

Can Microorganisms assist Crop Plants in Combating Climate

Change Associated Variabilities?

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Introduction

Climate change in IPCC usage refers to a change in the state of the climate that can be identified by changes in the mean and/or the variability of its properties, and that persists for an extended period, typically decades or longer. It refers to any change in climate over time, whether due to natural variability or as a result of human activity. This usage differs from that in the United Nations Framework Convention on Climate Change (UNFCCC), where climate change refers to a change of climate that is attributed directly or indirectly to human activity that alters the composition of the global atmosphere and that is in addition to natural climate variability observed over comparable time period.

Increases in sea level are consistent with warming. Global average sea level rose at an average rate of 1.8 mm per year over 1961 to 2003 and at an average rate of about 3.1 mm per year from 1993 to 2003. Whether this faster rate for 1993 to 2003 reflects decadal variation or an increase in the longer-term trend is unclear. Since 1993 thermal expansion of the oceans has contributed about 57% of the sum of the estimated individual contributions to the sea level rise, with decreases in glaciers and ice caps contributing about 28% and losses from the polar ice sheets.

Today, temperatures are monitored at many thousands of locations, over both the land and ocean surface. Indirect estimates of temperature change from such sources as tree rings and ice cores help to place recent temperature changes in the context of the past. In terms of the average surface temperature of Earth, these indirect estimates show that 1983 to 2012 was probably the warmest 30-year period in more than 800 years. The average temperature in the Indian sub-continent has risen by 0.57⁰C in the last 100 years and models project that it is likely to rise further to a maximum of 2.5C by 2050 and 5.8C by 2100 A warming of climate and decreasing soil moisture can also result in increasing need for irrigation. Irrigation requirement in arid and semi-arid regions is estimated to increase by 10% with every 1C rise in temperature. Besides high temperature, droughts, elevated CO₂, extreme rainfall events, more floods, cold waves, heat waves, and cyclones are the other important natural disasters that cause serious economic losses, are likely to be witnessed as a result of global warming.

Effect of warming on plants

High temperature which results due to global warming affects the plants adversely. It can

denature the proteins and can cause peroxidation.



Under HT conditions, plants exhibit various mechanisms for surviving which include long-term evolutionary phenological and morphological adaptations and short-term avoidance or acclimation mechanisms such as changing leaf orientation, transpirational cooling, or alteration of membrane lipid compositions. Closure of stomata and reduced water loss, increased stomatal and trichomatous densities, and larger xylem vessels are common heat induced features in plant. In many crop plants, early maturation is closely correlated with smaller yield losses under HT, which may be attributed to the engagement of an escape mechanism. Plants growing in a hot climate avoid heat stress by reducing the absorption of solar radiation. This ability is supported by the presence of small hairs (tomentose) that form a thick coat on the surface of the leaf as well as cuticles, protective waxy covering. In such plants, leaf blades often turn away from light and orient themselves parallel to sun rays (paraheliotropism)

Effect of high CO₂ on plants

As CO₂ concentrations increase, plants can maintain high photosynthetic rates with relatively low stomatal conductance. Across a variety of FACE experiments, growth under elevated CO₂ decreases stomatal conductance of water by an average of 22%. This would be expected to decrease overall plant water use, although the magnitude of the overall effect of CO₂ will depend on how it affects other determinants of plant water use, such as plant size, morphology, and leaf temperature. Overall, FACE experiments show decreases in whole plant water use of 5–20% under elevated CO₂. This in turn can have consequences for the hydrological cycle of entire ecosystems, with soil moisture levels and runoff both increasing under elevated.

Effect of salinity on plants

All carbohydrate, fatty acids and protein are adversely affected by salinity.

Physiological damage that occurs due to salt stress are

- Water deficiency,
- Ion cytotoxicity,
- Osmotic stress
- Disruption of cell organelle and metabolism
- Nutrient imbalance in plants.

Salinity effects photosynthetic processes by two ways:--

- Stomatal closure due to salinization
- Decreased carbon dioxide fixation due to osmotic stress

Effect of drought on plants

Water limitation is one of the major threats in crop production and this condition is projected to get considerably worse in coming decades. metabolic regulation including regulation of photosynthesis and accumulation of osmolytes in the drought stress response [43, 44]. Urano et al. [28] reported metabolomic changes in Arabidopsis leaves under drought condition. The accumulation of many metabolites was observed, including amino acids such as proline, raffinose family oligosaccharides, γ -amino butyrate (GABA) and tricarboxylic acid (TCA) cycle metabolites, which are known to respond to drought stress in plants. The authors also investigated the nc3-2 mutant, which lacks the NCED3 gene involved in the dehydration-inducible biosynthesis of abscisic acid (ABA), in order to assess the effect of ABA in the metabolic response to drought stress.

Effect of Climate change on microorganisms

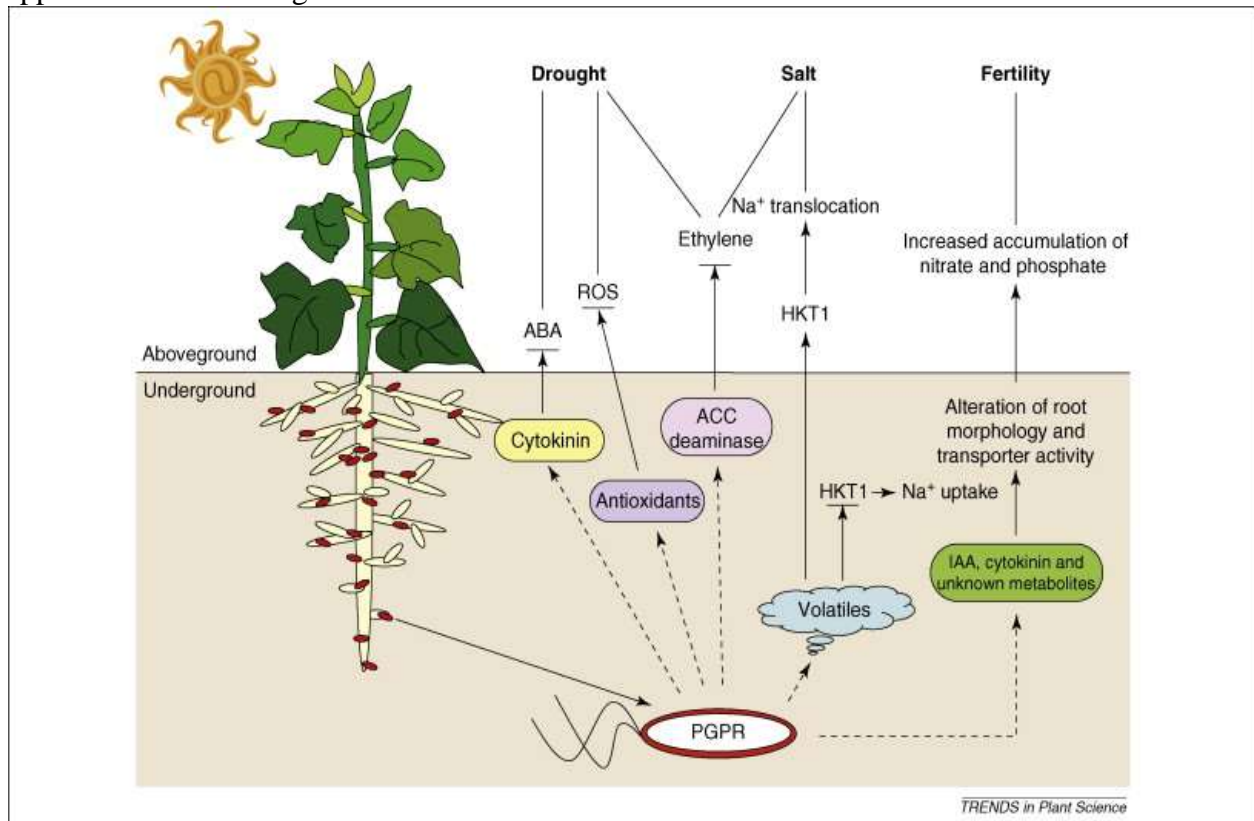
On the other hand, increased recalcitrance of litter and root detritus, as a consequence of higher C:N and increased lignification, can also lead to immobilization of soil N in CO₂-enriched environments thereby inducing nutritional limitations to microbial metabolism which might slow organic matter decomposition rates.

Effects of atmospheric CO₂ enrichment on mycorrhizal fungi are often profound. A meta-analysis recently indicated that exposure to elevated CO₂ elicited a 47% average increase in mycorrhizal abundance and that mycorrhizae were stimulated disproportionately more than roots. Another meta-analysis reported that the mass of

ectomycorrhizal (EM) fungi increased by 34% in CO₂-enriched environments, whilst that of AM (endomycor-rhizal) fungi increased by 21%. The extent to which mycorrhizae benefit from atmospheric CO₂ enrichment will probably depend heavily on the P and N status of both the plant and the symbiont. In general, plant carbon investment to support symbionts is inversely related to soil nutrient availability. Therefore, the increase in proportional allocation to soil fungi in plants growing in CO₂-enriched atmospheres is attributed to the combination of higher photosynthesis along with progressive nutrient limitations that sometimes accompany greater plant biomass production.

How microorganisms help in alleviating abiotic stress

Besides developing mechanisms for stress tolerance, microorganisms can also impart some degree of tolerance to plants towards abiotic stresses like drought, chilling injury, salinity, metal toxicity and high temperature. Bacteria belonging to different genera including *Rhizobium*, *Bacillus*, *Pseudomonas*, *Pantoea*, *Paenibacillus*, *Burkholderia*, *Achromobacter*, *Azospirillum*, *Microbacterium*, *Methylobacterium*, *Variovorax*, *Enterobacter* etc. have been reported to provide tolerance to host plants under different abiotic stress environments. Use of these microorganisms per se can alleviate stresses in agriculture thus opening a new and emerging application of microorganisms.



Role of microorganisms in alleviating abiotic stress

A variety of mechanisms have been proposed behind microbial elicited stress tolerance in plants.

IAA:- IAA synthesized by bacteria may be involved at different levels in plant-bacterial interactions. In particular, plant growth promotion and root nodulation are both affected by IAA. The role of IAA that was synthesized by the *Pseudomonas putida* GR12-2 in the development of canola roots was studied following the construction of an IAA-deficient mutant of this strain. Seed inoculation with wild-type *P. putida* GR12-2 induced the formation of roots that were 35–50% longer than the roots from seeds treated with the IAA-deficient mutant and the roots from uninoculated seeds. Inoculation of mung bean cuttings with a mutant of the same strain, which overproduces IAA, yielded a much greater number of shorter roots compared with controls. This result was explained by the combined effect of auxin on growth promotion and inhibition of root elongation by ethylene. The bacterial IAA that was incorporated by the plant stimulated the activity of the enzyme ACC synthase, resulting in increased synthesis of ACC, and a subsequent rise in ethylene that inhibited root elongation. Overall, bacterial IAA increases root surface area and length, and thereby provides the plant has greater access to soil nutrients. In addition, bacterial IAA loosens plant cell walls and as a result facilitates an increasing amount of root exudation that provides additional nutrients to support the growth of rhizosphere bacteria.

Cytokinin:- Cytokinins are compounds with a structure resembling adenine that are named based on their ability to promote cytokinesis or cell division in plants. They are produced by plants, some yeast strains and by a number of soil bacteria. Transgenic plants that overproduce cytokinins, especially during periods of abiotic stress, are significantly protected from the deleterious effects of those stresses. Some microbial strains produce cytokinin and antioxidants, which result in abscisic acid (ABA) accumulation and degradation of reactive oxygen species. Isopentenyladenine (iP) is secreted by *Paenibacillus polymyxa* in stationary phase. Isopentenyladenine riboside (iPR) and some additional cytokinin-like substances are secreted by yeast. Other rhizobacteria in which cytokinin secretion are detected are *Azotobacter* spp., *Rhizobium* spp., *Pantoea agglomerans*, *Rhodospirillum rubrum*, *Pseudomonas fluorescens*, *Bacillus subtilis*.

Ethylene:- The plant hormone ethylene is one of the simplest molecules with biological activity. *Achromobacter piechaudii* ARV8 which produced 1-aminocyclopropane-1-carboxylate (ACC) deaminase, conferred IST against drought and salt in pepper and tomato (Mayak et al. 2004). Many aspects of plant life are regulated by ethylene levels and the biosynthesis of ethylene is subjected to tight regulation, involving transcriptional and post-transcriptional factors regulated by environmental cues, including biotic and abiotic stresses (Hardoim et al. 2008). In the biosynthetic pathway of ethylene, S-adenosylmethionine (S-AdoMet) is converted by 1-aminocyclopropane-1-carboxylate synthase (ACS) to 1-aminocyclopropane-1-carboxylate (ACC), the immediate precursor of ethylene. Under stress conditions, the plant hormone ethylene endogenously regulates plant homeostasis and results in reduced root and shoot growth. In the presence of ACC deaminase producing bacteria, plant ACC is sequestered and degraded by bacterial cells to supply nitrogen and energy. Furthermore, by removing ACC, the bacteria reduce the deleterious effect of ethylene, ameliorating plant stress and promoting plant growth (Glick 2007). Saleem et al. (2007) have reviewed the role of microorganisms containing ACC deaminase, in stress agriculture. Inoculation with ACC deaminase containing bacteria induce longer roots which might be helpful in the uptake of relatively more water from deep soil under drought stress conditions, thus increasing water use efficiency of the plants under drought conditions.

Antioxidant enzymes:- Antioxidant enzymes secreted by rhizobacteria and fungi are

1. Catalase
2. Super oxide dismutase
3. Peroxidase
4. Glutathion reductase

These enzymes scavenges the ROS which is accumulated during stress condition.

Osmolytes:- Under stress condition rhizobacteria produce osmolytes such as potassium, glutamate, trehalose, proline, glycine, betanine etc. These osmolytes help in survival of bacteria under stress condition. Proline protects membranes and proteins against the adverse effects of high concentration of inorganic ions and temperature extremes. It also functions as a protein-compatible hydrotope, and as a hydroxyl radical scavenger. Trehalose is a nonreducing disaccharide, an α -1,1-glucoside, consisting of two molecules of α -glucose, that is widely distributed in nature. It is found in bacteria, yeast, fungi, plants, insects, and invertebrates. High levels of trehalose can act as a protectant against several different abiotic stresses including drought, high salt, and extremes of temperature. Trehalose, a highly stable molecule that is resistant to both acid and high temperature and can form a gel phase as cells dehydrate, replacing water and, as a result, decreasing damage from drought and salt. In addition, trehalose can prevent some of the protein degradation and aggregation that often occurs under both high and low temperature stresses.

Gene involved in alleviation of abiotic stress

- ❖ HKT gene --regulated by bacterial VOC
- ❖ AcdS gene--responsible for encoding ACC deaminase enzyme which is 650bp long.
- ❖ Drought stress Responsive genes– Which results in dehydration- responsive element binding protein (DREB2A), catalase (CAT1), and dehydrin (DHN) are found in bacteria.
- ❖ proBA gene derived from *Bacillus* sp. is responsible for proline accumulation in transgenic plants.

ERD gene:- The ERD genes are defined as those genes that are rapidly activated during drought stress. The encoded proteins show a great structural and functional diversity and constitute the first line of defense against drought stress in plants. To date, a total of 16 complementary DNAs (cDNAs) for ERD genes have been isolated from 1-h-dehydrated *Arabidopsis thaliana* and only half of these are characterized in soybean. These genes encode proteins that include ClpA/B adenosine triphosphate (ATP)-dependent protease, heat shock protein (HSP) 70-1, S-adenosyl-methionine-dependent methyltransferases, membrane protein, proline dehydrogenase, sugar transporter, senescence-related gene, glutathione-S-transferase, group II LEA (Late Embryogenesis Abundant) protein, chloroplast and jasmonic acid biosynthesis protein, hydrophilic protein, and ubiquitin extension protein.

Timmusk and Wagner (1999) were among the firsts to show that inoculation of *Paenibacillus polymyxa* confers drought tolerance in *A. thaliana* through the induction of drought responsive gene, ERD15 (EARLY RESPONSE TO DEHYDRATION 15). ERD15 from *Arabidopsis* has been functionally characterized as a common regulator of the abscisic acid (ABA) response and salicylic acid (SA)-dependent defense pathway [35]. Overexpression of ERD15 reduced ABA

sensitivity, as the transgenic plants had reduced drought tolerance and failed to increase their freezing tolerance in response to hormone treatment [35]. In contrast, loss of ERD15 function due to gene silencing caused hypersensitivity to ABA, and the silenced plants displayed enhanced tolerance to both drought and freezing. Inoculation of *Azospirillum brasilense* Sp245 in wheat (*Triticum aestivum*) under drought stress resulted in a better water status and an additional “elastic adjustment” resulting in better grain yield and mineral quality (Mg, K and Ca) at harvest.

Exopolysaccharide:- Microbial polysaccharides can bind soil particles to form microaggregates and macroaggregates. Plant roots and fungal hyphae fit in the pores between microaggregates and thus stabilize macroaggregates. The complex and dynamic interactions among microorganisms, roots, soil and water in the rhizosphere induce changes in physicochemical and structural properties of the soil. Plants treated with EPS producing bacteria display increased resistance to water stress due to improved soil structure (Sandhya et al. 2009). EPS can also bind to cations including Na, thus making it unavailable to plants under saline conditions. Chen et al. (2007) correlated proline accumulation with drought and salt tolerance in plants. Introduction of proBA genes derived from *Bacillus subtilis* into *A. thaliana* resulted in production of higher levels of free proline resulting in increased tolerance to osmotic stress in the transgenic plants. Increased production of proline along with decreased electrolyte leakage, maintenance of relative water content of leaves and selective uptake of K ions resulted in salt tolerance in *Zea mays* coinoculated with Rhizobium and Pseudomonas (Bano and Fatima 2009). Proline protects membranes and proteins against the adverse effects of high concentration of inorganic ions and temperature extremes.

References (if any)

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