



# National Seminar

on

**Maize for Crop Diversification under  
Changing Climatic Scenario**

9-10 FEBRUARY, 2020



**Organized by:**

**Maize Technologists Association of India**

**In collaboration with**

**ICAR-Indian Institute of Maize Research, Ludhiana &  
Punjab Agricultural University, Ludhiana**

### I-37 ESTIMATION OF GENETIC DIVERSITY AMONG NEWLY DEVELOPED WINTER MAIZE INBRED LINES

**Singh S.B.<sup>1</sup>, Chikkappa G. Karjagi<sup>2</sup>, Kumar S.<sup>1</sup>, Kumar K.<sup>3</sup>, Yathish, K.R.<sup>3</sup>, Jat B.S.<sup>4</sup>, Kasana R.K.<sup>1</sup>, Kumar A.<sup>1</sup> and Rakshit S.<sup>4</sup>**

<sup>1</sup>Regional Maize Research and Seed Production Centre, ICAR –Indian Institute of Maize Research, Begusarai

<sup>2</sup>Delhi Unit Office, ICAR –Indian Institute of Maize Research, New Delhi

<sup>3</sup>Winter Nursery Centre, ICAR –Indian Institute of Maize Research, Hyderabad

<sup>4</sup>ICAR –Indian Institute of Maize Research, Ludhiana  
[singhsb1971@rediffmail.com](mailto:singhsb1971@rediffmail.com)

Maize (*Zea mays* L.), the queen of cereals, holds unmatched fitness across diverse environments due to the high level of plasticity in its genome. Maize is gaining exponential rise in global demand even over the wheat and rice reflecting the substantial growth of maize in developing as well as industrial countries. Exploitation of hybrid vigor in maize has gained much significance in view of tremendous increase in its yield but still it demands the continuous development of better than the best hybrids to fulfill these rising demands in terms of yield as well as quality. Looking into the above facts, genetic diversity study at the morphological as well as molecular level with the help of forty polymorphic markers was made using 140 newly developed and 13 parental inbreds of released maize hybrids at Regional maize Research & Seed Production Center ICAR-IIMR, Begusarai, Bihar during Rabi, 2018-19. This study was conducted to understand the diverse nature among these lines and subsequently to use the desirable diverse parents in maize breeding program to produce superior hybrids, segregating populations with high variability and introgression of desirable traits/genes. D square study revealed the twenty clusters among which three clusters comprised 92, 21 and 23 genotypes while 17 genotypes falls in 17 different clusters individually. The highest inter-cluster distance was found between the cluster 17 & 19 (IMLSB-955-1 & IMLSB-2094) followed by cluster 13 & 17 (IMLSB-423-1 & IMLSB-955-1) and 14 & 17 (IMLSB-81-1 & IMLSB-955-1). Among the first three clusters highest inter-cluster distance was found between cluster 2 & cluster 3 and highest intra-cluster distance was observed within cluster 2. This reveals that the crosses among these distant genotypes may harness greater level of heterosis. Molecular diversity study with the help of 40 polymorphic markers which displayed clear size differences and total of 873 alleles were generated through these primers with an average polymorphism information content value of 0.8367. The primer *bnlg* 1614 and *bnlg*1642 was found as the best marker for identification of

genotypes as revealed by PIC values (0.9838 & 0.9737 respectively). The Jaccard's dissimilarity index showed the highest value of 1.00 among the genotypes IMLSB-274-1 & LM-16 followed by IMLSB-123-1 & LM-16 (0.981), IMLSB-119-2 & LM-14 (0.978), IMLSB-114-1 & HKI-1128 (0.978) and IMLSB-106-2 & HKI-1128 (0.978). The Jaccard's dissimilarity index classified the total genotypes in two major clusters and eight sub clusters. The high D square distance found among the genotypes IMLSB-955-1 & IMLSB-2094, IMLSB-423-1 & IMLSB-955-1 and IMLSB-81-1 & IMLSB-955-1 also recorded high Jaccard's dissimilarity coefficient value of 0.906, 0.798 & 0.840 respectively. These diverse genotypes can be used in further breeding program in the development of high yielding single cross maize hybrids as well as segregating population with high variability and introgression of desirable traits/genes.