



Germplasm for enhanced genetic gains in the dry land crops

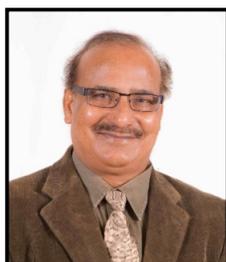
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BIO DATA

Dr. Hari D Upadhyaya is the Head, of the ICRISAT Genebank and Principal Scientist, ICRISAT, India. He is also Adjunct Professor, Department of Agronomy, Kansas State University, Manhattan, USA (2009-till date) and Professor, The University of Western Australia, Institute of Agriculture, Crawley WA 6009, Australia (2014- Contd.).

He is a well-known genetic resources specialist and a successful groundnut breeder with over 37 years of experience. His merit and competence has been recognized worldwide. He has received numerous national awards such as 'Harbhajan Singh Memorial Award' and many international awards including from Crop Science Society of America awards, fellow of the American Society of Agronomy and Crop Science Society of America, the winner of Frank N Meyer Medal award for Plant Genetic Resources, Crop Science Research Award and International Service in Crop Science Award. Dr Upadhyaya was elected Honorary Fellow of Indian Society of Plant Genetic Resources. He was recognized by the Uttar Pradesh Academy of Agricultural Sciences (UPAAS) as Fellow 2017, by the UPAAS for outstanding contribution in the field of Natural Resource Management (Biodiversity). UPAAS also instituted an award in his name as "Hari Deo Upadhyaya Best Agricultural Scientist Award - Germplasm Conservation and utilization". He has published over 830 research papers including several in high impact factor journals including Nature Biotechnology, Proceedings of National Academy of Sciences (USA), Nature Scientific Reports, Journal of Experimental Botany, and Science Advances. His work on conceptualizing and developing mini core collection and utilizing this resource for identifying new sources of variations for climate resilient traits has brought a paradigm shift among germplasm curators and crop breeders about the utility of such resource in identifying new sources of variations for use in crop improvement. The concept and process of developing mini core collection has been recognized in CGIAR systems as an 'International Public Good'. Dr Upadhyaya as groundnut breeder has developed large number of early-maturing, drought tolerant, high oil containing, and aflatoxin resistant high yielding breeding lines, of which 27 has been released as cultivars in 18 countries in Africa and Asia. He has also registered 23 advanced lines as elite genetic stocks with improved characteristics in Crop Science. His seminal work on genetics of wilt resistance, bringing together the two recessive genes which individually delay the wilting result in complete resistance, in chickpea has laid sound breeding program for wilt resistance in chickpea. Dr Upadhyaya is a great mentor, the scientists, students, and technicians from Asia, Africa, Europe and USA have benefitted greatly from scientific rigor and training he has imparted to them. He strongly believes in partnerships and collaborations which enabled him bagged many large-grants in the field of genetic resources and utilization.



Lecture Summary:

Abstracts: Agriculture faces daunting challenges in providing sufficient food, feed, fibre and fuel for a growing population. Adoption of improved technologies including seed, productivity of maize, rice and wheat has been drastically increased, while such a dramatic increase was not observed in the dryland crops. Genetic gain is defined as the annual increase in yield realized through crop breeding. Literature reveals $<1.0 \text{ year}^{-1}$ genetic gains through breeding in many crops. Therefore, there is a need to double the genetic gains in most dryland crops for future global food security. Enhanced genetic gains through use of genetic and genomics resources is the way forward for global food security. Globally, 7.4 million accessions are conserved in about 1,800 genebanks. ICRISAT genebank at Patancheru, India has the largest collection (125,083 accessions) of its mandate crops (sorghum, pearl millet, finger millet, chickpea, pigeonpea and groundnut), from 144 countries (www.icrisat.org). Low use of germplasm ($<1\%$) is a major concern globally leading to a narrow genetic base in most crop cultivars including ICRISAT mandate crops. For example, 50% of wheat, 75% of potato, 50% of soybean cultivars grown in USA trace back to 9, 4 and 6 genotypes in their pedigrees, respectively. Large size of collections and lack of reliable data on traits of economic importance, which show high genotype x environment interactions are considered as the main reasons for low use of genetic resources. Enhanced use of germplasm can be achieved through developing representative core (10% of entire collection) and mini core (10% of core or 1% of entire collection) collections, facilitating extensive evaluation of germplasm and identification of genetically diverse accessions with beneficial traits for use in crop improvement programs. At ICRISAT, systematic evaluation of mini core collections resulted in identification of a number of germplasm lines with agronomically and nutritionally beneficial traits in addition to resistance/tolerance to abiotic and biotic stresses. Multiple stress resistant and nutrient dense (oil, protein, Fe, Zn, Oleic acid) groundnut, multiple stress resistant, high sugar stalk and nutrient dense sorghum germplasm, downy mildew resistant pearl millet or nutrient dense finger and foxtail millets are some of the examples. Crop wild relatives harbour genes for stress tolerance, seed yield and nutritional traits. ICRISAT has made efforts to infuse diversity from wild relatives to enhance resistance to pod borer in chickpea and pigeonpea, and to rust and leaf spots in groundnut. In groundnut, wild species through amphidiploid has been successfully used to enhance 100-seed weight, pod yield and traits related to drought tolerance such as specific leaf area and SPAD chlorophyll meter reading. Researchers are now using high throughput phenotyping and genotyping platforms to dissect the genetic and physiological basis of trait expression and deployment to accelerate genetic gains in crop breeding. Sequencing genomes of diversity panels (for example, 3000-chickpea or 1000-groundnut genomes) and its comparison with reference genome is expected to associate sequence difference with agronomically beneficial traits. The enhanced use of the genetic and genomic resources have enabled researchers to identify significant marker-trait associations or candidate genes associated with agronomic traits. The use of groundnut germplasm lines identified from mini core collection as parents, have resulted in developing exceptionally high oil (up to 63%, compared to ~48% in control cultivar) and high-yielding breeding lines, indicating that new germplasm sources contribute to enhancing genetic gains. Enhanced use of plant genetic resources would drive accelerated genetic gains in dryland crops to meet the adverse effects of climate change on global agriculture.

Key words: Crops, Genetic gains, Germplasm, Traits, Genebank