Study of Yield Parameters and Kernel Micronutrient Genetic Diversity in Maize (*Zea mays L.*)

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Abstract

Forty-eight maize inbred lines were evaluated for thirteen traits for the genetic diversity study. The research experiment was conducted in randomized complete block design (RCBD) with three replications. All the 48 genotypes were grouped into 4 clusters. Cluster II consist of largest cluster comprising of 22 maize genotypes followed by cluster II (14) and cluster IV (11). cluster I comprise least number of genotype (1). Cluster distances indicated by the average inter and intra cluster distance are the approximate measure of the cluster divergence. Genotypes of cluster III show high intra cluster distance indicating high degree of divergence among the genotypes studied. It can be inferred that crossing between these genotypes may result in good recombinants for successful breeding program.

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Keywords: Cluster analysis, yield, iron, zinc, maize

Introduction

In India, maize is the third most important food crops after rice and wheat. India's maize production fluctuates between 10-14 million tons, with 80-90% of the production being in the *kharif* season. Major states that contribute in Maize productions are Karnataka, Andhra Pradesh, Bihar, Punjab, Uttar Pradesh and Madhya Pradesh. Maize in India, contributes nearly 9% in the national food basket and more than Rs.100 billion to the agricultural GDP at current prices apart from the Generating employment to over 100 million man-days at the farm and downstream agricultural and industrial sectors. In addition to staple food for human being and quality feed for animals, maize serves as a basic raw material as an ingredient to thousands of industrial products that includes starch, oil, protein, alcoholic beverages, food sweeteners, pharmaceutical, cosmetic, film, textile, gum, package and paper industries etc (Tripathia *et al.*, 2016).

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Zinc act as cofactor for more than 300 enzymes and it also constituent of many vital enzymes which is involved in RNA synthesis, DNA replication, cellular growth and metabolism. According to International Zinc Nutrition Consultative Group, mild to moderate zinc deficiency is prevalence around the world, while one third of global population at high zinc deficiency

particularly in developing countries. Zinc deficiency causes impaired growth, development and immunity, increase rate of mortality and morbidity, undesirable pregnancy outcomes and child death, and abnormal neurobehavioral development (Ashish Sharma *et al*., 2013).

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Iron (Fe) deficiency is a worldwide problem that is directly correlated with poverty and food insecurity. Approximately, one-third of the world's population suffer from Fe deficiency-induced anaemia, 80% of which are in developing countries (Boccio and Iyengar, 2003).In India about 51% of population suffering from anaemia. The consequences of Fe deficiency include increased death rates, diminished cognitive abilities of children and reduced labour productivity in women (Caballero, 2002). Fe is less available for absorption into the human body from vegetarian as opposed to non-vegetarian diets, Hunt (2003). Thus, evaluating the bioavailability of Fe is a necessity in order to improve the Fe nutritional quality in staple food crops. Given the high cost of quantifying Fe bioavailability via human and animal studies, in vitro screening of food samples represents the most feasible system for phenotyping.

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The genetic variation of iron and zinc concentration in the maize has the potential to improve it through plant-breeding. The maize-breeding programme of the CIMMYT has focused on identifying white grained maize germplasm that has the potential to address iron and zinc deficiencies in humans through increased kernel iron and zinc concentrations. There is need to research on the genetic variation of iron and zinc concentrations in the grain of maize and the potential to improve it through plant-breeding. CIMMYT has focused on study identifying white grained maize genotypes that has the potential to replenish iron and zinc deficiencies in humans, mainly in developing and under developing through increased kernel iron and zinc concentrations.

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Research Methodology

Genetic materials and field evaluation

The experiment was involving a set of forty-eight maize inbreds obtained from CIMMYT, Hyderabad and Maize Improvement Program, Institute of Agricultural Sciences, BHU, Varanasi. The details of maize genotypes used in the study given in (Table 1). Experiment was conducted

during *Rabi* 2017-18 in RCBD with two replications. Each genotype was sown into two rows of 3 m each with 70 cm row to row and 20 cm plant to plant distance. The soil of the experimental plot was fertile, alluvial loam and was characterized as the type of soil of Indo-Gangetic plains. Standard agronomic practices were performed for raising and maintenance of the healthy plants.

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Table 1. List of maize inbred lines used in the experiment

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S.N.	Genotypes	S.N.	Genotypes
1	DML 221	25	VL-1231
2	DQPM -1	26	VL-1018604
3	CML -162	27	VL-1016210
4	CML-163	28	VL-1016211
5	CML-164	29	VL-1248
6	CML-187	30	VL-1010923
7	CML- 229	31	VL-055199
8	CML -326	32	VL-1018148
9	CML -425	33	VL-108720
10	CML- 433	34	VL-1030
11	CML- 470	35	VL-1028
12	CML -70	36	VL-108725
13	DQPM -2	37	SNL-153277
14	DQPM -3	38	VL-108866
15	DQPM -4	39	VL-108162
16	DQPM -5	40	VL-062605
17	CM-140	41	VL 109309
18	CM-150	42	VL- 109452
19	CM-152	43	VL-109582
20	CM-212	44	VL-109800
21	CM-145	45	VL-12196
22	VL-1033	46	VL-1012837
23	VL-1037	47	VL-106210
24	VL-1056	48	SNL-153292

Observations recorded

Total 13 important traits were considered of maize, five randomly selected competitive plants from each plot and each replication, and their mean values were recorded. Observations were taken for: days to 50% tasseling, days to 50% silking, plant height (cm), tassel length (cm), cob length without husk (cm), cob diameter without husk (cm), number of kernel rows per cob, number of kernels per row, test weight (g), grain yield per plant (g), kernel iron content (mg/kg) and kernel zinc content (mg/kg). Biochemical analysis of iron and zinc concentration in maize kernels was done at the Department of Soil Science and Agricultural Chemistry, Institute of Agricultural Sciences, BHU, Varanasi. Triplicate milled samples of each genotype was digested with 9:4 diacid mixture (HNO3:HClO4) followed by atomic absorption spectrometry (AAS) using (Agilent 240FS AA) as per the procedure described by Zarcinas *et al*. (1987) with some revisions recommended by Singh *et al*. (2005).

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Results and Discussion

D2 analysis

Genetic divergence among forty-six maize inbreds were studied based on Mahalanobis D2 statistics revealed presence of considerably diversity among the 48 inbreds. Detail insight into the diversity is therefore, important in order to select desirable genotype / parents for utilizing in breeding programmes.

Grouping of maize inbreeds into different cluster

Forty-eight maize inbreds were grouped into four distinct clusters by Wards's method as shown in (Table 2 and Figure 1). In Cluster II highest number of inbred identified as largest cluster with 22 inbreds and followed by the cluster III (14) and cluster IV(11) and the minimum number of inbreds found in the cluster I(1). Among the different clusters, the cluster II with 22 inbred lines emerged as the largest cluster.

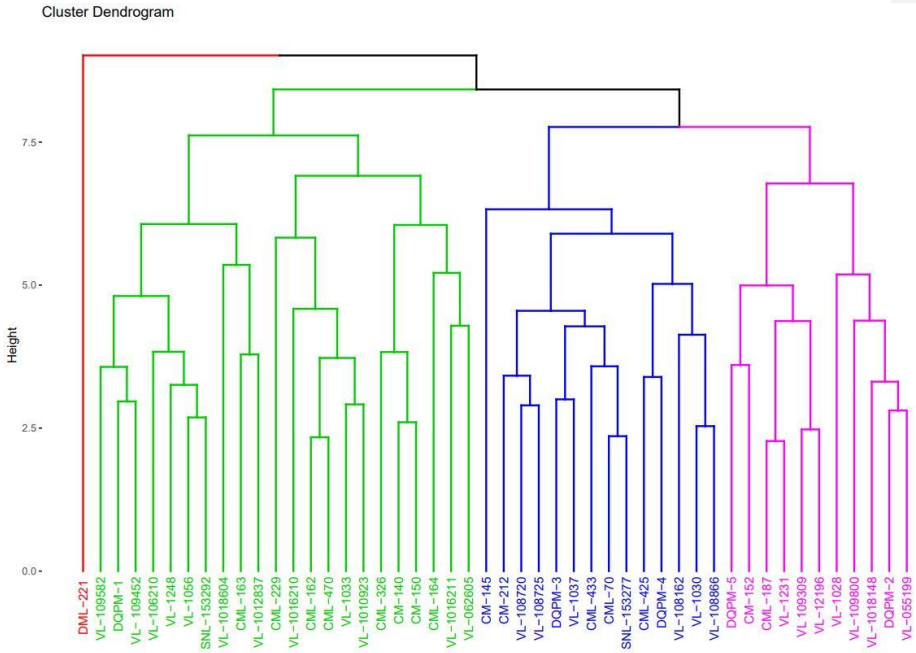

Fig 1. Dendrogram showing genetic diversity among forty-eight maize genotypes

Table 2. Grouping of forty-eight maize inbreds into four clusters by Ward's method

Cluster	No. of inbreds	Name of the maize inbreds
I	1	DML-221
II	22	VL-109582, DQPM-1, VL-109452,VL-1248, SNL-153292,VL-1018604, CML- 163, VL-1012837, CML-229, VL-1016210, CML-162, CML-470,VL-1033, VL-1010923, CML-326, CM-140, CM-150, CML-164,VL-1016211, VL-062605
III	14	CM-145, CM-212, VL-108720, VL-108725, DQPM-3, VL-1037, CML-433, CML-70, SNL-153277, CML-425, DQPM-4, VL-108162, VL-1030, VL-108866
IV	11	DQPM-5, CM-152, CML-187, VL-1231, VL-109309, VL-12196, VL-1028, VL-109800, VL-1018148, DQPM-2, VL-055199

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