

Al concentration, crystallographic nature of the product can be tuned from FCC to FCC/BCC and to BCC phases. Detailed tensile testing of the deposited coatings reveals strong texture developed during solidification. He pointed out that the area of additive manufacturing of multi-component alloys is still in the nascent stage and there exists opportunity for suitable applications. S. V. S. Narayan Murty (VSSC, Thiruvananthapuram) highlighted the problems of HEMs with regard to their commercial applications. He further stressed upon the formulation of proper direction of work for future prospects. Some of these problems are related to cost, ease of manufacturing, recyclability, etc.

Overall, the workshop led to many stimulating discussions among the delegates on various fundamental aspects of advanced research on HEMs as well as the existing challenges. Many distinguished materials scientists participated in the brain-storming discussions, on the use of thermodynamics database, precise chemical composition at different stages

of processing, defects characterization during deformation and diffusion data analysis in these multicomponent systems. It emerged that high-purity elements and precise processing lead to cost escalation of developing new alloys centred on high-entropy concepts. It was also suggested that the starting materials may be HEAs, but subsequently it may decompose to low-entropy phases. It was realized that first-principles calculation along with other computational tools should be used to understand the phase stability and phase selection. However, research in this area is exciting due to the possibility of developing and substituting strategic components using HEMs, which can eventually provide better services. It was agreed that collaboration among various groups would be important to resolve several fundamental issues. It may be noted that a website on HEA (<https://mme.iitm.ac.in/hea/>) is maintained at IIT-Madras to share information of latest publications and the groups working in India. The next workshop will be held in 2019 at IIT-Kanpur.

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MEETING REPORT

Breeding for crop improvement*

A one-day dialogue on breeding strategies for crop improvement was held on 10 July 2017.

V. Praveen Rao (Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad) opened the dialogue stating that the purpose was to integrate fundamental knowledge on breeding for crop improvement with what new technologies offer to raise crop production. The World War II imposed a severe shortage of food. Technology that was generated then, quickly came to the rescue of humanity in mid-1950s to mid-1960s. Two outstanding scientific developments are dwarf plant types in wheat and rice to produce more harvestable grain yields

which helped India reach self-sufficiency in food and other necessities for a comfortable life. Global population and food production have increased by several folds. The Indian population has also grown to 1.3 billion. We need 370–425 million tonnes by 2050 to feed our population. Rao further stated that this programme was aimed to address the major challenges to agriculture in the world today: (i) How to remain self-sufficient in food and other needs? (ii) How to reach the targeted crop production with less resources and in an economically acceptable and ecologically sustainable manner? (iii) How to face climate change, especially the frequent occurrences of droughts, floods, unpredictable weather vagaries near harvest and rising temperatures? T. Mohapatra (ICAR, New Delhi) chaired the dialogue and suggested the need for innovative technologies in agriculture to double farmers' income. Science has advanced from Mendelian

genetics to molecular breeding, transgenic breeding and genomics-associated breeding. He called for intensified trait discovery; breeding strategies to manipulate postharvest traits in crops and find ways to reduce the use of resources like fertilizers and water to get optimized yield. Zikang Li (Institute of Crop Sciences, China) delivered a keynote address on the 3K Rice Genome Project and its implication to future rice improvement. His group has identified 42 million single nucleotide polymorphisms (SNPs) in Rice Pan Genome and >12,000 novel genes that are absent in single reference genome. They have also detected structural variation, and transposition and deletions as predominant structural changes. The haplotype diversity will be used to understand gene function and large-scale gene/quantitative trait loci (QTL) discovery and allele mining by GWAS (genome wide association studies). E. A. Siddiq (PJTSAU) emphasized on the

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need for more investment and amending policy on agriculture and agricultural research to provide adequate funds for strategic research to all the national partners, including State Agricultural Universities. He also stressed on the need for clearly defining regulatory policies with respect to GM crops and genome editing of crop plants by the Government. Breeders still depend on naturally occurring variability and he emphasized on the creation of new variability by Targeting Induced Local Lesions IN Genomes (TILLING), interstitial mutagenesis, etc. to break the yield barriers.

P. B. Kirti (University of Hyderabad, UOH) explained activation tagging, wherein multiple enhancer elements are used to activate genes near the site of integration and study the effects of their overexpression on plant phenotype. A large activation-tagged population was developed in rice variety, Samba Mahsuri that grew well under limited water conditions without compromising on yield, and the corresponding genes were identified. N. Sarla (ICAR-Indian Institute of Rice Research (IIRR), Hyderabad) stated that chromosome segment substitution lines (CSSLs) are a genetic resource with complete genome of a distant genotype as overlapping segments in the background of a cultivar. A CSSL, significantly different from the parent, is used to map QTL or causal genes for the trait. Kuldeep Singh (ICAR-National Bureau of Plant Genetic Resources, New Delhi) mentioned that plant species have an antiquity of genome doubling followed by diploidization and repeated polyploidization. Significant progress has been demonstrated to study the origin of polyploids for the creation of new species. R. P. Sharma and P. Gupta (UOH) described how TILLING relies on random mutagenesis and assays to recover induced novel sequence variants. Reverse genetic strategies are used further to identify new allelic series of mutations in genes of

interest. They have used TILLING to identify tomato mutants with improved shelf-life and nutrient content. H. D. Upadhyaya (International Crops Research Institute for Semi-Arid Tropics (ICRISAT)) described on how transfer of genes from wild *Arachis* into cultivated groundnut is valuable, but challenging due to ploidy differences and genomic incompatibility between species. His group has developed introgression lines, using synthetic groundnut with high pod yields, high 100-seed weight and drought tolerance. R. K. Varshney (ICRISAT) proposed sequencing-based next generation breeding for genetic gains in grain legumes. Jauhar Ali (IRRI, Philippines) mentioned that temperature-sensitive genic male sterility (TGMS) facilitated hybrid rice breeding. Two-line hybrid rice seed production system using TGMS offers several advantages over cytoplasmic male sterility (CMS)-based three line system. S. R. Bhatt (ICAR-National Research Centre on Plant Biotechnology, New Delhi) described how uniparental genome elimination in wide crosses results in the production of haploids. Haploid inducer lines were generated by manipulating conserved gene coding for centromere histone 3 (*CENH3*) protein or a *BABYBOOM* Like gene. Precision breeding by CRISPR/Cas assisted genome editing was discussed by Amitabh Mohanty (DuPont, Hyderabad, and DuPont Pioneer, USA). The development of targeted genome editing by clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated protein 9 (Cas9) has created much interest. CRISPR/Cas, acting as sequence-specific nuclease, generates precise double-stranded breaks at the target DNA sequence to allow deletions, insertions or editing in the target native genes. Mohanty offered CRISPR/Cas technology for collaboration with researchers.

Anil Grover (University of Delhi South Campus, New Delhi) discussed breeding for high temperature resistance

in rice plants by transgenic approach. An important class of heat stress-induced upregulated proteins are chaperones, which interact with and assist the non-native proteins to acquire their functionally active state during and following heat stress. Hsp100 family represents a major class of Hsps with the role of removing protein aggregates in post-stress recovery phase. He discussed the possible repercussions of altering levels of Hsp100 proteins in heat tolerance response in rice plants. P. Anandakumar (ICAR-IIRR) presented efforts at transgenic breeding in rice nitrogen input use efficiency. Plants that do not form associations with bacteria must get nitrogen from the soil. Only 30–50% of the applied nitrogen is absorbed by the plants. Some assimilated nitrate is lost from crop canopies through ammonia volatilization. Nitrogen leaching contributes to algal bloom and hypoxia, and loss of aquatic biodiversity. R. V. Sonti (CSIR-Centre for Cellular and Molecular Biology) discussed on innate immunity and disease management. The first line of defence involves pattern recognition receptors that are located in the plasma membrane and that recognize pathogen-associated molecular patterns or damage-associated molecular patterns. He provided a broad overview of plant innate immune responses with specific examples. Narendra Tuteja (International Center for Genetic Engineering and Biotechnology, New Delhi) suggested the use of beneficial fungus (root endophyte *Piriformospora indica*). His group has cloned several salinity-tolerant genes from *P. indica*. They have shown that transgenic tobacco plants overexpressing fungal *PiCypA* provide high salinity tolerance.

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