



The World Bank

University of Agricultural Sciences, Bangalore

An online refresher course on

“Prequels to Plant Breeding by Design & Prediction”

28 January 2021 – 18 February 2021

Link for Registration: <https://forms.gle/WLxXYwLPGtT2LeXF9>

Zoom meeting links from 28.01.2021 to 18.02.2021

<https://us02web.zoom.us/j/9530179153?pwd=QVJ2MWJlU0hlkNW5Va0drdWxQQnppQT09>

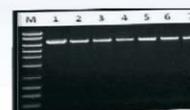
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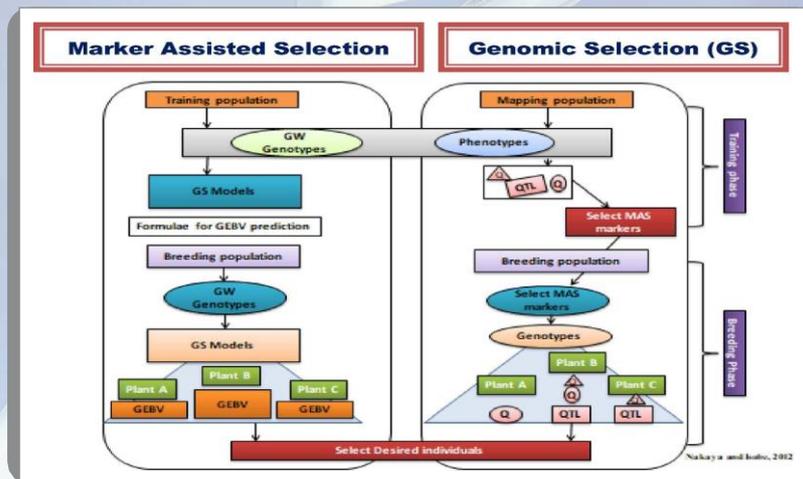
Meeting ID: 953 017 9153 Passcode: 12345

Conventional pre-genomics plant breeding based on phenotypic selection has resulted in perceptible genetic gains and has been effective in enhancing economic value of major crop plants. The pace of genetic gains in yield and other complex traits is difficult to sustain if only pre-genomics technologies are used. While conventional pre-genomics plant breeding has been, and will be successful in improving the economic worth of the crops, the application of genomic resources such as DNA markers will further accelerate the genetic gains realized by conventional plant breeding. The most commonly used DNA markers in the field of plant breeding and genetics are based on Simple Sequence Repeats (SSR), Cleaved Amplified Polymorphic Sequence (CAPS) and Single Nucleotide Polymorphism (SNP). The genomic resources help enhance pace and precision of developing improved crop cultivars by facilitating rapid genetic gain per breeding cycle through Marker Assisted Selection (MAS) and Genomic Selection (GS). Hence, the MAS and GS are regarded as precision crop breeding tools.

Implementation of MAS requires *a priori* detection and validation of Quantitative Trait Loci (QTL) controlling traits of economic importance. Bi-parent/multi-parent cross derived family and natural population-based

mapping are the two commonly used approaches to detect and validate QTL in crop plants. The two approaches are popularly referred to as Linkage Mapping (LM) and Association Mapping (AM), respectively. The LM and AM are not mutually exclusive but rather complementary. MAS is a design approach and has been effective only for traits controlled by major effect genes/QTL. However, majority of economically important traits are controlled by a large number of minor effect genes/QTL with significant cross-over genotype by environment interaction and exhibit complex inheritance. A predictive approach rather than design approach is useful for genetic improvement of such traits. In predictive approach, a large number of markers are used to predict and select the best individuals that exist in a breeding population. This predictive approach is referred to as GS. GS is a form of MAS of desired phenotypes early in the breeding cycle without laborious, time consuming mapping and validating QTL controlling target traits. GS is a predictive approach rather than a design approach like MAS. The use of MAS for traits controlled by major effect genes/QTL and GS for those controlled by minor effect genes/QTL enable enhanced pace, efficiency and precision of crop breeding.



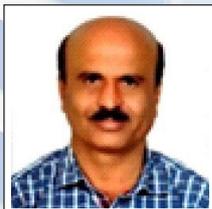


Objectives of the refresher course: To sensitize and update the knowledge and skills of the participants on the use of precision breeding tools in crop improvement.

Target beneficiaries: Graduates and young faculty of plant breeding and biotechnology from farm universities.

About the speakers

Dr. S. Ramesh is currently serving as a professor in the Department of Genetics and Plant Breeding, College of Agriculture, UAS, Bangalore. During 1995 to 1998, he started his professional career as sunflower breeder in the UAS, Bangalore. During this period, he contributed to the development of two sunflower hybrids, KBSH 41 and KBSH 42. Of these two hybrids, KBSH 41 is being exported to African countries. Subsequently, he served as a Visiting Scientist in sorghum breeding at ICRISAT from 2004 to 2007. During his stint at ICRISAT, he contributed to the development and sharing of a large number of grain and sweet sorghum trait-specific hybrid parents as testified by publications in reputed national and international journals. The hybrid parents along with the strategic information content of the published articles helped enhance research capabilities of sorghum breeders in India. During his tenure as Professor in the Departments of Plant Biotechnology and Genetics and Plant Breeding from 2008 to till date, he is offering advanced PG courses such as Quantitative Genetics, Population Genetics, Advances in Quantitative Genetics and Marker Development and Gene Mapping. During this period, as one of the coordinators, he trained entry-level teachers and researchers of State Agricultural Universities on the use



of genomic tools in plant breeding. He has also developed and validated several SSR markers in genomic resources limited crops like dolichos bean. Considering his contribution in teaching, and supervising thesis research by PG students, UAS, Bangalore conferred him “ICAR best teacher award” during 2016-2017. He has also been conferred “Best Research Supervisor Award” by GRAB’s Global Educational Trust, Chennai in 2019.

Dr. A. Mohan Rao is currently Professor and Head in the Department of Genetics and Plant Breeding, University of Agricultural Sciences, Bangalore. He contributed to the development, release and popularization of the crop varieties such as MAS 946-1 and MAS 26 (Aerobic rice), ML 365 (Finger millet), KBCH1 (Green Chilli Hybrid), Paustic 1 (Protein Rich rice), Paustic 7 (Iron Rich rice) and Paustic 9 (Zinc rich rice). He is the recipient of ICAR Best Teacher Award during the year 2013 for his teaching skills and awarded the Netherlands Fellowship under NFP twice by the Ministry of Development & Cooperation, Government of Netherlands. He has undergone post-doctoral training on Molecular Breeding/Molecular Marker Techniques twice at John Innes Centre, Norwich, UK sponsored by Kirkhouse Trust, UK. His contribution towards collection and characterization of 130 *Colletotrichum capsici* / *Colletotrichum gleosporoides* isolates causing fruit rot in chilli from across India are deposited in Institute of Microbial type culture collection and Gene Bank, Chandigarh. He is also the Principle Investigator for DBT, New Delhi Accredited Test Laboratory for genetic Fidelity Testing and virus indexing of Tissue Culture Raised Plants and Hot Pepper Improvement Unit at UASB.



Sponsored by

ICAR-NAHEP under Centre for Advanced Agricultural Science & Technology (CAAST) programme – Activity 1B
(NGT in Precision Crop Breeding including use of Advanced Genomic Tools & Introgressiomics)
(ICAR-NAHEP; F. No. NAHEP/CAAST/2017-18 dated 20.03.2018)

OUR TEAM



Dr. S. Rajendra Prasad
Vice-Chancellor and PI (CAAST Project), UAS, Bangalore



Dr. E. Gangappa
Professor and Coordinator
(CAAST Project - Activity 1B)
Department of Genetics and
Plant Breeding, College of Agriculture
GKVK, Bengaluru



Dr. S. Ramesh
Professor
Dept. of Genetics and
Plant Breeding
College of Agriculture
GKVK, Bengaluru



Dr. A. Mohan Rao
Professor and Head
Dept. of Genetics and
Plant Breeding
College of Agriculture
GKVK, Bengaluru



Dr. D.L. Savithamma
Dean (Agriculture)
College of Agriculture
GKVK, Bengaluru



Dr. M.P. Rajanna
Special Officer
College of Agriculture
Chamarajanagara



Dr. R.L. Ravikumar
Professor and Head
Dept. of Plant Biotechnology
College of Agriculture, GKVK, Bengaluru

SCHEDULE OF LECTURES OF ONLINE REFRESHER COURSE

Sl. No.	Date	Time	Topic
Inauguration			
1	28.01.2021	15.00 to 15.05 Hrs	Welcome and about the course by Dr. E. Gangappa , Professor of Genetics and Plant Breeding, UASB and Course Director
		15.05 to 15.10 Hrs	Remarks by Dr. N. Srinivasa , Dean (PGS), UASB
		15.10 to 15.20 Hrs	Address by Dr. S. Rajendra Prasad , Vice-Chancellor and PI, CAAST Project, UASB
		15.20 to 16.20 Hrs	Introduction to marker system
		16.20 to 16.30 Hrs	Coffee Break
		16.30 to 17.30 Hrs	Introduction to marker system (Contd...)
2	29.01.2021		Basic tenet's of SNP and CAPS marker systems
3	01.02.2021		Basic tenet's of SSR marker systems
4	02.02.2021		Application of marker systems
5	03.02.2021		Marker based diversity analysis
6	04.02.2021		Concept of linkage and estimation of recombination frequency
7	05.02.2021		Concept of linkage and estimation of recombination frequency (Contd...)
8	08.02.2021		Principle of linkage map construction
9	09.02.2021		Principle of linkage map construction (Contd...)
10	10.02.2021		Demonstration of softwares for linkage map construction
11	11.02.2021		Principle and analytical tools of QTL mapping
12	12.02.2021		Principle and analytical tools of QTL mapping (Contd...)
13	15.02.2021		Demonstration of softwares for QTL mapping
14	16.02.2021		Concept of Association Mapping
15	17.02.2021		Principle and workflow of Genomic selection
			Revision and valedictory
Valedictory programme			
16	18.02.2021	17.30 to 17.35 Hrs	Remarks by Dr. N. Srinivasa , Dean (PGS), UASB
		17.35 to 17.45 Hrs	Sample distribution of E-Certificates and Presidential remarks by Dr. S. Rajendra Prasad , VC and PI, CAAST Project, UASB
		17.45 to 17.50 Hrs	Vote of thanks by Dr. E. Gangappa , Professor of Genetics and Plant Breeding, UASB and Course Director

Convenor and refresher course Director

Dr. E. Gangappa

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E-Certificate will be issued for the participants with at least 80% attendance

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