

Estimates of heritability, genetic advance and correlation study for yield and its attributes in maize (*Zea mays* L.)

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Abstract: A study of heritability, genetic advance and correlation was undertaken at College of Agricultural farm; Rajendranagar under rain fed condition in 2002-2003 randomized block design with three replications. It was done using twenty four hybrids with their parents (six lines and four testers) including two checks namely Mandhuri and DHM 105. The characters plant height, ear height, number of seeds per row, 100 seed weight, protein content, and grain yield per plot revealed higher values of heritability. High genetic advance coupled with heritability was observed for plant height, grain yield per plot and protein content. Thus selection based on these traits will be effective in maize breeding program. Correlation study showed negative and significant association between grain yield and oil content at genotypic level.

Keywords: Correlation, Genetic Advance, Heritability and Maize

1. Introduction

Maize (*Zea mays* L.) is a sturdy, annual plant of North American origin belonging to Poaceae sub-family Maydeae. It is a very versatile crop growing in all sorts of altitudinal and fertility conditions. This makes it to be an important cereal crop having global importance [1]. It is used as a basic staple food crop and produced on nearly 100 million hectares in developing countries [2 and 3]. It is one of the most traded cereals with a total estimated global production of 885.3 million tons [1].

Together with rice and wheat, maize provides at least 30% of the food calories of more than 4.5 billion people in 94 developing countries [3]. Indeed, it is an excellent source of protein and food quality oil. It is more complete in nutrients in comparison to other cereals though all cereals including maize tend to be low in two essential amino acids that are lysine and tryptophan [4]. However, CIMMYT has developed maize with essential amino acid lysine and tryptophan named Quality Protein Maize (QPM). The protein of QPM has a nutritional value of nearly equivalent to cow's milk (18 and 19).

The genetic improvement of yield and its component depends up on the nature and the magnitude of variability present in genotypes. Most of the characters of breeders' interest are complex and polygenically controlled. A

successful selection program depends not only on heritability of desirable characters but also on the information on association among various yield component characters and their association with grain yield [5 and 6].

Accordingly, the present study on genetic analysis for grain yield, protein and oil improvement in selected quality protein maize (QPM) inbreds and hybrids was carried out with the objective of generating information on heritability, genetic advance and to investigate extent of character association between yield and its attribute in order to select superior genotypes among the material.

2. Material and Methods

2.1. The Genotypes, Study Area and Experimental Design

Twenty four F₁ hybrids along with their parents six lines namely B-QPM-104, B-QPM-105, B-QPM-108, B-QPM-112, B-QPM-114, B-QPM-117 and four testers namely B-QPM-118, B-QPM-122, B-QPM-124, B-QPM-128 including two checks Madhuri and DHM-105 (Table 1) were studied in randomized block design with three replications at College of Agricultural farm, Rajendranagar under rain fed condition in 2002-2003. Each plot consisted of one row with 5 m length a spacing of 75 cm x 20 cm was adopted.

2.2. Data Collection

Observation was recorded on selected five plants in each genotype for twelve important characters. These characters were days to 50 percent silking, days to 50 percent maturity, plant height, ear height, ear length, ear girth, number of seeds per row, number of seeds per row cob, 100 seed weight, grain yield per plot, oil percent and protein content. The mean of five plants of each genotype in each replication was used for statistical analysis. The analysis of variance, correlations, estimates of heritability and genetic

advance were calculated for all pairs of characters.

Oil content in grain was assessed using Nuclear Magnetic Resonance (NMR) spectroscopy. Kernels of each entry in each replication were dried in hot air to the moisture content of 4.5%. Fifteen grams of the sample was then used for assessing oil content, using NMR spectroscopy against a standard reference sample. Protein content in grain was assessed by multiplying the total nitrogen content of grain estimated by Kjeldahl method with a factor of 6.25.

Table 1. Pedigree history and morphological characters of QPM inbreds

line	Pedigree Origin	Days to 50% tasseling	Days to 50% silking	Protein (%)	Oil (%)
1	B-QPM-104 CML*-162xCML-165 QPM ¹ hybrids	49.33	54.33	9.26	10.42
2	B-QPM-105 CML-162xCML-165 QPM ¹ hybrids	50.00	55.00	10.24	11.24
3	B-QPM-108 CML-164xCML-166 QPM ¹ hybrids	49.57	55.00	8.64	10.24
4	B-QPM-112 CML-164xCML-166 QPM ¹ hybrids	48.67	55.67	8.54	10.05
5	B-QPM-114 CML-164xCML-120 QPM ¹ hybrids	53.33	58.00	8.34	10.44
6	B-QPM-117 CML-162xCML-165 QPM ¹ hybrids	53.67	58.33	10.61	9.89
7	B-QPM-118 Line derived from Shaki composite (QPM)	53.00	58.00	7.94	11.10
8	B-QPM-122 Line derived from Shaki composite (QPM)	53.67	58.67	9.84	10.52
9	B-QPM-124 CML-166xCML-211 QPM hybrids	53.33	58.67	9.28	9.76
10	B-QPM-128 CML-166xCML-211 QPM hybrids	52.67	58.00	8.63	10.25

Note: *CML=CIMMYT maize lines¹ QPM= Quality protein maize Shakati composite= QPM varieties Line 1, 2 and 3 are QPM high yielding hybrids

2.3. Statistical Analysis

2.3.1. Phenotypic and Genotypic Correlation

Phenotypic and genotypic correlations were calculated for the characters by working out the variance components of each character and the covariance components for each pair of characters using the formulae [7].

$$\text{Genotypic correlation coefficient (rg)} = \frac{\text{Cov xy (genotypic)}}{\sqrt{\text{Var (x).Var (y) (genotypic)}}} \quad (1)$$

$$\text{Genotypic variance} = \frac{\text{Treatment MS-Error MS}}{\text{Number of replications}} \quad (2)$$

$$\text{Genotypic Covariance} = \frac{\text{Treatment Covariance-Error covariance}}{\text{Number of replication}} \quad (3)$$

$$\text{Genotypic Covariance} = \frac{\text{Cov xy (phenotypic)}}{\sqrt{\text{Var (x).Var (y) (genotypic)}}} \quad (4)$$

To test the significance of correlation coefficients, the estimated values were compared with the table values of correlation coefficients [8] at 5% of significance with (n-2) degree of freedom where 'n' is the number of genotypes used in the experiment

2.3.2. Heritability

$$\text{Heritability (H)} = \text{Vg/Vp} = \text{Vg}/(\text{vg} + \text{ve}) \quad (5)$$

$$\text{Genetic advance (Gs)} = (\text{K}) (\text{vp}) (\text{SD P}) \quad (6)$$

Where vg, vp, ve and Gs are genotypic, phenotypic and environmental components of variance and genetic advance respectively under selection. K is the selection differential,

SD P is the phenotypic standard deviation of base population and H is the heritability of the character under selection.

3. Results and Discussion

Heritability estimates along with genetic advance is more helpful in predicting the genetic gain under selection than heritability estimates alone [9]. In present study the character plant height, ear height, number of seed per row, 100 seed weight, protein content and grain yield per plot revealed higher values of heritability. The characters plant height, number of seed row per cob, 100 seed weight, ear height, grain yield per plot, oil percent and protein percent recorded high genetic advance. High genetic advance coupled with heritability was observed for plant height, grain yield per plot and protein percent. Therefore selection based on these last three mentioned traits will be effective (Table 2). Similarly, it was reported that high to moderate heritability with moderate estimates of genetic advance for grain yield per plant and plant height [20].

In plant breeding, correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield [10]. Genotypic correlation coefficient is the heritable association between two variables [11]. However phenotypic correlation includes both phenotypic and environmental effect. Hence significant phenotypic

correlation without significant genotypic correlation has no value.

In the present study correlation showed negative and significant association between grain yield and oil content at genotypic level (Table 3). Grain yield was also negatively and significantly correlated with days of 50% silking, days of 50% tasseling and days of 50% maturity a genetic level while they were negatively correlated at phenotypic level but not significant. There was negative and significant association at genotypic level between 100 seed weight and oil content. While, phenotypic association

was negative but not significant due to masking effect of environment. Earlier studies also revealed that negative association of grain yield per plot and 100 seed weight to oil content [12]. Similarly negative association of oil percent with grain yield per plot was reported [13]. In this study, grain yield per plot was associated significantly and positively with to plant height, ear height, ear girth, number of seeds per row and 100 seed weight at genotypic level. These results are in agreement with earlier reports [14 and 15].

Table 2. Mean heritability and genetic advance for grain yield component characters, oil and protein content in maize

S. No	Traits	Mean	Heritability	Genetic advance (%)
1	Days to 50% tassling	51.90	0.369	3.074
2	Days to 50% silking	57.34	0.232	1.477
3	Days of 50% maturity	93.42	0.209	2.768
4	Plant height (cm)	188.99	0.591	14.957
5	Ear height (cm)	86.19	0.395	23.210
6	Ear length (cm)	13.94	0.337	12.067
7	Ear girth (cm)	12.47	0.405	10.740
8	Number of seeds per row	30.11	0.427	18.348
9	Number of seed rows per cob	13.62	0.035	0.857
10	100 seed weight (g)	28.12	0.416	15.026
11	Oil content %	10.28	0.108	1.943
12	Protein content %	9.19	0.961	15.015
13	Grain yield per plot (kg)	2.26	0.558	36.199

Table 3. Phenotypic and genotypic correlation coefficients of grain yield, yield component characters, oil and protein content in maize

Source	Days of 50% tasseling	Days of 50% silking	Days of 50% maturity	Plant height (cm)	Ear Height (cm)	Ear Length (cm)	Ear Girth (cm)	No. of Seeds Per row	No. seed Rows per cob	100 seed weight (g)	Oil content (%)	Protein Content (%)	Grain Yield Per Plot (kg)
Days of 50% tasseling		0.918**	0.06	-0.21	-0.04	-0.25	-0.13	-0.34*	0.08	-0.13	0.19	0.19	-0.23
Days of 50% silking	0.97**		0.08	-0.12	0.003	-0.20	-0.09	-0.28	0.13	-0.03	0.15	0.13	-0.12
Days of 50% maturity	0.88	0.15		0.05	-0.003	0.17	0.18	0.16	0.21	0.01	-0.002	0.12	0.09
Plant height (cm)	-0.38*	-0.19	0.27		0.46**	0.39*	0.44*	0.44*	0.33	0.30	0.02	-0.05	0.48*
Ear Height (cm)	-0.16	0.042	0.37*	0.88**		0.27	0.40*	0.34	0.20	0.12	-0.167	-0.21	0.32
Ear Length (cm)	-0.46**	-0.27	0.29	0.91**	0.82**		0.57**	0.77**	0.31	0.46**	-0.02	0.06	0.67**
Ear Girth (cm)	-0.19	0.06	0.54	0.93	0.96	0.71		0.58**	0.38*	0.54**	0.04	-0.01	0.63*
No. of Seeds Per row	-0.59**	-0.31	0.43*	1.01**	1.02**	0.94**	0.76**		0.20	0.37*	-0.06	-0.09	0.78*
No. seed Rows per cob	-0.20	0.12	-0.16	1.34**	1.73**	0.91**	1.16**	1.48**		0.19	0.04	0.03	0.44**
100 seed weight (g)	-0.63**	-0.60**	-0.07	0.67**	0.62**	0.67**	0.82**	0.50**	0.53**		-0.02	-0.18	0.71**
Oil content (%)	0.29	0.05	-0.01	-0.61**	-0.44*	-0.1**	-0.48**	-0.69**	-2.01**	-0.73**		-0.002	-0.7
Protein Content (%)	0.25	0.21	0.19	-0.08	-0.29	0.09	-0.05	-0.13	0.08	-0.28	0.01		-0.14
Grain Yield Per Plot (kg)	-0.54	-0.34	0.36*	0.91*	0.90**	0.98**	0.96**	0.96**	1.48**	0.81**	-0.89**	-0.18	

Note: Values at upper diagonals is phenotypic and lower diagonal is genotypic coefficients. *significant difference at 5% level **significant difference at 1 % level

The previous study of character association with thirty four genotypes of green maize also supports these results. It was indicated that strong correlation of yield with plant height, ear length and ear diameter [16]. Similarly former researches also reported the presence of high positive correlation between yields with that of plant height [17].

4. Conclusion

Heritability estimates along with genetic advance is more helpful in foresee the genetic gain under selection than heritability estimates alone. High genetic advance joined with heritability was observed for plant height, grain yield and protein percent. Therefore selection of genotypes based on these indicated traits will be effective. The correlation study revealed that selection based on traits plant height, ear height, number of seeds per row and 100 seed weight would be needed for improvement of maize grain yield.

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