

COTTON *Innovate*



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Annual Review Workshop of TMC MM I for Central Zone

A meeting of PI/CCPIs of three TMC MM I projects (TMC MM 1.4, TMC MM 1.6 & TMC MM 1.7) for central zone was held at Central Institute for Cotton Research, Nagpur on 19th May, 2014 to review the progress of work and to discuss the technical programme for the year 2014-15. The meeting started with welcome of the participants by Dr. M.V. Venugopalan Head PME, CICR, Nagpur. In his introductory remarks Dr. K. R. Kranthi, Member Secretary TMC MM I & Director, CICR explained about the purpose of the meeting. The action plan for the implementation of IRM-HDPS and HDPS demonstrations at various locations during 2014-15 were discussed and finalized based on the availability of seeds at various centres. The meeting ended with the vote of thanks by Dr. J. H. Meshram, In-charge TMC Cell, CICR, Nagpur.



Scientific Talk



Dr. Nandini Gokte-Narkhedkar, Principal scientist, CICR Nagpur, presented a wild idea titled “Green Vaccination-Helping plants for war against nematodes” under the aegis of Innovation Cell on May 24, 2014. In her talk, she suggested that Plant Immunization - Systemic Acquired Resistance (SAR) can be used as a strategy for nematode control. She listed major elicitors of SAR as Jasmonic acid and Salicylic acid among others. Salicylic acid is also part of the Mi-1-mediated defense response to root-knot nematode in tomato. Aspirin (Acetylsalicylic acid) releases salicylic acid on hydrolysis. Aspirin water was reported to activate SAR and improve plant growth in a variety of crops. Talk also focussed on using other sources of salicylic acid for induction of SAR for nematode control.

Dr. Suman Bala Singh, Head I/C, Crop Improvement Division, CICR, Nagpur presented a wild idea on “Cotyledons in Cotton: a boon ..” under the aegis of Innovation Cell on May 24, 2014. Ever since the release of the first hybrid, the area under hybrids has been constantly increasing and has reached to 94 per cent. Both inter and intra specific hybrids of diploid and tetraploid cotton have been developed and released. These hybrids have been developed through conventional and unconventional methods of hybrid seed production. Both the approaches have their own advantages and disadvantages. Conventional method of hybrid production is tedious, costly and requires skilled manpower. Cytoplasmic genetic male sterility (CMS) system has an adverse effect on fibre properties of the hybrids while use of genetic male sterility (GMS) system requires uprooting of plants which affects the plant population in seed production plot. However, of the two methods viz., CMS and GMS, GMS system has an edge over CMS. Morphological / molecular markers are required for detection of sterile plants in early stage of the crop which will help in maintaining the population in the hybrid seed production plot.



Scientific Talk



One such character which can be very effectively utilized is spotless cotyledons. This character can be incorporated through mutation, introgressed breeding or through biotechnology. The spotless cotyledons can be identified at emergence and will be male sterile while those with spotted cotyledons will be fertile and can be uprooted. The gaps created upon rouging can be immediately filled and this will not affect the plant growth much as there will be hardly 6-7 days difference in age of plant. The plant population thus can be maintained in GMS based hybrid seed production plot which is a major concern in using this system.

Literature Scan

Quantitative variation in maize kernel row number is controlled by the FASCIATED EAR2 locus

Peter Bommert, Namiko Satoh Nagasawa & David Jackson from Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, USA.

Variation in Kernel Row Number (KRN) in maize is controlled by the variation in inflorescence meristem and an increase in the size of the inflorescence meristem would enhance maize yields by increasing KRN. Based on association analysis, QTL mapping, TILLING, sequencing and expression studies, combined with the phenotypic validation efforts, authors could prove that *FEA2* loci can increase KRN (15-20%) without any undesirable effects. Basis of this increase was found to be differential gene expression of alleles owing to probable changes in gene regulatory sequences. Authors have also identified primers/restriction enzymes for tracing favorable *fea2* alleles

Practical implication of the discovery

Even with most of the area under single cross hybrids, India struggles to achieve even half of world's maize productivity. KRN is an important yield attributing trait in maize. Most of the maize cultivars generally have 14-18 kernel rows while *FEA2* mutants were found to have more than 20 KRN without any undesirable effects. The identified *fea2* allele can significantly increase the maize yields by increasing KRN and linked markers identified can be used for accelerated marker assisted maize breeding. Outcome of this systematic scientific study has potential to produce 'quantum jump' in maize production.

References : Nature Genetics, Mar 2013; 45 (3) :334-7.

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