

Study of Third Order Statistics in Maize Genotypes



Agriculture

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ABSTRACT

An investigation was carried out using forty maize genotypes belonging to grain maize, baby corn, sweet corn, pop corn and quality protein maize, to study the measures of symmetry (skewness), which is a descriptive statistics. The third order statistics, skewness revealed that nine traits were skewed negatively and sixteen traits were skewed positively, indicating additive and non additive gene action respectively.

Introduction:

Maize is the third most important food crop next to rice and wheat. It is the staple diet of low income families in several parts of India. About 66 per cent of the maize produced in the globe is used as feed, 17 per cent as food and as industrial produce and the remaining as seed. It has several industrial uses and is one of the crops whose advantageous features were realized and exploited from time immemorial (CIMMYT, 2000).

Crop improvement in maize has passed through several phases. Selection as a method of breeding probably dates back to the beginning of domestication (Mukherjee, 1997). Other breeding methods for maize improvement are mass selection, ear to row selection, varietal hybridization, development of synthetics and composites and heterosis breeding. Among these methods, varietal hybridization, development of synthetics, composites and hybrids, which take advantage of the allogamous nature of the crop, have gained much importance.

Generally all of our current quantitative genetic theories are based on first and second order statistics. Fisher *et al.*, (1932) emphasized the usefulness of third order (skewness) statistics in the study of quantitative traits. Hence a study was conducted in maize, to study the measures of symmetry (skewness), which is a descriptive statistics.

Materials and methods:

A collection of forty maize germplasm belonging to grain maize, baby corn, sweet corn, pop corn and quality protein maize were selected at random, but keeping in view that they represent the different types of maize, classified based on the grain characters and chemical composition (Table 1). The selfed progenies of the selected genotypes were raised at the Millet Breeding Station, TNAU in a randomized block design with two replications.

Table 1. List of genotypes used for the study

Sl. No	Genotype	Type	Sl.No	Genotype	Type
1.	CO1	Grain maize	21.	USC-5	Sweet corn
2.	UMC-12	Grain maize	22.	USC-7	Sweet corn
3.	UMC-13	Grain maize	23.	USC-9	Sweet corn
4.	UMH-15	Grain maize	24.	USC-10	Sweet corn
5.	UMH-26	Grain maize	25.	QPM-9114	QPM
6.	UMH-40	Grain maize	26.	QPM-9120	QPM
7.	UMH-42	Grain maize	27.	QPM-9122	QPM
8.	COH (M)-4	Grain maize	28.	QPM-9127	QPM
9.	COBC-1	Baby corn	29.	QPM-3	QPM
10.	BC-Local	Baby corn	30.	QPM-4	QPM
11.	BC-5	Baby corn	31.	QPM-5	QPM
12.	BC-7	Baby corn	32.	QPM-8	QPM
13.	BC-8	Baby corn	33.	9101 PC	Popcorn
14.	2KBC-6	Baby corn	34.	9102 PC	Popcorn
15.	2KBC-7	Baby corn	35.	9103 PC	Popcorn
16.	2KBC-8	Baby corn	36.	UPC-1	Popcorn
17.	USC-1	Sweet corn	37.	UPC-2	Popcorn
18.	USC-2	Sweet corn	38.	UPC-3	Popcorn
19.	USC-3	Sweet corn	39.	Bangalore Popcorn	Popcorn
20.	USC-4	Sweet corn	40.	Amber Popcorn	Popcorn

Observations for twenty five quantitative characters viz., Days to 50 per cent tasseling (Dt), Days to 50 per cent silking (Ds), Plant height (H), Ear height (Eh), Leaf number (Ln), Number of leaves above the upper most cob(Lac), Leaf length (Ll), Leaf width (Lw), Tassel length (Tl), Tassel branch (Tb), Cob length (Cl), Cob diameter (Cod), Number of grain rows per cob (Gr), Number of grains per row (Gpr), Number of grain per cob (Gpc), Hundred grain weight (Sw), Grain yield per plant (Y), Weight of the cob (Wc), Shelling percentage (Sp) and Days to maturity (Dm), were recorded on five randomly selected plants for each genotype in both the replications. Data of all these traits were recorded as per the NBPGR descriptor. Total Sugar, Starch Content, Carotene content, Crude protein content and Oil content were also estimated in two replicates.

The mean values of the genotypes for twenty five characters over two replications were subjected to descriptive statistics analysis using STATISTICA package.

Results and Discussion

The gene action for the quantitative traits in the germplasm collection of maize was found out based on the frequency distribution of traits through skewness which is a third order statistics skewness describes the degree of departure of a distribution from symmetry. Skewness could result when certain combinations of genes are lethal, presence of incomplete linkage of certain genes, presence of epistasis and one gene has a much larger effect than others.

Sign of skewness helps us to draw the conclusion about the gene action for a particular trait. The positive skewness indicated the presence of complementary epistatic gene action for that trait. The gain is slower with the mild selection and faster with intensive selection for that particular trait. The negative skewness indicated the presence of duplicate epistatic gene action and the gain is faster with mild selection and less rapid with intense selection. (Snape and Riggs, 1975).

The data recorded on twenty quantitative and five biochemical characters were subjected to descriptive statistics and properties of quantitative traits such as measures of central tendency (mean, median and mode), measures of dispersion or variability (range, variance, standard deviation and standard error) and measures of symmetry (skewness) were analysed and their respective values are furnished in the Table 2.

This third order statistics exhibited maximum positive value for oil content (1.72) and minimum positive value for shelling percentage (0.004). In the negative direction it showed maximum value for tassel branch (-0.59) and minimum value for number of grain rows per cob (-0.09).

Out of the twenty five characters investigated, nine traits viz., leaf number, number of leaves above the uppermost cob, leaf length, leafwidth, tassel branch, cob length, cob diameter, number of grain rows per cob and carotene content showed negative skewness values. Hence in the frequency distribution curves, most of the genotypes for these traits were distributed in the right hand direction (Figure 1 and 2). This indicates the presence of additive

gene action for these traits and hence they can be utilized as selection criteria while selecting the parents for hybridization programmes.

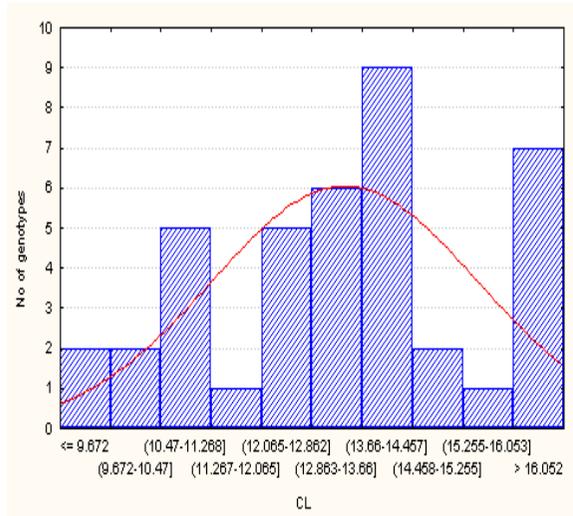


Fig 1. Frequency distribution of 40 maize genotypes for cob length

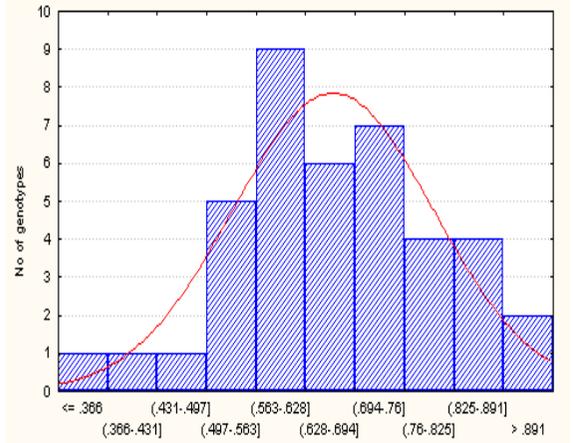


Fig 2. Frequency distribution of 40 maize genotypes for carotene content

The remaining sixteen characters such as days to 50 per cent tasseling, days to 50 per cent silking, plant height, ear height, tassel length, number of grains per row, number of grains per cob, hundred grain weight, grain yield per plant, weigh of the cob, shelling percentage, days to physiological maturity, total sugars, starch, protein content and oil content were skewed positively. Thus in the frequency distribution curves most of the genotypes were distributed in the left direction (Figure 3 and 4), indicating the presence of non additive gene action for these characters. These positively skewed characters can be used as selection indices for selecting the line for development of composites and synthetics in maize.

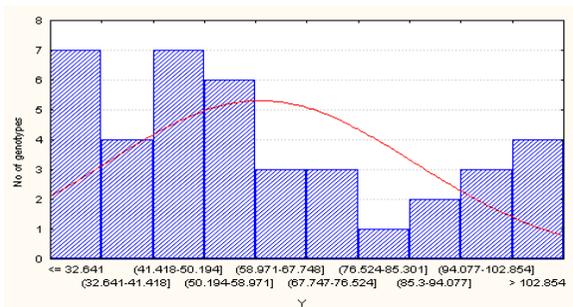
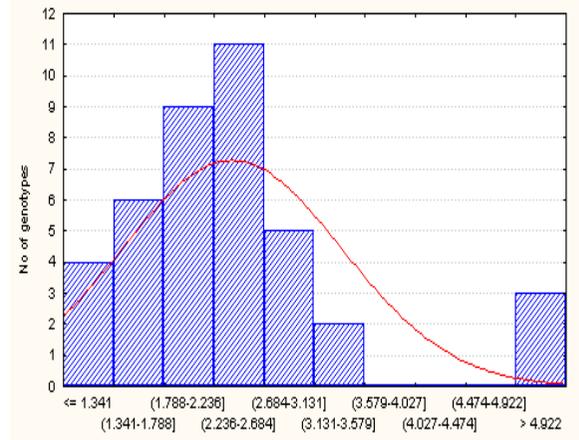


Fig 3. Frequency distribution of 40 maize genotypes for grain yield per plant

Conclusion

The third order statistics, skewness revealed that nine traits were skewed negatively and sixteen traits were skewed positively, indicating additive and non additive gene action respectively. Characters with additive gene action such as cob length, cob diameter, leaf number, leaf length, leaf width etc can be used as selection criteria for selection of parents for hybridization programme. Whereas the characters with non additive gene action such as plant height, ear height, number of grain rows per cob, number of grains per row etc can be used as selection indices for selecting lines for development of composites and synthetics.

Fig 4. Frequency distribution of 40 maize genotypes for oil



content

Table 2. Descriptive statistics of 25 characters in 40 maize genotypes

Characters	Mean	Median	Minimum	Maximum	Range	Variance	S.D	S.E	Skewness
Dt	57.46	57.25	53.00	63.00	10.00	4.45	2.11	0.33	0.67
Ds	60.03	59.75	56.00	66.00	10.00	5.79	2.41	0.38	0.40
H	124.20	118.85	94.70	167.30	72.60	403.16	20.08	3.18	0.77
Eh	60.25	56.30	35.00	100.00	65.00	228.53	15.12	2.39	0.62
Ln	12.51	12.55	9.50	14.30	4.80	1.18	1.08	0.17	-0.57
Lac	5.08	5.20	3.60	6.20	2.60	0.32	0.57	0.09	-0.57
Ll	59.273	58.65	46.00	71.60	25.60	38.63	6.22	0.98	-0.17
Lw	7.601	7.58	5.30	9.40	4.10	0.98	0.99	0.16	-0.26
Tl	28.95	27.93	22.50	37.40	14.90	13.73	3.71	0.59	0.55
Tb	16.58	16.75	10.60	20.40	9.80	5.03	2.24	0.36	-0.59
Cl	13.38	13.49	8.88	16.85	7.98	4.43	2.11	0.33	-0.20
Cod	3.74	3.80	2.43	5.18	2.75	0.43	0.66	0.10	-0.16
Gr	14.83	15.00	11.00	18.90	7.90	2.15	1.47	0.23	-0.09
Gpr	26.72	26.05	19.00	37.00	18.00	19.87	4.46	0.71	0.41
Gpc	358.21	354.30	216.70	492.20	275.50	5063.82	71.16	11.25	0.01
Sw	19.16	17.82	11.64	28.20	16.57	21.65	4.65	0.74	0.22
Y	59.77	51.71	23.87	111.63	87.77	695.422	26.37	4.17	0.66
Wc	72.07	64.18	29.37	131.39	102.02	908.06	30.13	4.77	0.58
Sp	82.29	82.30	75.17	88.52	13.35	6.94	2.64	0.42	0.004
Dm	103.68	103.25	98.00	111.00	13.00	7.60	2.76	0.44	0.94
Sug	4.52	2.93	1.70	8.50	6.80	6.73	2.59	0.41	0.44
Sta	73.90	75.60	62.95	88.40	25.45	33.31	5.77	0.91	0.06
Car	0.66	0.67	0.30	0.96	0.66	0.02	0.13	0.02	-0.12
Pro	11.41	11.08	9.49	13.41	3.93	1.18	1.09	0.17	0.26
Oil	2.40	2.31	0.89	5.37	4.48	0.97	0.98	0.16	1.72

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