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Genetic variability assessment on yield attributing traits in maize (Zea mays L.) inbred lines

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Abstract

In the present investigation, 33 maize inbred lines were evaluated for 12 traits to assess the mean performance and genetic parameters relevant to adoption of a breeding strategy. Grain yield/plant, single cob weight, number of grains/cob, ear height and plant height which exhibited moderately high variability, high GCV, heritability and genetic advance, are the most important characters to be considered for effective selection of hybrid as these traits are highly genetically controlled and less affected by environments indicating additive genetic effects. The study identified six promising inbred lines on the basis of their mean performance, the following inbred lines CML 509, CML-505, CML 167, CML 163-D, CML-511 and DMR QPM 102 having best yield contributing and cob characters and could be tested in different agro-ecologies to identify those that could be introgressed for further breeding programmes.

Keywords: Character association, maize, inbred lines, positively correlated

1. Introduction

Maize (*Zea mays* L.) is the third most important cereal grain of the grass family *Poaceae*. Globally, maize is known as queen of cereals because of its highest genetic yield potential. It has also a potential to be bred (by benefitting from its hybrid vigor) and the ability to develop new varieties with superior traits. They provide humankind with more nourishment than any other food class and nearly half of the total caloric requirement. Maize is not only an important human nutrient, but also a basic element of animal feed and raw material for manufacture of many industrial products. Together with rice and wheat, maize is an essential source of at least 30% of the food calories of more than 4.5 billion people in about 94 developing countries (Shiferaw *et al.*, 2011)^[1]. It is one of the most versatile emerging crops having wider adaptability. Maize, which is the only food cereal crop that can be grown in different seasons requires moderate climate for growth

In India, it is estimated that maize demand will continue to increase because of its diversified uses and increasing population. To meet the growing demand, enhancement of maize yield in coming years across all the growing locations in India is a big challenge in the era of climate change. Meeting such challenge will only be possible through science-based technological interventions like single cross hybrid technology and application of novel molecular tools and techniques in maize improvement.

For inbred lines that serve as the seed parent in a production field, the evaluation of the grain yield and yield components of the inbred line per se is a way of estimating the profitability of commercial seed production for a maize hybrid (Pinnisch *et al.*, 2011) ^[2]. Any trait that contributes to the stable production of large quantities of hybrid seed in a seed production field will be of interest to plant breeders. Knowledge of the amount and distribution of genetic variation and relationships between and within plant populations is indispensable for classifying parental lines and predicting future hybrid performance (Acquaah, 2007) ^[3]. The identification of the potential genotype is pre-requisite for taking up an efficient breeding programme Thapa *et al.*, (2016) ^[4]. So it is necessary to produce maize varieties which are high-yielding in order to increase the production and productivity of maize, and more nutritious to supplement protein-deficient diets of the people than traditional varieties.

2. Materials and Method

The experiment was conducted during 2017rabi season, comprised 33 maize inbred lines

among which sixteen of the inbred lines were obtained from the International Maize and Wheat Improvement Center (CIMMYT), India and 17 from the Directorate of Maize Research (DMR), New Delhi. Evaluation trial was conducted on 1st week of December, 2017 at the Experimental Farm of University of Calcutta at Baruipur, South 24 Parganas. Each inbred was grown within plot of single rows of 3m long with three replications and row to row spacing of 60 cm and plant to plant spacing of 20 cm respectively. Recommended package of agronomic practices and plant protection measures were adopted. Prior to flowering each row of inbred lines were covered separately with nets made of muslin cloth, in order to prevent outcrossing. Harvesting was carried out from the last week of April, 2018.

Data was recorded on five randomly selected plants excluding border plant from each replication for twelve traits like: Days to tasseling (50%), Days to silking (50%), Plant Height (cm), Ear height (cm),Cob Length (cm),Cob Diameter (cm), Number of grain rows/cob, Number of grains/row, Number of grains/cob,100 grain weight (g),Single cob weight (g), Grain Yield/Plant Mean performance and Genetic parameters were performed using different statistical tools.

Mean sum of squares (MSS) from analysis of variance (ANOVA) of twelve different characters were taken. The mean performance of the thirty three maize inbred lines evaluated for the above mentioned characters. Genotypic Coefficient of variance (GCV), Phenotypic Coefficient of variance (PCV), Heritability (H%), Genetic Advance (GA) and Genetic advance % of Mean (GA% of Mean) of the above mentioned traits of the thirty three maize genotypes were evaluated using Windosta t[®] ver. 8.5 software for statistical data analysis.

3. Result and Discussion

The extent of variability with respect to twelve quantitative characters in thirty-three germplasm measured in term of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance and genetic advance as percent of mean are given in (Table 3). For all of the characteristics investigations, analysis of variance indicated significant variations among germplasm, showing the presence of significant variability in the materials that can be exploited by selection (Table 2). The creation of hybrids required the selection of genetically divergent inbred lines with substantial genetic variability and heritability in the base population. Similar observations were reported by Sokolov and Guzhva (1997) ^[5]. Naushad et al., (2007) ^[6] who reported significant variability among maize cultivars for cob length, kernel rows per cob, kernel weight and grain yield. Saikia and Sharma (2000)^[7] Matin et al., (2017)^[8] Bhadru et al., (2020)^[9] Kharel et al., (2017)^[10] for different maize traits like plant height, ear height and grain yield per plant. The goal of the study was to produce higher producing cultivars than those already available. Thapa et al., (2018) [11]. The available genetic variety in the gene pool allows for the selection of superior types.

A wide range and significant variability was observed for most of the traits studied. Among all the twelve traits studied, no. of grains/cob showed maximum range followed by single cob weight and grain yield/plant. Phenotypic Coefficient of Variation (PCV) slightly higher than Genotypic Coefficient of Variation (GCV) for all the traits, indicating the less influence of environment in expression of the traits. Highest phenotypic and genotypic coefficient of variation (PCV and GCV) was observed for single cob weight (34.41 and 25.83) followed by Grain Yield/plant (33.31 and 26.65) and No. of grains/cob (28.53 and 22.45). Rafiq *et al.*, (2010) ^[12] reported similar results i.e. high estimates of GCV and PCV for single cob weight, grain yield/plant, number of grains/cob, number of grains/row, ear height, cob length, plant height, number of grain rows per cob, cob diameter, days to silking and days to tasseling. High PCV and GCV values for grain yield per plant and ear height in maize were reported by Singh *et al.*, (2003) ^[13] and Abirami *et al.*, (2005) ^[14]. Vashistha *et al.*, (2013) ^[15] also reported higher GCV and PCV estimates for the traits grain yield per plant, ear height and 100 grain weight.

The lowest value for PCV and GCV was shown by Days to 50% silking (6.36 and 5.26) followed by Days to 50% tasseling (6.79 and 5.12). As seen by the tight difference between genotypic and phenotypic coefficients of variation, environmental effect on the expression of these traits was minimal.

Higher broad sense heritability of traits revealed that larger portion of variations is heritable to offspring, in our experiment broad sense heritability revealed highest value for 100 grain weight(96.41) followed by Grain Yield/plant(63.98) and No. of grains/cob (61.96) where similar reports were made by Similar results have been reported by Vashistha et al., (2013)^[15] in maize for 100 grain weight, days to silking, number of grains per cob, number of grains per row, days to tasseling, single cob weight, number of grain rows per cob, cob length, plant height, ear height, and cob diameter. Magar et al., (2021) ^[16] reported similar high heritability for grain yield per plant and 100 grain weight at par with our studies. Rafiq *et al.*, (2010) ^[12] for plant height, ear height, grain yield/plant, grains/row, ear length and 100 grain weight. Ojo et al., (2006) ^[17] observed high heritability in maize for grain vield, and 100 kernel weight. Estimates of genetic advance are more useful in selection than the heritability.

Genetic advance as percentage of mean showed that these parameters were under control of additive genes. Heritability estimates coupled with genetic advance would be more reliable and useful in formulating selection procedure. Genetic advance was estimated and transferred into genetic advance as per cent of mean for all the traits (Table 3). The trait no. of grains/cob (104.15) registered the highest genetic advance followed by single cob weight (39.44), and grain yield/plant (33.92). High heritability with moderate genetic advance as percent of mean were observed for 100 grain weight, number of grains/cob and number of grains/row would prove quite effective since these characters seemed to be governed by additive gene action. An earlier work by Alake *et al.*, (2008) ^[18] reported similar observations in maize for grain yield per plant.

Lowest genetic advance was observed cob diameter and no. of grain rows/cob. High heritability along with high genetic advance recorded for the traits like no. of grains/cob, grain yield/plantand single cob weight, suggesting that these characters can be considered as favourable attributes for improvement through selection and this may due to additive gene action.

Low genetic advance and heritability for cob diameter and cob length indicates that these traits are chiefly controlled by non-additive gene action and the characters are highly influenced by environmental effects and selection would be ineffective. (Singh and Narayanan, 1993)^[13].

Table 1: List of the Inbred lines used in the experiment

No.	Genotypes	Туре	Category	Grain Colour	Source
1	Cml 161	Qpm	Inbred Line	Yellow	Cimmyt
2	Cml 163	Qpm	Inbred Line	Yellow	Cimmyt
3	Cml171	Qpm	Inbred Line	Yellow	Cimmyt
4	Cml193	Qpm	Inbred Line	Yellow	Cimmyt
5	Cml502	Qpm	Inbred Line	White	Cimmyt
6	Cml504	Qpm	Inbred Line	White	Cimmyt
7	Cml505	Qpm	Inbred Line	White	Cimmyt
8	Cml507	Qpm	Inbred Line	White	Cimmyt
9	Cml508	Qpm	Inbred Line	White	Cimmyt
10	Cm1509	Qpm	Inbred Line	White	Cimmyt
11	Cml510	Qpm	Inbred Line	White	Cimmyt
12	Cml511	Qpm	Inbred Line	White	Cimmyt
13	Cml536	Non Qpm	Inbred Line	White	Cimmyt
14	Cml537	Qpm	Inbred Line	White	Cimmyt
15	Cml 538	Non Qpm	Inbred Line	White	Cimmyt
16	Cml 539	Non Qpm	Inbred Line	White	Cimmyt
17	Cml 153	Qpm	Inbred Line	White	Dmr
18	Cml154-2	Qpm	Inbred Line	White	Dmr
19	Cml161-D	Qpm	Inbred Line	Yellow	Cdmr
20	Cml163-D	Qpm	Inbred Line	Yellow	Dmr
21	Cml165	Qpm	Inbred Line	Yellow	Dmr
22	Cml167	Qpm	Inbred Line	Yellow	Dmr
23	Cml169	Qpm	Inbred Line	Yellow	Dmr
24	Cml170	Qpm	Inbred Line	Yellow	Dmr
25	Cml179	Qpm	Inbred Line	White	Dmr
26	Cml451 Q	Qpm	Inbred Line	Yellow	Dmr
27	Dmr Qpm 102	Qpm	Inbred Line	Yellow	Dmr
28	Dmr Qpm 103	Qpm	Inbred Line	Yellow	Dmr
29	Dmr Qpm 03-104	Qpm	Inbred Line	Yellow	Dmr
30	Dmr Qpm 03-113	Qpm	Inbred Line	Yellow	Dmr
31	Dmr Qpm 03-121	Qpm	Inbred Line	Yellow	Dmr
32	H.K.I 163	Qpm	Inbred Line	Yellow	Dmr
33	H.K.I 193 - 1	Qpm	Inbred Line	Yellow	Dmr

Table 2: Analysis of variance for 12 yield traits in Maize inbreds

C No	Channelter	Mean Sum of Squares			
S. No.	Characters	Replication	Treatment	Error	
1	Days to tasseling (50%)	10.39	85.98**	17.38	
2	Days to silking (50%)	9.83	88.60**	11.76	
3	Plant height (cm)	2464.82	2273.94**	804.08	
4	Ear height (cm)	248.26	1225.08**	443.39	
5	Cob Length (cm)	2.81	13.21**	3.67	
6	Cob Diameter (cm)	1.23	2.99**	1.27	
7	No. of grain rows/cob	0.81	5.99**	1.25	
8	No. of grains/row	37.9	91.31**	18.27	
9	No. of grains/cob	1363.7	24061.37**	4087.51	
10	100 grain weight (g)	0.26	47.87**	0.58	
11	Single cob Weight (g)	523.31	2945.26**	604.88	
12	Grain Yield/plant(g)	255.6	2359.23**	372.68	

Table 3: Estimates of variability parameters for 12 yield attributes in Maize in breds

Traits/Parameters	GCV	PCV	Н%	GA (5%)	GA as % of Mean 5%
Days to tasseling (50%)	5.12	6.79	56.81	5.59	1.99
Days to silking (50%)	5.26	6.36	68.54	7.15	2.48
Plant height (cm)	10.84	17.61	37.86	17.26	2.82
Ear height (cm)	14.33	23.55	37.01	12.31	3.64
Cob Length (cm)	12.23	17.96	46.39	1.70	3.89
Cob Diameter (cm)	5.57	10.01	31.05	0.43	1.19
No. of grain rows/cob	9.43	12.63	55.77	1.44	3.61
No. of grains/row	17.95	23.75	57.13	5.81	7.04
No. of grains/cob	22.45	28.53	61.96	104.15	9.55
100 grain weight (g)	14.62	14.89	96.41	7.89	9.68
Single cob Weight (g)	25.83	34.41	56.32	39.44	11.65
Grain Yield/plant(g)	26.65	33.31	63.98	33.92	11.71

4. Conclusion

Hence in this study grain yield/plant, single cob weight, number of grains/cob, ear height and plant height which exhibited moderately high variability, high GCV, heritability and genetic advance, are the most important characters to be considered for effective selection of hybrid as these traits are highly genetically controlled and less affected by environments indicating additive genetic effects in the following inbred lines CML 509, CML-505, CML 167, CML 163-D, CML-511 and DMR QPM 102 having best yield contributing and cob characters and could be tested in different agro-ecologies to identify those that could be introgressed for further breeding programmes.

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6. Conflicts of Interest

The authors declare no conflict of interest.

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