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Heritability and genetic advance estimates for certain quantitative traits in maize (*Zea mays* L.)

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Abstract
In the present investigation, 77 maize genotypes including 54 F1s, 18 lines, 3 testers and 2 check varieties were evaluated in relation to genetic variability, heritability and genetic advance for different quantitative traits. Significant variability was reported in the genotypes for all the characters studied. Low to high estimates of GCV and PCV were reported for different characters. In general estimates of PCV were higher than that of GCV but the difference was very less for all the traits. Indicated less environmental influence on the expression of all the traits. High estimates of GCV and PCV (>20%) were reported for grain yield per plant, cob weight, kernels per cob and kernels per row. Heritability for different quantitative traits is most important aspect in plant breeding. However, heritability estimate alone does not provide sufficient evidence regarding the amount of genetic progress. Heritability estimates along with the estimates of genetic advance gives more reliable information. In the present investigation all the characters were showed high estimates of heritability (>61%). High estimates of genetic advance as percent of mean (>20%) were recorded for grain yield per plant, cob weight, kernels per cob, kernels per row, cob length, 100-kernel weight, cobs per plant, kernel rows per cob and plant height. The characters that had high GCV, heritability and genetic advance should be utilized in making selection strategy for yield improvement in maize.

Keywords: Heritability, genetic advance, quantitative traits and maize (*Zea mays* L.)

Introduction
Maize (*Zea mays* L.) is the third major cereal crop in the world after wheat and rice. It is one of the most important cereal crops of India. (Ambikabathy *et al*., 2019) [1]. Maize grain is used for three main purposes: as a staple food, as feed for livestock and poultry, and as a raw material for many industrial products. The main maize-based industrial products are breakfast products such as cornflakes, starch, sugar and oil. Its main component, starch, is used for human consumption or made into syrup or alcohol. Poultry, livestock, fish as well as wet dry milling industries, growing fast day by day, resulting in increased demand of maize. Therefore, there will be requirement of high yielding maize cultivars. Breeding for high yield crops requires information on the nature and magnitude of variation in the available materials and the proportion of total variability which is heritable in nature. Robinson *et al*., 1949 [15] have also suggested that the knowledge of heritability of a character is important as it indicates the possibility and extent to which improvement is possible through selection Therefore, in the present investigation, heritability and genetic advance estimates for certain quantitative traits were estimated.

Materials and Methods
For this experiment, 54 F1s were obtained through crossing of 18 lines (females) with 3 testers (males) in line x tester mating design during *Kharif* 2018. Resulting 54 F1 s along with their 21 parental lines and two check varieties were evaluated at Student Instructional Farm CS Azad University of Agriculture and Technology, Kanpur-208002 (U.P.), India during *Rabi* 2018-19. All the treatments were grown in a randomized complete block design (RCBD) in one row plots of 4m length with 60x25cm spacing and replicated three times. Observations pertaining to plant height at maturity, number of cobs/plant, number of kernel rows/cob, number of kernels/row, cob length (cm), cob diameter (cm), cob weight (g), number of kernels/cob, 100-kernel weight (g), grain yield/plant (g) and shelling percentage (%) were recorded on 5 randomly selected plants per entry per replication however, in case of days to 50% tasselling, days to 50% silking, days to 75% dry husk data were recorded on plot basis. All recommended cultural practices were done to raise a good crop.

The mean values of recorded data were used for Analysis of variance for Randomized Complete Block Design (Panse and Sukhatme, 1985) [13], Phenotypic, genotypic, and environmental coefficients of variation for different characters (Burton and de Vane, 1953) [5], heritability in broad sense (h^2b) (Hanson, 1963) [6], the expected genetic advance (Ga) and genetic advance as percent of mean (Johnson *et al.*, 1955) [9].

Result and Discussion:

Variability is the prerequisite for any breeding programme, but the effectiveness of any breeding programme depends on heritable portion of total variability present in the population for different traits. Thus, heritability for different quantitative traits is most important aspect in breeding. However, heritability estimate alone does not provide sufficient evidence regarding the amount of genetic progress. Heritability estimates along with the estimates of genetic advance gives more reliable information.

Analysis of variance for different quantitative traits is presented in table 1. Significant variability was observed among all the genotypes for all the characters under study. Mhoswa *et al.* (2016) [12], Thakur *et al.* (2016) [19], Shengu (2017) [17], Bisen *et al.* (2018) [4], Beulah *et al.* (2018) [3], Bartaula *et al.* (2019) [2], Prakash *et al.* (2019) [14], Ubi *et al.* (2019) [20], Islam *et al.* (2020) [8] and Taiwo *et al.* (2020) [18] also reported significant differences among all the characters under study. The estimates of genotype coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are presented in Table 2. Lower to higher estimates of GCV and PCV were reported for different characters. In general estimates of PCV were higher than that of GCV but the difference was very less for all the traits. Indicated that environment had negligible effect on the expression of all the characters. Beulah *et al.* (2018) [3], Bisen *et al.* (2018) [4] and Shengu (2017) [17] have also reported similar findings. High estimates of GCV (>20%) were exhibited by grain yield per plant (33.959), cob weight (29.7), kernels per cob (25.2) and kernels per row (22.694).

The information regarding to transmissibility of characters from parents to their offspring obtained through heritability estimates; hence it becomes crucial to know the extent of heritability of a trait for efficient selection strategy. In the present investigation, all the characters were showed high estimates of heritability (>61%). High estimates of genetic advance as percent of mean (>20%) were recorded for grain yield per plant, cob weight, kernels per cob, kernels per row, cob length, 100-kernel weight, cobs per plant, kernel rows per cob and plant height. The characters that had high GCV, heritability and genetic advance should be utilized in making selection strategy for yield improvement in maize. Similar findings have also been reported by Maruthi and Rani (2015) [11], Kinfe and Tsehaye (2015) [10], Sandeep *et al* (2015) [16], Thakur *et al.* (2016) [19], Prakash *et al.* (2019) [14], Hussain *et al.* (2019) [7], Ubi *et al.* (2019) [20], Islam *et al.* (2020) [8] and Taiwo *et al.* (2020) [18].

Table 1: Analysis of variance for different quantitative traits in maize

Source of variation	d.f.	Days to 50% tasseling	Days to 50% silking	Days to 75% dry husk	Plant height (cm)	Number of cobs/plant	Cob length (cm)	Cob diameter (cm)
Replication	2	4.628	10.602	5.727	4.257	0.004	2.063	1.262
Treatment	76	61.830**	66.057**	72.915**	1109.846**	0.066**	19.226**	3.939**
Error	152	4.180	4.431	5.096	4.915	0.002	1.140	0.421

Source of variation	d.f.	Cob weight (g)	Number of kernel rows/cob	Number of kernels / row	Number of kernels /cob	100-Kernel weight (g)	Shelling percentage (%)	Grain yield/plant (g)
Replication	2	0.974	0.557	1.476	7.041	0.494	0.437	5.245
Treatment	76	2729.318**	7.401**	89.955**	20434.191**	33.300**	115.092**	2789.363**
Error	152	1.937	0.193	0.497	9.729	0.581	4.294	7.328

*, ** significant at 5% and 1% level, respectively

Table 2: Estimates of GCV, PCV, heritability and genetic advance for different quantitative traits in maize

	Range Lowest	Range Highest	General Mean	GCV	PCV	h^2 (Broad Sense) %	Ga (5%)	Gen. Ad. as % of Mean (5%)
Days to 50% tasseling	106.33	130.33	117.178	3.741 L	4.128 L	82.1 H	8.184	6.984 L
Days to 50% silking	110.67	134	121.147	3.741 L	4.125 L	82.3 H	8.468	6.99 L
Days to 75% dry husk	143.67	167.67	154.896	3.07 L	3.398 L	81.6 H	8.848	5.712 L
Plant height (cm)	120.81	215.44	180.519	10.631 M	10.702 M	98.7 H	39.273	21.756 H
Number of cobs/ plant	1	1.38	1.13	12.921 M	13.393 M	93.1 H	0.29	25.68 H
Cob length (cm)	11.07	21.16	16.272	15.089 M	16.455 M	84.1 H	4.638	28.505 H
Cob diameter (cm)	9.54	14.25	12	9.026 L	10.519 M	73.6 H	1.914	15.954 M
Cob weight (g)	47.5	173.99	101.521	29.7 H	29.731 H	99.8 H	62.047	61.117 H
Number of kernel rows/ cob	9.42	17.62	13.633	11.369 M	11.818 M	92.5 H	3.072	22.531 H
Number of kernels /row	12.26	37.72	24.062	22.694 H	22.882 H	98.4 H	11.156	46.364 H
Number of Kernels/cob	125.94	531.04	327.426	25.2 H	25.218 H	99.9 H	169.852	51.875 H
100-Kernel weight (g)	15.71	33.9	24.328	13.575 M	13.932 M	94.9 H	6.629	27.249 H
Shelling percentage (%)	58.99	86.96	78.115	7.78 L	8.22 L	89.6 H	11.849	15.169 M
Grain yield/plant (g)	28.63	183.1	89.674	33.959 H	34.093 H	99.2 H	62.485	69.681 H

References

1. Ambikabathy A, Selvam N.J, Selvi DT, Dhasarathan M, Vairam N, Renganathan VG *et al*. Determination of Combining Ability and Heterosis for Yield and Yield Related Traits in Maize Hybrids Based on Line × Tester Analysis. Res. Jr. of Agril. Sci. 2019; 10(1):215-220.
2. Bartaula S, Panthi U, Timilsena K, Acharya SS, Shrestha J. Variability, heritability and genetic advance of maize

(*Zea mays* L.) Genotypes. Res. Agric. Livest. Fish. 2019; 6(2):163-169.
3. Beulah G, Marker S, Rajasekhar D. Assessment of quantitative genetic variability and character association in maize (*Zea mays* L.). Journal of Pharmacognosy and Phytochemistry. 2018; 7(1):2813-2816.
4. Bisen N, Rahangdale CP, Sahu RP. Genetic Variability and correlation studies of yield and yield component in maize hybrids (*Zea mays* L.) under kymore plateau and satpura hill region of Madhya Pradesh. International Journal of Agriculture, Environment and Biotechnology. 2018; 11(1):71-77.
5. Burton GM, de Vane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron. J. 1953; 45:471-481.
6. Hanson WD. Heritability in: WD Hanson and HF Robinson (Eds.) Statistical Genetics and Plant Breeding Publ. 982, Washington, DC National Academy of Science, National Research Council, 1963, 125-139.
7. Hussain MA, Askandar HS, Khether AA, Saaed RI. Evaluation of maize genotypes for yield and yield components and constructing selection index. Tikrit Journal for Agricultural Sciences. 2019; 19(4):76-82.
8. Islam NU, Ali G, Dar ZA, Maqbool S, Baghel S, Bhat A. Genetic variability studies involving drought tolerance related traits in maize (*Zea mays* L.) in breds. International Journal of Chemical Studies. 2020; 8(1):414-419.
9. Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybeans. Agronomy Journal. 1955; 47: 314-318.
10. Kinfe H, Tsehaye Y. Studies of Heritability, Genetic Parameters, Correlation and Path Coefficient in Elite Maize Hybrids. Acad. Res. J Agri. Sci. Res. 2015; 3(10):296-303.
11. Maruthi RT, Rani KJ. Genetic variability, heritability and genetic advance estimates in maize (*Zea mays* L.) inbred lines. Journal of Applied and Natural Science. 2015; 7(1):149-154.
12. Mhoswa L, Derera J, Quabe FNP, Musimwa TR. Diversity and path coefficient analysis of Southern African maize hybrids. Chilean Journal of Agricultural Research. 2016; 76(2):143-15.
13. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers. 4th Ed. ICAR, New Delhi, 1985, 361.
14. Prakash R, Ravikesavan R, Vinodhana N, Kumari SA. Genetic variability, character association and path analysis for yield and yield component traits in maize (*Zea mays* L.) Electronic Journal of Plant Breeding. 2019; 10(2):518-524.
15. Robinson HF, Comstock RE, Harvey PH. Estimates to heritability and degree of dominance in corn. Agron. J. 1949; 41:353-359.
16. Sandeep S, Bharathi M, Narsimha Reddy V, Eswari KB. Genetic variability, heritability and genetic advance studies in inbreds of maize (*Zea mays* L.). Eco. Env. & Cons. 2015; 21(Suppl.):S445-S449.
17. Shengu MK. Genetic Study of Some Maize (*Zea mays* L.) Genotypes in Humid Tropic of Ethiopia. International Journal of Scientific and Research Publications. 2017; 7(1):281-287.
18. Taiwo OP, Nwonuala AI, Isaiah BF. Variability in yield and yield components of selected pro-vitamin a maize (*Zea mays* L.) varieties in a humid environment of Port Harcourt, Nigeria. Asian Journal of Agricultural and Horticultural Research. 2020; 5(3):1-10.
19. Thakur S, Sinha SK, Mehta N, Thakur D. Genetic analysis of yield and its components in maize (*Zea mays* L.) inbred lines using line x tester analysis. International Journal of Agriculture Sciences, 2016; 8(53):2768-2773.
20. Ubi GM, Onabe MB, Kalu SE. Path coefficient analysis, character association and variability studies in selected maize (*Zea mays* L.) genotypes grown in Southern Nigeria. Annual Research & Review in Biology. 2019; 33(3):1-6.