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Studies on heritability and genetic advance estimates of Maize (*Zea mays* L.) under diverse ecosystem

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Abstract
15 diverse inbred lines, 3 testers of Maize and 45 F_1s were derived using 15 X 3 Line X Tester design were evaluated in a RBD in three replication in two locations (Kanpur and Aligarh) and two seasons (Kharif and Rabi) along with composite and hybrid checks at Kanpur and Aligarh. The data were collected on five randomely selected plants from each parent and their F_1s in each replication for 13 yield attributed traits namely Days to 50% tasseling, Days to 50% silking, Days to 75% dry husk, Plant height (cm), Number of cobs per plant, Cob weight (g), Number of grain rows per cob, Number of grains per row, Grain weight per cob (g), Shelling percentage (%), 100 kernel weight (g), Grain yield per plant and Seed vigour index. The data so generated were subjected for statistical analysis as usual procedure while heritability in narrow sense (Crumpacker and Allard 1962), broad sense as per Burton and de Vane (1953) and simillary genetic advance as per (Robinson *et al.* 1949). Heritability estimates were high for Cob weight, Number of grain rows per cob, Grain weight per cob and Grain yield per plant while moderate to low for rest of the characters. Results revealed low estimate of heritability for all the characters over the environments. Days to 75% dry husk, Plant height, Cob weight, Number of grain rows per cob, Grain weight per cob, Shelling percentage and Grain yield per plant showed moderate heritability. Estimates of genetic advance revealed low/ moderate estimate for all the thirteen characters over the environments. Therefore, improvement in these characters through selection seems to be very limited as low heritability coupled with low genetic advance reflected that almost all these characters were influenced by non-additive gene action

Keywords: Maize, heritability and genetic advance

Introduction
Maize (*Zea mays* L.) has a prominent position over the crops and supplying more than 30% calories consumed by the human being, billions of dollars providing annually to agriculture economy (Shiferaw *et al.* 2011). Due to diverse uses it can be cultivated with elevation ranging from sea level to up to 3000 m above mean sea level under tropical, sub-tropical and temperate conditions.

Maize is cultivated across 169 countries under different complex agro climatic conditions, with a total worldwide harvest area of approximately 194 million hectares, and producing 1148 million tonnes (Anonymous, 2021). Additionally, it is also cultivated for baby corn, sweet corn, silage making and as green cob as roasted one.

In India maize is cultivated in an area of about 9.03 mha with an annual production of 28.64 mt. during 1950-51, maize production of India was only 1.73 million tonnes (mt), which has increase 2019-20 about 28.64 mt. This achieved by increase of area and productivity of superior cultivars, especially of single cross hybrids. Due to diverse uses like feed, food, industrial products, bio fuel and bio plastic, forage and silage, maize demand is expected to increase from the current level to up to 45 mt by 2030 (Maize Vision 2020; IIMR).

Keeping in view the studied on heritability and genetic advance for yield and yield attributing traits on maize was conducted in two locations (Kanpur and Aligarh) and two seasons (Kharif and Rabi) to compute the genetic estimates of different traits aiming for selection of superior genotypes.

Materials and Methods
The base material for present study comprises 15 diverse inbred lines namely WiN-19, WiN-21, WiN-22, WiN-26, WiN-29, WiN-30, WiN-31, WiN-32, WiN-33, WiN-34, WiN-35, WiN-36, WiN-38, WiN-39, WiN-40 of maize and 3 testers *viz*. TSK-4, TSK-44 and D-15 of Maize,

selected on the basis of variability for various characters available in genetic material maintained in the section of maize, Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur-(UP). 45 F_1s were derived using 15 X 3 Line X Tester design to produce single crosses during Rabi (2017-18). All the crosses along with parents were evaluated in a replicated experiment during Kharif (2018) and Rabi (2018-19) at two diverse environments along with one composite (Azad Uttam) and one hybrid (DKC 9108) checks at Kanpur and Aligarh. The observations were recorded on g yield and maturity traits namely; Days to 50% tasseling, Days to 50% silking, Days to 75% dry husk, Plant height (cm), Number of cobs per plant, Cob weight (g), Number of grain rows per cob, Number of grains per row, Grain weight per cob (g), Shelling percentage (%), 100 kernel weight (g), Grain yield per plant and Seed vigour index. Observations were recorded on plot basis. The data so generated were pooled and all the onward calculation was carried out on based on pooled basis. Heritability in narrow sense was calculated using the formula as suggested by Crumpacker and Allard (1962), which is based on genetic components of variance analysis and in broad sense as per Burton and de Vane (1953). Similarily genetic advance at 5% selection intensity was calculated based on formula as suggested by Robinson *et al.* (1949).

Results and Discussion

The analysis of variance of experiments pooled is presented in Table-1 which revealed that the treatments were highly variable for the characters indicating the presence of high level of variability among the selected genotypes/inbreds and their crosses derived from it.

The orthogonal partitioning of treatments revealed that the lines, testers, F1s, lines vs F1s, lines vs testers and testers vs F1s were also showed significant values for all the characters indicating the variability in lines, testers and their interactions were also highly variable for all the characters in the material studied implying that the genotypes can be deployed in the development of varieties adapted to different environments (Allard, 1999) [2]. The parents chosen for the present study produced high yielding hybrids besides exhibiting high amount of variance for yield contributing traits. Similar trends for variances and its components in maize were reported by Lal and Kumar (2012), Anusheela *et al.*(2013), Abrha *et al.* (2013), Singh *et al.*(2013), Motamedi *et al.*(2014), Rajesh *et al.*(2014), Rastgari *et al.* (2014), Kuchanur *et al.* (2014), Ruswandi (2015), Kumar *et al.* (2016) and Ertiro *et al.* (2017) [15, 5, 1, 24, 16, 18, 19, 13, 9] for yield, quality, and maturity characters.

In present study Heritability, Genetic advance and genetic advance in percent over mean were calculated based on both narrow sense and broad sense respectively and presented in Table-2 and 3.

From the table it is clear that broad sense heritability and genetic advance both are higher than the heritability estimates in narrow sense in the entire environment and pooled over environment.

Higher heritability coupled with high genetic advance in broad sense was observed only for Seed vigour index while moderate to low for rest all the characters.

Based on narrow sense both heritability and genetic advance were comparatively lower in values than broad sense it showed that narrow sense heritability estimates were high for Cob weight, Number of grain rows per cob, Grain weight per cob and Grain yield per plant while moderate to low for rest of the characters.

In the present investigation, the results revealed low estimate of heritability for all the characters over the environments. Days to 75% dry husk, Plant height, Cob weight, Number of grain rows per cob, Grain weight per cob, Shelling percentage and Grain yield per plant showed moderate heritability similar results were also reported by Nzuve *et al*. (1014) Begum *et al*. (2016), Ribeiro *et al.* (2016) and Kharel *et al*. (2017 [17, 20, 12]).

The genetic advance in percent over mean was estimated for all the traits pooled over environments which ranged from (0.27%) number of cobs per plant to (10.73%) for grain yield per plant. In the present investigation, the results revealed low/ moderate estimate of genetic advance for all the thirteen characters over the environments. Therefore, improvement in these characters through selection seems to be very limited as low heritability coupled with low genetic advance reflected that almost all these characters were influenced by non-additive gene action. Similar results were reported by Zahid Mahmood *et al.* (2004), Thanga Hemavathy *et al.* (2008), Jawaharlal *et al.* (2011) and Anshuman *et al.* (2013) [25, 10, 11, 4].

Table 1: Analysis of variance for 13 quantitative characters over the environments in maize

	DF	Days to 50% tasseling	days to 50% sinking	Days to 75% dry husk	Plant height (cm)	Number of cobs per plant	COB weight (g)	Number of grain rows per cob
Replicates	2	3.462 **	4.354 **	5.565 **	36.513	0.109 **	1323.189 **	2.940 *
Environments	3	306635.600 **	310206.800 **	305930.700 **	206814.100 **	0.410 **	133308.300 **	183.931 **
Rep * Env.	6	0.830	0.556	1.383 *	1432.487 **	0.033	209.667	0.838
Treatments	62	58.375 **	66.705 **	111.274 **	6311.033 **	0.057 **	8062.825 **	8.726 **
Parents	17	41.658 **	45.355 **	90.914 **	1042.576 **	0.075 **	821.037 **	4.675 **
Parents (Line)	14	45.776 **	50.470 **	100.012 **	1124.966 **	0.021	759.073 **	4.842 **
Parents(Testers)	2	11.861 **	18.694 **	42.583 **	65.636	0.314 **	561.770 *	0.927
Parents (L vs T)	1	43.601 **	27.075 **	60.208 **	1843.001 **	0.348 **	2207.062 **	9.838 **
Parent vs Crosses	1	1887.001 **	2209.467 **	2259.483 **	308466.400 **	0.078 *	428018.100 **	249.087 **
Crosses	44	23.275 **	26.254 **	70.318 **	1479.405 **	0.049 **	1316.351 **	4.828 **
Line effect	14	33.407	38.641	144.403 **	3076.707 **	0.036	1720.879 *	6.929 *
Tester effect	2	12.669	18.502	98.052	613.390	0.020	6290.083 **	14.018 *
Line * Tester effect	28	18.966 **	20.615 **	31.294 **	742.612 **	0.058 **	758.820 **	3.121 **
Env * Treat	186	22.694 **	22.115 **	39.072 **	524.805 **	0.031 **	760.696 **	1.739 **
Env * Parents	51	22.993 **	23.595 **	37.324 **	636.824 **	0.029 *	793.362 **	2.372 **
Env * Parents (L)	42	17.698 **	16.978 **	39.763 **	591.040 **	0.016	725.705 **	1.873 **
Env * Parents (T)	6	7.417 **	9.806 **	35.287 **	197.995	0.070 **	203.634	4.433 **
Env * PAR (L vs T)	3	128.278 **	143.816 **	7.245 **	2155.461 **	0.130 **	2920.010 **	5.241 **

Env * Parent vs Cross	3	145.589 **	124.392 **	197.423 **	4433.814 **	0.085 **	6660.121 **	1.106
Env * Crosses	132	19.785 **	19.219 **	36.148 **	392.683 **	0.030 **	613.997 **	1.508 **
Env * Line effect	42	31.784 **	31.000 **	66.658 **	475.930	0.028	679.449	1.947
Env * Tester effect	6	18.935	17.225	9.857	227.796	0.059	363.090	0.841
Env * L * T effect	84	13.847 **	13.471 **	22.771 **	362.838 **	0.030 **	599.193 **	1.336 **
Error	496	0.429	0.390	0.507	162.950	0.019	173.302	0.861
Total	755	1229.102	1243.808	1234.740	1587.855	0.027	1498.240	2.456

Table 1: Continue…..

	Df	Number of Grains per row	Grain weight Per cob (g)	Shelling Percentage (%)	100 kernel Weight (g)	Seed vigour Index	Grain yield per Plant (g)
Replicates	2	36.254	1024.281 **	0.475	2.218	33729.880	1421.993 **
Environments	3	872.273 **	84889.510 **	144.060 **	1106.233 **	66434.580 **	97101.640 **
Rep * Env.	6	57.179	184.834	9.932	6.435	10784.830	280.192
Treatments	62	207.180 **	6236.380 **	69.063 **	70.142 **	1145589.000 **	6808.107 **
Parents	17	54.612 *	576.245 **	54.319 **	44.594 **	57440.600 **	676.068 **
Parents (Line)	14	62.685 **	561.335 **	44.641 **	40.091 **	64665.290 **	631.682 **
Parents(Testers)	2	5.078	361.329	146.484 **	62.111 **	1259.661	261.389
Parents (L vs T)	1	40.659	1214.803 **	5.480	72.593 **	68656.760 *	2126.836 **
Parent vs Crosses	1	8955.568 **	328194.400 **	2195.509 **	2206.224 **	62532190.000 **	349642.900 **
Crosses	44	67.299 **	1106.022 **	26.432 **	31.466 **	170859.400 **	1385.603 **
Line effect	14	70.812	1510.481 *	37.267	43.039	186370.700	1742.305
Tester effect	2	61.780	5415.365 **	53.782	4.591	21603.420	6463.892 **
Line * Tester effect	28	65.938 **	595.983 **	19.060 **	27.599 **	173764.900 **	844.517 **
Env * Treat	186	34.442	584.841 **	15.559 **	19.080 **	35319.590 **	638.455 **
Env * Parents	51	24.082	608.123 **	21.041 **	25.087 **	9437.388	630.369 **
Env * Parents (L)	42	25.417	565.330 **	19.764 **	26.630 **	7726.121	613.867 **
Env * Parents (T)	6	0.330	148.144	32.014 **	16.852 *	19790.600	133.490
Env * PAR (L vs T)	3	52.893	2127.179 **	16.978 *	19.953 *	12688.710	1855.146 **
Env * Parent vs Cross	3	51.494	5016.127 **	30.113 **	141.222 **	45975.270 **	5941.498 **
Env * Crosses	132	38.057 *	475.134 **	13.110 **	13.984 **	45077.360 **	521.056 **
Env * Line effect	42	31.612	512.164	17.692 *	15.715	58004.610	547.684
Env * Tester effect	6	47.340	323.908	5.728	41.576 **	26758.780	515.136
Env * L * T effect	84	40.616 *	467.421 **	11.346 **	11.147 **	39922.210 **	508.165 **
Error	496	28.555	123.134	5.391	7.077	11225.350	161.161
Total	755	48.274	1078.591	13.698	19.563	110589.600	1214.068

* Signficant at 5%, ** Signficant at 1%

Table 2: Estimates of population mean and heritability for 13 quantitative characters in Maize

Character	Population mean					Heritability									
	Kharif Kanpur	Kharif Aligarh	Rabi Kanpur	Rabi Aligarh	Pooled	Kharif Kanpur		Kharif Aligarh		Rabi Kanpur		Rabi Aligarh		Pooled	
						NS	BS	NS	BS	NS	BS	NS	BS	NS	BS
Days to 50% tasseling	61.646	54.313	126.4	128.539	92.724	19.079	0.972	17.898	0.962	24.782	0.963	48.893	0.921	5.033	0.404
Days to 50% silking	64.877	57.544	130.185	132.046	96.163	17.831	0.971	17.689	0.963	25.097	0.972	50.745	0.944	6.244	0.446
Days to 75% dry husk	99.431	92.097	164.508	166.308	130.586	34.349	0.952	31.954	0.973	30.946	0.982	39.760	0.982	14.845	0.423
Plant height (cm)	125.232	120.583	169.453	188.098	150.841	51.797	0.836	16.994	0.854	11.489	0.726	8.815	0.75	17.924	0.65
Number of cobs per plant	1.038	1.041	1.105	1.13	1.078	21.865	0.25	12.091	0.013	3.355	0.267	16.373	0.33	1.296	0.117
Cob weight (g)	76.992	75.226	123.443	120.918	99.145	36.422	0.836	37.271	0.84	21.992	0.815	21.624	0.798	24.586	0.654
Number of grain rows per	12.295	11.979	13.627	14.007	12.977	12.890	0.539	8.367	0.56	43.948	0.452	40.682	0.479	28.295	0.36
Number of grains per row	27.483	26.843	31.031	30.791	29.037	0.593	0.148	8.275	0.55	20.666	0.604	41.596	0.567	6.881	0.327
Grain weight per cob (g)	64.408	62.644	100.947	99.531	81.883	38.561	0.836	39.560	0.841	25.522	0.834	21.441	0.826	25.961	0.663
Shelling percentage (%)	83.086	82.691	81.132	81.783	82.173	21.771	0.532	22.260	0.522	19.190	0.546	12.226	0.741	14.120	0.374
100 kernel weight (g)	25.81	25.338	29.138	30.379	27.667	14.911	0.562	14.001	0.661	46.253	0.6	9.334	0.364	5.530	0.319
Seed vigour index	2731.504	2703.656	2747.353	2729.827	2728.09	12.101	0.839	13.441	0.889	12.394	0.987	11.559	0.883	6.136	0.838
Grain yield per plant (g)	65.691	63.723	104.533	103.35	84.324	38.743	0.82	40.547	0.827	26.840	0.803	18.355	0.787	26.724	0.648

Table 3: Estimates of genetic advance and genetic advance over mean for 13 quantitative characters in Maize

Character	Genetic advance										Genetic advance in % over mean									
	Kharif Kanpur		Kharif Aligarh		Rabi Kanpur		Rabi Aligarh		Pooled		Kharif Kanpur		Kharif Aligarh		Rabi Kanpur		Rabi Aligarh		Pooled	
	NS	BS	NS	BS	NS	BS	NS	BS	NS	BS	NS	BS	NS	BS	NS	BS	NS	BS	NS	BS
Days to 50% tasseling	1.19	7.49	0.58	6.34	1.68	7.56	2.18	4.35	0.29	2.76	1.93	12.15	1.08	11.67	1.33	5.98	1.69	3.38	0.32	2.98
Days to 50% silking	1.09	7.40	0.61	6.44	1.72	8.07	2.31	4.73	0.37	3.13	1.68	11.41	1.07	11.19	1.32	6.20	1.75	3.58	0.38	3.25
Days to 75% dry husk	1.93	7.01	2.35	9.70	2.498	10.07	3.15	8.58	1.18	3.87	1.94	7.05	2.56	10.54	1.51	6.12	1.89	5.16	0.9	2.97
Plant height (cm)	12.80	35.08	7.04	50.68	2.50	46.63	1.95	43.46	4.86	36.71	10.22	28.01	5.84	42.03	1.47	27.52	1.03	23.11	3.22	24.34
Number of cobs per plant	0.04	0.06	0.02	0.00	0.01	0.10	0.04	0.13	0.003	0.04	4.13	5.87	2.01	0.31	0.99	9.14	3.71	11.33	0.27	3.50
Cob weight (g)	13.63	46.32	13.55	45.47	8.28	64.15	6.86	51.95	8.56	41.95	17.7	60.17	18.01	60.44	6.71	51.97	5.67	42.96	8.63	42.31
Number of grain rows per	0.27	1.45	0.13	1.31	0.86	1.36	0.64	1.31	0.46	0.97	2.22	11.77	1.15	10.94	6.33	9.98	4.58	9.33	3.55	7.50
Number of grains per row	0.07	2.84	0.62	5.92	1.39	7.51	1.71	5.93	0.41	4.47	0.28	10.33	2.33	22.06	4.49	24.20	5.52	19.24	1.43	15.39
Grain weight per cob (g)	13.07	40.83	12.98	39.93	8.51	56.79	6.12	47.29	8.22	37.14	20.29	63.39	20.72	63.75	8.42	56.26	6.15	47.52	10.03	45.35
Shelling percentage	1.18	3.84	1.23	3.88	0.79	4.31	0.49	5.40	0.68	2.79	1.43	4.63	1.49	4.69	0.97	5.31	0.59	6.61	0.82	3.39
100 kernel weight (g)	0.82	4.34	0.75	4.69	2.65	5.22	0.41	3.14	0.27	2.57	3.17	16.80	2.95	18.50	9.09	17.92	1.37	10.32	0.98	9.30
Seed vigour index	41.13	562.02	43.52	640.07	46.58	647.83	38.69	592.42	21.07	569.31	1.5	20.58	1.6	23.67	1.69	23.58	1.41	21.70	0.77	20.87
Grain yield per plant (g)	14.44	42.19	14.66	41.07	9.56	58.38	5.71	47.17	9.05	38.32	21.99	64.22	23.01	64.46	9.15	55.85	5.53	45.64	10.73	45.44

References

1. Abrha SW, Zeleke HZ, Gissa DW. Line x tester analysis of maize inbred lines for grain yield and yield related traits. Asian journal of plant science. 2013;3:12-19.
2. Allard RW. Principles of Plant Breeding. 2nd edition, John Wiley and Sons, Inc. USA. 1999.
3. Anonymous. 2021. http://www.fao.org/faostat/en/#data/QC, accessed on 7 April, 2021.
4. Anshuman V, Dixit NN, Dipika, Sharma SK, Marker S. Studies on heritability and genetic advance estimates in Maize genotypes. Bioscience Discovery. 2013;4(2):165-168.
5. Anusheela V, Muthiah AR, Johnjoel A. Heterosis in quality protein maize. International Journal of Scientific Research. 2013; 2(11):567-570.
6. Begum S, Ahmed A, Omy SH, Rohman MM, Amiruzzaman M. Genetic variability, character association and path analysis in maize (*Zea mays* L.). Bangladesh Journal of Agricultural Research. 2016;41:173-182.
7. Burton GW, De Vane EH. Estimating heritability in tall fescue (Fistvea arundiancea) from replicated clonal material. Agronomy Journal. 1953;45:284-291.
8. Crumpacker DW, Allard RW. A diallel analysis of heading date in wheat. Hilgardia. 1962;32:275-278.
9. Ertiro BT, Beyene Y, Das B, Mugo S, Olsen M, Oikeh S, *et al.* Combining ability and testcross performance of drought-tolerant maize inbred lines under stress and non-stress environments in Kenya. Plant Breeding. 2017; 136:197-205.
10. Hemavathy AT, Balaji K, Ibrahim S, Anand, G, Sankar D. Genetic variability and correlation studies in maize (*Zea mays* L.). Agricultural Science Digest. 2008;28(2):112-114.
11. Jawaharlal J, Lakshmikantha Reddy G, Sai Kumar R. Genetic variability and character association studies in maize. Agriculture Science Digest. 2011;31(3):173-177.
12. Kharel R, Ghimire SK, Ojha BR, Koirala KB. Estimation of genetic parameters, correlation and path coefficient analysis of different genotypes of maize (*Zea mays* L.). International journal of agriculture innovations and research. 2017;6:191-195.
13. Kuchanur PH, Salimath PM, Kattimani SH, Patil SS, Wali MC, Nidagundi JM, Praveenkumar B. Combining ability and heterosis of drought tolerant maize (*Zea mays* L.) under stress conditions. Bioinfolet. 2014;11:29-40.
14. Kumar SVVP, Babu DR. Combining ability and heterosis in maize (*Zea mays* L.) for grain yield and yield components. International journal of environment, agriculture and biotechnology. 2016;9:763-772.
15. Lal JJ, Kumar RS. Combining ability and heterosis for polygenic characters in maize (*Zea mays* L.). Madras Agricultural Journal. 2012;99(4-6):174-177.
16. Motamedi M, Choukan R, Hervan EM, Bihamta MR Kajouri FD. Investigation of genetic control for yield and related traits in maize (*Zea mays* L.) lines derived from temperate and subtropical germplasm. International Journal of Biosciences. 2014;5(12):123-129.
17. Nzuve F, Githiri S, Mukunya DM, Gethi J, Genetic variability and correlation studies of grain yield and related agronomic traits in maize. Journal of agricultural science. 2014;6(9):166-176.
18. Rajesh V, Kumar SS, Reddy NV, Shivshankar A. Heterosis studies for grain yield and its component traits in single cross hybrids of maize (*Zea mays* L.). International Journal of Plant, Animal and Environmental Sciences. 2014; 4(1):320-325.
19. Rastgari M, Ahmadi H, Zebarjadi AR. Combining ability analysis and gene effects in maize (*Zea mays* L.) using line x tester crosses. Research on Crops. 2014;15(3):621- 625.
20. Ribeiro LP, Teodoro PE, Corrêa CCG, de Oliveira EP, da Silva FA *et al.* Correlations and genetic parameters in maize hybrids. Bioscience Journal. 2016;32(1):48-54.
21. Robinson HF, Comstock RE, Harvey PH. Genetic and phenotypic correlations in corn and their implication in selection. Journal of agronomy. 1951;43:282-287.
22. Ruswandi D, Supriatna J, Makkulawu AT, Waluyo B, Marta H, Suryadi E, *et al.* Determination of combining ability and heterosis of grain yield components for maize mutants based on Line× Tester analysis. Asian journal of crop science. 2015;7:19-33.
23. Shiferaw B, Prasanna B, Hellin J, Banziger M. Crops that feed the world 6. Past successes and future challenges to the role played by maize in global food security. Food Security. 2011;3:307-327.
24. Singh A, Shahi JP, Langade DM. Combining ability

studies for yield and its related traits in inbred lines of maize (*Zea mays* L.). Molecular Plant Breeding. 2013;4:177-188.
25. Zahid M, Shahid RM, Raheel A, Tariq R. Heritability and genetic advance estimates from maize genotypes in Shishi Lusht a valley of Krakurm. International Journal of Agriculture and Biology. 2004;2(2):253-257.