014) Synergism and context dependency of interactions between arbuscular mycorrhizal fungi and rhizobia with a prairie legume. Ecology 95:1045–1054

Lau JA, Lennon JT (2012) Rapid responses of soil microorganisms improve plant fitness in novel environments. Proc Natl Acad Sci U S A 109:14058–14062

Lebeis SL (2014) The potential for give and take in plant-microbiome relationships. Front Plant Sci 5:287

Lebeis SL (2015) Greater than the sum of their parts: characterizing plant microbiomes at the community level. Curr Opin Plant Biol 24:82–86

Lebeis SL, Rott M, Dangl JL, Schulze-Lefert P (2012) Culturing a plant microbiome community at the cross-Rhodes. New Phytol 196:341–344

Lebeis SL, Paredes SH, Lundberg DS, Breakfield N, Gehring J, McDonald M, Malfatti S, Glavina del Rio T, Jones CD, Tringe SG, Dangl JL (2015) Salicylic acid modulates colonization of the root microbiome by specific bacterial taxa. Science 349:860–864

Lederberg I, McCray AT (2001) Ome sweet omics: a genealogical treasury of words. Scientist 15:8

Lee SW, Ahn PI, Sy S, Lee SY, Seo MW, Kim S, Sy P, Lee YH, Kang S (2010) *Pseudomonas* sp. LSW25R antagonistic to plant pathogens promoted plant growth and reduced blossom red rot of tomato roots in a hydroponic system. Eur J Plant Pathol 126:1–11

Leite MCBS, de Farias ARB, Freire FJ, Andreote FD, Sobral JK, Freire MBGS (2014) Isolation, bioprospecting and diversity of salt-tolerant bacteria associated with sugarcane in soils of Pernambuco, Brazil. Rev Bras Eng Agrıc Amb 18:S73–S79

Leveau JHJ, Uroz S, de Boer W (2010) The bacterial genus Collimonas: mycophagy, weathering and other adaptive solutions to life in oligotrophic soil environments. Environ Microbiol 12:281–292

Li D, Voigt TB, Kent AD (2016) Plant and soil effects on bacterial communities associated with miscanthus X giganteus rhizosphere and rhizomes. GCB Bioenergy 8:183–193

Lidbury ID, Murphy ARJ, Scanlan DJ, Bending GD, Jones AME, Moore JD, Goodall A, Hammond JP, Wellington EM (2016) Comparative genomic, proteomic and exoproteomic analyses of three Pseudomonas strains reveals novel insights into the phosphorus scavenging capabilities of soil bacteria. Environ Microbiol 18:3535–3549

Lim JH, Kim SD (2013) Induction of drought stress resistance by multifunctional PGPR *Bacillus licheniformis* K11 in pepper. Plant Pathol J 29:201–208

López-Baena FJ, Monreal JA, Pérez-Montaño F, Guash-Vidal B, Bellogín RA, Vinardell JM, Ollero FJ (2009) The absence of Nops secretion in *Sinorhizobium fredii* HH103 increases *GmPR1* expression in William soybean. MPMI 22:1445–1454

Lugtenberg B, Kamilova F (2009) Plant-growth-promoting rhizobacteria. Annu Rev Microbiol 63:541–556

Lundberg DS, Lebeis SL, Paredes SH, Yourstone S, Gehring J, Malfatti S, Tremblay J, Engelbrektson A, Kunin V, del Rio TG, Edgar RC, Eickhorst T, Ley RE, Hugenholtz P, Tringe SG, Dangl JL (2012) Defining the core *Arabidopsis thaliana* root microbiome. Nature 488:86–90

Luo SL, Chen L, Chen JI, Xiao X, Xu TY, Wan Y, Rao C, Liu CB, Liu YT, Lai C, Zeng GM (2011) Analysis and characterization of cultivable heavy metal-resistant bacterial endophytes isolated from Cd-hyperaccumulator *Solanum nigrum* L. and their potential use for phytoremediation. Chemosphere 85:1130–1138

Luo S, Xu T, Chen L, Chen J, Rao C, Xiao X, Wan Y, Zeng G, Long F, Liu C, Liu Y (2012) Endophyte-assisted promotion of biomass production and metal-uptake of energy crop sweet sorghum by plant-growth-promoting endophyte *Bacillus* sp. SLS18. Appl Microbiol Biotechnol 93:1745–1753

Luvizotto DM, Marcon J, Andreote FD, Dini-Andreote F, Neves AAC, Araújo WL, Pizzirani-Kleiner AA (2010) Genetic diversity and plant-growth related features of *Burkholderia* spp. from sugarcane roots. World J Microbiol Biotechnol 26:1829–1836

Ma Y, Prasad MNV, Rajkumar M, Freitas H (2011) Plant growth promoting rhizobacteria and endophytes accelerate phytoremediation of metalliferous soils. Biotechnol Adv 29:248–258

Ma Y, Rajkumar M, Zhang C, Freitas H (2016a) Inoculation of *Brassica oxyrrhina* with plant growth promoting bacteria for the improvement of heavy metal phytoremediation under drought conditions. J Hazard Mater 320:36–44

Ma Y, Rajkumar M, Zhang C, Freitas H (2016b) The beneficial role of bacterial endophytes in heavy metal phytoremediation. J Environ Manag 174:14–25

Mahmood S, Daur I, Al-Solaimani SG, Ahmad S, Madkour MH, Yasir M, Hirt H, Ali S, Ali Z (2016) Plant growth promoting rhizobacteria and silicon synergistically enhance salinity tolerance of mung bean. Front Plant Sci 7:876

Mani D, Kumar C, Patel NK (2016) Integrated micro-biochemical approach for phytoremediation of cadmium and lead contaminated soils using *Gladiolus grandiflorus* L. cut flower. Ecotoxicol Environ Saf 124:435–446

Mapelli F, Marasco R, Rolli E, Cappitelli F, Daffonchio D, Borin S (2012) Mineral-microbe interactions: biotechnological potential of bio-weathering. J Biotechnol 157:473–481

Mapelli F, Marasco R, Rolli E, Barbato M, Cherif H, Guesmi A, Ouzari I, Daffonchio D, Borin S (2013) Potential for plant growth promotion of rhizobacteria associated with Salicornia growing in Tunisian hypersaline soils. Biomed Res 2013:248078

Marasco R, Rolli E, Attoumi B, Vigani G, Mapelli F, Borin S, Daffonchio D (2012) A drought resistance-promoting microbiome is selected by root system under desert farming. PLoS One 7:e48479

Marasco R, Rolli E, Vigani G, Borin S, Sorlini C, Ouzari H, Zocchi G, Daffonchio D (2013) Are drought-resistance promoting bacteria cross-compatible with different plant models? Plant Signal Behav 8:e26741

Marasco R, Mapelli F, Rolli E, Mosqueira MJ, Fusi M, Bariselli P, Reddy M, Cherif A, Tsiamis G, Borin S, Daffonchio D (2016) *Salicornia strobilacea* (synonum of *Halocnemum strobilaceum*) growth under different tidal regimes selects rhizosphere bacteria capable of promoting plant growth. Front Microbiol 7:1286

Marquez LM, Redman RS, Rodriguez RJ, Roosinck MJ (2007) A virus in a fungus in a plant: three-way symbiosis required for thermal tolerance. Science 315:513–515

Marschner P, Crowley D, Rengel Z (2011) Rhizosphere interactions between microorganisms and plants govern iron and phosphorus acquisition along the root axis–model and research methods. Soil Biol Biochem 43:883–894

Martinez-Absalon S, Rojas-Solis D, Hernandez-Leon R, Prieto-Barajas C, Orozco-Mosqueda MC, Pena-Cabriales JJ, Sakuda S, Valencia-Cantero E, Santoyo G (2014) Potential use and mode of action of the new strain *Bacillus thuringiensis* UM96 for the biological control of the grey-mould phytopathogen *Botrytis cinerea*. Biocontrol Sci Tech 24:1349–1362

Martins SJ, Vasconcelos de Medeiros FH, Magela de Souza R, Vilela de Resende ML, Martins Ribeiro Junior P (2013) Biological control of bacterial wilt of common bean by plant growth-promoting Rhizobacteria. Biol Control 66:65–71

Marulanda A, Barea JM, Azcón R (2009) Stimulation of plant growth and drought tolerance by native microorganisms (AM fungi and bacteria) from dry environments: mechanisms related to bacterial effectiveness. J Plant Growth Regul 28:115–124

Masciarelli O, Llanes A, Luna V (2014) A new PGPR co-inoculated with *Bradyrhizobium japonicum* enhances soybean nodulation. Microbiol Res 169:609–615

Mastretta C, Taghavi S, Van Der Lelie D, Mengoni A, Galardi F, Gonnelli C, Barac T, Boulet J, Weyens N, Vangronsveld J (2009) Endophytic bacteria from seeds of *Nicotiana tabacum* can reduce cadmium phytotoxicity. Int J Phytoremediation 11:251–267

Mavrodi OV, Walte N, Elateek S, Taylor CG, Okubara PA (2012) Suppression of Rhizocto-nia and Pythium root rot of wheat by new strains of Pseudomonas. Biol Control 62:93–102

Mayak S, Tirosh T, Glick BR (2004) Plant growth promoting bacteria that confer resistance to water stress in tomato and pepper. Plant Sci 166:525–530

McLellan CA, Turbyville TJ, Wijerante EMK, Kerschen EV, Queitsch C, Whitesell L, Gunatilaka AAL (2007) A rhizosphere fungus enhances Arabidopsis thermtolerance through production of an HSP90 inhibitor. Plant Physiol 145:174–182

Meena RK, Singh RK, Singh NP, Meena SK, Meena VS (2015) Isolation of low temperature surviving plant growth–promoting rhizobacteria (PGPR) from pea (*Pisum sativum* L.) and documentation of their plant growth promoting traits. Biocatal Agric Biotechnol 4:806–811

Meena MK, Gupta S, Datta S (2016) Antifungal potential of PGPR, their growth promoting activity on seed germination and seedling growth of winter wheat and genetic variability among bacterial isolates. Int J Curr Microbial Appl Sci 5:235–243

Mendes R, Raaijmakers JM (2015) Cross-kingdom similarities in microbiome functions. ISME J 9:1905–1907

Mendes R, Kruijt M, de Bruijn I, Dekkers E, van der Voort M, Schneider JH, Piceno YM, DeSantis TZ, Andersen GL, Bakker PA, Raaijmakers JM (2011) Deciphering the rhizosphere microbiome for disease-suppressive bacteria. Science 332:1097–1100

Mendes R, Garbeva P, Raajimakers JM (2013) The rhizosphere microbiome: significance of plant beneficial, plant pathogenic and human pathogenic microorganisms. FEMS Microbial Rev 37:634–663

Mengual C, Schoebitz M, Azcón R, Roldán A (2014) Microbial inoculants and organic amendment improves plant establishment and soil rehabilitation under semiarid conditions. J Environ Manag 134:1–7

Miao B, Stewart BA, Zhang F (2011) Long-term experiments for sustainable nutrient management in China: a review. Agron Sustain Dev 31:397–414

Micallef SA, Shiaris MP, Colón-Carmona A (2009) Influence of *Arabidopsis thaliana* accessions on rhizobacterial communities and natural variation in root exudates. J Exp Bot 60:1729–1742

Miller JB, Oldroyd GD (2012) The role of diffusible signals in the establishment of rhizobial and mycorrhizal symbioses. In: Perotto S, Baluška F (eds) Signaling and communication in plant symbiosis. Springer, Berlin, pp 1–30

Miransari M (2011) Hyperaccumulators, arbuscular mycorrhizal fungi and stress of heavy metals. Biotechnol Adv 29:645–653

Mishra PK, Mishra S, Selvakumar G, Kundub S, Gupta HS (2009) Enhanced soybean (*Glycine max* L) plant growth and nodulation by *Bradyrhizobium japonicum*-SB1 in presence of *Bacillus thuringiensis*-KR1. Acta Agric Scand B Soil Plant Sci 59:189–196

Mishra PK, Bisht S, Mishra S, Selvakumar G, Bisht J, Gupta HS (2012) Co-inoculation of rhizobium leguminosarum-PR1 with a cold tolerant Pseudomonas sp. improves iron acquisition, nutrient uptake and growth of fieldpea (*Pisum sativum* L.). J Plant Nutr 35:243–256

Mitter B, Pfaffenbichler N, Flavell R, Compant S, Antonielli L, Petric A, Berninger T, Naveed M, Sheibani-Tezerji R, von Maltzahn G, Sessitsch A (2017) A new approach to modify plant microbiomes and traits by introducing beneficial bacteria at flowering into progeny seeds. Front Microbiol 8:11

Moe LA (2013) Amino acids in the rhizosphere: from plants to microbes. Am J Bot 100:1692–1705

Morel M, Castro-Sowinski S (2013) The complex molecular signaling network in microbe-plant interaction. In: Arora NK (ed) Plant microbe symbiosis: fundamentals and advances. Springer, NewDelhi, pp 169–199

Mueller UG, Sachs JL (2015) Engineering microbiome to improve plant and animal health. Trends Microbiol 23:606–617

Munns R, Gilliham M (2015) Salinity tolerance of crops–what is the cost? New Phytol 208:668–673

Murray JD (2011) Invasion by invitation: rhizobial infection in legumes. Mol Plant-Microbe Interact 24:631–939

Mus F, Crook MB, Garcia K, Costas AG, Geddes BA, Kouri ED, Paramasivan P, Ryu MH, Oldroyd GED, Poole PS, Udvardi MK, Voigt CA, Ané JM, Peters JW (2016) Symbiotic nitrogen fixation and the challenges to its extension to nonlegumes. Appl Environ Microbiol 82:3698–3710

Nadeem SM, Ahmad M, Zahir ZA, Javaid A, Ashraf M (2014) The role of mycorrhizae and plant growth promoting rhizobacteria (PGPR) in improving crop productivity under stressful environments. Biotechnol Adv 32:429–448

Naseem H, Bano A (2014) Role of plant growth-promoting rhizobacteria and their exopolysaccharide in drought tolerance in maize. J Plant Interact 9:689–701

Nautiyal CS, Srivastava S, Chauhan PS, Seem K, Mishra R, Sopory SK (2013) Plant growth-promoting bacteria *Bacillus amyloliquefaciens* NBRISN13 modulates gene expression profile of leaf and rhizosphere community in rice during salt stress. Plant Physiol Biochem 66:1–9

Navarro JM, Pérez-Tornero O, Morte A (2014) Alleviation of salt stress in citrus seedlings inoculated with arbuscular mycorrhizal fungi depends on the rootstock salt tolerance. J Plant Physiol 171:76–85

Naveed M, Hussain B, Zahir A, Mitter B, Sessitsch A (2014a) Drought stress amelioration in wheat through inoculation with Burkholderia phytofirmans strain PsJN. Plant Growth Regul 73:121–131

Naveed M, Mitter B, Reichenauer TG, Wieczorek K, Sessitsch A (2014b) Increased drought stress resilience of maize through endophytic colonization by *Burkholderia phytofirmans* PsJN and *enterobacter* sp. FD17. Environ Exp Bot 97:30–39

Neeraj KS (2011) Organic amendments to soil inoculated arbuscular mycorrhizal fungi and *Pseudomonas fluorescens* treatments reduce the development of root-rot disease and enhance the yield of *Phaseolus vulgaris* L. Eur J Soil Biol 47:288–295

Nelson EB (2018) The seed microbiome: origins, interactions, and impacts. Plant Soil 422:7–34

Ngumbi EN (2011) Mechanisms of olfaction in parasitic wasps: analytical and behavioral studies of response of a specialist (Microplitis croceipes) and a generalist (Cotesia marginiventris) parasitoid to host-related odor. Ph.D. dissertation, Auburn University, Auburn

Ngumbi E, Kloepper J (2016) Bacterial-mediated drought tolerance: current and future prospects. Appl Soil Ecol 105:109–125

Nonnoi F, Chinnaswamy A, García de la Torre VS, Coba de la Peña T, Lucas MM, Pueyo JJ (2012) Metal tolerance of rhizobial strains isolated from nodules of herbaceous legumes *Medicago* sp. and *Trifolium* sp. growing in mercury-contaminated soils. Appl Soil Ecol 61:49–59

Oburger E, Dell'Mour M, Hann S, Wieshammer G, Puschenreiter M, Wenzel WW (2013) Evaluation of an ovel tool for sampling root exudates from soil-grown plants compared to conventional techniques. Environ Exp Bot 87:235–247

Ofaim S, Ofek-Lalzar M, Sela N, Jinag J, Kashi Y, Minz D, Freilich F (2017) Analysis of microbial functions in the rhizosphere using a metabolic-network based framework for metagenomics interpretation. Front Microbiol 8:1606

Ofek M, Voronov-Goldman M, Hadar Y, Minz D (2014) Host signature effect on plant root-associated microbiomes revealed through analyses of resident *vs* active communities. Environ Microbiol 16:2157–2167

Oldroyd GED (2013) Speak, friend, and enter: signaling systems that promote beneficial symbiotic associations in plants. Nat Rev Microbiol 11:252–263

Oldroyd GED, Murray JD, Poole PS, Downie JA (2011) The rules of engagement in the legume-rhizobial symbiosis. Annu Rev Genet 45:119–144

Olivares J, Bedmar EJ, Sanjuan J (2013) Biological nitrogen fixation in the context of global change. Mol Plant-Microbe Interact 26:486–494

Orozco-Mosqueda MDC, Rocha-Granados MDC, Glick BR, Santoyo G (2018) Microbiome engineering to improve biocontrol and plant growth-promoting mechanisms. Microbiol Res 208:25–31

Ortiz N, Armada E, Duque E, Roldan A, Azcon R (2015) The contribution of arbuscular mycorrhizal fungi and/or bacteria to enhancing plant drought tolerance under natural soil conditions: effectiveness of autochthonous or allochthonous strains. J Plant Physiol 174:87–96

Ortiz-Castro R, Martinez-Trujillo M, Lopez-Bucio J (2008) N-acyl-L- homoserinelactones:a class of bacterial quorum-sensing signals alter post-embryonic root development in *Arabidopsis thaliana*. Plant Cell Environ 31:1497–1509

Pandey VC (2012) Phytoremediation of heavy metals from fly ash pond by *Azolla caroliniana*. Ecotoxicol Environ Saf 82:8–12

Pandey VC, Ansari MW, Tula S, Yadav S, Sahoo RK, Shukla N, Bains G, Badal S, Chandra S, Gaur AK, Kumar A, Shukla A, Kumar J, Tuteja N (2016) Dose dependent response of *Trichoderma harzianum* in improving drought tolerance in rice genotypes. Planta 243:1251–1264

Pankaj U, Verma SK, Semwal M, Verma RK (2016) Assessment of natural mycorrhizal colonization and soil fertility status of lemongrass crop in subtropical India. J Appl Res Med Arom Plants 5:41–46

Panke-Buisse K, Poole A, Goodrich J, Ley R, Kao-Kniffin J (2015) Selection on soil microbiomes reveals reproducible impacts on plant function. ISME J 9:980–989

Paredes SH, Lebeis SL (2016) Giving back to the community: microbial mechanisms of plant-soil interactions. Funct Ecol 30:1–10

Park JD (2010) Heavy metal poisoning. Hanyang Med Rev 30:319–325

Passari AK, Chandra P, Mishra VK, Leo VV, Gupta VK, Kumar B, Singh BP (2016) Detection of biosynthetic gene and phytohormone production by endophytic actinobacteria associated with *Solanum lycopersicum* and their plant growth-promoting effect. Res Microbiol 167:692–705

Patel U, Sinha S (2011) Rhizobia species: a boon for "plant genetic engineering". Indian J Microbiol 51:521–527

Paul D, Lade H (2014) Plant-growth-promoting rhizobacteria to improve crop growth in saline soils: a review. Agron Sustain Dev 34:737–752

Peiffer JA, Spor A, Koren O, Jin Z, Tringe SG, Dangl JL, Buckler ES, Ley RE (2013) Diversity and heritability of the maize rhizosphere microbiome under field conditions. Proc Natl Acad Sci U S A 110:6548–6553

Penuelas J, Terradas J (2014) The foliar microbiome. Trends Plant Sci 19:278–280

Pereira P, Ibáñez SG, Agostini E, Miriam Etcheverry M (2011) Effects of maize inoculation with *Fusarium verticillioides* and with two bacterial biocontrol agents on seedlings growth and antioxidative enzymatic activities. Appl Soil Ecol 51:52–59

Perez YM, Charest C, Dalpe Y, Seguin S, Wang X, Khanizadeh S (2016) Effect of inoculation with arbuscular mycorrhizal fungi on selected spring wheat lines. Sustain Agric Res 5:24–29

Perez-Montano F, Alías-Villegas C, Bellogin RA, del Cerro P, Espuny MR, Jimenez-Guerrero I, Lopez-Baena FJ, Ollero FJ, Cubo T (2014) Plant growth promotion in cereal and leguminous agricultural important plants: from microorganism capacities to crop production. Microbiol Res 169:325–336

Philippot L, Raaijmakers JM, Lemanceau P, van der Putten WH (2013) Going back to the roots: the microbial ecology of the rhizosphere. Nat Rev Microbiol 11:789–799

Pieterse CMJ, Van Wees SCM, Ton J, Van Pelt JA, Van Loon LC (2002) Signalling in rhizobacteria-induced systemic resistance in *Arabidopsis thaliana*. Plant Biol 4:535–544

Pineda A, Dicke M, Pieterse CMJ, Pozo MJ (2013) Beneficial microbes in a changing environment: are they always helping plants deal with insects? Funct Ecol 27:574–586

Pontigo S, Godoy K, Jiménez H, Gutierrez-Moraga A, Mora MDLL, Cartes P (2017) Silicon-mediated alleviation of aluminum toxicity by modulation of Al/Si uptake and antioxidant performance in ryegrass plants. Front Plant Sci 8:642

Porcel R, Zamarreno AM, Garcia-Mina JM, Aroca R (2014) Involvement of plant endogenous ABA in *Bacillus megaterium* PGPR activity in tomato plants. BMC Plant Biol 14:36

Porras-Alfaro A, Bayman P (2011) Hidden fungi, emergent properties: endophytes and microbiomes. Annu Rev Phytopathol 49:291–315

Pozo MJ, Azcon-Aguilar C (2007) Unraveling mycorrhiza-induced resistance. Curr Opin Plant Biol 10:393–398

Prashar P, Kapoor N, Sachdeva S (2014) Rhizosphere: its structure, bacterial diversity and significance. Rev Environ Sci Biotechnol 13:63–77

Prathap M, Ranjitha KBD (2015) A critical review on plant growth-promoting rhizobacteria. J Plant Pathol Microbiol 6:1–4

Premachandra D, Hudek L, Brau L (2016) Bacterial modes of action for enhancing plant growth. J Biotechnol Biomater 6:3

Prosser JI (2015) Dispersing misconceptions and identifying opportunities for the use of "omics" in soil microbial ecology. Nat Rev Microbiol 13:439–446

Prudent M, Salon C, Souleimanov A, Emery RJN, Smith DI (2015) Soybean is less impacted by water stress using *Bradyrhizobium japonicum* and thuricin-17 from *Bacillus thuringiensis*. Agron Sustain Dev 35:749–757

Qiang SW, Ming QC, Ying NZ, Chu W, Xin HH (2016) Mycorrhizal colonization represents functional equilibrium on root morphology and carbon distribution of trifoliate orange grown in a split-root system. Sci Hortic 199:95–102

Qin S, Zhang YJ, Yuan B, Xu PY, Xing K, Wang J, Jiang JH (2014) Isolation of ACC deaminase-producing habitat-adapted symbiotic bacteria associated with halophyte *Limonium sinense* (Girard) Kuntze and evaluating their plant growth promoting activity under salt stress. Plant Soil 374:753–766

Qin YY, Leung CKM, Lin CK, Wong MH (2015) The associations between metals/metalloids concentrations in blood plasma of Hong Kong residents and their seafood diet, smoking habit, body mass index and age. Environ. Sci Pollut Res 22:13204–13211

Qiu M, Li S, Zhou X, Cui X, Vivanco J, Zhang N, Shen Q, Zhang R (2014) De-coupling of root-microbiome associations followed by antagonist inoculation improves rhizosphere soil suppressiveness. Biol Fertil Soils 50:217–224

Quecine MC, Araujo WL, Tsui S, Parra JRP, Azevedo JL, Pizzirani-Kleiner AA (2014) Control of *Diatraea saccharalis* by the endophytic *Pantoea agglomerans* 33.1 expressing *cry1Ac7*. Arch Microbiol 196:227–234

Quiza L, St-Arnaud M, Yergeau E (2015) Harnessing phytomicrobiome signaling for rhizosphere microbiome engineering. Front Plant Sci 6:507

Raaijmakers JM, Leeman M, MMP VO, Van der Sluis I, Schippers B, PAHM B (1995) Dose-response relationships in biological control of fusarium wilt of radish by *Pseudomonas* spp. Phytopathology 85:1075–1081

Raajimakers JM (2015) The minimal rhizosphere microbiome. In: Lugtenberg B (ed) Principles of plant-microbe interactions. Springer International Publishing Switzerland, Heidelberg, pp 411–417

Rajkumar M, Ae N, Prasad MNV, Freitas H (2010) Potential of siderophore-producing bacteria for improving heavy metal phytoextraction. Trends Biotechnol 28:142–149

Rajkumar M, Sandhya S, Prasad MNV, Freitas H (2012) Perspectives of plant-associated microbes in heavy metal phytoremediation. Biotechnol Adv 30:1562–1574

Ramadan EM, AbdelHafez AA, Hassan EA, Saber FM (2016) Plant growth-promoting rhizobacteria and their potential for biocontrol of phytopathogens. Afr J Microbiol Res 10:486–504

Ramegowda V, Senthil-Kumar M, Ishiga Y, Kaundal A, Udayakumay M, Mysore KS (2013) Drought stress acclimation imparts tolerance to *Sclerotinia sclerotiorum* and *Pseudomonas syringae* in *Nicotiana benthamiana*. Int J Mol Sci 14:9497–9513

Ramond JB, Tshabuse F, Bopda CW, Cowan DA, Tuffin MI (2013) Evidence of variability in the structure and recruitment of rhizospheric and endophytic bacterial communities associated with arable sweet sorghum (*Sorghum bicolor* (L.) Moench). Plant Soil 372:265–278

Ramos Solano B, Barriuso Maicas J, Pereyra de la Iglesia MT, Domenech J, GutiérrezManero FJ (2008) Systemic disease protection elicited by plant growth promoting rhizobacteria strains: relationship between metabolic responses, systemic disease protection, and biotic elicitors. Phytopathology 98:451–457

Rasche F, Velvis H, Zachow C, Berg G, van Elsas JD, Sessitsch A (2006) Impact of transgenic potatoes expressing antibacterial agents on bacterial endophytes is comparable with the effects of plant genotype, soil type and pathogen infection. J Appl Ecol 43:555–566

Rashedul IM, Madhaiyan M, Deka Boruah HP, Yim W, Lee G, Saravanan VS, Fu Q, Hu H, Sa T (2009) Characterization of plant growth-promoting traits of free-living diazotrophic bacteria and their inoculation effects on growth and nitrogen uptake of crop plants. Microbiol Biotechnol 19:1213–1222

Rastogi G, Coaker GL, Leaveu JHJ (2013) New insight into the structure and function of phyllosphere microbiota through high-throughput molecular approaches. FEMS Microbiol Lett 348:1–10

Raza W, Ling N, Yang L, Huang Q, Shen Q (2016a) Response of tomato wilt pathogen *Ralstonia solanacearum* to the volatile organic compounds produced by a biocontrol strain *Bacillus amyloliquefaciens* SQR-9. Sci Rep 6:24856

Raza W, Yousaf S, Rajer FU (2016b) Plant growth promoting activity of volatile organic compounds produced by bio-control strains. Sci Lett 4:40–43

Redman RS, Sheehan KB, Stout RG, Rodriguez RJ, Henson JM (2002) Thermotolerance generated by plant/fungal symbiosis. Science 298:1581

Reyes-Darias JA, García V, Rico-Jiménez M, Corral-Lugo A, Lesouhaitier O, Juárez-Hernández D, Yang Y, Bi S, Feuilloley M, Muñoz-Rojas J, Sourjik V, Krell T (2015) Specific gamma-aminobutyrate chemotaxis in pseudomonads with different lifestyle. Mol Microbiol 97:488–501

Richardson AE, Barea JM, McNeill AM, Prigent-Combaret C (2009) Acquisition of phosphorus and nitrogen in the rhizosphere and plant growth promotion by microorganisms. Plant Soil 321:305–339

Riggs PJ, Chelius MK, Iniguez AL, Kaeppler SM, Triplett EW (2001) Enhanced maize productivity by inoculation with diazotrophic bacteria. Aus J Plant Physiol 28:829–836

Rodell M, Velicogna I, Famiglietti JS (2009) Satellite-based estimates of groundwater depletion in India. Nature 460:999–1002

Rodriguez H, Redman RS (2008) Effect of a nickel-tolerant ACC deaminase-producing pseudomonas strain on growth of nontransformed and transgenic canola plants. Curr Microbiol 57:170–174

Rodriguez H, Vessely S, Shah S, Glick BR (2008) Effect of a nickel-tolerant ACC deaminase-producing pseudomonas strain on growth of nontransformed and transgenic canola plants. Curr Microbiol 57:170–174

Rodriguez RJ, White JF Jr, Arnold AE, Redman RS (2009) Fungal endophytes: diversity and functional roles. New Phytol 182:314–330

Rolli E, Marasco R, Vigani C, Ettoumi B, Mapelli F, Deangelis MI, Gandolfi C, Casati E, Previtali F, Gerbino R, Pierotti Cei F, Borin S, Sorlini C, Zocchi G, Daffonchio D (2015) Improved plant resistance to drought is promoted by the root-promoted microbiome as a water stress dependent trait. Environ Microbiol 17:316–331

Rosenblueth M, Martinez-Romero E (2006) Bacterial endophytes and their interactions with hosts. Soil Biol Biochem 21:373–378

Rout ME, Callaway RM (2012) Interactions between exotic invasive plants and soil microbes in the rhizosphere suggest that everything is not everywhere. Ann Bot 110:213–222

Roy SJ, Negrao S, Tester M (2014) Salt resistant crop plants. Curr Opin Biotechnol 26:115–124

Ruiz KB, Biondi S, Martínez EA, Orsini F, Antognoni F, Jacobsen SE (2015) Quinoa – a model crop for understanding salt-tolerance mechanisms in halophytes. Plant Biosyst 150:357–371

Ruiz-Lozano JM, Peralvarez MC, Aroca R, Azcon R (2011) The application of a treated sugar beet waste residue to soil modifies the responses of mycorrhizal and non mycorrhizal lettuce plants to drought stress. Plant Soil 346:153–166

Ruiz-Lozano JM, Aroca R, Zamarreno AM, Molina S, Andreo-Jimenez B, Porcel R, Garcia-Mina JM, Ruyter-Spira C, Lopez-Raez JA (2016) Arbuscular mycorrhizal symbiosis induces strigolactone biosynthesis under drought and improves drought tolerance in lettuce and tomato. Plant Cell Environ 39:441–452

Ruy CM, Murphy JF, Mysore KS, Kloepper JW (2004) Plant growth-promoting rhizobacteria systemically protect *Arabidopsis thaliana* against cucumber mosaic virus by a salicylic acid and NPR1-independent and jasmonic acid-dependent signaling pathway. Plant J 39:381–392

Salvioli A, Bonfante P (2013) Systems biology and “omics” tools: a cooperation for next-generation mycorrhizal studies. Plant Sci 203:107–114

Salvioli A, Ghignone S, Novero M, Navazio L, Venice F, Bagnaresi P, Bonfante P (2016) Symbiosis with an endobacterium increases the fitness of a mycorrhizal fungus, raising its bioenergetic potential. ISME J 10:130–144

Sánchez-Cañizares C, Jorrín B, Poole PS, Tkacz A (2017) Understanding the holobiont: the interdependence of plants and their microbiome. Curr Opin Microbiol 38:188–196

Sandhya V, Ali SZ, Grover M, Kishore N, Venkateswarlu B (2009) Pseudomonas sp. strain P45 protects sunflowers seedlings from drought stress through improved soil structure. J Oilseed Res 26:600–601

Sandhya V, Ali SZ, Grover M, Kishore N, Venkateswarlu B (2010) Pseudomonas sp. strain P45 protects sunflowers seedlings from drought stress through improved soil structure. J Oilseed Res 26:600–601

Santi C, Bogusz D, Franche C (2013) Biological nitrogen fixation in non-legume plants. Ann Bot 111:743–767

Santoro MV, Bogino PC, Nocelli N, Cappellari LR, Giordano WF, Banchio E (2016) Analysis of plant growth promoting effects of fluorescent pseudomonas strains isolated from *Mentha piperita* rhizosphere and effects of their volatile organic compounds on essential oil composition. Front Microbiol 7:1–17

Santoyo G, Orozco-Mosqueda MC, Govindappa M (2012) Mechanisms of bio-control and plant growth-promoting activity in soil bacterial species of Bacillus and Pseudomonas: a review. Biocontrol Sci Tech 22:855–872

Santoyo G, Moreno-Hagelsieb G, Orozco-Mosqueda MC, Glick BR (2016) Plant growth-promoting bacterial endophytes. Microbiol Res 183:92–99

Santoyo G, Hernandez-Pacheco C, Hernandez-Salmeron J, Hernandez-Leon R (2017) The role of abiotic factors modulating the plant-microbe-soil interactions: towards sustainable agriculture, a review. Span J Agric Res 15:e03R01

Sarma R, Saikia R (2014) Alleviation of drought stress in mung bean by strain *Pseudomonas aeruginosa* GGRJ21. Plant Soil 377:111–126

Savary S, Ficke A, Aubertot JN, Hollier C (2012) Crop losses due to disease and their implications for global food production losses and food security. Food Secur 4:519–537

Schaeppi K, Bulgarelli D (2015) The plant microbiome at work. Mol Plant-Microbe Interact 28:212–217

Schenk PM, Carvalhais LC, Kazan K (2012a) Unraveling plant-microbe interactions: can multispecies transcriptomics help. Trends Biotechnol 30:177–184

Schenk ST, Stein E, Kogel KH, Schikora A (2012b) Arabidopsis growth and defense are modulated by bacterial quorum sensing molecules. Plant Signal Behav 7:178–181

Schlaeppi K, van Themaat EVL, Bulgarelli D, Schulze-Lefert P (2013) *Arabidopsis thaliana* as model for studies on the bacterial root microbiota. In: de Bruijin FJ (ed) Molecular microbial ecology of the rhizosphere. Kluwer Academic, Dordrecht, pp 243–256

Schlaeppi K, Dombrowski N, Oter RG, Ver Loren van Themaat E, Schulze-Lefert P (2014) Quantitative divergence of the bacterial root microbiota in *Arabidopsis thaliana* relatives. Proc Natl Acad Sci U S A 111:585–592

Schuhegger R, Ihring A, Gantner S, Bahnweg G, Knappe C, Vogg G, Hutzler P, Schmid M, Van Breusegem F, Eberl L, Hartmann A, Langebartels C (2006) Induction of systemic resistance in tomato by N-acyl-L-homoserine lactone-producing rhizosphere bacteria. Plant Cell Environ 29:909–918

Selvakumar G, Kundu S, Joshi P, Nazim S, Gupta AD, Mishra PK, Gupta HS (2008a) Characterization of a cold-tolerant plant growth-promoting bacterium *Pantoea dispersa* 1A isolated from a sub-alpine soil in the North Western Indian Himalayas. World J Microbiol Biotechnol 24:955–960

Selvakumar G, Mohan M, Kundu S, Gupta AD, Joshi P, Nazim S, Gupta HS (2008b) Cold tolerance and plant growth promotion potential of *Serratia marcescens* strain SRM (MTCC 8708) isolated from flowers of summer squash (*Cucurbita pepo*). Lett Appl Microbiol 46:171–175

Selvakumar G, Joshi P, Nazim S, Mishra PK, Bisht JK, Gupta HS (2009) Phosphate solubilization and growth promotion by *Pseudomonas fragi* CS11RH1 (MTCC 8984) a psychrotolerant bacterium isolated from a high altitude Himalayan rhizosphere. Biologia 64:239245

Selvakumar G, Joshi P, Suyal P, Mishra PK, Joshi GK, Bisht JK, Bhatt JC, Gupta HS (2010a) *Pseudomonas lurida* M2RH3 (MTCC 9245), a psychrotolerant bacterium from the Uttarakhand Himalayas, solubilizes phosphate and promotes wheat seedling growth. World J Microbiol Biotechnol 5:1129–1135

Selvakumar G, Kundu S, Joshi P, Nazim S, Gupta AD, Gupta HS (2010b) Growth promotion of wheat seedlings by *Exiguobacterium acetylicum* 1P (MTCC 8707) a cold tolerant bacterial strain from the Uttarakhand Himalayas. Ind J Microbiol 50:50–56

Senthilkumar M, Swarnalakshmi K, Govindasamy V, Young KL, Annapurna K (2009) Bio-control potential of soybean bacterial endophytes against charcoal rot fungus, *Rhizoctonia bataticola*. Curr Microbiol 58:288–293

Sessitsch A, Mitter B (2014) 21st century agriculture: integration of plant microbiome for improved crop production and food safety. Microb Biotechnol 8:32–33

Sessitsch A, Hardoim P, Döring J, Weilharter A, Krause A, Woyke T, Mitter B, Hauberg-Lotte L, Friedrich F, Rahalkar M, Hurek T, Sarkar A, Bodrossy L, van Overbeek L, Brar D, van Elsas JD, Reinhold-Hurek B (2011) Functional characteristics of an endophyte community colonizing rice roots as revealed by metagenomic analysis. Mol Plant-Microbe Interact 25:28–36

Shabala S, Hariadi Y, Jacobsen SE (2013) Genotypic difference in salinity tolerance in quinoa is determined by differential control of xylem Na^+ loading and stomatal density. J Plant Physiol 170:906–914

Shaharoona B, Arshad M, Zahir ZA (2006) Effect of plant growth promoting rhizobacteriacontaining ACC-deaminase on maize (*Zea mays* L.) growth under axenic conditions and on nodulation in mung bean (*Vigna radiata* L.). Lett Appl Microbiol 42:155–159

Shahzad R, Khan AL, Bilal S, Waqas M, Kang SM, Lee IJ (2017) Inoculation of abscisic acid-producing endophytic bacteria enhances salinity stress tolerance in *Oryza sativa*. Environ Exp Bot 136:68–77

Sharifi R, Ryu CM (2016) Are bacterial volatile compounds poisonous odors to a fungal pathogen *Botrytis cinerea*, alarm signals to Arabidopsis seedlings for eliciting induced resistance, or both? Front Microbiol 7:1–10

Sharma M, Ghosh R (2017) Heat and soil moisture stress differently impact chickpea plant infection with fungal pathogens. In: Senthil-Kumar M (ed) Plant tolerance to individual and concurrent stresses. Springer Press, New Delhi, pp 47–57

Sharma S, Kulkarni J, Jha B (2016) Halotolerant rhizobacteria promote growth and enhance salinity tolerance in peanut. Front Microbiol 7:1600

Sheng X, He L, Wang Q, Ye H, Jiang C (2008) Effects of inoculation of biosurfactant-producing *Bacillus* sp. J119 on plant growth and cadmium uptake in a cadmium-amended soil. J Hazard Mater 155:17–22

Sheng M, Tang M, Zhang F, Huang Y (2011) Influence of arbuscular mycorrhiza on organic solutesin maize leaves under salt stress. Mycorrhiza 21:423–430

Shirley M, Avoscan L, Bernuad E, Vansuyt G, Lemanceau P (2011) Comparison of iron acquisition from Fe-pyoverdine by strategy I and strategy II plants. Botany 89:731–735

Shrestha J (2016) A review on sustainable agricultural intensification in Nepal. Int J Bus Soc Sci Res 4:152–156

Shridhar BS (2012) Review: nitrogen fixing microorganisms. Int J Microbiol Res 3:46–52

Shuhegge R, Ihring A, Gantner S, Bahnweg G, Knappe C, Vogg G, Hutzler P, Schmid M, Van Breusegem F, Eberl L, Hartmann A, Langebartels C (2006) Induction of systemic resistance in tomato by N-acyl-homoserine lactone-producing rhizosphere bacteria. Plant Cell Environ 29:909–918

Shukla PS, Agarwal PK, Jha B (2012) Improved salinity tolerance of *Arachis hypogaea* (L.) by the interaction of halotolerant plant growth-promoting rhizobacteria. J Plant Growth Regul 31:195–206

Siddikee MA, Chauhan PS, Anandham R, Han GH, Sa T (2010) Isolation, characterization and use for plant growth promotion under salt stress, of ACC deaminase producing halotolerant bacteria derived from coastal soil. J Microbiol Biotechnol 20:1577–1584

Singh BK, Bardgett RD, Smith P, Reay DS (2010) Microorganisms and climate change: terrestrial feedbacks and mitigation options. Nat Rev Microbiol 8:779–790

Singh LP, Gill SS, Tuteja N (2011) Unraveling the role of fungal symbionts in plant abiotic stress tolerance. Plant Signal Behav 6:175–191

Singh B, Kaur T, Kaur S, Manhas RK, Kaur A (2016) Insecticidal potential of an endophytic Cladosporiumvelox against *Spodoptera litura* mediated through inhibition of alpha glycosidases. Pestic Biochem Physiol 131:46–52

Singh S, Tripathi DK, Singh S, Sharma S, Dubey NK, Chauhan DK, Vaculík M (2017) Toxicity of aluminium on various levels of plant cells and organism: a review. Environ Exp Bot 137:177–193

Sloan SS, Lebeis S (2015) Exercising influence: distinct biotic interactions shape root microbiome. Curr Opin Plant Biol 26:32–36

Smith RE, Read DJ (2008) Mycorrhizal symbiosis, 3rd edn. Elsevier, Academic, New York

Smith SE, Smith FA (2011) Roles of arbuscular mycorrhizas in plant nutrition and growth: new paradigms from cellular to ecosystem scales. Annu Rev Plant Biol 62:227–250

Spaink HP (2000) Root nodulation and infection factors produced by rhizobial bacteria. Annu Rev Microbiol 54:257–288

Spence C, Alff E, Johnson C, Ramos C, Donofrio N, Sundaresan V, Bais H (2014) Natural rice rhizospheric microbes suppress rice blast infections. BMC Plant Biol 14:130

Sreenivasulu N, Sopory SK, Kavi Kishor PB (2007) Deciphering the regulatory mechanisms of abiotic stress tolerance in plants by genomic approaches. Gene 388:1–13

Srivastava S, Yadav A, Seem K, Mishra S, Chaudhary V, Srivastava CS (2008) Effect of high temperature on *Pseudomonas putida* NBRI0987 biofilm formation and expression of stress sigma factor RpoS. Curr Microbiol 56:453–457

Stella T, Covino S, Èvanèarová M, Filipová A, Petruccioli M, D'Annibale A, Cajthaml T (2017) Bioremediation of long-term PCB-contaminated soil by white-rot fungi. J Hazard Mater 324:701–710

Strange RN, Scott PR (2005) Plant disease: a threat to global food security. Annu Rev Phytopathol 43:83–116

Su J, Hu C, Yan X, Jin Y, Chen Z, Guan Q, Wang Y, Zhong D, Jansson C, Wang F, Schnurer A, Sun C (2015) Expression of barley SUSIBA2 transcription factor yields high-starch low-methane rice. Nature 523:602

Suarez C, Cardinale M, Ratering S, Jung S, Montoya AMZ, Geissler-Palaum R, Schnell S (2015) Plant growth-promoting effects of Hartmannibacter diazotrophic on summer barley (*Hordeum vulgare* L.) under salt stress. Appl Soil Ecol 95:23–30

Sugiyama A, Yazaki K (2012) Root exudates of legume plants and their involvement in interactions with soil microbes. In: Vivanco JM, Baluška F (eds) Secretions and exudates in biological systems. Springer, Berlin, pp 27–48

Sugiyama A, Bakker MG, Badri DV, Manter DK, Vivanco JM (2013) Relationships between *Arabidopsis* genotype-specific biomass accumulation and associated soil microbial communities. Botany-Botanique 91:123126

Suhag M (2016) Potential of biofertilizers to replace chemical fertilizers. Int Adv Res J Sci Eng Technol 3:163–167

Swenson W, Wilson DS, Elias R (2000) Artificial ecosystem selection. Proc Natl Acad Sci U S A 97:9110–9114

Syed Ab Rahman SF, Singh E, Pieterse CMJ, Schenk PM (2018) Emerging microbial biocontrol strategies for plant pathogens. Plant Sci 267:102–111

Symanczik S, Gisler M, Thonar C, Schlaeppi K, Van der Heijden MG, Kahmen A, Boller T, Maeder P (2017) Application of mycorrhiza and soil from a permaculture system improved phosphorus acquisition in Nanranjilla. Front Plant Sci 8:1263

Tajini F, Trabelsi M, Drevon JJ (2012) Combined inoculation with *Glomus intraradices* and *Rhizobium tropici* CIAT899 increases phosphorus use efficiency for symbiotic nitrogen fixation in common bean (*Phaseolus vulgaris* L.). Saudi J Biol Sci 19:157–163

Tank N, Saraf M (2010) Salinity-resistant plant growth promoting rhizobacteria ameliorates sodium chloride stress on tomato plants. J Plant Interact 5:51–58

Tarkka M, Schrey S, Hampp (2008) Plant associated soil microorganisms. In: Nautiyal C, Dion P (eds) Molecular mechanisms of plant and microbe coexistence. Springer, Berlin, pp 3–51

Thao NP, Tran LS (2016) Enhancement of plant productivity in the post genomic era. Curr Genomics 17:295–296

Theocharis A, Bordiec S, Fernandez O, Paquis S, Dhondt-Cordelier S, Baillieul F, Clement C, Barka EA (2012) *Burkholderia phytofirmans* PsJN primes *Vitis vinifera* L. and confers a better tolerance to low nonfreezing temperatures. Mol Plant-Microbe Interact 25:241–249

Tian C, Kasiborski B, Koul R, Lammers PJ, Bulcking H, Shachar-Hill Y (2010) Regulation of the nitrogen transfer pathway in the arbuscular mycorrhizal symbiosis: gene characterization and the coordination of expression with nitrogen flux. Plant Physiol 153:1175–1187

Tian BY, Cao Y, Zhang KQ (2015) Metagenomic insights into communities, functions of endophytes, and their associates with infection by root-knot nematode, *Meloidogyne Incognita*, in tomato roots. Sci Rep 5:17087

Timmusk S, Nevo E (2011) Plant root associated biofilms. In: Meshwari DK (ed) Bacteria in agrobiology. Plant nutrient management, vol 3. Springer, Berlin, pp 285–300

Timmusk S, Wagner EGH (1999) The plant growth-promoting rhizobacterium *Paenibacillus polymyxa* induces changes in *Arabidopsis thaliana* gene expression: a possible connection between biotic and abiotic stress responses. Mol Plant-Microbe Interact 12:951–959

Timmusk S, Timmusk K, Behers L (2013) Rhizobacterial plant drought stress tolerance enhancement: towards sustainable water resource management and food security. J Food Secur 1:6–9

Timmusk S, El-Daim IA, Cpolovici L, Tanilas T, Kannaste A, Behers L, Nevo E, Seisenbaeva G, Stenstrom E, Niinemets U (2014) Drought-tolerance of wheat improved y rhizosphere bacteria from harsh environments: enhanced biomass production and reduced emissions of stress volatiles. PLoS One 9:e96086

Timmusk S, Behers L, Muthoni J, Aronsson AC (2017) Perspectives and challenges of microbe application for crop improvement. Front Plant Sci 8:49

Tiwari S, Singh P, Tiwari R, Meena KK, Yandigeri M, Singh DP, Arora DK (2011) Salt-tolerant rhizobacteria-mediated induced tolerance in wheat (*Triticum aestivum* L.) and chemical diversity in rhizosphere enhance plant growth. Biol Fert Soils 47:907–916

Tiwari S, Lata C, Chauhan PS, Nautiyal CS (2016) *Pseudomonas putida* attunes morphophysiological: biochemical and molecular responses in *Cicer arietinum* L. during drought stress and recovery. Plant Physiol Biochem 99:108–117

Tiwari S, Prasad V, Chauhan PS, Lata C (2017) *Bacillus amyloliquefaciens* confers tolerance to various abiotic stresses and modulates plant response to phytohormones through osmoprotection and gene expression regulation in rice. Front Plant Sci 8:1510

Tkacz A, Poole P (2015) Role of root microbiota in plant productivity. J Exp Bot 66:2167–2175

Tkacz A, Cheema J, Chandra G, Grant A, Poole PS (2015) Stability and succession of the rhizosphere microbiota depends upon plant type and soil composition. ISME J 9:2349–2359

Trabelsi D, Mhamdi R (2013) Microbial inoculants and their impact on soil microbial communities: a review. Biomed Res 2013:e863240

Tripathi DK, Singh VP, Prasad SM, Chauhan DK, Dubey NK, Rai AK (2015) Silicon-mediated alleviation of Cr (VI) toxicity in wheat seedlings as evidenced by chlorophyll florescence, laser induced breakdown spectroscopy and anatomical changes. Ecotoxicol Environ Saf 113:133–144

Tripathi DK, Singh S, Singh VP, Prasad SM, Chauhan DK, Dubey NK (2016) Silicon nanoparticles more efficiently alleviate arsenate toxicity than silicon in maize cultivar and hybrid differing in arsenate tolerance. Front Environ Sci 4:46

Tripathi DK, Singh S, Singh VP, Prasad SM, Dubey NK, Chauhan DK (2017) Silicon nanoparticles more effectively alleviated UV-B stress than silicon in wheat (*Triticum aestivum*) seedlings. Plant Physiol Biochem 110:70–81

Turner TR, James EK, Poole PS (2013) The plant microbiome. Genome Biol 14:209

Ubertino S, Mundler P, Tamini LD (2016) The adoption of sustainable management practices by Mexican coffee producers. Sustain Agric Res 5:1–12

Ulloa-Ogaz AL, Munoz-Castellanos LN, Nevarez-Moorillon GV (2015) Biocontrol of phytopathogens: antibiotic production as mechanism of control, the battle against microbial pathogens. In: Mendez Vilas A (ed) Basic science, technological advance and educational programs, vol 1, pp 305–309

Upadhyay SK, Singh DP, Saikia R (2009) Genetic diversity of plant growth promoting rhizobacteria from rhizospheric soil of wheat under saline conditions. Curr Microbiol 59:489–496

Upadhyay SK, Singh JS, Singh DP (2011) Exopolysaccharide-producing plant growth-promoting rhizobacteria under salinity condition. Pedosphere 21:214–222

Uroz S, Dessaux Y, Oger P (2009) Quorum sensing and quorum quenching: the yin and yang of bacterial communication. Chembiochem 10:205–216

Vacheron J, Desbrosses G, Bouffaud ML, Touraine B, Moënne-Loccoz Y, Muller D, Legendre L, Wisniewski-Dyé F, Combaret CP (2013) Plant growth-promoting rhizobacteria and root system functioning. Front Plant Sci 4:1–19

Valliyodan B, Nguyen H (2006) Understanding regulatory networks and engineering for enhanced drought tolerance in plants. Curr Opin Plant Biol 9:1–7

Van der Heijden MG, Bardgett RD, Van Straalen NM (2008) The unseen majority: soil microbes as drivers of plant diversity and productivity in terrestrial ecosystems. Ecol Lett 11:296–310

Van der Heijden MGA, Martin FM, Selosse MA, Sanders IR (2015) Mycorrhizal ecology and evolution: the past, the present and the future. New Phytol 205:1406–1423

van Loon LC (2007) Plant responses to plant growth promoting bacteria. Eur J Plant Pathol 119:243–254 van Loon LC, Bakker PAHM, Pieterse CMJ (1998) Systemic resistance induced by rhizosphere bacteria. Annu Rev Phytopathol 36:453–483

van Peer R, Niemann GJ, Schippers B (1991) Induced resistance and phytoalexin accumulation in biological control of Fusarium wilt of carnation by Pseudomonas sp. strainWCS417r. Phytopathology 91:728–734

Vandenkoornhuyse P, Quaiser A, Duhamel M, LeVan A, Dufresne A (2015) The importance of the microbiome of the plant holobiont. New Phytol 206:1196–1206

Vardharajula S, Ali SZ, Grover M, Reddy G, Bandi V (2011) Drought-tolerant plant growth promoting Bacillus spp.: effect on growth osmolytes, and antioxidant status of maize under drought stress. J Plant Interact 6:1–14

Vargas L, Santa Brigida AB, Mota-Filho JP, de Carvalho TG, Rojas CA, Vaneechoutte D, Van Bel M, Farrinelli L, Ferreiro PCG, Vandepoele K, Hemerly A (2014) Drought tolerance conferred to sugarcane by association with *Gluconacetobacter diazotrophicus*: a transcriptomic view of hormone pathways. PLoS One 9:e114744

Vejan P, Abdullah R, Khadiran T, Ismail S, Nusrulhaq Boyce A (2016) Role of plant growth-promoting rhizobacteria in agricultural sustainability: a review. Molecules 21:573

Velazquez-Hernandez ML, Baizabal-Aguirre VM, Cruz-Vazquez F, Trejo-Contreras MJ, Fuentes-Ramırez LE, Bravo-Patino A, Valdez-Alarcon JJ (2011) Gluconacetobacter *diazotrophicus levansucrase* is involved in tolerance to NaCl, sucrose and desiccation, and in biofilm formation. Arch Microbiol 193:137–149

Verhagen BW, Glazebrook J, Zhu T, Chang HS, van Loon LC, Pieterse CM (2004) The transcriptome of rhizobacteria-induced systemic resistance in Arabidopsis. Mol Plant-Microbe Interact 17:895–908

Verma JP, Yadav J, Tiwari KN, Lavakush, Singh V (2010) Impact of plant growth promoting rhizobacteria on crop production. Int J Agric Res 5:954–983

Verma JP, Yadav LJ, Tiwari KN, Kumar A (2013) Effect of indigenous Mesorhizobium spp. and plant growth promoting rhizobacteria on yields and nutrients uptake of chickpea (*Cicer arietinum* L.) under sustainable agriculture. Ecol Eng 51:282–286

Vidali M (2001) Bioremediation: an overview. Pure Appl Chem 73:1163–1172

Vinocur B, Altman A (2005) Recent advances in engineering plant tolerance to abiotic stress: achievements and limitations. Curr Opin Biotechnol 16:123–132

Wagg C, Bender SF, Widmer F, Van der Heijden MG (2014) Soil biodiversity and soil community composition determine ecosystem multifunctionality. Proc Natl Acad Sci U S A 111:5266–5270

Wallenstein MD (2017) Managing and manipulating the rhizosphere microbiome for plant health: a system approach. Rhizosphere 3:230–232

Walters DR, Ratsep J, Havis ND (2013) Controlling crop diseases using induced resistance: challenges for the future. J Exp Bot 64:1263–1280

Wang WX, Vinocur B, Altman A (2003) Plant responses to drought, salinity and extreme temperatures: towards genetic engineering for stress tolerance. Planta 219:1–14

Wang Y, Ohara Y, Nakayashiki H, Tosa Y, Mayama S (2005) Microarray analysis of the gene expression profile induced by the endophytic plant growth-promoting rhizobacteria, Pseudomonas fluorescens FPT9601-T5 in Arabidopsis. Mol Plant-Microbe Interact 18:385–396

Wang HG, Zhnag XZ, Li H, He HB, Fang CX, Zhang AJ, Li QS, Chen RS, Guo XK, Lin HF, Wu LK, Lin S, Chen T, Lin RY, Peng XX, Lin WX (2011) Characterization of metaproteomics in crop rhizospheric soil. J Proteome Res 10:932–940

Wang X, Mavrodi DV, Ke L, Mavrodi OV, Yang M, Thomashow LS, Zheng N, Weller DM, Zhang J (2015) Biocontrol and plant growth-promoting activity of rhizobacteria from Chinese fields with contaminated soils. Microbial Biotechnol 8:404–418

Wang R, Dungait JAJ, Buss HL, Yang S, Zhang Y, Xu Z, Jiang Y (2017) Base cations and micronutrients in soil aggregates as affected by enhanced nitrogen and water inputs in semi-arid steppe grassland. Sci Total Environ 575:564–572

Wani PA, Khan MS, Zaidi A (2008) Effect of metal tolerant plant growth-promoting rhizobium on the performance of pea grown in metal-amended soil. Arch Environ Contam Toxicol 55:33–42

Waqas M, Khan AL, Hamayun M, Shahzad R, Kim YH, Choi KS, Lee IJ (2015) Endophytic infection alleviates biotic stress in sunflower through regulation of defense hormones, antioxidants and functional amino acids. Eur J Plant Pathol 141:803–824

Webb BA, Helm RF, Scharf BE (2016) Contribution of individual chemoreceptors to *Sinorhizobium meliloti* chemotaxis towards amino acids of host and non-host seed exudates. Mol Plant-Microbe Interact 29:231–239

Wei G, Kloepper JW, Tuzun S (1991) Induction of systemic resistance of cucumber to *Colletotrichum orbiculare* by select strains of plant-growth promoting rhizobacteria. Phytopathology 81:1508–1512

Wei Y, Su Q, Sun ZJ, Shen YQ, Li JN, Zhu XL, Hou H, Chen ZP, Wu FC (2016) The role of arbuscular mycorrhizal fungi in plant uptake, fractions and speciation of antimony. Appl Soil Ecol 107:244–250

Wenzel WW (2009) Rhizosphere processes and management in plant-assisted bioremediation (phytoremediation) of soils. Plant Soil 321:385–408

Weston LA, Mathesius U (2013) Flavonoids: their structure, biosynthesis and role in the rhizosphere including allelopathy. J Chem Ecol 39:283–297

White RA III, Borkum MI, Rivas-Ubach A, Bilbao A, Wendler JP, Colby SM, Koberl M, Jansson C (2017) From data to knowledge: the future of multi-omics data analysis for the rhizosphere. Rhizosphere 3:222–229

Wicke B, Smeets E, Dornburg V, Vashev B, Gaiser T, Turkenburg W, Faij A (2011) The global technical and economic potential of bioenergy from salt-affected soils. Energy Environ Sci 4:2669–2681

Wirthmueller L, Maqbool A, Banfield MJ (2013) On the front line: structural insights into plant–pathogen interactions. Nat Rev Microbiol 11:761–776

Wu Q, Cui Y, Li Q, Sun J (2015) Effective removal of heavy metals from industrial sludge with the aid of a biodegradable chelating ligand GLDA. J Hazard Mater 283:748–754

Wu QS, Wang S, Srivastava AK (2016) Mycorrhizal hyphal disruption induces changes in plant growth, glomalin-related soil protein and soil aggregation of trifoliate orange in a core system. Soil Tillage Res 160:82–91

Wuana RA, Okieimen FE (2011) Heavy metals in contaminated soil: a review of sources, chemistry, risks and best available strategies for bioremediation. ISRN Ecol 2011:402647

Yadav LJ, Verma JP, Jaiswal DK, Kumar A (2014) Evaluation of PGPR and different concentration of phosphorus level on plant growth, yield and nutrient content of rice (*Oryza sativa*). Ecol Eng 62:123–128

Yadav UP, Ayre BG, Bush DR (2015) Transgenic approaches to altering carbon and nitrogen partitioning in whole plants: assessing the potential to improve crop yields and nutritional quality. Front Plant Sci 6:275

Yang J, Kloepper JW, Ryu CM (2009) Rhizosphere bacteria help plants tolerate abiotic stress. Trends Plant Sci 14:1–4

Yang Q, Tu S, Wang G, Liao X, Yan X (2012) Effectiveness of applying arsenate reducing bacteria to enhance arsenic removal from polluted soils by *Pteris vittata* L. Int J Phytoremediation 14:89–99

Yang AZ, Akhtar SS, Amjad M, Iqbal S, Jacobsen SE (2016a) Growth and physiological responses of quinoa to drought and temperature stress. J Agron Crop Sci 202:445–453

Yang AZ, Akhtar SS, Iqbal S, Amjad M, Naveed M, Zahir ZA, Jacobsen SE (2016b) Enhancing salt tolerance in quinoa by halotolerant bacterial inoculum. Funct Plant Biol 43:632–642

Yasmin H, Bano A, Samiullah A (2013) Screening of PGPR isolates from semi-arid region and their implication to alleviate drought stress. Pak J Bot 45:51–58

Yeoh YK, Paungfoo-Lonhienne C, Dennis PG, Robinson N, Ragan MA, Schmidt S, Hugenholtz P (2016) The core root microbiome of sugarcanes cultivated under varying nitrogen fertilizer application. Environ Microbiol 18:1338–1135

Yu XM, Ai CX, Xin L, Zhou GF (2011) The siderophore-producing bacterium, *Bacillus subtilis* CAS15, has a biocontrol effect on Fusarium wilt and promotes the growth of pepper. Eur J Soil Biol 47:138–145

Yuan J, Zhang N, Huang Q, Raza W, Li R, Vivanco JM, Shen Q (2015) Organic acids from root exudates of banana help root colonization of PGPR strain *Bacillus amyloliquefaciens* NJN-6. Sci Rep 25:13438

Yuan Z, Jiang S, Sheng H, Liu X, Hua H, Liu X, Hua H, Liu X, Zhang Y (2018) Human perturbation of the global phosphorus cycle: changes and consequences. Environ Sci Technol 52:2438–2450

Zamioudis C, Pieterse CMJ (2012) Modulation of host immunity by beneficial microbes. Mol Plant-Microbe Interact 25:139–150

Zamioudis C, Mastranesti P, Donukshe P, Blilou I, Pieterse CM (2013) Unraveling root development programs initiated by beneficial *Pseudomonas* spp. Bacteria. Plant Physiol 162:304–318

Zehr JP, Jenkins BD, Short SM, Steward GF (2003) Nitrogenase gene diversity and microbial community structure: a cross-system comparison. Environ Microbiol 5:539–554

Zhang F, Lynch DH, Smith DL (1995) Impact of low root temperatures in soybean [*Glycine max* (L.) Merr.] on nodulation and nitrogen fixation. Environ Exp Bot 35:279–285

Zhang F, Dashti N, Hynes R, Smith DL (1996) Plant growth promoting rhizobacteria and soybean [*Glycine max* (L.) Merr.] nodulation and nitrogen fixation at suboptimal root zone temperatures. Ann Bot 77:453–460

Zhang H, Sun Y, Xie X, Kim MS, Dowd SE, Pare PW (2009) A soil bacterium regulates plant acquisition of iron via deficiency-inducible mechanisms. Plant J 58:568–577

Zhang J, Wang LH, Yang JC, Liu H, Dai JL (2015) Health risk to residents and stimulation to inherent bacteria of various heavy metals in soil. Sci Total Environ 508:29–36

Zhao S, Zhou N, Zhao ZY, Zhang K, Wu GH, Tian CY (2016) Isolation of endophytic plant growth-promoting bacteria associated with the halophyte Salicornia europea and evaluating their promoting activity under salt stress. Curr Microbiol 73:574–581

Zheng YK, Qiao XG, Miao CP, Liu K, Chen YW, Xu LH, Zhao LX (2016) Diversity, distribution and biotechnological potential of endophytic fungi. Ann Microbiol 66:529–542

Ziegler M, Engel M, Welzl G, Schloter M (2013) Development of a simple root model to study the effects of single exudates on the development of bacterial community structure. J Microbiol Methods 94:30–36

Zilber-Rosenberg I, Rosenberg E (2008) Role of microorganisms in the evolution of animals and plants: the hologenome theory of evolution. FEMS Microbiol Rev 32:723–735

Zmora N, Zeevi D, Korem T, Segal E, Elinav E (2016) Taking it personally: personalized utilization of the human microbiome in health and disease. Cell Host Microbe 19:12–20

Zolla G, Badri DV, Bakker MG, Manter DK, Vivanco JM (2013) Soil microbiomes vary in their ability to confer drought tolerance to *Arabidopsis*. Appl Soil Ecol 68:1–9

Zuppinger-Dingley D, Schmid B, Petermann JS, Yadav V, De Deyn GB, Flynn DF (2014) Selection for niche differentiation in plant communities increases biodiversity effects. Nature 515:108–111