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Research Article

Estimation of variability, heritability, genetic advance and assessment of frequency distribution for morphological traits in intercross population of maize

C. Neelima[1], C. Sarankumar[2], M. Sudha[1], K. N. Ganesan[3], R. Ravikesavan[4] and N. Senthil[2*]

[1]Department of Plant Biotechnology. Centre for Plant Molecular Biology and Biotechnology,
[2]Department of Plant Molecular Biology and Bioinformatics, Centre for Plant Molecular Biology and Biotechnology,
[3]Department of Genetics and Plant Breeding,
[4]Department of Millets, Centre of plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
***E-Mail**: senthil_natesan@tnau.ac.in

Abstract

Genetic variability analysis is an essential criterion in the selection of crops for improvement programmes and components like Phenotypic Coefficient of Variation, Genotypic Coefficient of Variation, heritability and Genetic Advance as percent of Mean are useful for the exploitation of variability. Skewness and kurtosis indicate the type of gene action and the number of genes governing the trait and selection can be done based on these values. In the present study, variability, heritability, genetic advance, skewness and kurtosis were assessed for the intercross (IC$_2$) population of (UMI1200×CE477) × (UMI1200×VQL1). Fourteen biometrical traits were recorded and the mean values were used for further analysis. Higher PCV values were obtained compared to their respective GCV values for all the traits of the population. Cob length (83.28% and 2.09%) showed the highest heritability and genetic advance suggesting higher genetic gain, which can be improved with simple selection methods and hence, showing additive gene action. Single plant yield showed higher heritability (77.29%) with low genetic advance (0.80%) and hence, requires appropriate selection methods to improve the genetic gain. With the exception of days to tasseling, all the traits showed platykurtic distribution suggesting that the large number of genes are involved in governing the traits. Days to silking, tassel length, the number of tassel branches, leaf length, leaf breadth, cob length, the number of kernels per row, cob weight, 100 kernel weight and single plant yield showed positive skewness suggesting dominant based complementary epistasis and hence, rapid genetic gain can be obtained by intense selection. Days to tasseling, plant height, ear height and the number of kernel rows per cob negative skewness showing duplicate gene action and hence, the rapid genetic gain can be obtained by mild selection.

Keywords

Genetic variability, heritability and GAM, skewness, kurtosis, maize

INTRODUCTION

Maize is one of the primary cereal crops that is grown throughout the world for its binary relevance in diet as well as livestock feed (Gwirtz *et al.,* 2014). As a result of its nutritional importance, diversity, wide adaptability and higher productivity potential, maize is a staple in many parts of the world. Normal maize is low in Vitamin A and certain essential amino acids like lysine and tryptophan. Owing to its wide usage, there is an urgent need to fortify maize with the deficient nutrition. Several studies have been aimed at improving the nutrition in maize (Muthusamy *et al.,* 2014, Hossain *et al.,* 2018, Pukalenthy *et al.,* 2019 and Chandran *et al.,* 2019). The improvement of nutritional traits and selection of lines with higher beta carotene and Quality Protein Maize traits must be coupled with the selection of lines with higher yield characters and good agronomic performance.

A decisive analysis of the genetic variability is an essential criterion for the initiation of any crop improvement programme in order to adopt the appropriate selection strategies (Dhanwani *et al.,* 2013). Effective genetic improvement can be made through proper understanding of nature and degree of genetic variation that influence quantitative and economic traits. Variability parameters including range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and heritability are usually utilized for efficient exploitation of variability (Kishore *et al.,* 2015). Since plant characters are complex in nature and is often environment biased and controlled by several genes in different environments, PCV and GCV is useful not only for the comparison of the phenotypic and genotypic variation but also acts as a tool to measure the effectiveness of the appropriate selection procedure for improvement (Bello *et al.,* 2012). Heritability is often measured in terms of the phenotypic variation that occurs due to various genetic causes. It often focuses on the extent of transmissibility of a character from one generation to the other. Effective selection procedures that significantly influences the improvement of a character can be established through the measure of heritability (Samadia, 2005). Simple selection methods are enough to quickly fix characters with high heritability. But heritability alone does not offer any practical importance unless coupled with genetic advance. Genetic advance exhibits the proportion of genetic gain expected when a selective pressure is applied to a particular trait. Therefore, a trait showing high heritability and high genetic advance is likely to be the best condition for selection (Ramanujam and Thirumalachar, 1967).

Skewness is a measurement of symmetry of the population and is often used to indicate the nature of gene action for any trait (Fisher, 1932). Positive skewness corresponds to complementary gene action, whereas negative skewness corresponds to duplicate epistasis (Pooni *et al.,* 1977). Kurtosis designates the number of genes that is governing the trait of interest (Robson, 1956). Kurtosis is a measure of peakedness or tailness of a data and measuring whether it is right tailed or left tailed to the normal distribution. Kurtosis is manifested in three levels *viz.,* leptokurtic (positive kurtosis) signifying that the traits are controlled by fewer genes, mesokurtic (normal distribution at 0) and platykurtic (negative kurtosis) signifying that the traits are controlled by a larger number of genes (Kapur, 1981). Several studies have analyzed the variability and frequency distribution for the maize lines improved with enhanced nutritional content (Lal and Singh, 2014, Chandana *et al.,* 2018, Bharathi *et al.,* 2018, Nagalakshmi *et al*., 2018 and Sarankumar *et al.,* 2019). The present study focuses on the analysis of genetic variability through PCV, GCV, GAM and heritability and to estimate the descriptive statistics of the population and to identify the nature of gene action in an intercross population that is enhanced for both beta carotene and QPM traits.

MATERIALS AND METHODS

The intercross (IC_2) generation of (UMI1200×CE477) × (UMI1200×VQL1), used in the study, was developed by the intercross of BC_3F_1 progenies from two independent crosses (UMI1200×CE477 and UMI1200×VQL1). The BC_3F_1 progenies were crossed during kharif 2018 to yield the IC_1 generation. These were selfed during rabi Summer 2018-2019 to produce the IC_2 generation. The IC population was developed to introgress two nutrition traits beta carotene and QPM into a single genotype. The IC_2 generation was evaluated at the Department of Millets, TNAU, Coimbatore. The plants were raised with a spacing of 60 × 25 cm in four-meter rows. All the necessary agricultural and protection strategies were followed.

Fourteen agronomic traits including days to tasseling (DT) (days), days to silking (DS) (days), plant height (PH) (cm), ear height (EH) (cm), tassel length (TL) (cm), the number of tassel branches (NTB) (nos.), leaf length (LL) (cm), leaf breadth (LB) (cm), cob length (CL) (cm), the number of kernels per row (NK/R) (nos.), the number of kernel rows per cob (NKR/C) (nos.), cob weight (CW) (g), 100 kernel weight (100KW) (g) and single plant yield (SPY) (g) were recorded for 115 plants from the IC_2 generation. The flowering data and the other morphological trait measurements were made from the date of tasseling and the cob measurements were taken when the physiological maturity was attained. The mean values were considered for calculations. The descriptive statistics were performed using the SPSS 16.0 software package. Descriptive statistics included skewness, kurtosis, variance, mean, range and standard deviation.

They mean data were also used to determine the Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), heritability (h^2 in the broad sense), Genetic Advance (GA), and Genetic Advance as percent of Mean (GAM). The Phenotypic Coefficient of Variation and the Genotypic Coefficient of Variation were calculated based on the technique formulated by Burton (1952). Broad sense heritability was computed by the approach given by Lush (1940). The GA and GAM (%) was determined by the calculation formulated by Johnson *et al.,* (1955).

RESULTS AND DISCUSSION

Exploitation of variability in the form of Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV) and heritability is essential for proper selection of lines for any breeding programme (Kishore *et al.,* 2015). The estimates of variability are given in Table 1. PH recorded the highest mean value (154.02cm) followed by CW (119.59cm). A higher proportion of PCV to GCV value was obtained for all the traits suggesting an influence of the environment. The phenotypic coefficient

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Table 1. Estimation of variability in (UMI1200×CE477) × (UMI1200×VQL1)

Characters	Parents (mean)	Progenies (mean)	PCV	GCV	h^2	GAM
DT	57.90	57.92	0.98	0.81	68.86	0.80
DS	59.90	59.96	0.99	0.84	71.65	0.87
PH	154.71	154.02	0.72	0.64	80.50	1.82
EH	74.80	75.02	1.59	1.34	71.74	1.75
TL	20.10	19.96	6.34	5.66	79.86	2.07
NTB	8.90	8.92	7.77	6.91	79.19	1.13
LL	55.33	54.98	2.30	2.09	83.26	2.15
LB	6.41	6.39	1.86	1.63	77.16	0.19
CL	13.00	13.01	9.40	8.58	83.28	2.09
NK/R	25.10	24.99	4.84	4.27	77.93	1.93
NKR/C	11.80	11.32	8.42	7.55	80.43	1.57
CW	119.70	119.59	0.82	0.72	75.63	1.53
100 KW	27.74	27.83	1.69	1.44	72.95	0.70
SPY	99.79	99.75	0.51	0.45	77.29	0.80

Note: DT – Days to tasseling, DS – Days to silking, PH – Plant height, EH – Ear height, TL – Tassel length, NTB – Number of tassel branches, LL – Leaf length, LB – Leaf breadth, CL- Cob length, NK/R – Number of kernels per row, NKR/C – Number of kernel rows per cob, CW – Cob weight, 100KW – 100 kernel weight, SPY – Single plant yield.

of variation was low for all the traits and ranged from 0.51% (SPY) to 9.40% (CL) and the genotypic coefficient of variation was also low for all the traits and ranged from 0.45% (SPY) to 8.58% (CL). Sarankumar *et al.,* (2019) reported PH recorded lower PCV and GCV values (1.39% and 1.18%). Bello *et al.,* (2012) reported low PCV and GCV values for seedling emergence (6.78% and 6.25%) and for days to tasseling (5.95% and 6.45%). The low coefficient of variation values suggests low variability among the population. This could be due to the fact that the populations obtained for the development of the intercross population already attained homozygosity. The estimate of heritability is a predictive measure scrutinizing the reliability of the phenotypic data and genetic advance as percent of mean is evidence of the expected result of the application of a selection pressure on the pertinent population. Hence, the heritability along with GAM would offer a more consistent index for the selection value (Johnson *et al.,* 1955). Heritability is usually measured in three levels *viz.,* low (for characters showing heritability of <30%), moderate (for characters showing a heritability of 30-60%) and high (for characters showing a heritability of >60%) (Robinson *et al.,* 1949) whereas genetic advance is measured as low (for characters showing a GAM value of <10%), moderate (for characters showing a GAM value of 10-20%) and high (for characters showing a GAM value of >20%) (Johnson *et al.,* 1955). All the traits showed high heritability ranging from 68.86% (DT) to 83.28% (CL). The maximum heritability was obtained for CL (83.28%) followed by LL (83.26%) and PH (80.50%). Lal and Singh (2014) reported high heritability for all the traits with the highest being seed yield (97%) followed by ear length (90.55%) and plant height (90.35%). Highest GAM was obtained for LL (2.15%) followed by CL (2.09%) and TL (2.07%) and ranged from 0.19% (LB) to 2.15% (LL). Bharathiveeramani *et al.,* (2012) reported high GAM values for DT (8.36%), DS (9.22%), 100KW (6.52%). A high heritability and genetic advance were obtained for CL (83.28% and 2.09%) and LL (83.26% and 2.15%) followed by PH (80.50% and 1.82%) and TL (79.86% and 2.07%). Higher heritability increases the opportunity for genetic improvement via proper methods of selection and hence the coupling of higher heritability with higher GA leads to higher genetic gain with additive gene action. DT, DS and EH had lower heritability and GAM values (68.86% and 0.80%, 71.65% and 0.87%, 71.74% and 1.75% respectively) which suggests that the genetic gain can be increased through stringent selection. Chandana *et al.,* (2018) reported high heritability and high GAM values for CW (99.68% and 40.97%) followed by SPY (99.55% and 47.25%) and NK/R (98.68% and 62.94%).

The nature of gene action and the number of genes controlling the trait is usually measured by the critical analysis of distribution properties by third order statistics such as skewness and kurtosis which are more important than the first and second order statistics that unravel only the interaction effects (Rani *et al.,* 2016). Skewness indicates the cluster of deviation above and below the value of central tendency and defines the extent of deviation in the distribution. Positive skewness would indicate the traits to be controlled by dominant and complementary gene action whereas a negative skewness would indicate the traits to be controlled by dominant and duplicate epistasis. Kurtosis indicates the level of peakedness over the population with a leptokurtic distribution would mean that the trait in question is controlled by fewer genes whereas a platykurtic distribution would mean that the trait is governed by many genes.

The skewness and kurtosis along with the frequency distribution is furnished in Table 2 and Fig. 1. A wide variation was exhibited by CW and ranged from 117.5g to 121.5g. All the traits exhibited low variation and majority of the lines had the same range as that of the recurrent parent. This low variability occurred due to the fact that the intercross population was developed from two populations that have already attained a high level of homozygosity

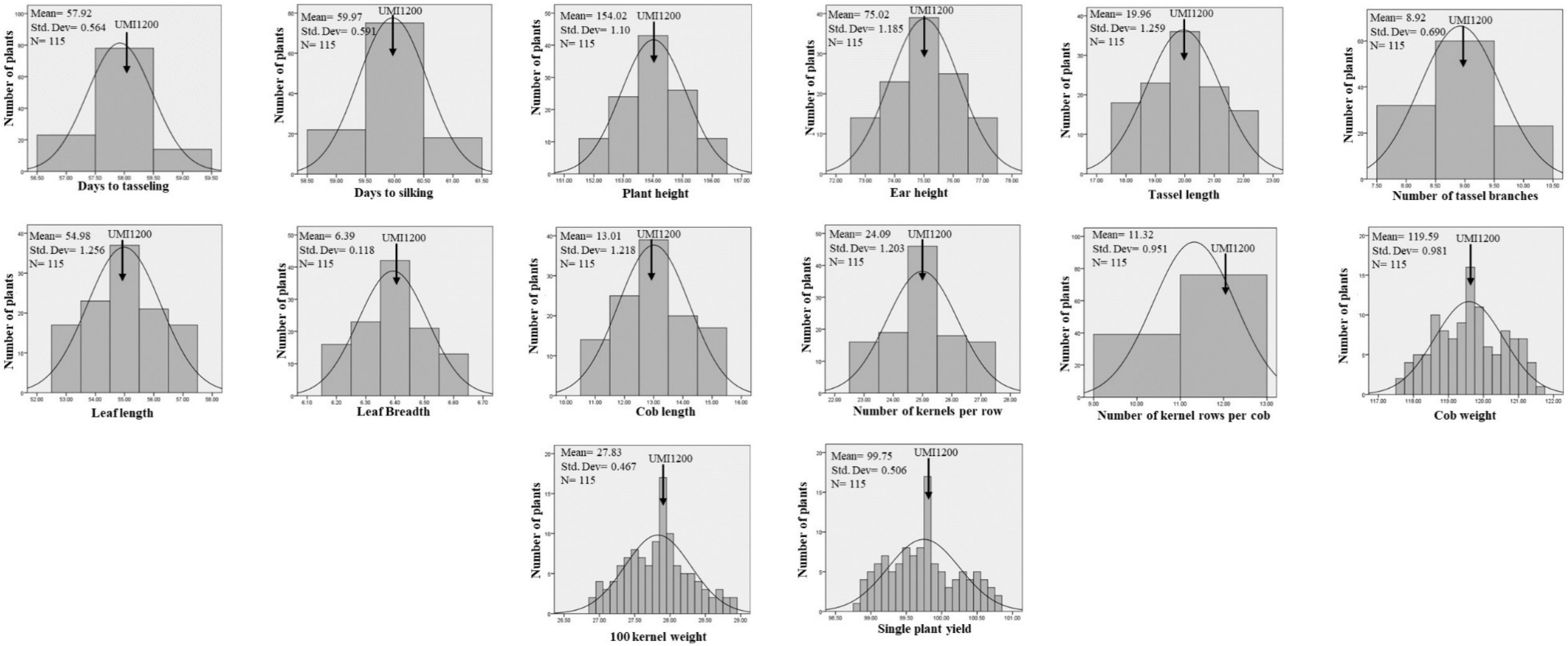

Fig.1. Frequency distribution for morphological traits in (UMI200×CE477)×(UMI1200×VQL1)

and had the same values as that of the recurrent parent. Hence, essentially majority of the intercross progenies are falling under the same graph as that of the recurrent parent. All the traits except DT showed platykurtic distribution, ranging from -0.94 (TL) to -0.10 (DS) with an average of -0.70, which indicates that the traits are governed by a large number of genes. Bharathi *et al.,* (2018) obtained platykurtic distribution for all the traits in the BC_2F_2 population ranging from -1.27 (SPY) to -0.17 (DS) for the cross UMI1200×VQL1. Nagalakshmi *et al.,* (2018) reported platykurtic distribution for DS (-0.17), CL (-0.23), CW (-0.22), NKR/C (-0.57), NK/R (-0.56) and SPY (-0.04). Skewness among the population ranged from -0.67 (NKR/C) to 0.22 (SPY). DT (-0.02), PH (-0.04), EH (-0.03) and NKR/C(-0.67) exhibited negative skewness whereas DS (0.01), TL (0.03), NTB (0.11), LL (0.03), LB (0.04), CL (0.07), NK/R (0.02), CW (0.02), 100KW (0.17) and SPY (0.22) exhibited positive skewness. Negatively skewed platykurtic distribution suggests that these traits are controlled by larger number of genes and displaying dominant and dominant based duplicate epistasis. Hence, rapid genetic gain can be obtained through mild selection for DT, PH, EH and NKR/C. Raghavendra and Hittalmani (2015) reported negatively skewed and platykurtic distribution for days to maturity (-0.39 and -0.19) and days to 50% flowering (-0.132 and -0.94). The positively skewed platykurtic distribution suggests that these traits are also controlled by larger number of genes but displaying dominant and dominant based complementary epistasis. Hence, rapid genetic gain can be obtained only through intense selection in DS, TL, NTB, LL, LB, CL, NK/R, CW, 100KW and SPY (Pooni *et al.,* 1977). Sumathi *et al.,* (2018) reported positively skewed platykurtic distribution for DT (0.12 and -1.61), DS (0.31 and -1.67), PH (0.21 and -0.82), NKR/C (0.73 and -0.40) and grain yield (0.67 and -1.43).

Table 2. Estimation of range, mean, standard deviation, variance, skewness and kurtosis in (UMI1200×CE477) × (UMI1200×VQL1)

Characters	Range		Mean	Standard Deviation	Variance	Skewness	Kurtosis
	Min	Max					
DT	57	59	57.92	0.57	0.32	-0.02	0.13
DS	59	61	59.96	0.59	0.35	0.01	-0.10
PH	152	156	154.02	1.10	1.22	-0.04	-0.56
EH	73	77	75.02	1.19	1.42	-0.03	-0.77
TL	18	22	19.96	1.26	1.60	0.03	-0.94
NTB	8	10	8.92	0.69	0.48	0.11	-0.89
LL	53	57	54.98	1.26	1.59	0.03	-0.92
LB	6.2	6.6	6.39	0.12	0.01	0.04	-0.71
CL	11	15	13.01	1.22	1.50	0.07	-0.83
NK/R	23	27	24.99	1.21	1.46	0.02	-0.68
NKR/C	10	12	11.32	0.95	0.91	-0.67	-1.57
CW	117.5	121.5	119.59	0.99	0.97	0.02	-0.80
100 KW	26.9	28.9	27.83	0.47	0.22	0.17	-0.40
SPY	98.8	100.8	99.75	0.51	0.26	0.22	-0.77

Note: DT – Days to tasseling, DS – Days to silking, PH – Plant height, EH – Ear height, TL – Tassel length, NTB – Number of tassel branches, LL – Leaf length, LB – Leaf breadth, CL- Cob length, NK/R – Number of kernels per row, NKR/C – Number of kernel rows per cob, CW – Cob weight, 100KW – 100 kernel weight, SPY – Single plant yield.

From the above results, CL showed the highest heritability and GAM values (83.28% and 2.09%) and hence, higher genetic gain and governed by additive gene action. SPY showed high heritability (77.29%) with low genetic advance (0.80%) and hence require appropriate selection methods to improve the genetic gain. All the traits except DT showed platykurtic distribution. DS, TL, NTB, CL, NK/R, CW, 100KW and SPY showed positive skewness indicating complementary epistasis governed by large number of genes and hence an intense selection is required for rapid genetic gain and DT, PH, EH and NKR/C showed negative skewness indicating duplicate gene action governed by large number of genes and hence a mild selection is required for a rapid genetic gain. The other traits have lower genetic gain and require proper selection methods to further improve the genetic gain in these traits. The IC population, therefore, shows significant genetic improvement in the agronomic characters based on the estimate of genetic gain and mode of gene action along with the desirable trait of increased nutrition and hence serve as a potential breeding material for further studies.

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