

Review Article

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## Perspectives of Plant Associated Microorganisms in Drought Management of Crops

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### ABSTRACT

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Cereals and legumes are largely grown under harsh rainfed conditions in India, which is further complicated by climate change and climate variability. Tropical drylands are experiencing deficit rainfall over the years. Due to this, agricultural production is affected in arid and semi arid regions. There is an urgent need to find low cost, ecofriendly, sustainable solutions to manage crop productivity under rainfed situations to help resource poor small and marginal farmers in particular. Plant microbiome interactions offer plants to tide over adverse conditions viz., biotic and abiotic stresses through their various activities. The mechanisms they employ under moisture stress conditions include; synthesis and accumulation of biochemical compounds like proline and sugars, regulation of ethylene synthesis, production of phytohormones and exopolysaccharides, enhancement of root growth, regulation of gene expression etc. In addition to water deficit stress, drylands are also deficient in various plant nutrients. Consortia of microorganisms with multiple improved functions such as nitrogen fixation, drought tolerance, nutrient mobilization and solubilization have a potential to improve drought tolerance, plant growth and development under rainfed conditions.

### Introduction

Water is the major limiting factor for crop production in arid and semi arid regions of the world (Daryanto *et al.*, 2016; Maheswari *et al.*, 2017). More than 50 % of arable lands are going to be affected by severe drought by 2050, threatening crop production and food security due to the increased frequency of droughts over the years. The climate change will further aggravate the problem in the near future making farming very difficult (Lobell *et al.*, 2011; Mancosu *et al.*, 2015; Sallam *et*

*al.*, 2019). Continuous drought over the years can cause severe water crisis, this would seriously affect agriculture dependent livelihoods and may even lead to food insecurity, famine and death (Karim *et al.*, 2014; Reid 2011). It is predicted that, drought would severely affect the maize, soybean and cotton growing regions across the globe (Ngumbi and Kloepper, 2016). About 40% deficit in water is causing 20-40 % reduction in yield of important crops such as wheat and maize (Daryanto *et al.*, 2016). In the United States, drought stress has resulted in around

67% of crop losses in the past 50 years (Comas *et al.*, 2013). Improving the agricultural productivity is of paramount importance to ensure food and nutritional security to ever increasing human population especially resource poor small and marginal farmers (Glick 2014; Naved *et al.*, 2014a). Cereals and legumes are largely grown under rainfed conditions in arid, semi-arid and sub humid regions (Creswell and Martin 1998; Farooq *et al.*, 2017).

Crop improvement through plant breeding and genetic engineering technologies help to develop crop plants tolerant to various biotic and abiotic stresses (Ngumbi and Kloepper, 2016; Reid 2011). However, conventional breeding methods are slow, labour intensive and sometimes lead to loss of useful traits. Genetic engineering although is faster but consumer acceptance level of genetically modified crops and their products varies across different countries (Ngumbi and Kloepper, 2016; Reid 2011). Under these circumstances, the pressing need of the hour is to find low cost, ecofriendly, sustainable solutions to manage the problem of water deficit stress without compromising the crop yield in rainfed agriculture (Chakraborty *et al.*, 2013; Ngumbi and Kloepper, 2016; Ruzzi and Aroca, 2015).

Plant beneficial microorganisms have tremendous potential to increase the drought tolerance and productivity of plants (Chanway and Holl, 1994; de Souza *et al.*, 2016; Kasim *et al.*, 2016). They display wide array of plant growth promoting characteristics, which aid in regulating the physiological responses to water deficit and improved survival and growth of plants under water stress conditions (Morasco *et al.*, 2012, 2013; Redman *et al.*, 2011).

The Plant Microbiome comprises of plant and soil associated microorganisms (Rout 2014).

The performance of plants in a given environment is influenced by their microbiome. Microbiome helps plants to overcome various biotic and abiotic stresses (Panke-Buisse *et al.*, 2015).

The plant associated microorganisms in rainfed crops are mainly grouped as;

**Rhizospheric microorganisms:** The microbes which are in close vicinity of roots and those which are positively affecting the plant growth and development are referred as plant growth promoting microorganisms (PGPMs) (Glick 2012; Kloepper and Schroth, 1978).

**Endophytic microorganisms:** Endophytic microorganisms are the one which found inside the tissues of plants without causing any harm (Naved *et al.*, 2014b; Schulz and Boyle, 2006).

**Epiphytic or phyllosphere microorganisms:** These are the microbes which are found on the above ground plant surfaces (Lindow and Brandl, 2003).

### **Factors affecting crop productivity**

Several biotic (pest and diseases) and abiotic (drought, salinity, cold, heat, nutrient deficiency, heavy metals, etc.) factors affect the agricultural production worldwide (Pandey *et al.*, 2017).

Amongst all, drought is the single most important factor causing severe yield losses in agriculture (Budak *et al.*, 2015; Daryanto *et al.*, 2016; Maheswari *et al.*, 2017; Naved *et al.*, 2014; Stromberger *et al.*, 2017).

In this communication, we discuss about the role of plant associated microorganisms in the management of drought stress in cereals and legumes of rainfed agriculture.

## **Roles of plant beneficial microorganisms**

The plant beneficial microorganisms help plant growth and development by several mechanisms (Backer *et al.*, 2018; Hardoim *et al.*, 2008; Vardharajula *et al.*, 2011). These include nitrogen fixation (Mirza *et al.*, 2001), solubilization and mobilization of phosphorus (Sridevi and Mallaiah, 2009), nutrient uptake (Mantelin and Touraine, 2004), phytohormone production (Naveed *et al.*, 2014), root growth (Somers *et al.*, 2004), alleviation of biotic (Compant *et al.*, 2005; Hill *et al.*, 1994) and abiotic stresses such as drought (Naveed *et al.*, 2014; Cohen *et al.*, 2009; Vilchez and Manzanera, 2011), salinity (Jha *et al.*, 2011) and yield improvement (Hameeda *et al.*, 2008).

## **Mechanisms of drought management in rainfed cereals and legumes**

### **Plant adaptations**

Plants being sessile organisms have developed certain mechanisms to cope up and survive under changing environmental conditions through various morpho-physiological modifications and evolutionary adaptations (Chmielewska *et al.*, 2016; Juenger, 2013).

### **Drought escape**

Annual herbaceous plants complete their life cycle before the onset of drought, there by escape moisture stress conditions for growth and development (Kooyers, 2015).

### **Drought avoidance**

Plants avoid ill effects of moisture stress by maintaining basic physiological functions and modifying a few or more morphological features like closure of stomata and increased synthesis and accumulation of wax on leaf

surfaces (Blum, 2005; Fang and Xiang, 2015; Tardieu, 2013; Zhang *et al.*, 2005)

### **Drought tolerance**

Plants withstand moisture stress conditions without affecting its growth and development, there would be a minimum loss in yield (Luo, 2010). Osmotic adjustment and accumulation of solutes play a very important role in adaptation of crop plants to moisture stress through cellular functions and turgor maintenance (Blum, 2017; Ullah *et al.*, 2017). The mechanisms include antioxidative stress metabolism and scavenging of reactive oxygen species. Plants accumulate various biochemical compounds such as sugars, amino acids, polyamines etc. to adapt to water stress conditions (Fang and Xiong, 2015).

Microorganisms help to enhance the drought tolerance of plants by various mechanisms;

### **Synthesis and accumulation of biochemical compounds**

Plants resort to elevated synthesis of sugars, amino acids and polyamines during drought stress conditions. Proline is a very important amino acid, it help plants to tolerate stress by maintaining cell turgor or osmotic balance, preventing electrolyte leakage by stabilizing cell membrane, reducing the concentration of reactive oxygen species (Farooq *et al.*, 2008; Hong *et al.*, 2000; Kiani *et al.*, 2007; Mansour 1998). Beneficial bacteria stimulate the synthesis of proline and sugars under stress conditions to prevent the damage to plants (Mafakheri *et al.*, 2010; Sandhya *et al.*, 2010; Silvente *et al.*, 2012). The *Bacillus* spp. improved the growth and development of maize (*Zea mays* L.) plants under water stress conditions by accelerating the synthesis of sugars, proline, amino acids and by restricting the electrolyte leakage, and increased the dry biomass by 46.6 % than uninoculated control

(Kavamura *et al.*, 2013; Vardharajula *et al.*, 2011). Inoculation of greengram (*Vigna radiata* L.) seeds with *Pseudomonas fluorescens* Pf1 boost the tolerance of plants to drought stress conditions upto 8 days by enhancing the synthesis of proline (Saravanakumar *et al.*, 2011). The *Pseudomonas aeruginosa* GGRJ21 enhances the tolerance level of mung bean (*Vigna radiata* L.) to drought by increasing shoot and root length by producing proline (Sarma and Saikia, 2014). Treatment of wheat seeds with *Pantoea alhagi*- strain LTYR-11Z<sup>T</sup> augment the plant growth by increasing the synthesis of soluble sugars and reducing the chlorosis of wheat (*Triticum aestivum* L.) leaves under drought stress conditions (Chen *et al.*, 2016). The *Bacillus subtilis* strain B26 enhanced the drought tolerance of plants by increasing the synthesis of total soluble sugars and starch whenever plants are under water stress (Gagne-Bourque *et al.*, 2015). Certain bacteria like *Bacillus megaterium* BOFC15 produce polyamines like spermidine for enhancing the drought adaptiveness of plants through increased synthesis of ABA, antioxidant enzymes and improving root growth (Zhou *et al.*, 2016).

### **Regulation of ethylene synthesis**

Ethylene is an important plant growth regulating hormone. It influences all the developmental stages of plants, its levels are low during growth and development stages but maximum at ripening and senescence period (Glick, 2005). The ethylene production in plants is affected by several factors such as drought, high temperature, pest and disease incidence, heavy metal etc. and its synthesis in plants increases during stress conditions (Abeles *et al.*, 1992). This increased level of ethylene synthesis lead to chlorosis, inhibition of shoot and root growth and early senescence of plants (Glick, 2005; Glick, 2014; Mayak *et al.*, 2004). The enzyme 1-aminocyclopropane

1-carboxylate (ACC) deaminase converts the ACC, the precursor of ethylene into ammonia and  $\alpha$ -ketobutyrate (Glick 2012; Honma and Shomomura, 1978). The ACC deaminase producing bacteria helps plants from drought and other environmental stress conditions by restricting the synthesis of ethylene under stress conditions (Gamalero and Glick, 2015). The *Serratia marcescens* (STJ5) and *Pseudomonas thivervalensis* (STF3) by their ACC deaminase activity improved the growth and development of maize (*Zea mays* L.) under field conditions (Shahzad *et al.*, 2013). The ACC deaminase producing *Serratia* and *Aerococcus* enhanced the shoot length (80.2%), root length (54.6%) and shoot dry weight (95.4 %) of wheat (*Triticum aestivum* L.) seedlings under water stress conditions (Bangash *et al.*, 2013). The consortium comprising of *Ochrobactrum pseudogrignonense* RJ12, *Pseudomonas* sp. RJ15 and *Bacillus subtilis* RJ46 improved the drought tolerance in *Vigna mungo* L. and *Pisum sativum* L. by decreasing ACC accumulation and down regulation of expression of ACC oxidase gene (Saikia *et al.*, 2018). Application of ACC deaminase producing *Bacillus amyloliquefaciens* and 30 Mg ha<sup>-1</sup> biochar with two irrigations increases the straw yield (75 %) and grain yield (77 %) of wheat over the control with four irrigations (Zafar-ul-Hye *et al.*, 2019).

### **Synthesis of exopolysaccharides (EPS)**

Biofilm is formed by the complex group of bacteria by attaching to various biotic and abiotic surfaces (Batool and Hasnain, 2005). Beneficial bacteria produce exopolysaccharides (EPS), a diverse polymer of sugars which aid in attachment of bacteria to different surfaces and subsequently development of biofilm. Biofilm retains more water around them, due to this, they could survive under water stress and other environmental variations (Batool and

Hasnain, 2005; Chenu and Roberson, 1996; Costerton *et al.*, 1987; Qurashi and Sabri, 2012; Roberson and Firestone, 1992). The EPS enabled the attachment of microorganisms to root surface and helped plants tolerate drought conditions by improving soil moisture content, root length and plant biomass (Bashan and Holguin, 1997). Inoculation of maize (*Zea mays* L.) seeds with EPS producing *Alcaligenes faecalis* (AF3), *Pseudomonas aeruginosa* (Pa2) and *Proteus penneri* (Pp1) improved the relative water content, sugar and proline levels and helped the plant to tide over drought stress conditions (Naseem and Bano, 2014). The *Rhizobium* sp. strain YAS34 by its EPS production helps sunflower (*Helianthus annus* L.) plants to grow under drought stress conditions by improving soil aggregation and adhesion of soil particles around roots (Alami *et al.*, 2000). The exopolysaccharide producing *Pseudomonas putida* improved the root growth and plant biomass of sunflower (*Helianthus annus* L.) seedlings under water stress conditions (Sandhya *et al.*, 2009). EPS producing bacterial strains *Planomicrobium chinense* strain P1 and *Bacillus cereus* strain P2 effectively reduced the negative effects of drought stress by improving, sugar, chlorophyll and protein contents of wheat grown as a rainfed crop (Khan and Bano, 2019).

### **Production of phytohormones**

Microorganisms are known to produce plant hormones viz., indole acetic acid (IAA), gibberlic acid (GA) and abscisic acid (ABA) which help plants tolerate drought conditions. The IAA whenever present at low concentration enhances cell elongation and root growth (Vilchez *et al.*, 2016). The ABA under drought situations prevented the loss of water by closure of stomata; it also increased the root growth and accumulation of solutes (Raschke, 2006). Several plant beneficial

bacteria synthesized these plant hormones IAA (Kuan *et al.*, 2016), GA (Bottini *et al.*, 2004) and ABA (Vurukonda *et al.*, 2016) and helped plant to tolerate drought stress (Glick, 1995; Marulanda *et al.*, 2009). The *Rhizobium phaseoli* (MR-2) and *Mesorhizobium ciceri* (CR-30 and CR-39) by the synthesis of IAA improved drought tolerance of wheat by increasing the root length (Hussain *et al.*, 2014). The *Azospirillum brasilense* increased drought tolerance level of pearl millet (*Pennisetum glaucum* L.) by enhancing the root length, lateral roots and root hairs (Tien *et al.*, 1979). Inoculation of *Pseudomonas* spp. strain AKM-P6 improved the survival of sorghum (*Sorghum bicolor* L.) seedlings at elevated temperatures (47-50°C day/30-33°C night) upto 15 days vis-à-vis 5 days of non-inoculated plants. It also enhanced the proline, sugar and amino acids and other metabolites (Ali *et al.*, 2009). The *Phyllobacterium brassicacearum* strain STM196 increased the drought tolerance of *Arabidopsis thaliana* by delaying the switch over of vegetative phase to reproductive phase and also by enhancing water use efficiency (Bresson *et al.*, 2013). Consortia of *Paenibacillus polymyxa* strain DSM 36, *P. polymyxa* strain Loutit and *Rhizobium tropici* (CIAT 899) helped the common bean (*Phaseolus vulgaris* L.) plants to alleviate drought stress by increasing the ABA concentration in shoots (Marcia *et al.*, 2008). The *Azospirillum lipoferum* improved the drought stress tolerance in maize (*Zea mays* L.) plants through the synthesis of ABA and GA (Cohen *et al.*, 2009).

### **Enhancement of root growth**

Increasing the water uptake capacity of plants is very essential to overcome water stress (Long *et al.*, 2008). Beneficial bacteria improved the water uptake of plants by increasing root length, lateral roots and root volume, so that, plants could take up water



from deeper layers under stress conditions (Armada *et al.*, 2014). Inoculation of maize (*Zea mays* L.) plants with endophytic bacteria viz., *Burkholderia phytofirmans* PsJN and *Enterobacter* sp. FD17 enhanced root growth, drought tolerance, plant biomass and yield (Naved *et al.*, 2014b). The *Bacillus thuringiensis* AZP2 improved the drought tolerance of wheat (*Triticum aestivum* L.) plants by increasing the length and density of roots (Timmusk *et al.*, 2014). Beneficial bacteria such as *Azospirillum brasilense* strain Az39 and *Brayrhizobium japonicum* strain E109 improved the germination of maize (*Zea mays* L.) and soybean (*Glycine max* L.) respectively (Cassan *et al.*, 2009). Consortia of *Pseudomonas striata*, *Azospirillum* and *Rhizobium* helped in enhancing nodule number, nodule dry weight, plant height and dry matter of pigeon pea (*Cajanus cajan* L.) (Devanand *et al.*, 2002). The combined application of *Rhizobium tropici* (CIAT 899) and *Paenibacillus polymyxa* (DSM 36) reduced the damages of drought and improved the nodulation, nitrogen content and plant growth in common bean (*Phaseolus vulgaris* L.) (Figueiredo *et al.*, 2008). The *Exophiala pisciphila* helps sorghum plants to tolerate drought stress conditions upto one month by improving plant height, shoot dry weight (Zhang *et al.*, 2016). Inoculation of sunflower with *Bacillus pumilus* SF3 increased root dry matter under water stress conditions (Forchetti *et al.*, 2010). Seed treatment of pigeon pea (*Cajanus cajan* L.) with *Enterobacter ludwigii* SRI-229 improved the root weight of pigeon pea (*Cajanus cajan* L.) by 16 % over untreated control (Gopalakrishnan *et al.*, 2016). The *Pseudomonas* spp. strain OG caused enhancement of root length of green gram by 53 % (Goswami *et al.*, 2013). Two bacterial isolates *Bacillus* sp. (12D6) and *Enterobacter* sp. (16i) increased the drought tolerance of maize and wheat by improving root length, root branching and root surface area (Jochum

*et al.*, 2019). *Sphingomonas* sp. Cra20 by accelerating the development of lateral roots and root hairs improved the drought tolerance of *Arabidopsis thaliana* (Luo *et al.*, 2019).

### Regulation of gene expression

Whenever plants experience stress conditions, they switch on /off certain genes for survival. Over expression of certain genes in plants under drought stress conditions enhanced the tolerance level and yield (Sakuma *et al.*, 2006). Trehalose triggers the expression of genes which encodes for stress tolerance, carbon and nitrogen metabolism in plants. Beneficial bacteria like *Rhizobium etli* causes over expression of trehalose-6-phosphate synthase gene (ReOtsA) in common bean (*Phaseolus vulgaris* L.) resulting in increased number of nodules, nitrogenase activity and crop biomass as compared to wild type *R. etli* (Suarez *et al.*, 2008). Inoculation of green gram (*Vigna radiata* L.) with *Pseudomonas aeruginosa* GGRJ21 results in increased tolerance to drought by elevated expression of drought responsive genes viz., dehydrin (DHN), catalase (CAT1) and dehydration responsive element binding protein (DREB2A) (Sarma and Saikia, 2014). Treatment of wheat cv. Sids1 with *Bacillus amyloliquefaciens* 5113 and *Azospirillum brasilense* NO40, led to over expression of drought responsive genes i.e., ascorbate peroxidase (*APX1*) of ascorbate–glutathione redox cycle (Kasim *et al.*, 2013). Real time PCR analysis of expression of dehydrin (drought responsive gene) in maize (*Zea mays* L.) showed that, the endophytes *Bacillus licheniformis* CRIDA MSEB 17, *Bacillus subtilis* CRIDA MSEB 78 and *Bacillus subtilis* CRIDA MSEB 72 enhanced the expression of dehydrin upto 30.51 %, 33.56 % and 40.32 % respectively in terms of relative quantification of the gene in relation to control, revealing that bacterial endophytes modify the response of host plant to drought

conditions (ICAR-CRIDA, 2017). The *Paenibacillus polymyxa* induced the expression of early response to dehydration (ERD 15), a drought responsive gene in *Arabidopsis thaliana* under drought stress conditions (Timmusk and Wagener, 1999). The *Bacillus subtilis* strain B26 protected the plants from moisture stress by upregulating the drought responsive genes such as DHN3-like, LEA-14-A-like and DREB2B-like genes in *Brachypodium distachyon* (Gagné-Bourque *et al.*, 2015).

### **Manipulation of microbiome**

Microbiomes represents extremely complex group of organisms (Rascovan *et al.*, 2016). Thorough knowledge of crop specific microbiome would help to modulate the microbiome in a way that would lead to better the growth and development of crop plants (De-la-Pena *et al.*, 2014; Laksmanan *et al.*, 2014; Rascovan *et al.*, 2016; Tkacz Poole *et al.*, 2015). Study of plant microbiome has been limited so far due to technical hiccups. With the advancement of high-throughput sequencing technologies like metagenomic analysis, large amount of information is available on the composition of microbial communities in the rhizosphere of different plants (Rascovan *et al.*, 2016) like rice (Edwards *et al.*, 2015), wheat (Donn *et al.*, 2015), maize (Aira *et al.*, 2010) and soybean (Mendes *et al.*, 2014). The composition of microbiome varies with crop, soil type and prevailing environmental conditions, for example Proteobacteria, Bacteroidetes and Actinobacteria were predominant and Chloroflexi and Firmicutes were absent in the barley (*Hordeum vulgare* L.) root microbiome (Burgarelli *et al.*, 2015). However, still a very little information is available on the effect of different abiotic stresses on the root microbiome of crop plants (Blee *et al.*, 2013; De-la-Pena *et al.*, 2014; Tkacz Poole *et al.*, 2015). Drought considerably changes the

composition of bacterial and fungal communities indicating that, this restructured microbiome might help the plant survival under adverse environmental situations (Santos-Medellin *et al.*, 2017). In case of rice, water stressed plants had the dominance of *Chloroflexi* and actinobacteria with severe reduction of delta-proteobacteria and acidobacteria in comparison with the well watered plants (Santos-Medellin *et al.*, 2017). Further research is required for the crop specific analysis of microbiome, since this would help to understand, explore and augment the level of drought responsive microorganisms in the overall composition of microbiome through external application. This enhanced level of drought responsive microorganisms would improve the adaptiveness of crop plants to water stress (Santos-Medellin *et al.*, 2017). The main challenge here was to select appropriate microbial species or their consortia to deal with the situation (Gopal and Gupta, 2016).

### **Omic approaches for the management of drought**

Several important drought responsive genes coding for proteins which protect the plants from abiotic stresses have been identified and characterized in different crops through functional genomics studies like transcriptomics, proteomics and metabolomics (Joshi *et al.*, 2016). Extensive studies on functional genomics of drought tolerance have been done on *Arabidopsis thaliana* (Yin *et al.*, 2014). However, functional genomics studies involving microorganisms and plants are mostly being done on salt stress (de Lorenzo *et al.*, 2009; Kapardar *et al.*, 2010; Zhao *et al.*, 2009), cold stress (Liljeqvist *et al.*, 2015) heavy metals and drought stress on crops like cucumber (Li *et al.*, 2014), tomato (Zhang *et al.*, 2011). These omic approaches have been discussed in a review by Meena *et al.*, (2017). These

kinds of studies in rainfed crops, involving microorganisms for drought tolerance are limited. Hence, in future, extensive functional genomics studies are required to understand the mechanisms and to enhance greater drought tolerance in dryland crops.

### **Metabolic modelling for mitigating drought in rainfed crops**

Plant metabolism is a source of various useful metabolites for pharmaceutical and biotechnological applications (Baghalian *et al.*, 2014). Metabolic engineering is a mechanism which involves the manipulation of metabolic pathways through regulation of gene expression (Jarboe *et al.*, 2010). Plants differ in synthesis and accumulation of biochemical compounds to cope up with moisture stress conditions, for example legumes exhibit high tolerance to drought (Ashraf and Iram, 2005; Ford, 1984). Plant associated microorganisms also regulate the synthesis, accumulation and composition of various metabolites in plants under stress conditions (Rasmussen *et al.*, 2012). Inoculation of *Bacillus subtilis* strain B26 to timothy (*Phleum pratense* L.) alters the plant metabolism under drought stress conditions leading to enhanced synthesis of sugars (sucrose and fructans) and amino acids (glutamic acid, asparagine) in roots and shoots when compared with non-inoculated plants (Gagne-Bourque *et al.*, 2016). By delineating the profile of various metabolites in drought tolerant and susceptible crop plants would help to know the biochemical pathways affected by water stress and subsequently in developing highly tolerant crop plants (Silvente *et al.*, 2012). Metabolic modelling helps to foresee and regulate plant metabolism to get desired outcome (Baghalian *et al.*, 2014; Stitt *et al.*, 2010). This can be achieved by inducing the accumulation of metabolites through regulation of gene expression.

Microorganisms also regulate the gene expression and synthesis of biochemical compounds in plants, which has been discussed in previous sections. Some of the available metabolic models include; AraCyc, a biochemical pathway database for *Arabidopsis* (Mueller *et al.*, 2003) and MoTo DB, for tomato (Grennan 2009).

### **Future Prospects**

Plants and microorganisms have long history of co-evolution (Backer *et al.*, 2018). From the aforementioned literature it is evident that, beneficial bacteria through different mechanisms help to enhance the drought tolerance of plants under water deficit conditions. The available literature indicates that, most of studies using drought tolerant microorganisms have done in maize and wheat. There is a necessity to explore and exploit the effectiveness of these beneficial microbes in other cereals, legumes and millets as well. Moreover, rainfed production systems have not been systematically explored to identify native drought tolerant bacteria to enhance drought tolerance of rainfed crops (Saleem *et al.*, 2018). It is true that, maize and wheat are the major staple food crops of the world after rice. The expected demand of these crops is around 3.3 billion tones by 2050 (FAO, 2016). This demand has to be met by overcoming catastrophic effects of climate change on agriculture such as loss of available arable land due to soil erosion, rise in sea level and with diminishing water resources. Moreover, cereal yields are stagnated all over the world (FAO, 2016). Under these circumstances, drought tolerant microorganisms provide an excellent option to improve the drought tolerance as well as of growth and yield of plants. Apart from improving soil health and crop productivity, biofertilizers and biopesticides also contribute to reducing the green house gas emissions into the atmosphere by helping in



downscaling the use of agrochemicals, this in turn lead to minimizing the use of fossil fuels in the manufacture of agrochemicals (Havukainen *et al.*, 2018). At present, most of these studies are confined to laboratory or research farms.

To enhance the outreach of these simple, low cost and eco-friendly technologies, more and more on-farm studies with active participation of farmers are required. With regard to consistency problem, identification of location specific microorganisms may help to overcome this. Since the microorganisms are well adapted to the prevailing conditions at their natural habitat such as pH, nutrients, soil moisture and other native organisms. Besides this, there is also need to develop formulations of consortia having several plant growth-promoting characteristics and standard utilization procedures of the same to improve drought tolerance of plants.

Enormous potential exist in this kind of technology and could be one of the important approaches to sustain agricultural production in less developed and developing countries (Barea, 2015; Zoppellari *et al.*, 2014). We need to integrate microbial technologies along with the agrochemicals in reduced quantities to sustain soil health and agricultural production (Ahmad *et al.*, 2018).

In conclusions the development and implementation of novel innovative technologies are necessary to address the problem of drought in rainfed areas. Plant beneficial microorganisms can provide low cost, environment friendly drought mitigation solutions for improving the crop productivity. Manipulation of microbiome with crop specific useful microorganisms would help to improve growth, health and productivity of crop plants. In future, exhaustive studies are required to understand the effect of abiotic stresses vis-à-vis normal conditions on the

composition of microbiome of rainfed cereals and legumes. This would help to manipulate the composition of microbiome, for example exploitation of drought tolerant microorganisms to get desired benefits in respect of crop growth and production. Metabolic modelling of rainfed crops under the influence of abiotic stress and microorganisms is also important, as this would helps to foresee and regulate plant metabolism to get expected outcome. Studies involving omic approaches and high-throughput phenotyping of plants under the influence of beneficial microorganisms under drought stress conditions are necessary to understand the mechanisms and to impart greater drought tolerance in dryland crops. In addition to water scarcity, drylands are also nutrient hungry with host of other problems. To address this issue in a comprehensive manner, a consortia of microorganisms with multiple functions such as nitrogen fixation, drought tolerance, nutrient solubilization and disease control is required to bring the multiple benefits under single umbrella. It would lead to greater acceptance and usage among the farmers. Further exploration of novel and efficient microorganisms with multiple benefits is necessary to sustain rainfed agricultural production. With the renewed push for organic agriculture, beneficial microorganisms being important component would play greater role in sustaining soil health, environment and agricultural production.

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