

International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
 ISSN Online: 2617-4707
 IJABR 2024; SP-8(6): 594-597
www.biochemjournal.com
 Received: 09-03-2024
 Accepted: 12-04-2024

Pargat Singh
 Department of Genetics and
 Plant Breeding, Institute of
 Agricultural Sciences, Banaras
 Hindu University, Varanasi,
 Uttar Pradesh, India

SP Singh
 Department of Genetics and
 Plant Breeding, Institute of
 Agricultural Sciences, Banaras
 Hindu University, Varanasi,
 Uttar Pradesh, India

Rajesh Singh
 Department of Genetics and
 Plant Breeding, Institute of
 Agricultural Sciences, Banaras
 Hindu University, Varanasi,
 Uttar Pradesh, India

Pavan Devesh
 Department of Genetics and
 Plant Breeding, Institute of
 Agricultural Sciences, Banaras
 Hindu University, Varanasi,
 Uttar Pradesh, India

M Shankar
 Department of Genetics and
 Plant Breeding, Institute of
 Agricultural Sciences, Banaras
 Hindu University, Varanasi,
 Uttar Pradesh, India

Corresponding Author:
Pargat Singh
 Department of Genetics and
 Plant Breeding, Institute of
 Agricultural Sciences, Banaras
 Hindu University, Varanasi,
 Uttar Pradesh, India

Dissection of genetic parameters for yield in relation to iron and zinc content in maize (*Zea mays* L.)

Pargat Singh, SP Singh, Rajesh Singh, Pavan Devesh and M Shankar

DOI: <https://doi.org/10.33545/26174693.2024.v8.i6Sh.1379>

Abstract

Maize (*Zea mays* L.), is of American origin and is one of the most multipurpose crop having wider adaptability under various agro-climatic conditions. Maize is known as queen of cereals because it has the highest genetic yield potential among the cereals. This experiment was conducted to estimate the genetic traits of forty-eight maize genotypes (inbred lines) collected from CIMMYT, Hyderabad and Banaras Hindu University (BHU), Varanasi. The research experiment was conducted in randomized complete block design (RCBD) with three replications at Agricultural Research Farm, Institute of Agricultural Sciences, BHU, Varanasi. ANOVA indicated a significant difference among maize genotypes for all the characters. Genotypic coefficient of variance (GCV) was lower than phenotypic coefficient of variance (PCV) for most of the traits. Highest heritability (bs) was detected for zinc content followed by test weight, kernel iron content, grain yield per plant mainly. Highest genetic advance was observed for test weight whereas, the highest genetic advance as percentage of mean (GAM) was observed for kernel zinc content followed by kernel iron content and grain yield per plant. The findings of the present investigation indicated the presence of enough genetic variability among the maize genotypes analyzed, which can be exploited for maize improvement programs and development of cultivars/hybrids to enrich iron and zinc content in maize kernels.

Keywords: Maize, PCV, GCV, heritability, iron, zinc

Introduction

Maize (*Zea mays* L.), is of American origin and is one of the most multipurpose crop having wider adaptability under various agro-climatic conditions. Maize is known as queen of cereals because it has the highest genetic yield potential among the cereals. It is cultivated on nearly 150 m ha in about 160 countries having wider diversity of soil, climate, biodiversity and management practices that contributes 36% (782 m t) in the global grain production. The United States of America (USA) is the largest producer of maize contributes nearly 35% of the total production in the world and maize is the driver of the US economy. The USA has the highest productivity ($>9.6 \text{ t ha}^{-1}$) which is double than the global average (4.92 t ha^{-1}). On the other hand, the average productivity in India is 2.43 ton/ha.

Micronutrient deficiency also called as hidden hunger is global burden especially in developing countries. Nutrient deficiency is due to inadequate intake of any of the essential nutrient in diet which impairs growth and development of affected individuals; probably increase rate of morbidity and mortality. Many of the regional and national surveys have identified that zinc, iron and vitamin A as most vital for human health among the 30 essential nutrients. The mineral elements most commonly lacking in human diets are zinc (Zn) and iron (Fe).

Zinc and iron malnutrition are global health problem. Zinc is very important micronutrient for human health. Zinc performs exclusively large number of key functions; as it is important for human health, it is also called "metal of life" (Kaur, Gupta, Saraf, & Saraf, 2014) [18]. Zinc behaves like anti-depressant to overcome the depression. Low level of zinc in body leads to the Alzheimer's and Parkinson's diseases. Zinc plays a significant role in the regulation of blood pressure. In case of arterial hypertension, amount of zinc in bones, blood serum and lymphocytes is decrease, while it is increased in erythrocytes, heart, liver, kidney, suprarenal glands and spleen. Zinc has key role in the inhibition of hepatitis and liver cirrhosis. Zinc also regulates the functioning of endocrine system through modulation of thymus gland activity.

There is need to research on the genetic variation of 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. In addition, Cornell University has focused on traits such as multiple aleurone layer (MAL), which can increase kernel zinc and lower the phytic acid concentration, which decrease the bioavailability of zinc. Low-phytic acid maize has reduced levels of phytate, zinc chelator, in the kernels. Consequently, high amount of zinc can be absorbed from the diet. There is also evidence that lysine in high concentrations in opaque or quality protein maize (QPM), enhance zinc absorption in human body.

Material and method

Research material and methodology

Forty-eighty maize inbred lines used in this study were obtained from CIMMYT, Hyderabad and Maize Improvement Program BHU, Varanasi (Table 1). The experimental trial was conducted in RCBD during *Rabi 2017-18* at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (25.18°N latitude; 83.03°E longitude and at an altitude of 123.23 m above the sea level). 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 characterized as the type of soil of Indo-Gangetic plains which is fertile and alluvial loam.

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) [25] with some revisions recommended by Singh *et al.* (2005) [23].

Statistical analysis

Analysis of variance and estimation of genetic parameters were done by using R software (version 4.1) package: variability (version 0.1). Broad sense heritability was

calculated according to the formula given by Johnson *et al.* (1955) [14]; Hanson (1961) [11]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated according to Burton (1952) [5]; Singh and Choudhury (1985) [24]. Genetic advance (GA) was calculated by the formula suggested by Johnson *et al.* (1955) [14]; Allard (1975) [2]. Genetic advance in per cent of mean (GMA) was calculated by the formula given by Comstock *et al.* (1952) [8].

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

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

Results and Discussion

Analysis of variance

Analysis of variance showed that, all the forty-eight maize inbred lines consist of a significant variation for all the thirteen traits (Table 2). Significant variance among genotypes demonstrated the existence of genotypic variations, emphasizing the significance of their genetic worth in identifying the ideal genetic makeup for a given condition and therefore providing a wider range of selection options. Patil *et al.* (2016) [26] also observe significant genetic variation in maize inbreds for days to 50% tasseling, days to 50% silking, plant height, cob length, cob diameter, number of kernel rows per cob, number of kernels per row, test weight and grain yield per plant. Significant variations in iron and zinc concentration in maize kernel were also observed by Banziger and Long (2000) [4]; Chakraborti *et al.* (2011) [7]; Agrawal *et al.* (2012) [11]; Guleria *et al.* (2013) [10]; Mallikarjuna *et al.* (2014) [18]; Sharma *et al.* (2021) [22]; Goredema-Matongera *et al.* 2023 [9].

Table 2: ANOVA for thirteen traits of forty-eight maize inbred lines

Source of variation	df	DFT	Mean Sum of DFS	Square ASI	PHT	CLWH	CDWH
Replication	1	3.76**	1.76	0.0417	26.42**	0.60*	0.002*
Treatment	47	19.81**	877.24**	25.50**	179.19**	4.96	0.92
Error	47	0.4413	32.74	0.95	3.57	0.111	0.061

Source of variation	df	NKPC	Mean Sum of NKPR	of Square NCPP	TW	GYPP	Fe	Zn
Replication	1	0.166	0.16	0.00	189.8**	0.60	1.55*	1.72**
Treatment	47	3.73**	15.92**	0.11**	143.3**	4.96**	69.62**	157.6**
Error	47	0.67	1.37	0.00	11.9	0.111	0.366	0.237

', *' indicates significant at 5% and 1% respectively

DFT - days to 50% tasseling, DFS - days to 50% silking, PHT - plant height (cm), TL - tassel length (cm), CLWH - cob length without husk (cm), CDWH - cob diameter without husk (cm), NKRPC - number of kernel rows per cob, NKPR - number of kernels per row, NCPP - number of cob per plant, TW - 1000 seed weight (g), GYPP - grain yield per plant (g), FE - iron content (mg/kg), ZN - zinc content (mg/kg).

Genetic Parameters

Genetic parameters play a significant role to determine the amount of variability in different traits in crops. In any crop species the phenotypic variability present in a genotype or a set of genotypes can be divided into genotypic and environmental components. The genotypic component is the heritable portion of the total variability, its magnitude on yield and yield attributing characters influence the selection schemes to be followed by the plant breeders. Thus the success of genetic improvement of crops for any trait depends on the nature of the variability present in the germplasm. In the present study, higher PCV was observed than GCV for all the characters (Table 2). It shows that environmental factors affect their phenotypic expression of traits. These findings are accordance with Patil *et al.* (2016) [26]; Hosamani *et al.* (2018) [13]. On the basis of magnitude of heritability Johnson *et al.* (1955) [14] classified heritability as low (>30%), medium (30-60%) and high (>60%). They also classified genetic advance as percentage of mean values,

low (0-10%), moderate (10- 20%) and high (>20%). Highest broad sense heritability was observed for found in zinc concentration(99.7%) followed by test weight(99.03%) and iron concentration(98.3%)and grain yield per plant (98.86%), High broad sense heritability for grain yield and zinc concentration also reported by Mageto *et al.* (2020) [17]. High broad sense heritability showed that traits are governed by the additive genetic variance. The highest genetic advance was reported only for test weight (95.24%) and rain yield per plant(45.8%) and on the other hand, genetic advance as percentage of mean (GAM) was observed for kernel zinc content (76.19%) followed by kernel iron content (49.38%), grain yield per plant (23.38%) and anthesis silking interval(42.68%). High heritability in broad sense (99.03%) with high genetic advance (95.24%) was found for test weight. Larik *et al.* (2000) [16] suggested that the most effective condition for selection is when high genetic advance with high heritability is present.

Table 3: Estimation of genetic parameters in thirteen traits of 48 maize inbred lines

Trait	Range		Grand Mean	PCV (%)	GCV (%)	h ² bs (%)	GA (%)	GAM
	Max.	Min.						
Days to 50% tasseling	58	45	51	6.2239	6.0869	95.6	6.2733	12.2630
Days to 50% silking	61.0	47.0	54.1	5.74	5.53	92.0	5.94	10.99
Anthesis silking interval	3	1.0	2.37	22.33	21.51	91.02	1.01	42.68
Plant height (cm)	164.0	121.0	136.0	6.86	7.03	96.0	18.92	13.86
Tassel length (cm)	16.4	8.9	12.21	13.0	12.74	95.6	3.13	25.67
Cob diameter without husk (cm)	5.9	3.2	4.39	16.0	14.97	87.6	1.26	28.88
Number of kernel per cob	420	160	258	22.07	21.34	93.42	10.77	42.48
Number of kernels per row	32.0	20.0	24	12.21	11.19	84.06	5.09	21.14
Number of cob per plant	2.0	1.0	1.2	19.64	19.64	98.2	0.49	40.46
Test weight (g)	292	115	223.32	20.81	20.76	99.03	95.24	42.65
Grain yield per plant (g)	124.2	50.2	79.4	22.13	22.1	98.86	35.79	45.8
Kernel zinc content (mg/kg)	72.3	14.2	23.94	37.09	37.04	99.7	18.24	76.19
Kernel iron content (mg/kg)	37.7	12.4	24.42	24.42	24.09	98.3	12.24	49.38

Conclusion and Future Prospective

Maize inbred lines used under study expressed a significant variation for all the traits studied. High heritability with high genetic advance was observed for test weight and grain yield per plant. On the basis of mean performance, robust maize inbreds were identified for kernel iron content *viz.*, DML-221, CML-164, CML-187, DQPM-5, VL-1018104 and VL-108866 and on the other hand for zinc content *viz.*, DML-221, CML-164, CML-229, DQPM-5, CM-152, and CM-212. These maize inbreds can be utilize for the improvement of iron and zinc content through

appropriate breeding methods in combination of conventional and molecular approaches. Identified maize inbred lines with high micronutrient can be used for the development of bio-fortified maize cultivars/hybrids to overcome the malnutrition problem in underdeveloped and developing countries.

Acknowledgement

The authors extend sincere thanks to CIMMYT and BHU for providing maize inbred lines and experimental land for conducting valuable research.

References

1. Agrawal PK, Jaiswal SK, Prasanna BM, Hossain F, Saha S, Guleria SK, *et al.* Genetic variability and stability for kernel iron and zinc concentration in maize (*Zea mays* L.) genotypes. *Indian J Genet Plant Breed.* 2012;72(4):421-428.
2. Allard RW. Principles of plant breeding. New York: John Wiley and Sons, Inc; c1975.
3. Anonymous. ICAR - Indian Institute of Maize Research (ICAR-IIMR), Ludhiana, Punjab, India; c2021.
4. Banziger M, Long J. The potential for increasing the iron and zinc density of maize through plant-breeding. *Food Nutr Bull.* 2000;21(4):397-400.
5. Burton GW. Quantitative inheritance in grasses. In: Proceedings of 6th International Grassland Congress; c1952. p. 277-283.
6. Cakmak I. Enrichment of cereal grains with zinc: agronomic or genetic biofortification. *Plant Soil.* 2008;302(1):1-17.
7. Chakraborti M, Prasanna BM, Hossain F, Mazumdar S, Singh AM, Guleria SK, Gupta HS. Identification of kernel iron- and zinc-rich maize inbreds and analysis of genetic diversity using microsatellite markers. *J Plant Biochem Biotechnol.* 2011;20:224-233.
8. Comstock R, Robinson H, Gowen J. Estimation of average dominance of genes. *Heterosis.* 1952;2:494-516.
9. Goredema-Matongera N, Ndhlela T, van Biljon A, Kamutando CN, Cairns JE, Baudron F, Labuschagne M. Genetic Variation of Zinc and Iron Concentration in Normal, Provitamin A and Quality Protein Maize under Stress and Non-Stress Conditions. *Plants.* 2023;12(2):270.
10. Guleria SK, Chahota RK, Kumar P, Kumar A, Prasanna BM, Hossain F, Agrawal PK, Gupta HS. Analysis of genetic variability and genotype x year interactions on kernel zinc concentration in selected Indian and exotic maize (*Zea mays*) genotypes. *Indian J Agric Sci.* 2013;83(8):836-841.
11. Hanson WD. Heritability, statistical genetics and plant breeding. Washington: National Academy of Science, National Research Council; c1961. p. 125-140.
12. Hindu V, Palacios-Rojas N, Babu R, Suwarno WB, Rashid Z, Usha R, *et al.* Identification and validation of genomic regions influencing kernel zinc and iron in maize. *Theor Appl Genet.* 2018;131(7):1443-1457.
13. Hosamani M, Kuchanur PH, Mahiboobsa M, Siddhesh R. Genetic variability for yield and yield attributing traits in maize (*Zea mays* L.). *J Pharmacogn Phytochem.* 2018;7(3):1964-1966.
14. Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybean. *J Agron.* 1955;47(7):314-318.
15. Khush GS, Lee S, Cho JI, Jeon JS. Biofortification of crops for reducing malnutrition. *Plant Biotechnol Rep.* 2012;6(3):195-202.
16. Larik AS, Malik SI, Kakar AA, Naz MA. Assessment of heritability and genetic advance for yield and yield components in *Gossypium hirsutum* L. *Sci Khyber.* 2000;13(1):39-44.
17. Mageto EK, Lee M, Dhliwayo T, Palacios-Rojas N, San Vicente F, Burgueño J, Hallauer AR. An evaluation of kernel zinc in hybrids of elite quality protein maize (QPM) and non-QPM inbred lines adapted to the tropics based on a mating design. *Agronomy.* 2020;10(5):695.
18. Mallikarjuna MG, Nepolean T, Hossain F, Manjaiah KM, Singh AM, Gupta HS. Genetic variability and correlation of kernel micronutrients among exotic quality protein maize inbreds and their utility in breeding programme. *Indian J Genet Plant Breed.* 2014;74(2):166-173.
19. Popat R, Patel R, Parmar D. variability: Genetic variability analysis for plant breeding research. R package version 0.1.0. <https://CRAN.R-project.org/package=variability>. Published; c2020.
20. Prasanna BM, Mazumdar S, Chakraborti M, Hossain F, Manjaiah KM, Agrawal PK, Guleria SK, Gupta HS. Genetic variability and genotype × environment interactions for kernel iron and zinc concentrations in maize (*Zea mays* L.) genotypes. *Indian J Agric Sci.* 2011;81(8):704-711.
21. R Core Team. R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing; c2020. URL <https://www.R-project.org/>.
22. Sharma D, Chhabra R, Muthusamy V, Zunjare RU, Hossain F. Molecular characterization of elite maize (*Zea mays* L.) inbreds using markers associated with iron and zinc transporter genes. *Genet Resour Crop Evol.* 2021;68(4):1545-1556.
23. Singh D, Chonkar PK, Dwivedi BS. Manual on soil, plant and water analysis. New Delhi: Westville Publishers; c2005.
24. Singh RK, Choudhury BD. Biometrical method in quantitative genetic analysis. Ludhiana, New Delhi: Kalyani Publishers; c1985. p. 54-57.
25. Zarcinas BA, Cartwright B, Spouncer LR. Nitric acid digestion and multi-element analysis of plant material by inductively coupled plasma spectrometry. *Commun Soil Sci Plant Anal.* 1987;18(1):131-146.
26. Patil P, Peng RD, Leek JT. What should researchers expect when they replicate studies? A statistical view of replicability in psychological science. *Perspectives on Psychological Science.* 2016 Jul;11(4):539-544.