The Pharma Innovation

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Assessment of genetic diversity analysis in maize (*Zea Mays* L.) for yield and yield attributing traits in Middle Gujarat condition

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Abstract
Maize is considered as queen of cereals. Present investigation is performed to investigate the presence of variability in the group of maize germplasms. Fifty-one genotypes were grown in two replicate with randomized complete block design. Analysis of variance revealed the presence of higher amount of genetic variability for most of the characters while further assessment through genetic variability analysis revealed that grain yield per plant and ears per plant mainly governed by the additive gene action with moderate heritability with high genetic advance while no of kernels per row was found low heritable with moderate genetic advance suggest the preponderance of the dominant gene action. These few characters were improved through exploitation of heterosis while rest of the characters governed by the additive gene action may improve by the selection from the segregating population.

Keywords: Maize, Variability, GCV, PCV, Heritability

Introduction

As the world's population grows, the scientific community must employ all available means to enable producers to fulfill the world's ever-increasing need for food and other resources. In this pursuit, modern breeding technologies show promise. Plant breeders like maize because of its high photosynthetic rates, high yield, and vast adaptability. In various regions of the world, it is a valuable food source for humans and cattle, as well as a source of biofuel and fiber (Xu *et al*., 2009) [2].

Maize (*Zea mays* L.) belongs to the tribe Maydeae of the grass family Poaceae, with chromosomal number 2n=20 and a genomic size of 2.36 Gb. *Zea mays* is an annual and perennial grass genus endemic to Mexico and Central America. Male and female flowers are present on distinct inflorescences on the same plant in a monoecious plant. Male inflorescences, known as tassels, are found at the apex of the plant and consist of a core spike and 10-50 lateral branches. A tassel spikelet comprises two florets, and each floret has three anthers. Pollen grains formed by anthers are very minute, hardly visible with the human eye, light in weight, and quickly carried away by the wind. Silk, cob, or ear female inflorescences appear halfway on the main stem. At the moment of initiation, axillary buds have two florets, but only the top one develops. Each functioning floret of an ear generates an ovary with a silk-covered elongated style (trichomes). It is typically protandrous, which means that male spikelets mature before female spikelets. Anemophily pollens and protandry increase cross-pollination, although only approximately 5% of self-pollination is documented (Hofmann *et al*., 2014) [3]. Grains grow in ears or cobs, frequently one on each stalk, and account for roughly 42% of a plant's dry weight.

Maize was grown over an area of 193.7 million ha worldwide, yielding 1,147.7 million tonnes of grain in 2019 with an average productivity of 5925 kg/ha (Anonymous, 2019) [4]. Maize is the third most significant cereal in India, after rice and wheat. The total cultivated land area was 9.13 million hectares. With 27.80 million tonnes of grain produced and an average productivity of 2509 kg/ha (Anonymous, 2019) [4]. At present prices, maize provides approximately 9% of the national food basket and more than $400 billion to agricultural GDP. The primary goal of most maize breeding programmes is the generation of widely adopted high-yielding cultivars. Since yield is a complicated property, selecting based on its component character may be more successful. Path coefficient analyses between yield and yield components are required before planning a useful breeding programme.

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Numerous researchers have sought to discover the link between the characteristics on which high-yielding choices may be performed, emphasizing the relevance of genetic component estimations in forecasting quantitative characters for selection as well as the associated response.

Materials and Methods
Experimental site
This experiment was conducted at the Experimental Farm, Department of Genetics & Plant Breeding, B. A. College of Agriculture, AAU, Anand, which is located in Gujarat state's Agro Climatic Zone-III (Middle Gujarat). Anand is located at 22° 35' N latitude and 72° 55' E longitude, at an elevation of 45.1 meters above mean sea level. The experimental site's soil is sandy loam, a typical "Goradu" soil (alluvial in origin and belongs to alfisol) of the "Charotar" tract with low organic matter content. It is rather deep, well drained, and moisture retentive. The climate of the region is tropical and semi-arid.

Experimental design and material
In a randomized complete block design with two replications, 51 different maize genotypes were evaluated. Each genotype was planted in a single row 5.0 m long, 30 cm apart, with a plant-to-plant spacing of 10 cm. The experiment was surrounded by boundary rows to prevent damage and border effects. Agronomical and plant protection procedures were implemented to ensure a good yield.

Studied characters
Plant height (PH), ear height (EH), ear length (EL) and ear girth (EG) were recorded in centimeters while ears per plant (EPP), number of kernel rows per ear (KRP), number of kernels per row (KPR), number of kernels per ear (NKE) were recorded on the basis of counting. Grain yield per plant was measured in grams. All observations were recorded on five randomly selected competitive plants of each genotype in each replication for various maize descriptors (IBPGR, 1991). On a plot basis, the phenological characteristics of tasselling (TA) and Silking (SI) were recorded.

Statistical analysis
The mean values were used to calculate the analysis of variance (Panse and Sukhatme, 1978) [16], genotypic and phenotypic coefficients of variation (Burton, 1952) [6],

heritability in general (Allard, 1960) [7], and genetic progress expressed as a percentage of mean (Johnson *et al*., 1955) [15]. The data were analyzed in R-studio using the "Variability" package (Popat *et al*., 2020) [8].

Result and Discussion
ANOVA and mean performance
Mean is a relatively simple measure used in plant breeding to assess phenotypic variability and it serves as the basis for screening desirable genotypes. The mean values of 51 genotypes of maize for all the 14 quantitative characters along with standard error of mean (S.E.M ±), critical difference (C.D) and coefficient of variation (C.V %) are given in Table 1. The analysis of variance found that the mean sum of squares owing to genotypes was very significant for all of the characters, demonstrating the presence of substantial genetic variability in the experimental material. Analysis of variance (ANOVA) may not disclose absolute variability, which may be obtained by normalizing the phenotypic and genotypic variances and calculating the coefficient of variability. The vast range of diversity allows plant breeders to pick superior and desired genotypes for further crop development. Aside from ANOVA, the level of variation may be evaluated and stated specifically in terms of genotypic variance, phenotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation, heritability, and genetic advance as a percentage the of the mean (Table 2).

All crops benefit from early blossoming. During days to 50% tasselling, there were significant variations between genotypes (Table 1). This trait's mean values varied from 55.50 to 77.50 days. At 55.50 days of sowing, the genotype GWQPM-40-5 displayed early tasseling, followed by GWQPM-46-2 (56.50 days) and GWQPM-47-1 (59.00 days). A similar pattern was seen for days to 50% Silking. Ear height is an essential agronomic feature in maize breeding because it influences plant development andyieldsd potential. I-07-66-4-1 (74.88 cm) and GWQPM-67-2 (78.97 cm) genotypes had the longest ears (72.06 cm). I-07-60-4-3 has the lowest ear placement recorded (23.42 cm). Grain yield, which ranged from 27.18 to 111.25 g, was shown to have a substantial genotypic difference. Among all the genotypes, GWQPM-22-5 (111.25 g) was significantly producing more grain yield which was followed by GWQPM-11 (102.09 g) and IL-17-28 (97.87 g).

Table 1: Mean performance, analysis of variance (ANOVA) and estimation of genetic variables for 19 characters of maize

Trait	Mean	S.E.M.	C.D. at 5%	CV%	Replication (DF = 01)	Genotypes (DF = 50)	Error (DF = 50)
Days to 50% tasseling	68.96	1.61	4.58	3.31	106.03**	58.65**	5.21
Days to 50% silking	75.18	1.73	4.29	3.25	148.32**	54.29**	6.00
Plant height (cm)	125.16	6.31	17.94	7.14	2033.23**	969.83**	79.86
Ear height (cm)	49.53	3.06	8.71	8.75	429.07**	281.00**	18.83
Ears per plant	1.45	0.20	0.58	20.05	0.21	0.20**	0.08
Ear length (cm)	13.49	0.82	2.32	8.59	3.22	9.87**	1.34
Ear girth (cm)	11.18	0.92	2.63	11.70	0.02	5.42**	1.71
Ear weight (g)	78.64	7.33	20.82	13.18	39.84	1477.28**	107.49
Number of kernel rows per ear	13.34	1.05	3.01	11.22	0.65	4.56**	2.24
Number of kernels per row	25.16	1.67	4.76	9.43	36.79*	56.95**	5.63
Number of kernels per ear	337.11	33.69	95.71	14.13	5153.00	14203.50**	2270.80
Shelling (%)	65.89	0.77	2.19	1.65	1.42	95.48**	1.19
Test weight (g)	17.59	2.45	6.98	19.76	190.29**	42.20**	12.09
Grain yield per plant (g)	63.17	10.56	30.00	23.64	3372.8**	801.7**	223.2

Table 2: Variability parameters of 14 characters of maize

Trait	σ^2_g	σ^2_p	GCV (%)	PCV (%)	H^2_b (%)	GA% Mean
Days to 50% tasseling	26.71	31.93	7.49	8.19	83.66	14.12
Days to 50% Silking	24.14	30.15	6.53	7.30	80.09	12.04
Plant height (cm)	444.98	524.84	16.85	18.30	84.78	31.96
Ear height (cm)	131.08	149.91	23.11	24.71	87.44	44.52
Ears per plant	0.06	0.14	16.82	26.17	41.32	22.28
Ear length (cm)	4.26	5.61	15.30	17.55	76.02	27.48
Ear girth (cm)	1.85	3.56	12.16	16.88	51.93	18.06
Ear weight (g)	684.89	792.38	33.27	35.79	86.43	63.73
Number of kernel rows per ear	1.15	3.40	8.06	13.82	34.01	9.68
Number of kernels per row	25.66	31.29	20.12	22.22	81.99	37.54
Number of kernels per ear	5966.39	8237.14	22.91	26.92	72.43	40.17
Shelling (%)	47.14	48.33	10.41	10.55	97.53	21.19
Test weight (g)	15.05	27.14	22.04	29.60	55.44	33.81
Grain yield per plant (g)	289.24	512.42	26.92	35.83	56.45	41.66

Genetic variability, heritability and genetic advance

The genetic and phenotypic variance values demonstrated the effect of the environment on the expression of any trait. GCV and PCV estimates were low, indicating little variability for days to tasselling and Silking, as reported by Murugan *et al*. (2010) [9] and Ogunniyan and Olakojo (2014) [10].

Similarly, heritability was found to be high (80.09%) with modest genetic advancement of 12.04 percent. It showed that the chosen attribute was dominated by additive gene activity and so could be enhanced by selection. These findings are consistent with those of Anshuman *et al*. (2013) [11], Kumar *et al*. (2014) [12], and Sandeep *et al*. (2015) [13]. Similar trend was observed for the days with 50% Silking. In the present investigation, plant height (GCV:16.85, PCV: 18.30), ear length (GCV:15.30, PCV:17.55), ears per plant (GCV:16.82, PCV:26.17), ear girth (GCV:12.16, PCV:16.88), no of kernel rows per ear (GCV: 8.06, PCV: 13.82), no of kernels per ear (GCV:22.9, PCV: 26.92), test weight (GCV: 22.04, PCV: 29.60) and grain yield per plant (GCV:26.92, PCV: 35.83) were highly influenced by the environment as they had higher PCV value than GCV value. Rajesh *et al.* (2013) [14], Kumar *et al*. (2014) [12], Ogunniyan and Olakojo (2014) [10] and Sandeep *et al.* (2015) [13], Murugan *et al.* (2010) [9], Anshuman *et al.* (2013) [11] and Abe *et al.* (2019) [1] reported the similar trend for the different cob characters.

Heritability was found to be moderate for no of kernels per row (34.01%) while genetic advance was found low (9.68%) which showed lower transmission ability in this environment. Hence, selection may be made in desired direction based on phenotypic performance for location. The results are in accordance with the findings of Murugan *et al.* (2010) [9], Idris and Mohammad (2012) [17], Anshuman *et al.* (2013) [11] and Sandeep *et al.* (2015) [13]. Ears per plant was governed by moderate heritability with higher genetic advance. Similar result was observed for grain yield per plant suggesting selection followed by hybridization to be carried out to accumulate desirable genes for this trait. Similar results were also found by Murugan *et al.* (2010) [9], Anshuman *et al.* (2013) [11], Kumar *et al*. (2014) [12] and Abe *et al.* (2019) [1]. While rest of the characters were governed by additive gene action, hence they showed high heritability with higher genetic advance.

Conclusion

Maize is an important staple food crop of the one third population of the world. In the present study, analysis of variance revealed the significant genotypic effect indicated the ample amount of variability was present in the population. ANOVA may not reveal absolute variability, which may be achieved by normalizing the phenotypic and genotypic variances and computing the coefficient of variability. Genotypic and phenotypic coefficient of variance indicated that character plant height, ear length, ears per plant, ear girth, no of kernel rows per ear, no of kernels per ear, test weight and grain yield per plant were influenced by the environment and few characters were governed by the additive gene action with high heritability coupled with high genetic advance may improve by the hybridization followed by selection.

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