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Studies on genetic parameters, correlation and path coefficient analysis in maize (*Zea mays* L.) hybrids under waterlogging condition

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Abstract

The screening of fifty-five CIMMYT maize hybrids was carried out to estimate the genetic variability, heritability, genetic advance as per cent of mean, correlation and path coefficient analysis of 15 characters contributing to yield per plant under excess soil moisture condition at Banaras Hindu University, Varanasi. The experiment was conducted in an alpha lattice design with two replications, and phenotypic data were analyzed using fifteen morphological and agronomic traits. Analysis of variance revealed significant differences among the genotypes for plant height, ear height, ears per plot, field weight, number of kernel rows per ear and number of kernels per row. Higher genotypic and phenotypic coefficients of variation observed in several surface roots followed by ear height and field weight suggested that selection can be effective for these traits. High heritability, coupled with high genetic advance noticed for ear height, and plant height indicated additive gene effects. Hence, simple selection could be useful for further improvement in these characters. Correlation analysis showed that yield per plant exhibited highest and positive significant correlation with the number of kernels per row followed by field weight, ear length, number of kernel rows per ear, plant height, ear per plant and ear height. Path coefficient analysis revealed that the highest positive direct effects on yield per plant were exhibited by field weight followed by the number of kernels per row, number of kernel rows per ear, ear length and number of nodes bearing brace roots. If the selection for waterlogging tolerant genotype is made for any of these components, the improvement in yield per plant could be achieved.

Keywords: Correlation, Genetic variability, Maize, Path analysis, Water logging

Introduction

Maize (*Zea mays* L.) is the most important cereal crop that ranks third in the world after wheat and rice (Pingali, 2001; Rani *et al.*, 2015; Chaudhary *et al.,* 2016). Karnataka has the highest area of 1.2 million hectares (m ha) and production of 3.3 million tons (mt), whereas Tamil Nadu has the highest productivity of 6.5 tons ha^{-1}. Maize ranks second in yield, third in production and area in India (Anonymous, 2016). Maize exhibits greater diversity in phenotypes than any other cereal crop (Kuleshov, 1933) and also in habitat from tropical to temperate regions of the world. Unlike wetland crops such as rice, maize plants do not have a gaseous exchange system between above-ground plant parts and inundated roots. Therefore, breeding of waterlogging tolerant maize varieties will likely to boost maize production both at fodder and grain yield beyond the present level.

Progress in different disciplines of plant breeding for increased resistance for biotic and abiotic stresses depends predominantly on the extent of genetic variability present in germplasm. This is easily measured as the phenotypic expression reflects non-genetic as well as genetic influences. Heritability and genetic advance are essential parameters for selecting a genotype. Heritability is a heritable portion of phenotypic variance (Hanson *et al.*, 1956; Falconer, 1996) and helps the researcher to select out elite genotype from a diverse genetic population. Genetic advance is the measure of genetic gain under selection and understanding the type of gene action for polygenic traits.

Correlation is the degree and direction of the association between two or more variables which can be useful in determining yield components and used for genetic improvement of grain and fodder yield. The standardized partial regression coefficient, *i.e.* path coefficient provides information about direct and indirect effects of the independent variable on the dependent variable. It reveals whether the association of these characters with yield is due to their direct impact on yield or a consequence of their indirect effects via other component characters. Keeping in view of these aspects, the present study was undertaken to assess the nature and magnitude of gene-

-tic variability and association of growth, earliness and yield parameters in maize.

Materials and Methods

***Experimental design and sample analysis*:** The experiment was carried out during crop season *Kharif* 2017 in alpha lattice design with two replications at the Agriculture Research Farm of Banaras Hindu University, Varanasi, India. The experimental material comprised of 53 maize hybrids along with two checks (900MG from Monsanto and P3502 from Pioneer) which were obtained from CIMMYT (International Maize and Wheat Improvement Center, Mexico) germplasm under the project 'Climate Resilient Maize for Asia (CRMA)' (Table 1). Each genotype was planted in two rows of three meters each in length with a spacing of 60 x 25 cm with ten plants per row. Waterlogging stress was imposed at approximately 2-3 inch depth for seven days at the V_6-V_7 growth stage/ knee height stage of crop growth (35 days after sowing). Proper bunding was done so that water remains within, and after seven days, water was drained out (Zaidi *et al.,* 2016). The crop was raised as per the recommended agronomic package of practices. The observations were recorded for fifteen characters *viz.* pre-harvest data like- number of surface roots (SR), number of nodes bearing brace roots (NBR), days to 50 per cent anthesis (DA), days to 50 per cent silking (DS), plant height (PH) (cm), ear height (EH) (cm) and post-harvest data like- plant population (PP), ears per plot (EPP), field weight (FW) (t/h), ear length (EL) (cm), ear diameter (ED) (cm), number of kernel rows per ear (NRE), number of kernels per row (NKR), 100 seed weight (SW) (g) and yield per plant (YPP) (g).

***Statistical analysis*:** Statistical analysis of data was carried out according to Paterson and Patterson (1984) for analysis of variance; Burton (1952) for calculation of GCV, PCV; Johnson *et al.* (1955) for heritability and genetic advance; Al-Jibouri *et al.* (1958) for correlation coefficient and Dewey and Lu (1959) for path analysis.

Results and Discussion

Analysis of variance: The analysis of variance for the 15 characters revealed significant differences among all the experimental genotypes for plant height, ear height, ears per plot, field weight, number of kernel rows per ear and number of kernels per row (Table 2). Thus the presence of variability among genotype in the present study indicated the ample scope for selection of genotypes for both fodder and grain yield, based on these traits. Similar results for these traits were also reported earlier (Saleem *et al.,* 2007; Nzuve *et al.*, 2014; Sharma *et al.*, 2014; Sravanti *et al.*, 2017).

***Genetic variability, heritability and genetic advance*:** The GCV and PCV measure the genotypic and phenotypic variability present in the genotypes (Table 3). High GCV coupled with high PCV were observed for characters *viz.* number of surface roots (20.30 and 30.20), ear height (21.50 and 23.20) and field weight (20.30 and 35.20) suggested that simple phenotypic selection methods can be effective for improving these traits. Similar findings were reported for the same traits earlier (Rafiq *et al.*, 2010); Reddy *et al.*, 2012; Najeeb *et al.,* 2009). Moderate GCV coupled with moderate PCV were observed with plant height (13.00 and 14.30), number of kernels per row (13.50 and 19.90) and 100 seed weight (12.80 and 16.00). Similar results were also observed by Nagabhushan *et al.* (2012). Low GCV and PCV observed in days to 50% anthesis (2.80 and 4.80) and days to 50% silking (0.20 and 3.20) indicating less variance for these traits, as reported earlier by Ghosh *et al.* (2014) and Nagabhushan *et al.* (2012). PCV values were higher than GCV values for all the characters thereby suggesting the role of experimental variance to the total variance (Reddy *et al.*, 2012; Sharma *et al.*, 2014). Most of the traits exhibited less difference between PCV and GCV, indicating the lesser influence of the environment (Ghosh *et al.*, 2014).

Table 1. List of fifty-five maize genotypes evaluated during the experiment

Maize genotypes						
ZH17506	ZH17495	ZH138267	ZH15553	ZH15561	ZH15562	ZH17509
ZH15550	ZH17230	ZH15546	ZH138269	ZH15565	ZH138278	ZH138260
ZH17504	ZH15548	ZH17505	ZH138294	ZH15568	ZH15554	ZH17500
ZH17507	ZH15547	ZH17494	ZH15551	ZH17229	ZH138303	VH11128
ZH17496	ZH17502	ZH17497	ZH17501	ZH15555	ZH15558	ZH17510
ZH138305	ZH17503	ZH15556	ZH15564	ZH17499	ZH15559	900MG
ZH15560	ZH15566	ZH17231	ZH17508	ZH138312	ZH17228	P3502
ZH17232	ZH17498	ZH15549	ZH15557	ZH15567	ZH15563	

Table 2. Analysis of variance (ANOVA) for fifteen characters in 55 hybrids of maize

Source	**Replication**	**Treatment**	**Block**	**Error**
Degree of freedom	1	54	20	34
		Mean sum of square		
SR	1.78	24.60	22.33	14.90
NBR	1.54	0.58	1.06	0.46
DA	64.15	13.52	12.73	11.48
DS	28.51	6.93	10.90	8.02
PH	3782.05	422.06*	121.08	95.85
EH	1082.05	217.15*	52.84	41.87
PP	3.28	9.44	11.62	7.64
EPP	224.08	20.95*	23.47	15.38
FW	1.32	0.27*	0.22	0.21
EL	4.81	4.19	2.59	3.94
ED	0.30	0.46	0.48	0.38
NRE	39.60	4.69*	4.06	2.83
NKR	48.98	21.42*	16.08	15.59
YPP	4.24	541.92	912.48	463.96
SW	19.44	33.46	23.44	12.00

**(P<0.05); SR: Surface roots; NBR: Number of nodes bearing brace roots; DA: Days to 50 per cent anthesis; DS: Days to 50 per cent silking; PH: Plant height; EH: Ear height; PP: Plant population; EPP: Ears per plot; FW: Field weight; EL: Ear length; ED: Ear diameter; NRE: Number of kernel rows per ear; NKR: Number of kernels per row; YPP: Yield per plant; SW: Seed weight (100)*

Table 3. Mean variability, heritability and genetic advance as per cent of mean for 15 traits in 55 maize hybrids

Traits	**Mean**	**Range**		**PCV**	**GCV**	**Heritability %**	**GAM**
		Min	**Max**				
SR	11.35	5.00	19.50	30.20	20.30	36.60	13.80
NBR	2.75	1.50	4.00	19.10	7.80	16.60	2.70
DA	61.07	56.00	68.50	4.80	2.80	33.10	1.90
DS	62.44	58.50	68.50	3.20	0.20	0.50	0.02
PH	116.86	77.50	147.50	14.30	13.00	82.70	22.10
EH	51.86	20.00	77.50	23.20	21.50	85.60	37.90
PP	13.66	7.00	18.00	16.40	8.00	23.70	3.90
EPP	13.66	6.00	21.00	24.60	13.90	31.90	9.10
FW	1.10	0.25	2.31	35.20	20.30	30.00	11.90
EL	12.12	8.94	15.63	13.10	6.10	21.90	2.80
ED	3.94	2.75	6.90	12.50	5.70	21.10	2.50
NRE	13.23	7.00	16.20	12.40	8.50	47.20	8.30
NKR	19.02	10.70	27.50	19.90	13.50	45.70	12.70
YPP	63.91	12.00	100.60	28.30	15.20	28.90	9.10
SW	25.55	18.28	48.16	16.00	12.80	64.1	16.9

GAM: Genetic advance as percent of mean

Burton *et al.* (1952) noticed that GCV, along with heritability analysis give the best roadmap of the extent of advance to be expected by selection. Solitary high heritability always not indicated the amount of genetic improvement. High heritability accomplished with high genetic advance as per cent of mean (GAM) always gives a more reliable conclusion (Johnson *et al.*, 1955; Nguyen *et al.,* 2019). High heritability with high genetic advance as per cent of mean was recorded in ear height (85.60 and 37.90) and plant height (82.70 and 22.10) indicating the role of additive gene effect and the possibility of improvement of these traits through simple selection method like mass selection. Like that of the present investigation, Kumar and Satyanarayana (2001), and Sharma *et al.* (2014) also reported the similar results for these traits. High heritability with moderate genetic advance for per cent of mean of 100 seed weight (64.10 and 16.90) and moderate heritability with moderate genetic advance for per cent of mean of the number of kernels per row (45.70 and 12.70), number of surface roots (36.60 and 13.80) and field weight (30.00 and 11.90), indicated that presence of both additive and non-additive gene actions. Hence the desired results might not be obtained by simple selection. Similar results were also reported earlier (Nzuve *et al.*, 2014; Maruthi and Rani, 2015; Begum *et al.*, 2016; Kapoor, 2017; Vishwanath *et al.*, 2018). Low heritability with low genetic advance for per cent of mean was recorded for the number of nodes bearing brace roots (16.60 and 2.70), days to 50% silking (0.50 and 0.02), plant population (23.70 and 3.90), ear length (21.90 and 2.80), ear diameter (21.10 and 2.50) and yield per plant (28.90 and 9.10). This indicated the operation of non-additive gene action and heritability due to the favourable influence of environment rather than genotype. Thus the improvement of these traits through heterosis breeding is possible. Similar results were observed earlier by Ghosh *et al.* (2014). Thus the study of genetic parameters like the GCV, PCV, heritability (broad sense) and genetic advance as per cent of a mean provides a clear cut picture about the magnitude of variability present in a plant population.

Character association: Studies on correlation coefficients of different plant traits are useful criteria to identify desirable traits that contribute to improving the dependent variable (yield per plant). The genotypic and phenotypic correlations among the traits studied revealed the existence of several statistically significant relationships (Table 4). Yield per plant showed significant and positive genotypic correlation with number of nodes

Table 4. Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficient among different traits in maize

Traits	SR	NBR	DA	DS	PH	EH	PP	EPP
SR	**1.0000**	-0.1038	-0.0249	0.0472	-0.0437	-0.0459	-0.1364	-0.2229*
NBR	0.4079	**1.0000**	0.0737	0.1409	-0.0686	0.0314	0.1243	-0.0277
DA	-0.1242	-0.9632	**1.0000**	0.6664**	0.1413	0.0671	0.0786	0.0486
DS	0.2304	0.2042	0.4087	**1.0000**	0.1146	0.1365	0.0559	0.0276
PH	0.2513	0.1649	-0.1577	-0.0126	**1.0000**	0.8368**	0.3002**	0.4828**
EH	0.0001	0.1762	-0.2404	0.0846	0.9571	**1.0000**	0.2226*	0.5201**
PP	0.9409	0.1524	0.3682	-1.2434	0.6383	0.0133	**1.0000**	0.5221**
EPP	0.6958	-0.2109	-0.9132	0.0514	0.0011	0.4545	-0.8188	**1.0000**
FW	0.3851	0.2716	0.1631	-0.3367	0.1917	0.1737	0.3990	0.3562
EL	-0.0225	-0.2141	-0.1080	0.3409	0.4176	0.1236	-0.7871	-0.9378
ED	-0.1279	0.8978	-0.6997	0.8643	0.0180	0.9909	0.2614	0.4967
NRE	0.8226	0.5926	0.3444	0.1985	0.8472	0.8192	0.1613	0.4177
NKR	-0.3344	0.4647	0.0167	-0.7224	0.5785	0.1080	-0.2412	-0.6826
SW	0.1346	-0.2595	-0.5331	0.8391	0.0754	0.0164	0.4094	0.4775
YPP	0.4125	0.7347	0.3395	-0.3280	0.5437	0.8657	-0.1653	-0.9966

Traits	FW	EL	ED	NRE	NKR	SW	YPP
SR	-0.1519	-0.1029	-0.0116	-0.0463	-0.0517	-0.0524	-0.0666
NBR	0.0548	-0.0486	-0.0679	-0.0572	-0.073	-0.0214	0.1041
DA	0.1533	0.2254*	0.0291	-0.0318	0.2954**	-0.076	0.1405
DS	0.0434	0.0011	0.0444	-0.0668	0.0635	-0.0802	-0.0374
PH	0.5531**	0.3199**	0.2095*	0.3405**	0.2435*	0.0842	0.3855**
EH	0.5317**	0.1668	0.2289*	0.3038**	0.1151	0.1003	0.3037**
PP	0.4446**	0.0886	-0.0986	0.2239*	0.068	0.0443	0.2553**
EPP	0.7304**	0.1798	0.1514	0.3120**	0.1492	0.121	0.3107**
FW	**1.0000**	0.5151**	0.2302*	0.3979**	0.4985**	0.1183	0.6579**
EL	0.3827	**1.0000**	0.1751	0.2950**	0.7202**	-0.0691	0.6526**
ED	0.6569	-0.4822	**1.0000**	0.3645**	0.1491	0.1098	0.2577**
NRE	0.4661	0.3803	0.2640	**1.0000**	0.1982*	0.1422	0.5255**
NKR	0.2817	0.9466	-0.0569	0.4345	**1.0000**	-0.109	0.6623**
SW	0.5224	-0.1687	0.1142	-0.0866	0.2701	**1.0000**	0.0397
YPP	0.3716	0.6372	0.9471	0.0799	0.8213	0.2796	**1.0000**

*(P<0.05); ** (P<0.01)

bearing brace roots, number of surface roots, days to 50 percent anthesis, plant height (Iqbal *et al*., 2011), ear height (Bello *et al*., 2010), field weight, ear length (Bello *et al*., 2010), ear diameter (Begum *et al.,* 2016), number of kernels per row (Begum *et al.,* 2016) and 100 seed weight (Ghosh *et al.,* 2014), while the remaining traits exhibited non-significant genotypic correlation. At phenotypic level all the traits evaluated, with the exception of number of kernels per row (Reddy *et al*., 2012; Seyedzavar *et al*., 2015), field weight, ear length (Bello *et al*., 2010), number of kernel rows per ear (Rafiq *et al*., 2010; Bello *et al*., 2010; Wannows *et al*., 2010), plant height (Ghosh *et al.,* 2014; Iqbal *et al*., 2011), ears per plot (Zaidi *et al.,* 2007), ear height (Ghosh *et al.,* 2014), ear diameter (Ali *et al.,* 2018) and plant population (Rafiq *et al*., 2010) exhibiting significant and positive correlation coefficients with yield per plant, showed weak phenotypic correlations with grain yield. The yield-related traits displaying positive and significant association with yield per plant suggested that yield can be improved through simultaneous selection for these traits (Ojo *et al*., 2006). The genotypic correlation is greater than the phenotypic correlation for almost all the assessed traits. These findings were in close conformity of Alake *et al.* (2008), who suggested that the low phenotypic correlation might result from the modifying effect of the environment on the association trait at the genetic level. Selection is generally based on phenotypic expression of traits. Hence, selection for the traits exhibiting positive significant genotypic and phenotypic correlation would be of major use in indirect and direct selection for grain yield, respectively (Alake *et al.,* 2008).

Table 5. Genotypic path coefficients (direct: on diagonal and indirect: off-diagonal) on yield per plant in maize

Traits	SR	NBR	DA	DS	PH	EH	PP	EPP	FW	EL	ED	NRE	NKR	SW
SR	**-0.6699**	-1.0890	0.3315	-0.6150	-0.6710	-0.2004	-1.1821	-0.8576	-1.0282	0.0602	0.3415	-0.1963	0.8928	-0.3594
NBR	0.3137	**0.9208**	-0.1022	0.6578	0.5311	0.5675	0.4909	-0.6792	0.8747	-0.6894	1.8918	0.9087	0.4967	-0.8357
DA	0.1386	0.3755	**-0.1166**	-0.4564	0.1761	0.2684	-0.4112	1.0197	-0.1821	0.1206	0.7814	-0.3845	-0.9353	0.5953
DS	-0.2683	-0.2379	-0.4760	**-1.1646**	0.0146	-0.0985	1.4480	-0.0598	0.3921	-0.3970	-1.0066	-0.2311	0.8413	-0.9772
PH	-1.3391	-1.1286	0.86	1.4666	**-0.1613**	-0.8676	-1.7218	-0.2043	-0.2882	-0.5186	-1.8334	-0.4863	-0.6996	-0.9081
EH	1.0043	0.6269	-0.6752	0.7000	0.5623	**0.9332**	2.3568	1.4484	0.4808	0.9481	0.6435	0.1589	0.4499	0.5248
PP	0.5935	0.5963	1.4407	-1.8645	0.4973	0.9642	**0.9123**	-0.2032	0.5609	-0.0794	0.9350	0.6312	-1.9435	1.6018
EPP	-0.2268	0.0687	0.2977	-0.0167	-1.3263	-0.9741	0.2669	**-0.3259**	-1.1161	0.3056	-0.4878	-0.1361	0.2225	-0.4816
FW	-0.9869	-0.6960	-0.9179	0.8628	-0.0541	-0.0079	-1.0225	-0.9128	**-0.5627**	-0.9808	-0.6834	-0.1944	-1.7220	-0.3389
EL	-0.1902	-1.8070	-0.9117	0.8777	0.5252	0.0437	-0.6445	-0.9164	0.2308	**0.4419**	-0.0704	0.2102	0.9913	-0.4240
ED	0.5241	-0.6791	0.8674	-1.5418	-1.1717	-1.0606	-0.1690	-0.1333	-1.6917	1.9759	**-0.0978**	-0.1795	0.2331	-0.5679
NRE	1.5953	1.7511	0.7608	0.5912	0.7928	0.5677	0.2936	1.3487	0.7367	0.0488	0.1337	**0.0175**	0.4837	-0.8944
NKR	-0.9349	2.6890	0.8834	-0.1803	0.3477	0.6252	-1.3956	-0.9501	1.6304	0.4778	-0.3291	0.5144	**0.7867**	1.9629
SW	0.8591	-0.6560	-1.9024	0.3552	0.4810	0.1049	0.6129	0.4292	0.3342	-1.0765	0.7287	-0.5528	0.7237	**1.3820**
YPP	0.4125	0.7347	0.3395	-0.3280	0.5437	0.8657	-0.1653	-0.9966	0.3716	0.6372	0.9471	0.0799	0.8213	0.2796

***Path analysis*:** The correlation is not sufficient to explain the real association as it does not indicate the cause and effect relationship. Therefore, the correlated traits were further analyzed for direct and indirect effects of specific components on yield. The results of genotypic and phenotypic path coefficient analysis and the direct and indirect effects of each coefficient were also recorded (Table 5-6). Yield per plant as the dependent variable was evaluated against other measured traits as independent variables. The highest genotypic direct effect on yield per plant was exhibited by 100-seed weight followed by plant population, ear height, number of kernels per row, number of nodes bearing brace roots, field weight and ear length. Shi *et al*. (2008) and Bello *et al.* (2010) also reported similar observations in maize. The residual effect of 0.6949 indicated that some more traits were contributing to the yield per plant, and it needs to be studied further. Phenotypic path analysis revealed that most of the traits had a positive direct effect on grain yield. The highest phenotypic direct effect on yield per plant was exhibited by field weight followed by the number of kernels per row, number of kernel rows per ear, ear length and number of nodes bearing brace roots. Similar results were found by Rafiq *et al*. (2010), Reddy *et al.* (2012) and Seyedzavar *et al.* (2015) for these traits. Days to 50% silking and ear per plant were exerted a direct and negative effect, as recorded earlier by Parimala *et al.* (2012) for this trait. In the present investigation, the residual effect at the phenotypic level was 0.5334, which indicated that the influence of other non-included factors on the yield per plant.

Table 6. Phenotypic path coefficients (direct: on diagonal and indirect: off diagonal) on yield per plant in maize

Characters	SR	NBR	DA	DS	PH	EH	PP
SR	**0.0284**	-0.0029	-0.0007	0.0013	-0.0012	-0.0013	-0.0039
NBR	-0.0142	**0.1370**	0.0101	0.0193	-0.0094	0.0043	0.0170
DA	-0.0001	0.0003	**0.0043**	0.0029	0.0006	0.0003	0.0003
DS	-0.0039	-0.0116	-0.0550	**-0.0826**	-0.0095	-0.0113	-0.0046
PH	-0.0002	-0.0003	0.0007	0.0005	**0.0047**	0.0040	0.0014
EH	-0.0013	0.0009	0.0019	0.0039	0.0236	**0.0282**	0.0063
PP	-0.0091	0.0083	0.0053	0.0037	0.0201	0.0149	**0.0669**
EPP	0.0362	0.0045	-0.0079	-0.0045	-0.0785	-0.0845	-0.0848
FW	-0.0537	0.0194	0.0542	0.0153	0.1955	0.1879	0.1571
EL	-0.0168	-0.0079	0.0367	0.0002	0.0521	0.0272	0.0144
ED	-0.0003	-0.0019	0.0008	0.0012	0.0059	0.0064	-0.0028
NRE	-0.0133	-0.0164	-0.0091	-0.0191	0.0976	0.0870	0.0642
NKR	-0.0176	-0.0248	0.1004	0.0216	0.0828	0.0392	0.0231
SW	-0.0007	-0.0003	-0.0011	-0.0011	0.0012	0.0014	0.0006
YPP	-0.0666	0.1041	0.1405	-0.0374	0.3855	0.3037	0.2553

Characters	EPP	FW	EL	ED	NRE	NKR	SW
SR	-0.0063	-0.0043	-0.0029	-0.0003	-0.0013	-0.0015	-0.0015
NBR	-0.0038	0.0075	-0.0067	-0.0093	-0.0078	-0.0100	-0.0029
DA	0.0002	0.0007	0.0010	0.0001	-0.0001	0.0013	-0.0003
DS	-0.0023	-0.0036	-0.0001	-0.0037	0.0055	-0.0052	0.0066
PH	0.0023	0.0026	0.0015	0.0010	0.0016	0.0012	0.0004
EH	0.0147	0.0150	0.0047	0.0065	0.0086	0.0033	0.0028
PP	0.0349	0.0297	0.0059	-0.0066	0.0150	0.0045	0.0030
EPP	**-0.1625**	-0.1187	-0.0292	-0.0246	-0.0507	-0.0242	-0.0197
FW	0.2582	**0.3534**	0.1820	0.0814	0.1406	0.1762	0.0418
EL	0.0293	0.0840	**0.1630**	0.0285	0.0481	0.1174	-0.0113
ED	0.0042	0.0065	0.0049	**0.0280**	0.0102	0.0042	0.0031
NRE	0.0894	0.1140	0.0845	0.1044	**0.2865**	0.0568	0.0407
NKR	0.0507	0.1695	0.2449	0.0507	0.0674	**0.3400**	-0.0372
SW	0.0017	0.0017	-0.0010	0.0015	0.0020	-0.0015	**0.0141**
YPP	0.3107	0.6579	0.6526	0.2577	0.5255	0.6623	0.0397

Conclusion

Yield is a complex character, governed by several major and minor genes. Yield per plant was increased with number of kernels per row, field weight, ear length, number of kernel rows per ear, plant height, ears per plot and ear height. The field weight, number of kernels per row, number of kernel rows per ear, ear length and number of nodes bearing brace roots had direct effect on yield per plant. The variability analysis revealed that the characters *viz.,* number of surface roots, ear height and field weight should be given importance in selection for the improvement of both fodder and grain yield, based on these traits. High heritability with high genetic advance was recorded in ear height and plant height, indicating greater importance of additive gene effect. Therefore, to obtain high yield per plant, one should consider these characters in maize breeding programme.

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