



ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.03
TPI 2019; 8(3): 87-91
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www.thepharmajournal.com
Received: 07-01-2019
Accepted: 12-02-2019

Priyanka Jaiswal
M.Sc.(Ag) Genetics and Plant
Breeding, IAS, BHU, Varanasi,
Uttar Pradesh, India

Banshidhar
M.Sc.(Ag) Genetics and Plant
Breeding, GBPUAT, Pantnagar,
Uttarakhand, India

Sonam Rani Agrahari
M.Sc.(Ag) Genetics and Plant
Breeding, IAS, BHU, Varanasi,
Uttar Pradesh, India

Rajesh Singh
Professor Genetics and Plant
Breeding, IAS, BHU, Varanasi,
Uttar Pradesh, India

Correspondence
Priyanka Jaiswal
M.Sc.(Ag) Genetics and Plant
Breeding, IAS, BHU, Varanasi,
Uttar Pradesh, India

Estimation of genetic parameters for yield related traits and grain zinc concentration in biofortified inbred lines of maize (*Zea mays L.*)

Priyanka Jaiswal, Banshidhar, Sonam Rani Agrahari and Rajesh Singh

Abstract

The present investigation was undertaken with the objective to assess variability (ANOVA, PCV and GCV), heritability, genetic advance, genetic advance as percentage of mean (GAM) and grain zinc concentration in 30 biofortified inbred lines of maize (*Zea mays L.*) for 11 traits. Trials were conducted during kharif 2017 at Agricultural Research farm, Institute of Agricultural Sciences in Randomized Block Design with three replications. Each entry was planted in row-to-row and plant-to-plant spacing of 60 cm x 20 cm. All the recommended packages of practices were followed to raise a good crop. The data were analyzed for variation using ANOVA. Over the year high GCV and PCV was observed for 100 seed weight followed by ear height, tassel length, Zn concentration, cob diameter, plant height and grain yield per plant. High heritability was observed for all the character except for days to 50% tasseling, days to 50% silking and cob length without husk. The high heritability coupled with high genetic advance as percent of mean was recorded for 100 seed weight, tassel length, ear height, Zn concentration, grain yield, plant height and cob diameter.

Keywords: Biofortified maize inbred, Variability, Heritability, Genetic Advance, Genetic Advance as percentage of mean

Introduction

Maize (*Zea mays L.*) is one of the three most important food crops grown in world. It is not only an important human food, but also a basic element of animal feed and raw material for manufacture of many industrial products. Maize is a member of poaceae family ($2n=2x=20$). Worldwide, approximately 21% of total produced maize is consumed directly as food while the rest part of produce is used in other purposes. In Latin America and Africa maize is mainly used for food while in Asia it is used for both food and feed. In many countries it is the basic staple food and an important ingredient in the diets of people. In India, it is third most important cereal next to wheat and rice and cultivated over an area of 8.69 million hectares, producing 21.81 million tons of grains with average productivity of 2509 kg /ha (2015-2016, Annual report DAC & FW). Karnataka, Rajasthan, Madhya Pradesh, Maharashtra, Andhra Pradesh, Uttar Pradesh, Bihar, Gujarat and Tamil Nadu are major maize producing state in India.

Maize kernels are good source of protein (9-10%), oil (2.5-4%), carbohydrate (65-70%), albuminoides (10.4%), crude fibre (2.3%) and ash (1.3%) (Cortez and Wild-Altamirano, 1972) [5]. The germ is relatively rich in minerals, with an average value of 11 percent as compared with less than 1 percent in the endosperm. The embryo consists the important genetic information, vitamin A, nicotinic acid, riboflavin, vitamin E and minerals for the plant to grow. Maize is the preferred food for one-third of all malnourished children and 900 million poor people worldwide mostly in major developing countries (Wadhvani, 2016) [27]. Hence, qualifies as a predominant crop in context of supplementing global nutrition by bridging the gap of malnutrition through "biofortification". Biofortification can be defined as a process to increase the bioavailability and the concentration of nutrients in crops through both conventional plant breeding (White and Broadley, 2008) [28] and recombinant DNA technology (Zimmermann and Hurrell, 2002) [29]. Biofortification programme initially involves exploration of available genetic resources for targeted micronutrient enhancement. Subsequently, the identified lines with higher concentration of targeted micronutrients can be used in hybridization programme for development of micronutrient enrich hybrids or varieties.

The knowledge of nature and magnitude of genotypic and phenotypic variability present in the crop species plays a vital role in formulating a successful breeding programme aimed at developing a desirable superior cultivar. The development of a high end plant breeding programme is dependent upon the existence of exploitable variability in the population and the extent to which the desirable traits are heritable. Thus, the assessment of existing variability becomes highly essential for a well oriented and high ended biofortification programme, hence the study of variability and genetic parameters for yield and yield contributing traits is absolutely essential. For selecting such improved genotypes from diverse genetic stock a vivid understanding and scientific knowledge on available variability, heritability and the expected genetic advance is necessary. Therefore, the present study was conducted with the aim to estimate variability and genetic parameters of different component traits towards the grain yield and grain zinc concentration so that the desired information can be obtained and used in the future maize breeding programmes.

Methodology

In this present investigation the experimental material is comprised of 30 biofortified inbred lines of maize which were analysed to assess the variability and estimating genetic parameters for yield attributing traits and grain zinc concentration. The field experiments were conducted in Randomized Block Design (RBD) with three replications during kharif 2017 at Agricultural Research farm, Institute of Agricultural Sciences, BHU Varanasi. Initially two seeds per hill were planted and later on thinning was done to maintain single plant per hill. Two border rows were also planted to avoid the border effect. The recommended packages of agronomic practices relevant to the crop were followed throughout the crop period. Biochemical analysis for kernel Zn concentrations was carried by atomic absorption spectrometry method.

Observed characteristics and sampling measurements

Observations for the pre and post-harvest parameter were recorded on five plants selected at random from each genotype for each replication. Days to 50 percent tasseling was recorded by counting number of days taken from the date of sowing to the date of 50 percent of plants shedding pollen. Days to 50 percent silking was recorded by counting number of days taken from the date of sowing to the date of 50 per cent of plants with silk emergence. Width of leaf was measured in centimeter using a scale. Length of tassel was measured and recorded in centimeters from the base of tassel (from the base to the tip of the tassel). Measurement of ear height was taken from the base of the plant to the node of the attachment of the lower most ear in centimeters. Height of the plant was measured in centimeters at maturity from the base of the plant (ground level) to the tip of the tassel. Length of cob and cob diameter was measured and recorded in centimeters after removing the husk. The weight of random sample of one hundred kernels was taken and was recorded with the help of electronic top pan balance. For recording grain yield per plant (g) cobs from five random plants were harvested and after shelling, the grain was dried to get uniform moisture of 15% and the weight was measured with the help of an electronic top pan balance. Biochemical analysis for kernel Zn concentrations was carried out on ground samples of seeds digested with diacid (HNO_3 and HClO_4) followed by atomic absorption spectrometry (AAS)

method as per the protocol described by Zarcinas *et al.* (1987)^[29] with some modifications suggested by Singh *et al.* (2005)^[23]. The principles of quantification in AAS based on the Beer-Lambert law; which describes a linear relationship between the absorbance and the concentration of element.

Biometrical analysis

There were 11 measurable traits which were recorded on five individual plants and average value were analyzed for variability assessment, estimation of genetic parameters and determining grain zinc concentration. The recorded data were analyzed to calculate genotypic and phenotypic coefficients of variation (GCV and PCV), heritability (broad sense), genetic advance and expected genetic advance as percent of mean. The analysis of variance for different traits was carried out using mean data in order to assess the genetic variability among the genotypes as given by Cochran and Cox (1957)^[4]. The level of significance was tested at 5% and 1% using F test. Genotypic components of variance were estimated by using the formula given by Cochran and Cox (1957)^[4]. Phenotypic variance (σ_p^2) was computed for each trait under study by using the formula, $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$. Genetic parameters were estimated for each character from ANOVA. Phenotypic and genotypic coefficients of variability for all traits were estimated using the formula of Burton and De Vane (1953)^[3] and were categorized as low (0-10), medium (10-20) and high (>20) as per Sivasubramanian and Madhava (1973)^[23]. The broad sense heritability (h^2_{bs}) was estimated for all traits as the ratio of genotypic variance to the total variance as suggested by Lush, (1949)^[12] and Hanson *et al.* (1956)^[7] and categorized as low, moderate and high as per Robinson (1949)^[22]. Genetic advance for each traits was estimated by using the formula given by Johnson *et al.* (1955)^[55]. Genetic advance was then expressed as percentage of the grand mean. Grain Zinc concentration was estimated following AAS based on the Beer - Lambert law using the relation Element concentration (mg/kg) = AAS reading \times dilution factor.

Results and Discussion

Analysis of Variance (ANOVA)

The analysis of variance (Table 1.1) showed highly significant differences for all eleven traits under study in 30 genotypes of maize. It is evident from the ANOVA that the treatment differences were highly significant for all the traits, which revealed that there is an inherent presence of sufficient genetic variability among the different genotypes under study and hence desirable improvement can be brought through selection. Genetic parameters were estimated for each character from ANOVA. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was estimated from these variances in terms of standard deviation as percentage of the grand mean and presented in table 1.2. The genetic variability as shown by the genotypic coefficient of variation (GCV) and phenotypic coefficient of variations (PCV), showed that the PCV was slightly higher than GCV for all the studied traits, indicating that these traits were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. The highest estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for 100 seed weight 22.29% and 21.96% respectively, followed by tassel length (PCV=15.88%, GCV=15.06%), ear height (PCV=14.42%, GCV=13.26%), Zn concentration (PCV=14.16%, GCV=12.75%), cob diameter

(PCV=13.24%, GCV=9.68%), leaf width (PCV=10.03%, GCV=9.54%), plant height (PCV=8.15%, GCV=6.33%), grain yield per plant (PCV=8.086%, GCV=6.480%), cob length without husk (PCV=7.69%, GCV=3.41%), days to 50% tasseling (PCV =5.55%,GCV=2.37%). The lowest PCV and GCV were observed for days to 50% silking 5.08% and 2.33%, respectively. High coefficient of variation provides great scope for the selection of desirable types. These findings were in accordance with earlier reports of Rafiq *et al.* (2010) [17], Jawaharlal *et al.* (2011) [8] and Rajesh *et al.* (2013) [18] and revealed presence of substantial variability for all traits studied. Grain yield, cob length, ear height, 100 grain weight and ear diameter had high GCV estimates. These findings were in accordance with those of Dixon *et al.* (2000) [6] and Queiroz *et al.* (2011) [16]. PCV and GCV is highest for 100 seed weight, similar finding was also reported by Mani *et al.* (1999) [13] for 100 grain weight and Kabdal *et al.* (2003) [10] for 100 grain weight and grain yield per plant. Days to 50% tasseling and days to 50% silking both had recorded the low PCV and GCV values, similar result was also obtained by Vashistha *et al.* (2013) [25]. Genotypic coefficient of variation provides information on the genetic variability present in various quantitative characters, but it is not possible to determine the amount of the variation that was heritable only from the genotypic coefficient of variation. Genetic coefficient of variation together with heritability estimates would give the best picture of the amount of advance to be expected from selection (Burton and Devane, 1953) [3]. Thus, the heritable portion of the variation could be more useful with the help of heritability estimates. The highest estimates of heritability in broad sense was for 100 seed weight(97%) followed by leaf width (90.40%), tassel length (89.90%), ear height (84.50%), Zn concentration (81.0%), grain yield per plant (64.2%), plant height (60.20%). High heritability for these traits demonstrated that these traits could be successfully transferred to offspring, and selection for such trait is easy and quick These traits can also be used for indirect selection of some other correlated traits that have low heritability and complex inheritance. Moderate heritability was observed for cob diameter (53.50%) and days to 50% silking (21.11%) while the low heritability was observed for cob length without husk (19.70%) and days to 50% tasseling (18.20) for which selection is not effective. These findings were in consonance with the reports made earlier in maize by Mulamba and Mock (1978) [15] for ear height, Sumalini and Manjulatha (2012) [21] for plant height, ear height, ear length, ear girth, kernel rows/ear, kernels/row, 100 kernels weight, grain yield/plant (g), Kashiani *et al.* (2014) [11] for ear height, plant height, number of kernels per row, 100 seed weight and ear length. The knowledge of heritability enables the plant breeder to decide the course of selection procedure to be followed under a given situation. However heritability values coupled with genetic advance would be more reliable and useful in formulating selection procedure. Genetic advance

was estimated at 5% selection intensity and for comparison among the traits it was transformed into genetic advance as percent of mean. Genetic advance as percent of mean was highest for 100 seed weight followed by tassel length, ear height, Zn concentration, cob diameter, grain yield per plant, plant height. Similar result was obtained by Saakyan and Khachtryan (1983) [19] for 100 seed weight and Aboyi *et al.* (2004) [1] and Rafiq *et al.* (2010) [17] for plant height. Maruthi *et al.* (2015) [14] reported similar results for grain yield per plant, ear height, plant height, number of kernels per row, 100 seed weight and ear length. Lowest genetics advance value was recorded for days to 50% tasseling and days to 50% silking. Similar result was reported by Sandeep *et al.* (2015) [20]. The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population (Vanniarajan *et al.*, 1996) [24].

The salient findings of the present study

- Analysis of variance revealed significant difference among genotypes for all the traits studied. The genotype VL109524 had highest grain yield per plant followed by VL1016211, VL1248, VL1016210, VL1231, VL1018604, VL1028, SNL153277 and VL05552.
- GCV% and PCV% were observed to be the highest for 100 seed weight followed by ear height, tassel length, Zn concentration, cob diameter, plant height and grain yield per plant indicating thereby that these traits should be given due consideration for effective selection.
- In general, the estimates of broad sense heritability and genetic advance were high for all the character except for days to 50% tasseling, days to 50% silking and cob length without husk.
- The high heritability coupled with high genetic advance as percent of mean was recorded for 100 seed weight, tassel length, ear height, Zn concentration, grain yield, plant height and cob diameter.
- Highest grain zinc concentration in mg/kg was reported for VL 1248 (39.53) followed by VL 057982 (38.47), VL 102 (37.17), VL 1010923 (37.1), VL 1010778 (36.07), VL 055199 (35.57) and VL 107657 (35.37).

Conclusion

From variability studies, maximum phenotypic and genotypic variability was observed for plant height, ear height, grain yield per plant, Zn concentration and 100 seed weight. Higher genotypic and phenotypic coefficient of variation was estimated for 100 seed weight followed by ear height, tassel length, Zn concentration, cob diameter, plant height and grain yield per plant. High heritability coupled with high genetic advance was recorded for 100 seed weight, tassel length, ear height, Zn concentration, grain yield, and plant height and cob diameter. The zinc concentration was found highest in VL1248 (39.53mg/kg) and lowest in HUZM78 (19.67 mg/kg) with mean value 32.18±1.14.

Table 1: Analysis of Variance (ANOVA) for eleven traits in thirty maize genotypes.

Source of variation	D.F.	Mean sum of square (MSS)										
		DTT (50%)	DTS (50%)	LW (cm)	TL (cm)	EH (cm)	PH (cm)	CLWOH (cm)	CD (cm)	100SW (gm)	Y/P (gm)	Zn (mg/kg)
Rep.	2	8.18	0.63	0.04	0.85	26.86	34.17	7.01	0.07	0.74	20.65	0.57
Trt.	29	11.90**	11.93**	1.73**	55.72**	117.59**	276.96**	3.50**	0.90**	58.10**	80.94**	54.42**
Error	58	7.14	6.62	0.06	2.02	6.76	49.96	2.02	0.20	0.59	12.68	3.94
S.E ±		1.54	1.48	0.14	0.82	1.50	4.08	0.82	0.25	0.44	2.05	1.14
C.V. (%)		5.02	4.51	3.10	5.06	5.67	5.14	6.89	9.02	3.85	4.84	6.17

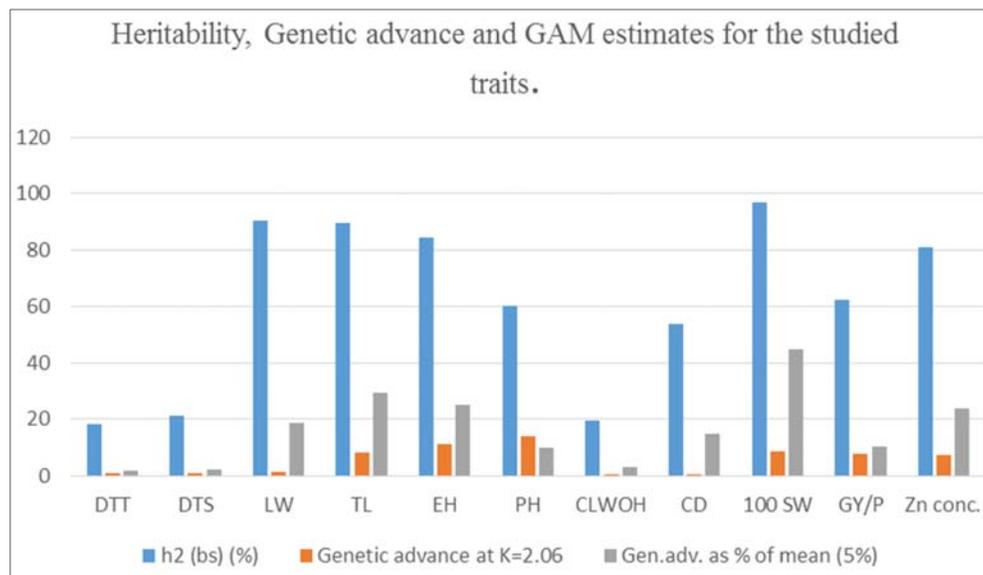
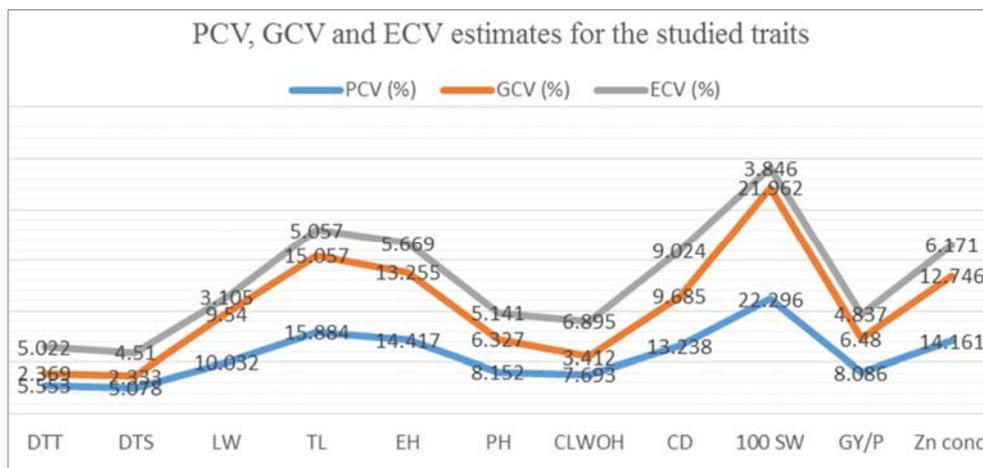
C.D. (5%)	4.37	4.20	0.39	2.32	4.25	11.55	2.32	0.73	1.25	5.82	3.24
C.D. (1%)	5.81	5.59	0.53	3.09	5.65	15.37	3.09	0.98	1.67	7.74	4.32

**and*Significant at 1% and 5% level of significance, respectively. Where PH (cm) = plant height, DTT (50%) = days to 50% tasseling, DTS (50%) = days to 50% silking, LW(cm)=leaf width, EH(cm) = ear height, TL(cm) = tassel length, CLWOH(cm) =cob length without husk, CD(cm) = cob diameter, 100SW(g)=100 seed weight, Y/P = yield per plant, Zn (mg/kg)=Zinc concentration

Table 2: Estimates of variability, heritability and genetics advance as per cent of mean for eleven traits in thirty maize genotype.

Traits/Parameter	DTT	DTS	LW	TL	EH	PH	CLWOH	CD	100SW	GY/P	Zn conc.	
Range	Max	56.000	60.667	9.133	37.133	56.833	154.900	23.500	5.900	29.300	82.963	39.533
	Min	49.933	53.300	6.300	22.033	37.533	119.967	18.633	4.100	14.100	64.750	19.667
Grand mean	53.192	57.050	7.825	28.099	45.856	137.491	20.612	4.987	19.936	73.612	32.182	
Phenotypic variance	8.724	8.392	0.616	19.919	43.702	125.630	2.514	0.436	19.758	35.430	20.769	
Genotypic variance	1.588	1.771	0.557	17.900	36.945	75.666	0.494	0.233	19.171	22.753	16.826	
Environmental variance	7.136	6.621	0.059	2.019	6.757	49.964	2.020	0.203	0.588	12.677	3.943	
PCV (%)	5.553	5.078	10.032	15.884	14.417	8.152	7.693	13.238	22.296	8.086	14.161	
GCV (%)	2.369	2.333	9.540	15.057	13.255	6.327	3.412	9.685	21.962	6.480	12.746	
ECV (%)	5.022	4.510	3.105	5.057	5.669	5.141	6.895	9.024	3.846	4.837	6.171	
C.V.(%)	5.022	4.510	3.105	5.057	5.669	5.141	6.895	9.024	3.846	4.837	6.171	
h ² (bs) (%)	18.20	21.10	90.42	89.86	84.54	60.23	19.67	53.52	97.02	62.22	81.01	
Genetic advance at K=2.06	1.108	1.259	1.462	8.262	11.513	13.907	0.642	0.728	8.884	7.874	7.606	
Gen.adv. as% of mean (5%)	2.082	2.207	18.687	29.404	25.106	10.115	3.117	14.596	44.564	10.697	23.633	

Where PH (cm) = plant height, DTT (50%) = days to 50% tasseling, DTS(50%) = days to 50% silking, LW(cm)=leaf width, EH(cm) = ear height, TL(cm) = tassel length, CLWOH(cm) =cob length without husk, CD(cm) = cob diameter, 100SW(g)=100 seed weight, Y/P = yield per plant, Zn (mg/kg)=Zn concentration.



Acknowledgement

We should duly acknowledge Institute of Agricultural Sciences, BHU for financial support. We should also pay our special gratitude to Dr. S.K.Singh Professor Genetics and Plant Breeding, BHU, Varanasi and Dr. Satish Kumar Singh Asst. Professor Genetics and Plant Breeding, Dr. RPCAU, Pusa for their valuable guidance and generous help for the completion of this work.

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