



Research Article

HARNESSING THE GENETIC VARIABILITY AND TRAITS ASSOCIATION FOR MAIZE (*ZEAMAYS* L.) IMPROVEMENT

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Abstract: Analysis of variance (ANOVA) indicated that the mean sum of squares due to genotypes were highly significant for all the traits. The magnitude of GCV and PCV was observed high for the characters viz., harvest index followed by 100 seeds weight, days to 50% maturity, biological yield/plant and seed yield/plant. It indicates that selection of desired germplasm for these traits may be worthwhile for improving seed yield in future breeding programme. Broad sense heritability was estimated for all the characters under study. High heritability was observed for most of the traits and it was noted highest for cob ear weight, biological yield per plant, seed yield per cob, number of seeds per cob, days to 50% maturity, 100 seeds weight, days to 50% tasselling, shelling percent and seed yield per plant. Seed yield per plant shows significant positive correlation with seed yield per cob and harvest index. Seed yield per plant shows significant negative correlation with days to 50% tasselling, days to 50% silking. The maximum direct positive genotypic path on grain yield per plant was observed in followed by seed yield per cob, shelling percent, 100 seeds weight, number of leaves per plant, number of seeds per cob, number of rows per cob, cob ear weight, number of cobs per plant, plant height and days to 50% tasselling. Maximum direct negative effect on grain yield per plant was observed in followed by harvest index, biological yield per plant, cob length, days to 50% maturity, days to 50% silking and cob diameter.

Keywords: Genetic variability, Heritability, Correlation, Path analysis

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Introduction

Maize (*Zea mays* L.) $2n=20$, is the third most important cereal crop after rice and wheat in the world. It is referred to as "Miracle Crop" and "Queen of the Cereals" due to its high productivity potential compared to other Poaceae family members. It is believed to have originated in Southern Mexico or Northern Guatemala [1]. It has two close relatives, among the American Maydis viz., genus *Tripsacum* (gamagrass) and *Teosinte* (euchlena). The suitability of maize to diverse environments is unmatched by any crop.

Maize as an allogamous crop is an important cereal which is used as food for human consumption as well as feed for animal and poultry. It is the third most widely distributed crop of the world being grown in diverse season and ecologies. It is used world-wide for feed, food and serves as source of basic raw material of number of industries viz., oil, starch, protein, food, alcoholic beverages, sweeteners, cosmetics and bio-fuels etc. It is principal field crop of the country. About 59 percent of the total production is used as feed, while the remaining is used as industrial raw material (17%), food (10%), export (10%) in other purpose (4%) [2]. Globally it is grown in 184 mha across 175 countries, with total production of 1016 MMT, and average production of 5.52 t/ ha [3].

The ratio of genotypic variance to the phenotypic variance or total variance is known as heritability. It is generally expressed in percentage. Thus, heritability is the heritable portion of phenotypic variance. Estimates of heritability are useful in predicting the transmission of character from the parents to their off springs. Estimates of heritability are free from genetical assumptions. Heritability estimates are based on empirical results. The broad sense heritability can be estimated from parental as well as hybrid populations. Heritability helps in the selection of elite types from the mixed parental population or segregating populations. Narrow sense heritability gives an idea about the additive genetic variance. Heritability estimates can be worked out from both in-breeders as well as out-breeders. Correlation studies provide information about yield contributing characters.

This information is useful to plant breeder in selection of elite genotypes from diverse genetic populations [4]. Mass selection has been used to improve grain yield in several crops through indirect selection of highly heritable traits which are associated with yield. Path coefficient analysis helps in indirect selection for genetic improvement of yield. Selection for a component trait for yield improvement is called indirect selection. While, straight selection for is termed as direct selection. The entire success of plant breeding, programme in any crop largely depend on the range of Genetic variability owing to genetic and non-genetic causes present in crop. Grain yield in maize is a complex character controlled by many factors. Selection for desirable genotypes is done based on grain yield and its other component characters. Studies on correlation coefficients of different characters are useful criteria to identify desirable traits that contribute to improve the dependent variable.

Materials and methods

Fifteen genotypes were sown in a Randomized Block Design (RBD) with three replications. Each entry in each replication consisted of single row of 3m length. Genetics and Plant Breeding Research Farm, AKS University, Satna, M.P. during *kharif* 2021. Spacing between rows and between plants was 60 cm and 20 cm respectively. Initially 2 seeds per hill were sown and later thinning was practiced to maintain single plant per hill. Recommended dose of fertilizers (NPK-120:60:40 Kg/Ha) were applied for raising healthy and uniform crops. The crop was raised as per the recommended package of practices. Two border rows were also planted to minimize border effect.

Results and Discussion

The Analysis of variance (ANOVA) indicated that the mean sum of squares due to genotypes were highly significant for all the traits [Table-1]. The similar finding has been reported by many researchers [5-7].

Table-1 Analysis of variance for 17 different traits in 15 genotypes of maize

Characters	Mean sum of squares		
	Replication (df=2)	Treatment (df=14)	Error (df=28)
Days to 50% tassling	36.96	61.28	5.67
Days to 50% silking	15.76	20.40	4.33
Number of cobs / plants	0.08	0.06	0.19
Plant height	44.20	149.68	16.00
Cob length	0.54	4.62	2.26
Cob diameter	0.03	0.29	0.21
Number of rows/cob	0.83	3.64	2.37
Cob ear weight	3.49	7655.88	9.99
Seed yield/cob	3.28	262.08	6.29
Shelling percent	45.44	289.45	27.77
Number of leafs/plant	0.68	4.29	1.04
Number of seeds/cob	95.30	1845.51	47.76
100 seeds weight	1.17	59.48	4.75
Days to 50% maturity	15.02	64.09	4.76
Biological yield/plant	8.11	1375.41	20.29
Harvest index	34.86	122.96	49.62
Seed yield/plant	3.30	211.34	20.13

Table-2 Genetic parameters for 17 characters of 15 maize genotypes

Traits	Genotypic Coefficient of variation	Phenotypic coefficient of variation	Heritability (%) (Broad Sense)	Genetic Advance	Genetic Advance as % of Mean 5%
Days to 50% tassling	8.38	8.80	0.91	8.45	16.45
Days to 50% silking	3.94	4.44	0.79	4.23	7.20
Number of cobs/plant	13.50	9.59	0.67	0.60	39.20
Plant height	3.79	4.01	0.89	13.00	7.38
Cob length	3.81	5.33	0.51	1.31	5.61
Cob diameter	8.89	16.34	0.30	0.19	9.97
Number of rows/cob	6.99	11.81	0.35	0.80	8.52
Cob ear weight	10.57	10.58	1.00	103.93	21.77
Seed yield/cob	27.37	27.70	0.98	18.79	55.70
Shelling percent	22.85	24.03	0.90	18.29	44.76
Number of leafs/plant	13.17	15.14	0.76	1.87	23.61
Number of seeds/cob	14.71	14.90	0.97	49.77	29.90
100 seeds weight	16.19	16.88	0.92	8.44	31.99
Days to 50% maturity	4.99	5.18	0.93	8.81	9.88
Biological yield/plant	13.81	13.92	0.99	43.46	28.25
Harvest index	20.94	27.12	0.60	7.87	33.32
Seed yield/plant	19.26	20.25	0.91	15.64	37.75

Coefficient of Variation

The phenotypic coefficient of variation (PCV) was higher in magnitude than that of genotypic coefficient of variation for all the characters under study. The highest PCV was recorded for seed yield per cob, harvest index, shelling percent, seed yield per plant and the characters viz., days to 50% silking, plant height and showed low phenotypic coefficient of variation. Many researchers also find the highest PCV for most of the character like biological yield, seed yield per cob and lowest for days to 50% silking [8-10]. Genotypic coefficient of variation (GCV) was recorded highest for seed yield per cob, harvest index, shelling percent, and the characters viz., days to 50% silking and plant height showed low genotypic coefficient of variation. Many researchers also find the reported high estimates of GCV for seed yield per cob [11-12] [Table -2].

Heritability (%) and genetic advance

Broad sense heritability was estimated for all the characters under study. high heritability was observed for most of the traits and it was noted highest for cob ear weight, biological yield per plant, seed yield per cob, number of seeds per cob, days to 50% maturity, 100 seeds weight, days to 50% tassling, shelling percent (90.40% and seed yield per plant (90.50%). Many researchers also find the similar results for days to 50% maturity, cob ear weight and thousand seed weight [13-15]. Genetic advancement was recorded highest for cob ear weight, number of seeds per cob, biological yield per plant, seed yield per cob, shelling percent, seed yield per plant, plant height and the characters viz., days to 50% silking, number of leaves per plant, number of cobs per plant, number of rows per cob, cob diameter showed low genetic advance.

The high genetic advance as percent of mean was recorded for seed yield per cob, shelling percent, number of cobs per plant, seed yield per plant, harvest index, seeds weight and the characters viz., plant height, days to 50% silking, cob

length exhibited low genetic advance as per cent of mean. The results revealed that the estimates of genotypic correlation coefficients were higher in magnitude than their corresponding correlation coefficient at phenotypic level [Table-2].

Correlation and path analysis

Seed yield per plant shows significant positive correlation with seed yield per cob and harvest index. Seed yield per plant shows significant negative correlation with days to 50% tassling, days to 50% silking. Non-significant positive correlation with plant height, cob length, cob diameter, days to 50% maturity, biological yields per plant, cob ear weight and shelling percent. Non-significant negative correlation with number of cobs per plant, number of rows per cob, number of leaves per plant, number of seeds per cob and 100 seeds weight [Table-3].

The maximum direct positive genotypic path on grain yield per plant was observed in followed by seed yield per cob, shelling percent, 100 seeds weight, number of leaves per plant, number of seeds per cob, number of rows per cob, cob ear weight, number of cobs per plant, plant height and days to 50% tassling. Maximum direct negative effect on grain yield per plant was observed in followed by harvest index, biological yield per plant, cob length, days to 50% maturity, days to 50% silking and cob diameter. The maximum indirect positive genotypic path in number of cobs per plant observed through shelling percent, 100 seeds weight, number of seeds per cob, number of rows per cob, number of cobs per plant, days to 50% tassling, biological yield per plant, cob length, days to 50% maturity and cob diameter [Table-4]. The grain yield or economic yield, almost in all the crops, is referred to as super character which results from the interactions of several component characters that are termed as yield and yield contributing components. Thus, genetic construction of seed yield, in chickpea as well as in other crops, is based on the balance or overall net effect construct by various yield components directly or indirectly by interacting with each other.

Table-3 Genotypic Correlation of 17 traits of Maize

Traits	DFT	DFS	NCP	PH	CL	CD	NRC	CEW	SYC	SP	NLP	NSC	HSW	DFM	BYP	HI	SYP
DFT	1.000	0.738**	0.102	-0.466	-0.238	-0.287	0.104	0.079	-0.546	0.154	-0.158	0.470	0.118	-0.154	-0.284	-0.115	-0.595*
DFS		1.000	-0.104	-0.414	-0.419	-0.407	-0.235	0.092	-0.315	-0.252	0.373	-0.237	0.073	-0.121	0.055	-0.585*	-0.624*
NCP			1.000	-0.207	0.146	0.082	0.161	-0.039	-0.148	0.199	-0.498	0.111	0.216	0.028	0.032	-0.334	-0.011
PH				1.000	-0.422	0.472	-0.314	-0.038	-0.022	-0.077	0.511	0.090	-0.033	-0.266	-0.005	0.260	0.321
CL					1.000	0.410	-0.271	-0.445	0.762**	0.947**	-0.6429*	0.157	-0.038	0.530	-0.033	1.000	0.369
CD						1.000	-1.038	0.380	0.365	0.572*	0.338	0.287	0.919	-0.161	0.204	1.094	0.095
NRC							1.000	-0.249	-0.672*	-0.257	-0.563*	-0.048	-0.292	0.692**	-0.316	-0.872**	-0.375
CEW								1.000	0.013	-0.422	0.295	0.045	0.555	-0.244	-0.205	0.171	0.246
SYC									1.000	0.426	-0.096	-0.437	-0.101	0.384	0.522	0.760**	0.849**
SP										1.000	-0.398	0.248	-0.152	0.226	0.311	0.768**	0.184
NLP											1.000	-0.064	0.247	-0.760**	-0.109	-0.025	-0.217
NSC												1.000	0.160	-0.375	-0.674*	0.339	-0.351
HSW													1.000	-0.508	-0.175	-0.179	-0.187
DFM														1.000	0.357	0.067	0.300
BYP															1.000	0.016	0.389
HI																1.000	0.656*
SYP																	1.000

Table-4 Genotypic path of traits with seed yield of Maize

Traits	DFT	DFS	NCP	PH	CL	CD	NRC	CEW	SYC	SP	NLP	NSC	HSW	DFM	BYP	HI
DFT	2.817	2.081	0.288	-1.313	-0.671	-0.808	0.293	0.223	-1.538	0.435	-0.444	1.325	0.333	-0.433	-0.800	-0.324
DFS	-0.844	-1.142	0.118	0.472	0.478	0.464	0.269	-0.106	0.360	0.288	-0.426	0.270	-0.084	0.138	-0.063	0.669
NCP	0.001	-0.001	0.012	-0.003	0.002	0.001	0.002	-0.001	-0.002	0.003	-0.006	0.001	0.003	0.000	0.000	-0.004
PH	-1.499	-1.331	-0.667	3.218	-1.356	1.517	-1.009	-0.121	-0.072	-0.248	1.644	0.290	-0.105	-0.856	-0.015	0.835
CL	0.448	0.787	-0.274	0.792	-1.880	-0.770	0.509	0.836	-1.433	-1.781	1.208	-0.294	0.072	-0.997	0.061	-1.880
CD	1.039	1.473	-0.296	-1.709	-1.485	-3.623	3.762	-1.378	-1.321	-2.075	-1.225	-1.041	-3.329	0.583	-0.737	-3.964
NRC	0.363	-0.821	0.562	-1.095	-0.946	-3.627	3.494	-0.870	-2.350	-0.897	-1.969	-0.166	-1.020	2.420	-1.102	-3.049
CEW	0.114	0.132	-0.056	-0.054	-0.637	0.545	-0.356	1.432	0.018	-0.604	0.422	0.065	0.795	-0.349	-0.293	0.244
SYC	-5.985	-3.458	-1.627	-0.244	8.359	3.998	-7.376	0.138	10.966	4.672	-1.053	-4.788	-1.104	4.209	5.726	8.339
SP	0.638	-1.040	0.821	-0.319	3.916	2.368	-1.062	-1.742	1.761	4.134	-1.646	1.025	-0.628	0.932	1.283	3.175
NLP	-0.419	0.992	-1.324	1.359	-1.710	0.899	-1.499	0.784	-0.255	-1.059	2.659	-0.171	0.655	-2.022	-0.290	-0.067
NSC	1.884	-0.948	0.443	0.361	0.627	1.151	-0.191	0.180	-1.750	0.993	-0.257	4.007	0.639	-1.504	-2.704	1.358
HSW	0.327	0.203	0.600	-0.090	-0.106	2.545	-0.809	1.537	-0.279	-0.421	0.683	0.442	2.770	-1.408	-0.486	-0.496
DFM	0.016	0.012	-0.003	0.027	-0.054	0.017	-0.071	0.025	-0.039	-0.023	0.078	0.038	0.052	-0.102	-0.037	-0.007
BYP	0.025	-0.005	-0.003	0.000	0.003	-0.018	0.028	0.018	-0.047	-0.028	0.010	0.060	0.016	-0.032	-0.090	-0.001
HI	0.480	2.442	1.395	-1.083	-4.171	-4.564	3.640	-0.712	-3.172	-3.204	0.106	-1.414	0.748	-0.280	-0.065	-4.171

Therefore, correlation studies are of considerable importance in understanding the relationship of any two given characters or any number of characters with each other. A positive correlation between desirable characters is helpful to the plant breeder because it helps in simultaneous improvement of both the characters. Negative correlation on the other hand, will hinder the parallel expression of both characters. In the present study, correlation coefficients were worked out for all possible pairs of characters particularly the seed yield per plant and its components at genotypic and phenotypic levels.

In the present findings, the magnitudes of genotypic correlation coefficient were greater than corresponding phenotypic correlation coefficient (in general also) similar findings by Many researchers [16-19].

Conclusion

The magnitude of GCV and PCV was observed high for the characters viz., harvest index followed by 100 seeds weight, days to 50% maturity, biological yield/plant and seed yield/plant. The maximum direct positive genotypic path on grain yield per plant was observed in followed by seed yield per cob, shelling percent, 100 seeds weight, number of leaves per plant, number of seeds per cob, number of rows per cob, cob ear weight, number of cobs per plant, plant height and days to 50% tasseling.

Application of research: Study of grain yield per plant by harvest index, biological yield per plant, cob length, days to 50% maturity, days to 50% silking and cob diameter.

Research Category: Genetics and Plant Breeding

Abbreviations: RBD- Randomized Block Design
ANOVA-Analysis of variance

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Study area / Sample Collection: Genetics and Plant Breeding Research Farm, AKS University, Satna, 485001

Cultivar / Variety / Breed name: Maize (*Zea mays* L.)

Conflict of Interest: None declared

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References

- [1] Anwar T.S., Abellandsa A.L. and Cauny R.L. (2009) *Agron. Abstr. American Soc. Agron.*, 82, 391-393.
- [2] Bhatiya F., Bajaj K. and Prasanna B.M. (2006) *Euphytica*, 129.
- [3] Bineeta Devi (2020) *International Journal of Agriculture Sciences*, 12 (2), 9445-9447.
- [4] Choudhary M., Cochran D. and Cox H. (2015) *Orissa J. Agric. Res.*, 5, 10-16.
- [5] Desheva B., Singh S.V. and Shashi J.P. (2015) *Orissa J. Agric. Res.*, 5(1/2), 10-16.
- [6] Chaitali G. and Bini P. (2007) *Functional Plant Bot.*, 30, 239-264.
- [7] Hushan S., Shariflou M.R. and Sharp P. (2013) *Maydica*, 49(2), 97-103.

- [8] Jhonson S.K., Johnson R.R. and Boyer J.S. (1955) *Agron. J.*, 70, 678-688.
- [9] Kaddem M., Kabra N. and Rao N.Y. (2014) *Transactions of Indian Society of Desert Technology and University Centre of Desert Studies*, 10, 97-99.
- [10] Kalimullah H.S., Geetha K. and Ibrahim S.M. (2012) *Ele. J. Plant Breed.*, 20(1), 1067-1072.
- [11] Mehendi S., Singh C.M. and Kushwaha V.K. (2013) *The Bioscan*, 8(4), 1481-1484.
- [12] Mehendi S., Singh I.P., Bohra A. and Singh C.M. (2015) *Legume Research*, 38(6), 758-762.
- [13] Kamani B., Magari R. and Kang M.S. (2009) *Genotype-environment interaction: Progress and prospects. In M. S. Kang (Ed.), Quantitative genetics, genomics, and plant breeding. CABI Publications, Wallingford, Oxon, UK*, 221-243.
- [14] Mecha N., Lal H. and Kumar G. (2014) *Crop Sci.*, 43, 2018-2027.
- [15] Rajdeep S., Padmanaban J. and Manirajan S. (2014) *Int. J. Plt. Sci.*, 5(1), 290-29.
- [16] Rajpoot A.A., Fahmi A.I. and Salma S.A. (2013) *J. Genet. Plant Breed.*, 53, 119-127.
- [17] Shah K., Praveenkumar B. and Sri Devi O. (2017) *Trends Biosci.*, 7(16), 2279-2290.
- [18] Sharaan G., Prashanth Y., Narsimha R.V., Sudheer K.S. and Venkateshwara R.P. (2017) *Intl. J. Appl. Biol. Pharma. Technol.*, 5(1), 257-260.