

Dr. Sishta Venkata Seetharama Shastry

Memorial Lecture - 2021



“Rice Improvement: New Breeding Technologies”

by

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Dr. Sishta Venkata Seetharama Shastry (1928 – 2019)

Dr. S.V.S. Shastry was born on 4th November 1928. His early education was in Guntur and Peddapuram, Bachelor's degree from Agriculture College, Bapatla and his Master of Science and Doctoral degree from University of Wisconsin in 1958. He started his career as Assistant Professor (Cytogenetics) in 1958-61 and Botanist, 1961-1966 at the Indian Agricultural Research Institute (IARI), New Delhi. His research spanned wide range of subjects including Cytogenetics, Taxonomy, Genetics, Plant Breeding, Physiology, Crop Science, Agronomy, Extension and Development.



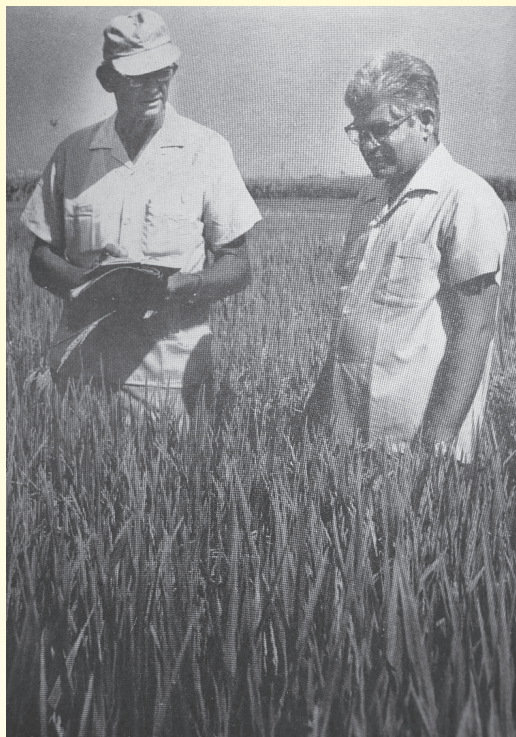
He took over as the Project Coordinator (Rice) in 1966 and served till 1975. He developed high yielding rice varieties namely Jaya, Phalguna, Prakash and Sona. All of these varieties were very popular among the farmers and noteworthy among these is Jaya, which is still popular with the farmers. Later on, he joined as Senior Agricultural Officer, Agricultural Production and Protection and then as Executive Secretary, International Rice Commission, F.A.O., Rome from 1975-1977. He served as Director of Research, International Institute of Tropical Agriculture (IITA), Nigeria from 1977-1983. He also served as the Honorary Trustee and Vice-Chairman of the Programme Committee of IRRI during 1970-73 and Chairman, Steering committee and Member, Scientific and Technical Committee, West Africa Rice Development Association (WARDA) from 1977-82. Recognising his monumental contributions in the area of science and technology especially in rice research, the President of India honoured him with the Padma Shri award in 1971. He has also been bestowed with several awards including Borlaug Award, 1974; Janna Reddy Venkatareddy Prize, 1974; Tonnage Club Medal, 1974; West Godavari Farmers' Trophy, 1975. He was elected as Fellow of two prestigious science academies of India namely Indian National Science Academy (INSA) and National Academy of Agricultural Sciences (NAAS). He had a pleasing personality and has been a role model for many of us and future generation of rice workers.

Seminal contributions of Dr. SVS Shastry in rice

Taking forward the expertise gained on pachytene analysis in *Melilotus* species at the University of Wisconsin, he published the seminal report on the pachytene stage of rice chromosomes (Shastry et al., 1960). He published a series of papers on cytology of cultivated and wild species, their interspecific hybrids and re-interpretation of species relationships in the genus, *Oryza* (Shastry and Mishra, 1961; Shastry *et al.*, 1961; Shastry

and Rang Rao, 1961; Shastry 1964a, b). Through his exhaustive biosystematic analysis, he could delineate two new species of *Oryza* namely, *Oryza nivara* and *O. collina* (Sharma & Shastry 1965a, b). Based on their studies, they proposed that *O. nivara* is the progenitor of cultivated rice (Shastry and Sharma, 1973). One of the collections of *O. nivara* was found to be resistant to grassy stunt virus disease of rice at International Rice Research Institute (IRRI), Philippines which helped the development of grassy stunt virus resistant rice varieties.

Through his futuristic vision, he has been instrumental in planning and establishment of the then All Indian Coordinated Rice Improvement Project (AICRIP) at Rajendranagar, Hyderabad which later evolved as Directorate of Rice Research



Dr Wayne Freeman and Dr S V S Shastry



**First Review meeting in 1967 with AICRIP Cooperators
(Dr S V S Shastry, Dr Wayne Freeman and Dr D V Sheshu)**

(DRR). The state-of-the-art rice quality lab and glass house facilities developed by him at the present day ICAR-Indian Rice Research Institute (ICAR-IIRR) is a standing testimony of his monumental contribution for the rice fraternity as outstanding researcher and administrator.

“Rice Improvement: New Breeding Technologies”

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It is a great privilege for me to be invited to deliver the Dr. S.V.S. Shastry Memorial Lecture of 2021 at the ICAR-Indian Institute of Rice Research (ICAR-IIRR). I express my sincere gratitude to the Director and Organizing Committee, ICAR-Indian Institute of Rice Research (ICAR-IIRR) and Society for Advancement of Rice Research (SARR), Hyderabad for inviting me on this important occasion of Foundation Day of ICAR-IIRR. I am honored to be the part of the lecture series, which have been delivered by eminent scientists and great personalities associated with rice research in the past. The fact that I represent the ‘Rice Community’ makes me even more conscious of this honour. Connecting today’s challenges of agriculture with the vision of Dr. S.V.S. Shastry, there cannot be a better subject than improving rice production and productivity through new breeding technologies. I feel proud and humble in delivering the lecture as a tribute to the eminent rice researcher, visionary, leader, and the first Project Coordinator of All India Coordinated Rice Improvement Project (AICRIP), Dr. S.V.S. Shastry.

Rice being the primary staple food crop is grown in more than 150 million hectares globally and India occupies nearly 1/3rd of global area (i.e. 44 million hectares). However, the production of rice in India (~ 120 million tonnes) is approximately 1/5th of global rice production (~ 503 million tonnes). Globally, our country ranks first in area and 2nd in production of rice. Rice is not only calorie source of more than >70% of population in India, but also a major livelihood for millions of farmers. This one cereal crop has helped India to achieve food security from a situation of hunger, starvations, and famines immediately after the independence. The rice production in India after independence was ~20.5 million tonnes from the cultivated area of ~31 m hectares. The estimate of rice production in India for 2020-21 is 120.32 million tons. The innovations in agriculture, appropriate scientific interventions, quality seeds, better management practices, government policies together with the hard work of Indian farmers helped India to attain goal of not only self-sufficiency in food production, but also a major exporter of agriculture commodities. Despite huge domestic consumption, India exports ~17.73 million tons of rice worth Rs. 65326/- crores.

A total of 1436 improved rice varieties including 127 hybrids have been released from public and private sectors of India, till June 2021. In this regard, the All India Coordinated Rice Improvement Project (AICRIP) has played a central role in not only systematic

evaluation of entries/genotypes but also in spreading/extension of the improved genetic material to the remote places and adverse ecologies, where breeders could use these lines for improvement of the cultivars grown and adapted to local ecologies. Despite appreciable gain in production of rice, the productivity (yield kg/ha) has been a major concern. With an exception of last 3-4 years, the country is witnessing stagnation during the last two decades, as far as rice productivity is concerned. This could be partly due to the favourable climatic conditions in last 3-4 years along with the introduction of new agriculture technologies.

There is great disparity of rice productivity in different states of India. It ranges from 1.70 t/ha in Mizoram to 4.03 t/ha in Punjab. In addition, the productivity of states occupying significant area under rice cultivation, i.e. UP, West Bengal, Assam, Bihar, Chhattisgarh, Odisha, and M.P (total 25.22 mha) is a matter of concern. While, this can be attributed to the adverse ecosystems and problematic soil/ecologies, e.g. upland, rainfed lowland, hills, deep water, saline, acidic, and alkaline soils in the above mentioned states, it also indicated an opportunity for improvement through development of improved rice varieties and hybrids suited to these stress prone ecologies.

Rice is the first crop genome which was sequenced in 2005 and I was the part of -International Rice Genome Sequencing Project (IRGSP) from NIPB, those days NRCPB. It is among very few multi-national plant genome sequencing efforts where Indian flag was depicted on chromosome 11 along with flags of several other countries shown on the different chromosomes of rice. Since then, the progress in rice genome sequencing and genomics and other 'omics' sciences have been tremendous. In 2011, 40 cultivated accessions and 10 accessions of *Oryza rufipogon* and *Oryza nivara* were re-sequenced to discover markers and genetic variants of agronomically important genes (Xu et al, 2011). Another landmark in this area was re-sequencing of 3,000 rice accessions from 89 countries (Wang et al, 2018,). This information is being used by rice researchers for the discovery of novel alleles and deploying them for developing novel breeding materials and varieties. Later, several efforts were made to sequence the wild rice relatives, basmati, aromatic, and coloured rice etc. Some of the recent advancements like re-sequencing of 1,143 indica rice accessions (Lv et al, 2020) have helped in developing indica genome based SNP markers for trait improvement. In another such development, International Rice Research Institute (IRRI), Chinese Academy of Agricultural Science (CAAS), and Beijing Genomics Institute (BGI) have joined hands to sequence 10000 rice accessions under the "Rice 10,000 Genome Project". This will not only reveal the global diversity of rice but also help immensely the breeding programs. The massive data generated from sequencing of DNA and RNA of rice is being managed by several databases like-Rice Annotation Project Data Base (RAP-DB), Gramene, RPAN: Rice Pan-genome Browser, and Rice Expression Profile Database (RiceXPro) etc. These databases help in retrieving the genes, markers,

and protein information. These databases are highly useful in structural and functional genomics of rice.

I understand and appreciate the fact that ICAR-IIRR, a premier national institute under ICAR has developed very useful genomic resources of rice. More than 30 mapping populations for yield, phosphorus use efficiency, nitrogen use efficiency, high grain Fe/Zn, bacterial blight, blast, sheath blight resistance; brown plant hopper and leaf folder resistance etc. are precious resources for QTL/gene mapping, cloning, functional analysis and breeding programs. Ethyl methane sulfonate (EMS) induced mutants of BPT5204 and Nagina 22 are useful genetic resources for gene discovery and development of novel phenotypes/traits. Similarly, chromosome segment substitution lines (CSSLs) derived from wild rice species developed at ICAR-IIRR are national genetic resource of rice. These lines can be used to tap the useful genes of wild rice species, their functional analysis and utilization in breeding programs for development of climate resilient rice genotypes. ICAR-IIRR has also generated genome and transcriptome sequences of several rice cultivars and cloned more than 22 genes. Functional characterization of these genes in near future will enable breeders to use them in breeding programs.

Another important area of rice research, which has made significant dent in the last decade is the development and utilization of genetic markers in rice. Since 1980s, various DNA marker technologies have progressed from restriction fragment length polymorphism (RFLP) and randomly amplified polymorphic DNA (RAPD) to high-throughput next-generation sequencing technologies that have facilitated the development of large quantities of single-nucleotide polymorphism (SNP) markers along with simple-to-use PCR based functional markers. Till date, 46 genes conferring resistance against different strains of the bacterial blight pathogen and more than 100 genes conferring resistance against blast pathogen are available. Among these, the genes identified for bacterial leaf blight resistance (*Xa1*, *Xa2*, *Xa3*, *Xa4*, *Xa5*, *Xa10*, *Xa13*, *Xa21*, *Xa33*, *Xa38*), blast resistance (*Pi-1*, *Pi 2*, *Pi 4(t)*, *Pi 5*, *Piz-5*, *Pi 5(t)*, *Pi 7*, *(t)*, *Pi 10 (t)*, *Pi-b*, *Pi54*, *Pi21*, *Pia Pi1*, *Pi2*, *Pi54*, *Pi40*, *Pi9*, *Pi5*, *Pita*, *Pizt*, *Pi68*), and sheath blight resistance QTLs (*qShB1*, *qShB2-1*, *qSB5*, *qShB6*, *qShB9-2*) are being used extensively in disease resistance breeding programs. Among insect resistance genes, 11 Gall midge resistance genes (*Gm1*, *Gm2*, *Gm4(t)*, *Gm5(t)*, *Gm6(t)*, *Gm7(t)*, *Gm8(t)*, *Gm9(t)*, *Gm10(t)*, *Gm11(t)*), 35 Brown Planthopper resistance genes (*Bph1*, *Bph2*, *Bph3*, *Bph4*, *Bph5*, *Bph6*, *Bph7*, *Bph8*, *Bph9*, *Bph10(t)*, *Bph20(t)*, *Bph21(t)*, *Bph12(t)*, *Bph13(t)*, *Bph14*, (*Qbp1*) and *Bph15 (Qbp2)*, *Bph33t*) and GLH resistance genes (*Glh-1*, *Glh-2*, *Glh-3*, *Glh-4*, *Glh-5*, *Glh-6*, *Glh-7*, *Glh-8*, *Grh4*, *Grh2*) have been identified. We were the first to map and clone a major gene *Pi54* for rice blast resistance in 2005 (Sharma et al, 2005). This gene being effective against many strains of *Magnaporthe oryzae*, has been

used in marker assisted selection. This gene has already been transferred in more than 40 varieties of rice using MAS and has created a silent revolution in rice breeding program. Some of these genes are widely used in India and abroad for breeding them into the many susceptible rice cultivars and hybrids with the help of DNA markers and I am happy to note that ICAR-IIRR has fine-mapped, cloned and characterized a few of these genes/QTLs, thus expanding the repertoire of genes/QTLs available for improvement through marker-assisted breeding (MAB).

The wild relatives of rice are an important source of agronomically useful traits that have been extensively used in rice improvement programs. India being the centre of origin for rice, has large diversity of wild accessions collected and preserved in different institutes such as NBPGR, New Delhi, ICAR-IIRR, Hyderabad, ICAR-NRRI, Cuttack and in a few state agricultural Universities such as IGKV, Raipur etc. Several important genes such as *Xa21*, *Xa23*, *GS*, *Xa38*, *Xa29(t)*, *Xa27*, *Pi9*, *Pi40*, *bph11*, *bph12*, *Bph14*, *Bph15*, *Bph20*, *Bph21*, *Bph10*, *Bph18*, *Wbph7(t)*, *Wbph8(t)*, WA cytoplasm were identified from wild rice accessions. I am very happy to note that ICAR-IIRR has a well-structured programme to rapidly develop and evaluate wild rice derived introgression lines for various traits like resistance against bacterial blight, blast, BPH, sheath blight, DSR-related and yield related traits.

The progress of research related to development and utilization of molecular markers in India has been spectacular and more than 43 marker-assisted selection (MAS) derived varieties have been developed for resistance/tolerance to various biotic and abiotic stresses. These include, for bacterial blight resistance (Improved Samba Mahsuri, Improved Pusa Basmati 1, DRR Dhan 53, DRR Dhan 59, Improved Lalat, Improved Tapaswini etc.), blast resistance (DRR Dhan 51, PRR78), bacterial blight and blast resistance (DRR Dhan 62), submergence tolerance (Swarna Sub1, Ranjit Sub1, Bahadur Sub1, CR1009 Sub1 etc.), drought tolerance (DRR Dhan 42), drought and submergence tolerance (DRR Dhan 50), bacterial blight and salinity tolerant (DRR Dhan 58) & bacterial blight and low P tolerance (DRR Dhan 60). I understand that ICAR-IIRR and ICAR-IARI, New Delhi have contributed significantly in this area and has developed a number of MAS derived varieties.

Along with the food security, nutritional security is very critical for development of the country. Genetic engineering is the viable approach for enhancing nutrients in rice. Golden Rice to help combat vitamin A deficiency has been recently approved for commercial cultivation in Philippines in 2021. Golden rice event GR2E identified for the release was developed by genetic transformation of *Zea mays* phytoene synthase (*psy*) in combination with the *Erwinia uredovora* carotene desaturase (*crtI*). Genetically engineered golden rice has high levels of beta carotene to meet up to 30%-50% of the estimated average requirement of vitamin A in young children of 5-6 years of age. This has been released by

joint efforts of Philippine Rice Research Institute and International Rice Research Institute (IRRI). The Golden Rice was first conceptualized by Ingo Potrykus and Peter Beyer in the late 1980s. Similar to Vitamin A, Fe deficiency is very prevalent in women and children of developing world. In most of the developing world, rice is primarily consumed as staple food, therefore, it is a most desirable target crop for Fe biofortification. Due to accumulation of most of the grain iron in aleurone layer, it is lost after polishing. Therefore, transgenic approach can be one of the pragmatic approach for Fe biofortification of rice. This can be achieved by either over-expression of genes associated in Fe storage, transport, influx, uptake and translocation etc. More than 90 Fe QTLs have been identified over the 12 rice chromosomes. It is necessary to utilize these QTLs in breeding programs aiming Fe biofortification. Unlike Fe, increasing Zinc through breeding approach is very much possible. ICAR-IIRR has developed four high Zn rice varieties possessing high yield and good grain quality (DRR Dhan 45, DRR Dhan 48, DRR Dhan 49 and DRR Dhan 63) for commercial cultivation. I understand that being the coordinating center for consortia research platform (CRP) on biofortification, ICAR-IIRR is playing significant catalytic role in nutritional improvement of not only rice but also other crops like wheat, maize, pearl millet, sorghum and minor millets and these efforts have culminated in development and release of more than 80 biofortified crop varieties.

Genome editing or gene editing, one of the important new breeding tools is the cleanest breeding technology, enabling the most precise modifications in genome. This Nobel prize winning technology is dependent on breaking the double stranded DNA with sequence specific nucleases such as ZFN, TALENs, and Cas9 followed by DNA repair by non-homologous end-joining (NHEJ) or homology-directed repair (HDR) resulting in target nucleotides disruption or insertion, respectively. Clustered regularly interspersed short palindromic repeats (CRISPR)/CRISPR associated (Cas) technology has been widely used for genome editing in recent times. This technology enables specific genetic modifications in a shortest possible time. Besides being highly specific, genome editing does not require continuous expression of foreign elements, therefore, all the reagents can be segregated out after the desired mutations occur. Hence, in all means CRISPR/Cas9 can be considered as a biological mutagen. While cross breeding (including marker-assisted breeding), mutation breeding and transgenic breeding require 6-12 years of time for delivery of final product and release as a commercial cultivar, genome editing makes it possible to breed the new varieties in as early as 3-4 years. The plants derived from ZFN and TALEN technology of genome editing have already been commercialized in USA, e.g. herbicide resistant canola and oleic acid rich soybean. Using CRISPR/Cas9 technology of genome editing, several plants edited for novel traits such as high levels of gamma-aminobutyric acid (GABA)

containing tomato in Japan, waxy corn, non-browning lettuce and mushroom in USA are about to be released soon. In our country also, several research groups are using genome editing for traits improvement and functional genomics. When I served as the director at NABI-Mohali, β -carotene-enriched Cavendish banana was developed using the CRISPR/Cas9. ICAR laboratories are also using genome editing for various traits in different crops. One such collaborative network was developed under the funding of ICAR-NASF and ICAR-IIRR, a network partner, has developed genome edited lines of premium grain quality rice cultivar Samba Mahsuri with durable bacterial blight resistance and high grain number. In future, commercialization of these lines can enhance income of millions of farmers growing Samba Mahsuri, which is an export quality rice variety. Biosafety guidelines for genome edited plant products are still under consideration of DBT, Government of India. While Canada, USA, Columbia, Argentina, Chile, Brazil, Israel, Japan and Australia have deregulated the genome edited crops (specifically where there is no foreign DNA), several Asian and African countries are drafting the regulations. I sincerely hope that the Government will soon implement the simple guidelines developed for evaluation of biosafety aspects and agronomic worth of such genome edited crops

India needs to produce 168 million tons of rice by 2050 to feed the projected 1.62 billion populations. It has to be achieved with reduced land, water, and other resources. Achievement of these targets become more difficult under the new challenges of climate change, deteriorating soil health, emergence of new biotic agents, changing pest and pathogen dynamics, shortage of farm labour and increasing cost of cultivation.

Strategies to address the challenges in rice improvement

- a. Breeding for improvement of yield, grain and nutritional quality, durable stress resistance and nutrient use efficiency in irrigated rice ecosystem through increased application of molecular tools in consonance with conventional breeding and speed breeding.
- b. Application of hybrid rice technology for breaking yield ceiling barriers in irrigated rice through deployment of novel biotechnological tools.
- c. Among ~35000 protein coding genes, only ~800 genes have been cloned and functionally characterized in indica rice. There are several miracle genes/alleles, which need to be uncovered. They need to be cloned and characterized for meeting the global challenges of rice production in near future.
- d. Development of novel crop production and processing technologies for enhancing rice production, improving resource use efficiency and sustainability of DSR, customized mechanization of rice cultivation, developing cultivars and hybrids

suiting DSR and mechanization, thus increasing profits in irrigated ecosystem in the realm of climate change.

- e. Concerted efforts are required to mine alleles and orthologues of important genes in the local rice landraces and wild species.
- f. Evaluation and identification of germplasm lines in which micronutrients like Fe and Zn should be present in the endosperm of the grain.
- g. More efforts are required to identify high protein and resistant starch containing germplasm for utilization in the biofortification project.
- h. More projects are required to be implemented in the NARS system on 'Genome Editing' of rice for different traits.
- i. Development of protection technologies for the holistic management of existing and emerging multiple biotic stresses in irrigated rice
- j. Adoption of novel strategies to accelerate the diffusion of rice technologies among farmers and other stake holders and to assess their impact assessment.
- k. Application of new technologies like AI, IoT, sensors and big data analytics for phenotyping of large population and management of various production and protection technologies.

In conclusion, I would like to mention that application of new technologies in breeding and other disciplines can certainly help us to produce more quantity of rice in a lesser area, using less of water and other resources and in an eco-friendly and sustainably manner. I am sure that ICAR-IIRR will continue to strive towards meeting these objectives in a pragmatic manner. I wish all the staff of ICAR-IIRR, both working and retired staff along with AICRIP partners a very happy Foundation Day.

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Prof. Tilak Raj Sharma, a well-known Plant Molecular Biologist, is presently leading the Indian agriculture sector as Deputy Director General (Crop Science), ICAR, Government of India. Earlier he contributed in the establishment and development of several prominent Indian institutes like National Agri-Food Biotechnology Institute, Mohali (Executive Director), Center of Innovative and Applied Bioprocessing (Chief Executive Officer), National Institute for Plant Biotechnology (Project Director) and Indian Institute of Agricultural Biotechnology (OSD).

He obtained Post Doctorate training on Genome analysis and bioinformatics at University of Alberta, Edmonton, Canada (1994) and Cold Spring Harbor Laboratory, NY, USA (2001 & 2004), and Ph D from CSK HPKVV, Palampur in 1990.

For his outstanding research contributions Dr. Sharma has been Awarded various awards like; University Gold Medal and Certificate of Honour in Ph.D, 1990, Young Scientist Award, NAAS, 1998; ICAR Young Scientist Award (Crop Sciences), 1999; Prof. Umakant Sinha Memorial Award in Biochemistry, Biophysics and Biotechnology, Indian Science Congress Association, 2001; International World Technology Award for Biotechnology (jointly to Int. Rice Genome Sequencing Team) in 2003, DBT National Bioscience Award for Career Development, 2007. NAAS Recognition Award 2008; VASVIK Award 2011, Rafi Ahmed Kidwai Award-ICAR, 2011, NASI-Reliance Industries Platinum Jubilee Award, 2013, J C Bose National Fellowship, 2013 & 2018 and Prof MGK Menon Lecture Award (NASI) 2017., Prof. Bishan Singh Samundari Memorial lecture award (Guru Nanak Dev University Amritsar) -2017-18 and Prof. K.S. Bilgrami Memorial Medal (INSA)-2018.

Dr. Sharma is the fellow of all four national academies viz; Indian National Science Academy, Indian Academy of Sciences, National Academy of Sciences and National Academy of Agricultural Sciences.

His major research interests are in the areas of Genomics and plant disease resistance. Dr. Sharma has contributed extensively to the improvement of rice for over 30 years and cloned a new rice blast resistance gene *Pi54* which has been deployed in more than 40 rice varieties in India and abroad. He has been associated with the decoding of complete genomes of rice, tomato, Pigeon pea, Jute, mango, tea and many plant pathogens. Dr. Sharma has guided 25 Ph.D students in Agricultural Biotechnology. He has published more than 180 research papers, have four patents and associated in the development of three blast resistant rice varieties Pusa 1637, HPR2880, and Pusa Sambha



**Dr. W H Freeman; Dr. D V Sheshu; Dr. S V S Shastry with Dr Norman E Borlaug at
AICRIP Farm, Rajendranagar**

**Society for
Advancement of
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