Electronic Journal of Plant Breeding

Research Note

Genetic analysis of polygenic traits in maize

Rajan Prasad Mishra[1*], Sandeep Kumar[1], Ashok Kumar[2] and Tarkeshwar[3]

[1]Institute of Agriculture Sciences, Department of Genetics and Plant Breeding, Bhagwant University, Ajmer, Rajasthan
[2]Department of Genetics and Plant Breeding, Bundelkhand University, Jhansi (U.P.)
[3]Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.)
*E-Mail: rajanmishrask@gmail.com

Abstract
Maize is one of the important cereals in the world. It is a good source of carbohydrates (70-87%) and protein (6-13%). To develop a high-yielding variety of any crop, heritability and genetic advance are important selection parameters for the selection of yield and yield attributes. In this regard, the present investigation was carried out at the Namdeo Umaji Agri Tech India Private Limited, Pune, during *Kharif,* 2022 to study the extent of variability among maize genotypes. Observations were recorded on 19 polygenic traits and the mean values were subjected to statistical analyses. High GCV and PCV were recorded for anthesis and silking interval, number of leaves, lodging percentage, number of kernels per row and grain yield per plant. High heritability accompanied by high genetic advance was noted for anthesis and silking interval, lodging percentage, grain yield per plant, number of leaves per plant, number of kernels per row, number of tassel branches, leaf width, days to 50% silking, protein content, leaf length, number of kernel rows per cob, cob diameter and cob length. It indicates that these traits are governed by additive gene action and selection will be rewarding for improving these traits in maize.

Keywords: Heritability, Variability, Genetic Advance, GCV, PCV, Zea mays.

Maize (*Zea mays* L.) is the third most important crop next to Wheat and Rice. It is mostly cultivated in tropical, subtropical, and temperate highlands. The indigenous people of southern Mexico cultivated maize (2n=20) for the first time about 8000 years ago. It is a C4 crop and is a member of the *Maydae* tribe and the *Poaceae* family. It is a tall, monoecious, day neutral with a deterministic growth pattern. The genus *Zea* comprises of four wild species namely, *Z.luxurians* (2n = 20), *Z.maxicana* (2n = 20), *Z.perennis* (2n = 40) and *Z. diploperennis* (2n = 20) (Nartam *et al*., 2015).

Maize has one of the highest yield potential of all cereals, maize has earned the title "Queen of Cereals." Maize is also referred to as a "contingency crop" since it may be used during any of its growth stage, as tender green fodder in the early stages, as baby corn in the very early

stages of cob development, as green cob in the slightly later stages, and as maize grain in the fully developed stages (Yadav *et al*., 2014). In 1951, the area under maize in India was 3.31 million hectares and it has risen to more than 9.2 million hectares during 2022. The spread of maize farming in non-traditional regions like Andhra Pradesh, Karnataka, Maharashtra, and Tamil Nadu is the primary reason for the increase in area. Over the past 60 years, a variety of breeding techniques, including single cross hybrids, double cross hybrids, and composite breeding, have been used to boost maize yield. However, single cross-hybrids received top focus over the past ten years, which led to a noticeable increase in maize yield (Sharma, 2021).

Heritability and genetic advance are two crucial concepts in the field of genetics and plant breeding, shedding light

on the inheritance and improvement of traits in crops. These concepts are indispensable in modern agriculture, enabling us to make informed decisions regarding crop breeding and selection (Falconer and Mackay, 1996). Heritability is a measure of the proportion of phenotypic variation in a trait that is attributable to genetic factors. It helps us understand the degree to which genes influence the expression of a particular trait. Genetic advance is a measure of the expected improvement in a trait that can be achieved through selective breeding. It quantifies the potential gain that can be made by choosing the best-performing individuals as parents for the next generation (Hallauer *et al*., 2010).

Understanding the genetic mechanisms involved in the inheritance of different quantitative and quality features is crucial for successful manipulation through breeding strategies, which would improve yield and quality indices. Keeping the facts in view the present study was conducted to understand the tendency of various variability parameters.

The investigation was conducted during *Kharif,*2022 at Namdeo Umaji Agri Tech India Private Limited in Pune, India. The experimental site was located at 560 meters above sea level, between 24 degrees 54' and 10 degrees 24' North latitude and 73 degrees 19' and 75 degrees 10' East longitude, with hot, semi-arid climate (BSh) and annual average temperatures ranging from 19 to 33°C. A total of 10 genetically diverse maize genotypes were used as parents (**Table 1**). A total of 45 crosses were synthesised by crossing the parents in diallel mating fashion (excluding reciprocals) during *Kharif* 2021. The resultant 45 F_1s were evaluated along with parents and the standard check Aravali Makka-1, in randomised block design with three replications, during *Kharif,* 2022 .

Each entry was planted in five rows each of three meters long, with a row-to-row spacing of 60 cm and a plant-to-plant spacing of 20 cm. All the recommended agronomic practices were followed for crop cultivation.

Observations for 19 metric traits *viz*., leaf length (leaf attached to the cob) (cm), leaf width (leaf attached to the cob) (cm), number of tassel branches, number of leaves above upper cob, plant height (cm), lodging percentage, cob length (cm), cob diameter (cm), number of kernel rows per cob, number of kernels per row, 100-seeds weight (g), grain yield per plant (g), seed moisture content (%) and protein content (%), were recorded on five randomly selected competitive plants of each entry in each replication, while for days to 50 percent tasselling, days to 50 percent silking, anthesis to silking interval, days to 75 percent brown husk, days to maturity, and lodging percent, observations were recorded on the plot basis. Analysis of variance (ANOVA) for Randomized Block Design as proposed by Panse and Sukhatme (1967), heritability in broad sense as proposed by Hanson (1963), genetic advance as proposed by Allard (1960) and the genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV) as proposed by Burton and de Vane (1953), were calculated based on mean data.

The ANOVA revealed significance of mean squares for all the traits suggesting the existence of sufficient variability among the genotypes for all the examined traits (**Table 2**) .Significant difference was also noted between parents and hybrids for all the traits studied. This is intune with the reports of Reddy *et al*. (2012), Rahman *et al*. (2015), Pandey *et al*. (2017), and Alhessein and Suliman (2022).

Broad-sense heritability is a measure that quantifies the proportion of phenotypic variation within a population that can be attributed to all genetic factors, including additive, dominant, and epistatic genetic interactions. It provides a broader view of the genetic contribution to a trait's variation. For all the 19 characters, the estimates of heritability (broad sense) and genetic advance in percent over the mean were calculated (**Table 3**). Heritability estimates varied from 66.80% (days to maturity) to 99.85% (seed moisture percent). The estimates of heritability in broad sense were observed to be high for seed moisture percent

Table 1. List genotypes and their collection sites

S. No.	Inbred/ Variety	Mode of collection	Collection Place
1	HM 10	Agri Asia seed Pvt. ltd	Pune
2	Vivek 21	Sayaji seed LLP	Jalna
3	PM-5 (Pratap Makka-5)	Tierra seed tech Pvt ltd.	Buldhana
4	Vivek Hybrid 15	ProFarm seed Pvt ltd	Aurangabad
5	Navjot	Killi seed and Fertilizer Ltd	Uruli Kanchan
6	PMH-1	Agrovet seed Zambia ltd	Nrayan Gao
7	PMH-2	C P seed Pvt ltd	Pune
8	HM-8	Signature biotech Pvt ltd	Hadapsar
9	Aravali Makka -1	UPL India Ltd	Pune
10	PEHM-2	Kaveri seed Pvt ltd	Jalna

Table 2. ANOVA for randomized block design for 19 traits of maize

Source of variation	Replications	Treatments	Error
	2 DF	54 DF	108 DF
Leaf length (Leaf attached to cob) (cm)	0.22	188.27**	5.56
Leaf width (Leaf attached to cob) (cm)	0.09	2.59**	0.07
Days to 50% Tassel flowering	5.81	38.84**	4.02
Days to 50% silking	7.8	195.20**	4.86
Days to 75 % dry husk	56.95	101.74**	9.94
Days to maturity	12.93	105.93**	15.06
Anthesis and Silking Interval	0.22	6.69**	0.04
No. of Tassel branches	2.17	16.52**	0.34
No. of leaves (Above upper cob)	0.03	7.61**	0.07
Plant height (cm)	50.87	517.85**	54.57
Lodging percentage	0.01	23.70**	0.19
Cob length (cm)	0.04	11.68**	0.46
Cob Diameter (cm)	0.00	2.04**	0.07
No. of kernels/row	0.07	98.52**	1.08
No. of kernels row/cob	0.56	12.77**	0.4
Seed Moisture (%)	0.24	959.41**	0.47
100 Seed weight (g)	6.39	29.12**	1.42
Protein content (%)	0.13	4.82**	0.13
Grain yield per plant (g)	78.12	8797.05**	70.13

*,**Significant at 5% and 1% probability level respectively.

Table 3. Mean, Range, heritability, genetic advance, GCV and PCV for 19 traits in maize

Characters	Mean	Min	Max	Var (g)	Var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)	% Contribution
Leaf length (Leaf attached to cob) (cm)	60.91	45.60	74.10	60.90	66.47	91.63	15.39	25.26	12.81	13.38	6.93
Leaf width (Leaf attached to cob) (cm)	6.34	4.00	8.10	0.84	0.91	92.17	1.81	28.58	14.45	15.06	6.25
Days to 50% Tassel flowering	53.38	48.00	63.00	11.61	15.62	74.30	6.05	11.33	6.38	7.40	8.12
Days to 50% silking	57.45	51.00	70.00	63.45	68.31	92.88	15.81	27.52	13.86	14.39	7.37
Days to 75 % dry husk	91.60	83.00	104.00	30.60	40.54	75.48	9.90	10.81	6.04	6.95	7.52
Days to maturity	97.98	87.00	110.00	30.29	45.35	66.80	9.27	9.46	5.62	6.87	7.84
Anthesis and Silking Interval	5.25	3.00	9.00	2.22	2.26	98.29	3.04	57.87	28.34	28.58	4.91
No. of Tassel branches	15.26	10.50	19.50	5.39	5.73	94.03	4.64	30.39	15.21	15.69	6.40
No. of leaves	5.82	2.50	9.10	2.51	2.58	97.46	3.23	55.42	27.25	27.60	4.54
Plant height (cm)	181.87	150.10	204.80	154.43	209.00	73.89	22.00	12.10	6.83	7.95	6.71
Lodging percentage	9.05	5.50	15.56	7.85	8.00	98.20	5.72	63.24	30.98	31.26	4.13
Cob length (cm)	16.89	13.00	22.10	3.74	4.20	88.96	3.76	22.25	11.45	12.14	4.35
Cob Diameter (cm)	6.13	3.98	7.80	0.66	0.73	90.24	1.59	25.88	13.22	13.92	4.72
No. of kernels/row	25.86	15.00	38.00	32.48	33.56	96.79	11.55	44.66	22.04	22.40	3.62
No. of kernels row/cob	15.35	13.00	24.66	4.12	4.52	91.16	3.99	26.02	13.23	13.86	4.31
Seed Moisture (%)	17.66	8.75	23.5	19.65	20.11	99.85	36.80	20.45	10.26	10.34	3.87
100 Seed weight (g)	29.76	24.00	36.40	9.23	10.66	86.64	5.83	19.58	10.21	10.97	4.06
Protein content (%)	9.00	6.56	11.23	1.56	1.69	92.25	2.47	27.48	13.89	14.46	1.93
Grain yield per plant (g)	203.39	121.50	325.40	2908.97	2979.10	97.65	109.79	53.98	26.52	26.84	2.42

(99.85%), anthesis and silking interval (98.29%), lodging percentage (98.20%), grain yield per plant (97.65%), number of leaves (97.46%), number of kernels per row (96.79%), number of tassel branches (94.03%), days to 50% silking (92.88%), protein content (92.25%), leaf width (92.17%), leaf length (91.63%), number of kernels row per cob (91.16%), cob diameter (90.24%), 100-seeds weight (86.64%), cob length (88.96%) and days to 75% dry husk (75.48%). If broad-sense heritability is high, it indicates that a significant portion of the phenotypic variation is due to genetic factors. Consequently, selecting individuals based on their trait values should result in substantial improvements in the population mean for that trait. Similar findings were reported by Reddy *et al.* (2012), Begum *et al.* (2016), Pandey *et al.* (2017), Vishwanath *et al.* (2018), Nagalakshmi *et al.* (2018), Alhessein and Suliman (2022) and Sahu *et al.* (2022).

Moderate values of heritability were observed for days to 50% flower tasseling (74.30%), plant height (73.89%) and days to maturity (66.80%). The low heritability estimates were not noted for any of the traits under investigation. Conversely, if broad-sense heritability is low, it suggests that the genetic component, including non-additive genetic effects, has a limited impact on the trait's variation. In such cases, even if selection is applied, the expected genetic advance may be smaller because the genetic contribution to the trait's variation is modest. Kara (2001) also noted low heritability estimates for some traits.

The genetic advance represents the expected improvement in the mean of a trait within a population after one generation of selection. The estimates of genetic advance in percent over mean were determined for all the characters under estimation. The estimates of genetic advance in percent over the mean for the characters ranged from 9.46% (days to maturity) to 63.24% (lodging percentage). High estimates for genetic advance were recorded for lodging percentage (63.24%), anthesis and silking interval (57.87%), number of leaves per plant (55.42%), grain yield per plant (53.98%), number of kernels per row (44.66%), leaf length (25.26%), number of tassel branches (30.39%), leaf width (28.58%), days to 50% silking (27.52%), protein content (27.48%), cob diameter (25.88%), cob length (22.25%) and number of kernel rows per cob (20.45%), respectively. A high genetic advance indicates the potential for significant and rapid improvement in a trait through selective breeding. Similar results were observed by Devi *et al.* (2015), Begum *et al.* (2016), Vishwanath *et al.* (2018) and Pradhan *et al.* (2022) also.

Moderate genetic advance was observed for days to 50% tasselling (11.33%), days to 75% dry husk (10.81%), plant height (12.10%) and 100-seeds weight (19.58%) while low amount of genetic advance in percent of mean was observed only for the trait days to maturity (9.46%). A moderate or low genetic advance indicates that selective

breeding or selection for a specific trait is likely to result in slower or more limited improvements in that trait within the population. Ojo *et al.* (2006) also reported low heritability and genetic advance for days to harvest.

The GCV quantifies the relative genetic variability of a trait within a population of plants due to genetic reasons. The PCV assesses the total variability of a trait within a population, including genetic and environmental sources of variation. The higher values of genotypic coefficient of variation (GCV) along with phenotypic coefficient (PCV) were recorded for anthesis and silking interval (28.34% and 28.58%), number of leaves (27.25% and 27.60%), lodging percentage (30.98% and 31.26%), number of kernels per row (22.04% and 22.44%) and grain yield per plant (26.52% and 26.84%) as presented in **Table 2**. The combination of high GCV and high PCV suggests that the trait has significant genetic diversity and is responsive to selective breeding. Plant breeders can potentially achieve substantial improvements in the trait by selecting and breeding plants with desirable trait values. These findings were also supported by earlier workers like Rahman *et al.* (2015), Bhusal *et al.* (2017) and Neelima *et al.* (2020). -

Moderate GCV along with PCV were noted for the traits leaf length (12.81% and 13.38%), leaf width (14.45% and 15.06%), days to 50% silking (13.86% and 14.39%), number of tassel branches (15.21% and 15.69%), cob length (11.45% and 12.14%), cob diameter (13.22% and 13.92%), number of kernel rows per cob (13.23% and 13.86%), seed moisture (10.26% and 10.34%), 100-seeds weight (10.21% and 10.97%) and protein content (13.89% and 14.86%). Low values of GCV and PCV suggest that such traits are primarily influenced by environmental factors. Traits with low GCV and PCV are often considered stable because they exhibit minimal variation across different individuals and environments. This stability can be valuable when consistency in trait expression is essential. Vishwanath *et al.* (2018) also studied moderate PCV and GCV were observed for cob diameter and cob length in the F_1 generation. The rest of the traits like days to 50% tassel flowering, days to 75% dry husk, days to maturity and plant height, showed low PCV and GCV for these traits. Munawar *et al.* (2013) found a low GCV and PCV for number of kernel rows per ear and the number of kernels per row. Yadesa *et al.* (2022) detected low GAM values (less than 10%) in agronomic variables such as days to 50% anthesis, days to 50% silking, days to maturity, number of rows per ear, and ear length.

In conclusion, the high heritability accompanied with high genetic advance was observed for lodging percentage, anthesis, and silking interval, number of leaves per plant, grain yield per plant, number of kernels per row, leaf length, number of tassel branches, leaf width, days to 50% silking, protein content, cob diameter, cob length and number of kernel rows per cob which indicated that there

was additive gene action involved for the expression of such traits. Phenotypic selection for such traits could be be highly rewarding.

REFERENCES

Alhessein, M.B. and Suliman, S.H. 2022. Performance, heritability and correlation studies on maize (*Zea mays* L) genotypes under irrigated condition in central Sudan. *Environ Sci Ecol: Curr Res,* **3**:1061. [Cross Ref]

Allard, R.W. 1960. Principle of Plant Breeding. John Wiley and Sons. pp.154.

Archana, K.A., Kuchanur, P.H., Zaidi, P.H., Mandal, S.S., Arunkumar, B., Patil, A., Seetharam, K. and Vinayan, M.T. 2018. Stability for grain yield and other traits in tropical maize (*Zea mays* L.) under heat stress and optimal conditions. *Int. J. Curr. Microbio. App. Sci.*, **7**(11):815-823. [Cross Ref]

Begum, S., Ahmed, A., Omy, S.H., Rohman, M.M. and Amiruzzaman, M. 2016. Genetic variability, character association and path analysis in maize (*Zea mays* L.). *Bangladesh Journal of Agricultural Research*, **41**(1):173-182. [Cross Ref]

Bhusal, T., Lal, G.M., Marker, S. and Synrem, G.J. 2017. Genetic variability and traits association in maize (*Zea mays* L.) genotypes. *Annals of Plants and Soil Research*, **19**(1):59-65.

Burton, G.W. and de Vane, E.H. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, **45**:478-481. [Cross Ref]

Devi, E.L., Verma, S.S., Sundip, K. and Singh, N.K. 2015. Genetic variability studies for yield and contributing traits under two plant densities and molecular diversity analysis in maize (*Zea mays* L). *Maydica*, **60**(4):37.

Ellis, R.H., Summerfield, R.J., Edmeardes, G.O. and Robert, E.H. 1992. Photoperiod, temperature and the interval from sowing to tassel initiation in diverse cultivars of maize. *Crop Sci.,* **32**: 1225-1232. [Cross Ref]

Falconer, D. S. and Mackay, T. F. C. 1996. Introduction to Quantitative Genetics (4th ed.). Pearson.

Hallauer, A.R. and Miranda, J.B. 1988. Quantitative genetics in maize breeding 2nd edition. Iowa State University Press, Ames, pp.267-294.

Hallauer, A. R., Miranda Filho, J. B. and Carena, M. J. 2010. Quantitative Genetics in Maize Breeding (3rd ed.). *Springer*. [Cross Ref]

Hanson, W.D. 1963. Heritability. *Statistical Genetics and Plant Breeding*, NAS-NRC, Washington, Publ., **982**, pp.125-140.

Kara, S.M. 2001. Evaluation of yield and yield component traits in inbred maize lines. *Turkish Journal of Agriculture and Forestry*, **25**: 383-391.

Nartam, A.T., Moon, M.K., Sapakal, S.A., Patil, S.R. and Peshattiwar, P.D. 2015. Combining ability studies in maize (*Zea mays* L.). *J. Soils Crops,* **25**(1):109-115.

Neelima, C., Sarankumar, C., Sudha, M., Ganesan, K. N., Ravikesavan, R. and Senthil, N. 2020. Estimation of variability, heritability, genetic advance and assessment of frequency distribution for morphological traits in intercross population of maize. *Electronic Journal of Plant Breeding,* **11**(2):574-580. [Cross Ref]

Nagalakshmi, R.M., Ravikesavan, R., Paranidharan, V., Manivannan, N., Firoz, H., Vignesh, M. and Senthil, N. 2018. Genetic variability, heritability and genetic advance studies in backcross populations of maize (*Zea mays* L.). *Electronic Journal of Plant Breeding,* **9**(3):1137–1145. [Cross Ref]

Ojo, D.K., Omikunle, O.A., Oduwaye, O.A., Ajala M.O. and Ogunbayo S.A. 2006. Heritability, character correlation and path coefficient analysis among six inbred lines of maize (*Zea mays* L.). *World Science Research Journals*, **2**(3):352-358.

Pandey, Y., Vyas, R.P., Kumar, J., Singh, L., Singh, H.C. and Yadav, P.C. 2017. Heritability, correlation and path coefficient analysis for determining interrelationships among grain yield and related characters in maize (*Zea mays* L.). *International Journal of Pure Applied Bioscience*, **5**(2):595-603. [Cross Ref]

Panse, V.G. and Sukhatme, P.V. 1967. Statistical methods for agricultural workers. II Edn. pp.152-157.

Pradhan, P., Thapa, B., Ghosh, A., Subba, V., Sahu, C.R. and Kundagrami, S. 2022. Genetic variability assessment on yield attributing traits in maize (*Zea mays* L.) inbred lines. *The Pharma Innovation Journal*, **11**(5):1642-1645.

Rahman, M.W., Talukder, M.A.I., Mamun, M.A.A., Hanif M.A. and Uddin M.J. 2015. Studies on genetic variability, correlation and path analysis of yield attributes in maize genotypes (*Zea mays* L.). *Journal of Chemical, Biological and Physical Sciences*, **5**(4):3964-3971.

Reddy, V.R., Jabeen, F., Sudarshan, M.R. and Rao, A.S. 2012. Studies on genetic variability, heritability,

correlation and path analysis in maize (*Zea mays* L.) over locations. *International Journal of Applied Biology and Pharmaceutical Technology*, **4**(1):196-199.

Sahu, J., Sinha, S.K., Chaudhari, P., Giri, S.K. and Sathish, K. 2022. Evaluation of maize (*Zea mays* L.) genotypes to estimate the genetic parameters of variability for various polygenic traits. *The Pharma Innovation Journal*, **11**(9):668-672.

Sharma, P. 2021. Line × tester analysis of yield and its contributing traits in maize (*Zea mays* L.). Thesis submitted at Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishwavidyalaya Palampur, Himanchal Pradesh.

Vishwanath, Singh, L., Yadav, P. C., Kumar, S., Singh, H. C., Yadav, R. K., Pandey, Y. and Gupta, S. 2018. Assessment of genetic variability and selection parameter for yield contributing traits in maize (*Zea mays* L.). *IOSR Journal of Pharmacy,* **8**(8):1-31.

Yadav, O.P., Karjagi, C.G. and Dhillon, B.S. 2014. Overview of maize improvement. *Indian Farming*, **64**(4):5-11.

Yadesa, L., Abebe, B. and Tafa, Z. 2022. Genetic variability, heritability, correlation analysis, genetic advance, and principal component analysis of grain yield and yield related traits of quality protein maize (*Zea mays* L.) inbred lines adapted to mid-altitude agroecology of Ethiopia. *EAS J Nutr Food Sci*, **4**(1):8-17. [Cross Ref]