

Original Research Article

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Estimation of Association among Yield and Yield Attributing Traits of Maize (*Zea mays* L.)

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ABSTRACT

Keywords

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In the present investigation, phenotypic and genotypic correlation coefficients were estimated among 19 characters of 51 maize genotypes, to find out the association between grain yield and its contributing characters. Grain yield per plant significantly and positively correlated with plant height, ear height, number of kernels per row, number of kernels per ear, shelling percentage and test weight at genotypic and phenotypic basis. Observable correlations among different traits was confirmed through phenotypic correlation, actual correlation could be known through genotypic correlation only, which eliminates environmental influence. Genotypic correlation permits prediction of correlated response and evaluation of relative influence of one character on other. Genotypic correlation in particular is helpful in construction of selection indices.

Introduction

As the world population continues to increase, the scientific community must use all avenues available to enable growers to meet its ever-increasing demand for food and other resources. Modern breeding technologies hold promise in this quest. Maize with its high photosynthetic rates, good yield and wider adaptability make a choice of crop for plant breeders. It is a valuable food source, to mankind and livestock, as well as a source of biofuel

and fiber in some parts of the world (Xu *et al.*, 2009). Maize is a C4 plant, *i.e.* it is physiologically more efficient. Morphologically it has greater phenotypic diversity than any other grain crop. Maize is widely cultivated as a *kharif* crop in India, but with the evolution of new improved varieties and assured availability of irrigation facility, it can be successfully grown during *rabi* in many parts of the country. The yield level of maize during *rabi* season is considerably higher than that in *kharif* due to higher water and fertilizer use efficiency.

Maize (*Zea mays* L.) is an important staple food crops and provide bulk of raw materials for the livestock and many agro-allied industries in the world. Plant breeders are interested in developing cultivars with improved yield and other desirable agronomic and phenological characters. In order to achieve this goal, the breeders had the option of selecting desirable genotypes in early generations or delaying intense selection until advanced generations (Puri *et al.*, 1982). Since grain yield in maize is quantitative in nature and polygenically controlled, effective yield improvement and simultaneous improvement in yield components are imperative (Bello and Olaoye, 2009). Selection on the basis of grain yield character alone is usually not very effective and efficient. However, selection based on its component characters could be more efficient and reliable (Muhammad *et al.*, 2003). Knowledge of association between yield and its component traits and among the component parameters themselves can improve the efficiency of selection in plant breeding. The traits influencing yield are understood through correlation studies to determine the nature and extent of relationships between yield and other yield attributing traits. Yield improvement and stability is the primary objective of a plant breeder. Therefore, correlation analysis of a particular trait with other trait attributing to yield is of great importance for selecting lines for higher yield.

Materials and Methods

Experimental site

The present investigation on genotypic and phenotypic correlation study was carried out at the Agricultural Research Station, Anand Agricultural University, Sansoli (Fig 1). Agricultural Research Station, Anand Agricultural University, Sansoli comes under middle Gujarat Agro Climatic Zone-III (Plate 3.4). Geographically, Sansoli is situated at 22°81'N Latitude and 72° 75' E Longitude with an elevation of 33 meter above mean sea level. The soil of the experimental site is sandy loam, the typical "Goradu" and alluvial in origin.

Experimental material and Design

Fifty-one genotypes were procured from Main Maize Research Station, Anand Agricultural University, Godhra (Table 2.1). These genotypes were evaluated using Randomized Complete Block Design (RCBD) with two replications. Maize genotypes were sown with 60 x 30 cm spacing with single row of 6 m for each genotype in two tire system.

Cultural Practices

Sowing date was done in *Rabi* season, 202021, after land preparation was done as the following: deep plowed first using chisel, harrowed by disc harrow, leveling and ridging. Thinning was carried out two weeks after seedling emergence to one plant per hill. A dose of fertilizer application, 2N (100 kg/ha) was add in split dose after emergence of two week and before flowering. Hand weeding was done to kept the plot free of weeds.

Phenotyping

Phenotyping was performed on five randomly selected competitive plants of each genotype in each replication for various characters like days to 50% tasseling and silking in days, plant height in cm, ear height in cm, ears per plant, ear length in cm, ear girth in cm, ear weight in gramme, number of kernel rows per ear, number of kernels per row, number of kernels per ear, shelling percentage, test weight in gramme, grain yield per plant in gramme, protein content in percentage, total soluble sugar in percentage, β - carotene in parts per million, lysine and tryptophan μ g per ml.

Statistical Analysis

Genotypic correlation coefficient (r_{gij})

The genotypic correlation is estimated as suggested by Hazel (1943) using variability v0.1.0 package developed by Popat *et al.*, (2020) through RStudio (RStudio team, 2020).

$$r_{g_i g_j} = \frac{\sigma_{g_i g_j}}{\sqrt{\sigma_{g_i}^2 \times \sigma_{g_j}^2}}$$

Where,

$r_{g_i g_j}$ = Genotypic correlation coefficient between i^{th} and j^{th} character

σ_{g_i} = Genotypic variance of i^{th} character

σ_{g_j} = Genotypic variance of j^{th} character

$\sigma_{g_i g_j}$ = Genotypic covariance between i^{th} and j^{th} characters

Phenotypic correlation coefficient ($r_{p_i p_j}$)

The genetic and environmental causes of correlation combined together gives phenotypic correlation coefficient ($r_{p_i p_j}$) and was estimated with the help of following formula.

$$r_{p_i p_j} = \frac{\sigma_{p_i p_j}}{\sqrt{\sigma_{p_i} \times \sigma_{p_j}}}$$

Where,

$r_{p_i p_j}$ = Phenotypic correlation coefficient between i^{th} and j^{th} character,

σ_{p_i} and σ_{p_j} = Phenotypic variances of i^{th} and j^{th} character, respectively.

$\sigma_{p_i p_j}$ = Phenotypic covariance between i^{th} and j^{th} character.

The values of genotypic and phenotypic correlation coefficients were tested against standardized tabulated values of r with $(g-2)$ and $(rg-2)$ degree of freedom at 0.05 and 0.01 levels of probabilities for genotypic and phenotypic correlation, respectively as per the suggestion given by Fisher and Yates, (1963).

Results and Discussion

The data revealed that correlation both at genotypic and phenotypic levels had same trend (Table 3.1). Values of genotypic correlation coefficients were found higher than those of their respective phenotypic correlation coefficients in most of the cases, suggesting strong and inherent association.

However, for some character pairs, phenotypic correlation were found higher than the respective genotypic correlation, which implied influence of the non-genetic causes *i.e.*, environmental influence.

Grain yield per plant exhibited significant and positive association with plant height, ear height, number of kernels per row, number of kernels per ear, shelling percentage and test weight at genotypic and phenotypic basis. Ear weight established positive and significant association with grain yield at both the levels. Number of kernel rows per ear showed positive and significant correlation at both levels. Days to 50 per cent tasseling and silking showed positive and significant correlation with grain yield at genotypic and phenotypic levels. Ears per plant establish significant and positive correlation with grain yield at both levels. While β -carotene content established phenotypically negative and significant correlation with grain yield.

Bello *et al.*, (2010) recorded significant correlation of grain yield in maize with days to 50 per cent tasseling and 50 per cent silking, ear height, number of kernels per plant and plant height. Similar results were also recorded by Selvaraj and Pothiraj (2011), Munawar *et al.*, (2013) and Gazal *et al.*, (2018).

Plant height exhibited higher and significant correlation with ear height, number of kernels per row, ear weight and test weight at both the levels in positive direction. Ear girth and shelling percentage exhibited positive and significant association with plant height at both genotypic and phenotypic levels.

Table.1 List of Genotypes

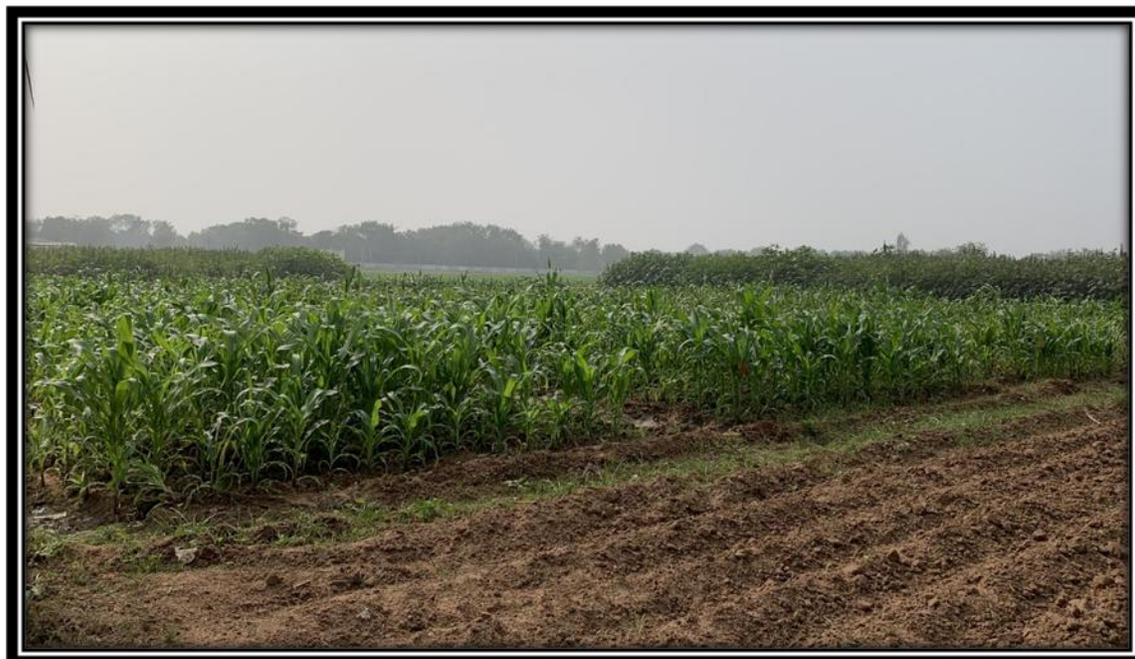
Sr. No.	Genotypes	Source
1	I-07-14-1-2	AAU, Godhra
2	I-07-28-3-2	AAU, Godhra
3	I-07-29-1-3	AAU, Godhra
4	I-07-66-1-2	AAU, Godhra
5	I-07-66-2-3	AAU, Godhra
6	I-07-66-3-2	AAU, Godhra
7	I-07-66-4-1	AAU, Godhra
8	I-07-56-4-3	AAU, Godhra
9	I-077-59-5	AAU, Godhra
10	I-07-60-4-3	AAU, Godhra
11	I-07-65-44-4	AAU, Godhra
12	I-07-6-4-4	AAU, Godhra
13	I-07-6-4-5	AAU, Godhra
14	I-07-9-5	AAU, Godhra
15	I-07-13-1-3	AAU, Godhra
16	IL-14-28	AAU, Godhra
17	IL-14-48	AAU, Godhra
18	IL-14-60	AAU, Godhra
19	IL-17-28	AAU, Godhra
20	IL-17-32	AAU, Godhra
21	IL-17-34	AAU, Godhra
22	IL-17-44	AAU, Godhra
23	GYL-10	AAU, Godhra
24	PFSR5-3-5	AAU, Godhra
25	IL-15-39	AAU, Godhra
26	IL-15-11	AAU, Godhra
27	IGI-1101	AAU, Godhra
28	IGI-1103	AAU, Godhra
29	GYL-2	AAU, Godhra
30	CML-307	AAU, Godhra
31	IGI-1102	AAU, Godhra
32	IGI-1104	AAU, Godhra
33	LTP-1-1	AAU, Godhra
34	LM-B-2	AAU, Godhra
35	LM-5	AAU, Godhra
36	H07R-1-3	AAU, Godhra
37	GWQPM-5-3	AAU, Godhra
38	GWQPM-11	AAU, Godhra
39	GWQPM-17-2	AAU, Godhra
40	GWQPM-22-5	AAU, Godhra
41	GWQPM-26-1	AAU, Godhra
42	GWQPM-26-3	AAU, Godhra
43	GWQPM-40-3	AAU, Godhra
44	GWQPM-40-5	AAU, Godhra
45	GWQPM-46-2	AAU, Godhra
46	GWQPM-47-1	AAU, Godhra
47	GWQPM-55-2	AAU, Godhra
48	GWQPM-67-2	AAU, Godhra
49	GWQPM-68-4	AAU, Godhra
50	I-07-54-3-2	AAU, Godhra
51	I-07-7-3-2	AAU, Godhra

Table.2 Genotypic and phenotypic correlation coefficients

		TA	SI	PH	EH	EPP	EL	KPR	EG	KRP	NKE	EW	SH	TW	Pro	TSS	LYS	TRP	Car	GY
TA	rg	1.00	0.98**	-0.01	0.15	-0.24	-0.03	-0.11	-0.26	-0.09	-0.14	-0.20	-0.31*	-0.50**	-0.36**	-0.06	-0.32*	-0.35**	0.14	-0.41**
	rp	1.00	0.97**	0.02	0.14	-0.13	0.00	-0.08	-0.23*	-0.09	-0.11	-0.17	-0.28**	-0.27**	-0.28**	-0.06	-0.26**	-0.33**	0.13	-0.36**
SI	rg		1.00	-0.03	0.14	-0.25	-0.01	-0.10	-0.23	-0.09	-0.12	-0.19	-0.27*	-0.49**	-0.31*	-0.07	-0.29*	-0.32*	0.14	-0.40**
	rp		1.00	0.00	0.13	-0.15	0.01	-0.07	-0.21*	-0.10	-0.11	-0.17	-0.26**	-0.26**	-0.26**	-0.07	-0.24*	-0.30**	0.13	-0.37**
PH	rg			1.00	0.89**	0.36**	0.64**	0.39**	0.51**	-0.01	0.28*	0.62**	0.30*	0.56**	-0.12	-0.12	-0.13	-0.14	0.05	0.42**
	rp			1.00	0.89**	0.25**	0.58**	0.35**	0.41**	-0.03	0.23*	0.52**	0.29**	0.43**	-0.13	-0.11	-0.12	-0.13	0.04	0.36**
EH	rg				1.00	0.34*	0.65**	0.40**	0.43**	-0.02	0.28*	0.52**	0.35*	0.36**	-0.15	-0.16	-0.19	-0.22	0.00	0.33*
	rp				1.00	0.23*	0.57**	0.35**	0.35**	-0.03	0.23*	0.43**	0.33**	0.25*	-0.16	-0.14	-0.18	-0.20*	-0.01	0.27**
EPP	rg					1.00	0.21	0.14	0.14	-0.06	0.08	0.08	0.21	0.30*	0.07	0.05	0.15	0.11	0.00	0.65**
	rp					1.00	0.16	0.10	0.14	0.00	0.09	0.07	0.17	0.17	0.04	0.05	0.15	0.08	-0.01	0.51**
EL	rg						1.00	0.67**	0.60**	-0.07	0.47**	0.60**	0.33*	0.53**	-0.02	-0.08	0.05	0.16	-0.32*	0.50**
	rp						1.00	0.69**	0.56**	-0.04	0.49**	0.59**	0.31**	0.41**	0.00	-0.08	0.06	0.15	-0.31**	0.49**
KPR	rg							1.00	0.53**	0.20	0.85**	0.37**	0.48**	0.36**	-0.10	-0.01	-0.09	-0.03	-0.18	0.64**
	rp							1.00	0.49**	0.20*	0.84**	0.38**	0.46**	0.29**	-0.08	-0.01	-0.08	-0.03	-0.18	0.62**
EG	rg								1.00	0.36**	0.57**	0.52**	0.32*	0.60**	0.00	-0.03	-0.02	0.09	-0.36**	0.59**
	rp								1.00	0.46**	0.60**	0.57**	0.28**	0.39**	0.01	-0.03	0.00	0.08	-0.33**	0.61**
KRP	rg									1.00	0.65**	-0.19	-0.09	-0.17	0.17	0.16	-0.15	-0.13	-0.08	0.32*
	rp									1.00	0.67**	-0.05	-0.08	-0.12	0.16	0.14	-0.12	-0.11	-0.08	0.37**
NKE	rg										1.00	0.23	0.29*	0.20	0.02	0.12	-0.12	-0.07	-0.20	0.66**
	rp										1.00	0.30**	0.28**	0.17	0.03	0.11	-0.09	-0.06	-0.19*	0.66**
EW	rg											1.00	0.34*	0.75**	-0.08	0.05	0.13	0.19	-0.27	0.34*
	rp											1.00	0.31**	0.55**	-0.06	0.04	0.13	0.18	-0.26**	0.39**
SH	rg												1.00	0.47**	-0.01	-0.06	0.00	0.12	0.09	0.35**
	rp												1.00	0.36**	-0.02	-0.05	0.01	0.12	0.08	0.33**
TW	rg													1.00	-0.13	0.15	0.25	0.25	-0.11	0.71**
	rp													1.00	-0.10	0.11	0.18	0.18	-0.08	0.50**
Pro	rg														1.00	0.01	0.32*	0.55**	-0.06	0.04
	rp														1.00	0.02	0.30**	0.50**	-0.06	0.05
TSS	rg															1.00	0.12	0.15	0.04	0.20
	rp															1.00	0.12	0.14	0.04	0.19
LYS	rg																1.00	0.87**	-0.32*	0.08
	rp																1.00	0.84**	-0.31**	0.07
TRP	rg																	1.00	-0.32*	0.14
	rp																	1.00	-0.31**	0.13
Car	rg																		1.00	-0.20
	rp																		1.00	-0.19*
GY	rg																			1.00
	rp																			1.00

*, ** Significant at 5% and 1% levels, respectively

Fig.1 Experimental site for maize genotype evaluation



Number of kernels per ear found significantly and positively correlated with plant height at genotypic and phenotypic level. Ear length was found positively associated with plant height at genotypic and phenotypic level. Ears per plant found positively associated with plant height at genotypic and phenotypic levels.

Similar results were recorded by Selvaraj and Pothiraj, (2011) and Bhiusal *et al.*, (2017) for ear girth with plant height in maize. Bello *et al.*, (2010) and Roy *et al.*, (2018) observed positive and significant correlation between plant height and number of kernels per ear in maize.

The yield was perfectly correlated with plant height, ear height, number of kernels per row, number of kernels per ear, shelling percentage and test weight at genotypic and phenotypic basis. The prime genetic cause of correlation is pleiotropy, though linkage is a cause of transit correlations particularly in a population derived from crosses between divergent strains. Enhanced repression of genes controlling different traits manifest correlation, while enhanced expression of one or more reveal

negative correlation. Observable association among different characters is confirmed through phenotypic correlation, whereas true association could be known through genotypic correlation only, which eliminates environmental influence. Genotypic correlation permits prediction of correlated response and evaluation of relative influence of one character on other. Genotypic correlation in particular is helpful in construction of selection indices.

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