



Prof. S. Kannaiyan Memorial Oration-Series:12

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Delivered during

**Inaugural Function of 14th NABS-National Conference on
"Innovations in Biology and Biotechnology
for their Application in Agriculture and
Animal Sciences for Food Security"**

held at

**Agricultural College and Research Institute,
Kudumiyanmalai
Tamil Nadu Agricultural University
on 28 January, 2025**



Pramod W. Ramteke

*Department of Molecular Biology & Genetic Engineering
RTM Nagpur University, Nagpur*

Topic of Oration:

Microbial Biotechnologies in Sustainable Agriculture

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I am deeply humbled and honored to receive the most prestigious and coveted **Prof. S. Kannaiyan Memorial NABS-Lifetime Achievement Award** for the year 2024. I would like to express my gratitude especially to NABS Executive Committee and all the members of NABS. Thank you for bestowing me with such an honour and this special award. This award solidifies my beliefs and inspires me to work even harder and motivates me to continue striving for excellence in all my endeavors.

Prof. S. Kannaiyan is a renowned world famous scientist in Agricultural Microbiology and Biotechnology. In addition to Founding Member of NABS, he has been former Vice - Chancellor of Tamil Nadu Agricultural University, Coimbatore and Chairman of National Biodiversity Authority, Govt. of India. His outstanding scientific contributions are remarkable and have been inspiration to many. However, I stand nowhere near to Prof. S. Kannaiyan.

Over the years I had an opportunity to work in the area agricultural microbiology and biotechnology and here I would like to share some of my work in the following paragraphs.

Introduction

Frequent famine had been a recurrent feature of life in India. During 1964–66, India experienced two severe droughts which led to food shortages and famines among the country's growing population. In India, the green revolution was launched under the guidance of geneticist Prof. M. S. Swaminathan, Father of the Green Revolution in India. This period was part of the larger Green Revolution endeavor initiated by Norman Borlaug, which leveraged agricultural research and technology to increase agricultural productivity in the developing world. It helped in increasing food production in the country. The green revolution's primary aim was to introduce high-yielding varieties (HYVs) of cereals to alleviate poverty and malnutrition. Not to deny, the green revolution was capable of mitigating hunger and malnutrition in the short term. After the green revolution, the production of cereal crops tripled with only a 30% increase in the land area cultivated. The green revolution helped India move from a state of importing grains to a state of self-sufficiency.

Although for around 30 years there was an increase in the production of crops, the rice yield became stagnant and further dropped to 1.13% in the period from 1995 to 1996. Similarly with wheat, production declined due to the decrease in its genetic potential and monoculture cropping pattern. The productivity of potato, cotton, and sugarcane also became stagnant. During the post-green revolution period, several notable negative impacts arose. Excessive and inappropriate use of fertilizers and pesticides polluted waterways and killed beneficial insects and wildlife. It has caused over-use of soil and rapidly depleted its nutrients. The rampant irrigation practices led to eventual soil degradation. Groundwater practices have fallen dramatically. Further, heavy dependence on few major crops has led to the loss of biodiversity of farmers and the increase of stubble burning cases since 1980. These problems were aggravated due to the absence of training to use modern technology and vast illiteracy leading to excessive use of chemicals.

In the years since Green Revolution was adopted, issues of sustainability have come up due to the adverse environmental and social impacts. Globally, agriculture is on an unsustainable track and has a high ecological footprint now. The green revolution, which was beneficial in ensuring food security, has unintended but harmful consequences on agriculture and human health. Therefore, adoption of organic ways of farming is a need for sustainable agricultural practices.

Climate change, driven by human activities has emerged the biggest global challenges of our time. As temperatures rise and weather patterns become increasingly erratic, we face several challenges as a society. India, being a predominantly agrarian economy, faces the adverse effects of climate change in the agricultural sector. One of the major implications of

climate change is global warming due to the accumulation of greenhouse gases in the atmosphere. The enhanced greenhouse effect leads to rising temperatures and alterations in weather patterns. Climate variability increases the frequency and intensity of extreme weather events like droughts, floods, cyclones, and heatwaves. These events can lead to substantial crop losses and disruption of farming practices. Besides, global warming intensifies extreme weather events, such as floods, cyclones, and heatwaves, leading to devastating implications on crops.

The Indian monsoon, a lifeline for agriculture, is highly sensitive to climate variability. Global warming affects the hydrological cycle, leading to changes in rainfall patterns and the timing of monsoons. Irregular monsoons, have a profound impact on rain-fed agriculture, affecting crop growth, water availability, and overall farm productivity.

The imbalanced water availability also result in depleted water resources for irrigation. The increase in average temperatures adversely affects crops, disrupting their growth, development, and yield potential. Rising temperatures and shifting climatic conditions present a favourable atmosphere for pests, leading to infections and crop damage. The moisture levels changing in a warmer climate also contribute to the emergence and spread of plant diseases. Likewise, floods pose ill-impact of climate change on crop production. They destroy standing crops, wash away fertile topsoil, and promote the spread of diseases, leading to substantial yield losses. Similarly, heatwaves reduce crop productivity, disrupt pollination, and increase water stress.

Besides global warming and climate variability, climate change also triggers environmental imbalance. Increased temperature and changing rainfall patterns

can also result in soil degradation. Erosion, nutrient depletion, and compaction are reasons for soil infertility, which affects crop growth and yield potential. Additionally, the rise in temperature enhances the evaporation rate, leading to increased soil moisture stress.

Environmental changes and expanding agricultural areas lead to biodiversity loss, which refers to the decline in the variety and abundance of species in ecosystems. The result is the loss of genetic diversity in crops, disruption of pollination, and imbalanced ecosystem services. Besides, biodiversity loss also increases pest and disease pressure, which affects soil health and nutrient cycling. All these factors pose a negative impact on agricultural productivity, resilience, and sustainability. The combined effects of global warming, climate variability, and environmental changes have resulted in several challenges for farming practices. Changing climate conditions and extreme weather events often lead to decreased crop yields, affecting food security and livelihoods for millions of farmers; pushing farmers into a cycle of poverty and debt.

To meet global food demand, food production must be doubled by 2050. At this crucial time, there is a pressing need to transition to more sustainable crop production practices, ones that concentrate more on promoting sustainable mechanisms, which enable crops to grow well in resource limited and environmentally challenging environments, and also develop crops with greater resource use efficiency that have optimum sustainable yields across a wider array of environmental conditions. The phytomicrobiome is considered as one of the best strategies; a better alternative for sustainable agriculture, and a viable solution to meet the twin challenges of global food security and

environmental stability (Ramteke, 2013; Kumar *et al.*, 2019; Sagar *et al.*, 2021; Chakraborty and Ramteke *et al.*, 2023). Use of the phytomicrobiome, due to its sustainable and environmentally friendly mechanisms of plant growth promotion, is becoming more widespread in the agricultural systems.

Isolation and characterization of Plant Growth Promoting Bacteria (PGPB)

From different rhizospheres bacterial with various plant growth promoting (PGP) traits were isolated. PGPB were isolated from rhizospheres of sugarcane (Parihar *et al.*, 2003), pigeon pea (Ramteke *et al.*, 2012; Singh *et al.*, 2013), maize (Kumari *et al.*, 2017) and sweet potato (Bordé-Pavlicz *et al.*, 2024); and medicinal plants *Withania somnifera* (Rathur *et al.*, 2012) and *Andrographis paniculata* (Tobit *et al.*, 2017). Also, PGPB were isolated from organic farm (Sagar *et al.*, 2017) sodic soil (Hafeez *et al.*, 2018) and sewage irrigated soils (Ramteke *et al.*, 2012; Singh *et al.*, 2014).

We observe rich bacterial diversity both in terms of their types and functional (PGP) traits. Bacterial diversity is represented by heterotrophs, coliforms (Sagar *et al.*, 2017), *Bacillus thuringensis* (Anandhi *et al.*, 2013); *Azotobacter* (Hafeez *et al.*, 2018; Reddy *et al.*, 2018, Sagar *et al.*, 2022), *Pseudomonas* spp. (Singh *et al.*, (2014, Zhumakayev *et al.*, 2022); *Rhizobium* (Singh **et al.**, 2013), *Bacillus* spp (Singh *et al.*, 2013, Sagar *et al.*, 2022, Bordé-Pavlicz *et al.*, 2024), *Enterobacter* spp. (Hafeez *et al.*, 2018; Sagar *et al.*, 2019, 2020); *Azospirillum* sp (Reddy *et al.*, 2018); *Mesorhizobium ciceri* (Pandey *et al.*, 2018) and *Erwinia* Species (Sagar *et al.*, 2018, 2020). Majority of these microorganisms display multiple PGP traits viz. production of ammonia (NH₃) (93.2%), indole acetic acid (IAA) (89.6), catalase (85.0), 1- aminocyclopropane- 1- carboxylate deaminase (ACCD) (78.6%), Hydrogen

Cyanide (73%) siderophore (69.0%); and Phosphate and potassium solubilizing activity. Richness of their functional characteristics further revealed by their tolerance to salinity and wide range of pH. Most of the isolates were tolerant to > 5 % NaCl and wide range of pH. Furthermore, majority of the nitrogen fixers (96-97%) displayed multiple PGP traits, tolerance to salinity and wide range of pH. Comparative analysis of L-aminocyclopropane-1-carboxylate (ACC) Deaminase (Singh et al., 2015) and production of Hydrogen Cyanide with Production of Siderophore and Phosphate Solubilization activity (Sagar et al., 2018) in PGPB was performed. Additionally, PGPB were tolerant to heavy metals (Rathur et al., 2012; Singh et al., 2013; Tobit et al., 2017), antibiotics (Pandey et al., 2018; Sagar et al., 2020) and UV-B (Rathur et al., 2012). Elimination of plasmid in the organism resulted in the loss of tolerance of heavy metal ions and trace elements, indicating the role of the plasmid in tolerance to heavy metals and antibiotics (Sagar et al., 2020; Pandey et al., 2018). Molecular aspects of symbiotic association between legumes and Rhizobia were extensively highlighted (Pandey et al., 2018).

Siderophore-mediated Fe-scavenging is an essential process in soil ecosystems that improves the bioavailability of iron and promote plant growth and play an important role in pathogen biocontrol. Our studies highlighted biosynthesis pathways, transport mechanisms, and biotechnological applications of fungal siderophores (Dhusia *et al.*, 2020; Kumeera *et al.*, 2021; Pecoraro *et al.*, 2022)

Rhizospheric Metagenomics

Microbial communities of the rhizospheric region undoubtedly play a central role in the nutrient cycling, plant productivity and growth promotion. In order to know how changes in the rhizospheric microbial

community can make an impact on overall crop function, wheat rhizospheric soil samples from three districts were subjected to metagenomic sequencing (Khan et al., 2020; Srivastava et al., 2020; 2021). Metagenome datasets of wheat rhizospheres were deposited in NCBI with accession numbers: 1. Ballia (SRR8468314), 2. Ghazipur (SRR8468865), and 3. Mau (SRR9326128). Also, individual promising bacterial isolates from different rhizosphere were further subjected to molecular characterization and 653 gene sequences deposited in NCBI.

PGPB assisted Crop Growth Promotion

Enhancement of growth and yield parameters of several crops employing PGPB both in the laboratory and field conditions was evaluated. Crops included wheat (Sagar et al., 2018), rice (Sagar et al., 2019), maize (Sagar et al., 2022), tomato (Reddy *et al.*, 2018; Rajput and Ramteke 2019), Cauliflower (Kumari *et al.*, 2017) and Kalmegh (Tobit *et al.*, V., 2017). Abiotic stress is a major deterrent to agricultural production. Under different stress conditions enhancement of growth and yield of crops employing PGPB both in the laboratory and field conditions was evaluated. Effect of PGPB on growth and yield of crops studied were: pH Stress Durum Wheat (Laloo *et al.*, 2017); drought stress Okra (Yadav et al., 2018); and salinity stress rice and millets (Sagar *et al.*, 2020). Also, we studied synergistic effect of PGPB on wheat under reduced level of NPK (Sagar *et al.*, 2018; 2020).

Plant Pathogens and PGPM as Biocontrol Agents

Citrus is the third most important fruit crop in India after mango and banana. Citrus greening (also known as HLB) caused by ‘*Candidatus Liberibacter*’, a noncultured, gram negative bacterium is a destructive disease of citrus worldwide including India. The study

was conducted to analyze molecular variability among the HLB isolates in different citrus species based on the nucleotide sequence analysis of the part of *rplA*-*rplJ* operon of 50S ribosomal protein gene sub-units (*rplA*-*rplJ*). The sequence analysis revealed that all isolates were closely related to 'Candidatus *Liberibacter asiaticus*' irrespective of their host. To our knowledge, this is the first study reporting the sequence analysis of ribosomal protein gene (*rplA*-*rplJ*) of 'Ca. *L. asiaticus*' infecting different citrus cultivars in western Maharashtra region (Bhose *et al.*, 2015). Additionally, nitrocellulose membrane (NCM) based DNA extraction method for simultaneous detection of *citrus mosaic badnavirus* (CMBV) and *Candidatus Liberibacter asiaticus* by duplex PCR was developed (Motghare *et al.*, 2017).

Karnal bunt (KB) of wheat is an internationally quarantined fungal pathogen disease caused by *Tilletia indica* (Ti) and affects the international commercial seed trade of wheat. We announce here the first improved draft genome (PKQB01000000) assembly of a monoteliosporic culture of the Ti fungus, consisting of 787 scaffolds with an approximate total genome size of 31.83 Mbp, which is more accurate and near to complete than the previous version (Kumar *et al.*, 2018). Also comparative genomic analysis of monosporidial and monoteliosporic cultures for unraveling the complexity of molecular pathogenesis of Ti pathogen of wheat was performed (Mishra *et al.*, 2019). The availability of a near-complete, more accurate, and nonredundant genome sequence serves as baseline data to provide ample opportunities to understand the pathogenic mechanisms as the model for the identification of the fungal pathogenic determinants involved in disease development, which will be used for devising effective crop protection strategies as part of the development of resistant wheat cultivars showing immunity against KB.

The use of *Trichoderma* isolates with efficient antagonistic activity represents a potentially effective and alternative disease management strategy to replace health hazardous chemical control. In this context, twenty isolates showing antagonistic activity against four fungal pathogens viz. *Fusarium oxysporum* f. sp. *lycopersici*, *Alternaria alternata*, *Colletotrichum gloeosporoides* and *Rhizoctonia solani* were studied for diversity analysis and comparative analysis of microsatellites (Rai et al., 2016; Rai et al., 2016a; 2019). *ERG-1* gene, encoding a squalene epoxidase has been used for the first time for diversity analysis. Phylogenetic analysis of *ERG-1* gene sequences also indicated the possibility of occurrence of squalene epoxidase driven triterpene biosynthesis as an alternative biocontrol mechanism in *Trichoderma* species.

Bacterial antagonistic potential of several isolates against plant diseases were evaluated. Native *Bacillus thuringiensis* (Berliner) isolates from diverse habitats showed wide spectrum of activities against cruciferous pastes (Anandhi et al., 2013). Antagonistic activity against phytopathogenic fungi *Fusarium oxysporum* was shown by *Mesorhizobium ciceri* (Pandey et al., 2018) and *Pseudomonas* spp, (Matikhaye et al., 2021). Glyphosate-tolerant *Pseudomonas resinovorans* SZMC 25872 strain showed antagonistic potential against the plant pathogenic bacterium *Agrobacterium tumefaciens* (Zhumakayev et al., 2022). Suppression of bacterial wilt of tomato (*Lycopersicon esculentum* Mill.) by PGRB was observed (Afaque et al., 2016; 2017).

***Azolla* as biofertilizer**

Due to high productivity, nitrogen fixation and photosynthesis, *Azolla* is important as biofertilizer in rice cultivation. Besides the plant has several other

uses such as green manure, fish and animal feed, water purifier and hydrogen gas producer. Increasing soil salinity is however, serious impediment in the popularization of *Azolla* as biofertilizer. However, there have been no attempts to understand the effect of salinity on the physiological, biochemical and molecular response of the plant. Our results offer new insights on the response of *A. microphylla* and *A. caroliniana* to salinity (Yadav et al., 2016; 2019; 2022). The results demonstrates significant differences with respect to the physiological attributes, antioxidant enzymes, nitrogen fixation and regulation of ion content and fluxes. Involvement of up regulation of important proteins related to protein synthesis and cell signaling was noted to adapt to short term salinity exposure.

Conclusion

As long as the human population continues to increase, the world will have to withstand the escalating demand for food. Considering the good impact of PGPR in terms of biofertilization, biocontrol, and bioremediation, all of which exert a positive influence on crop productivity and ecosystem functioning, encouragement should be given to its implementation in agriculture. Hoping for the betterment of technology in developing successful research and development, PGPR use will surely become a reality and will be instrumental to crucial processes that ensure the stability and productivity of agroecosystems, thus leading us towards an ideal agricultural system.

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I proudly accept this honour on behalf of every member of my team. I gratefully acknowledge the hard work, dedication, and sacrifices of all my students who were part of this work.

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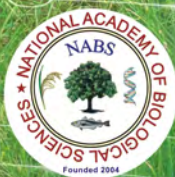
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National Academy of Biological Sciences

NABS-Secretariat, Room No. 209, Second Floor
CAS in Botany, University of Madras, Guindy Campus
Chennai- 600 025, Tamil Nadu, India Mobile: +91-94436 73155
E-mail : secretarynabs@gmail.com Visit : www.nabsindia.org

