GENETIC VARIABILITY AND TRAIT ASSOCIATION IN CIMMYT MAIZE HYBRIDS UNDER WATER SUBMERGENCE CONDITION

MANISH KUMAR CHOUDHARY, GAYATRI KUMAWAT*, JAI PRAKASH SHAHI, MUNNESH KUMAR, ASHOK SINGHAMSETTI AND GANESH KUMAR KOLI

Genetics and Plant Breeding Department,
Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, (U. P.), India
*(e-mail : kumawatgayatri10@gmail.com)

SUMMARY

The screening for water stress of seventy CIMMYT maize genotypes was carried out to estimate the genetic variability parameters, heritability, GAM, correlation and path coefficient analysis at Agriculture Research Farm, Institute of Agriculture Science, BHU, Varanasi. Analysis of variance revealed significant differences among the genotypes for surface root, anthesis-silking interval, plant height, ear height, number of plants per plot, number of ears per plot, ear length and number of kernels per row. Moderate to higher GCV and PCV coupled with high heritability and high GAM observed for surface root, ear height, number of plants per plot, number of ears per plot, field weight and yield per plant suggested that simple selection can be effective for these traits. Correlation analysis indicated that yield per plant exhibited highest and positive significant correlation with field weight, number of ears per plot, ear diameter, number of kernels per row, ear length, 100-seed weight, number of plants per plot and number of kernel rows per ear. Path coefficient analysis revealed that the highest positive direct effects on yield per plant were exhibited by 100-seed weight followed by field weight, number of kernels per row, ear height, ear length, ear diameter, days to 50% silking, number of ears per plot, number of kernel rows per ear and number of plants per plot. If the selection for water logging tolerant genotype is made for any of these component traits, the improvement in yield per plant could be achieved.

Key words : Maize, genetic variability parameters, correlation, path analysis and water stress

The major constraints for low productivity in the region especially in India, are biotic (disease and pests) and abiotic stresses such as drought, low nitrogen, salinity and excess soil moisture. Among the various abiotic stresses, water-logging, caused by unforeseen flooding, continuous rainfall and inadequate soil drainage or a high-water table, is one of the most imperative constraints for maize production in South Asia and many other countries of the world. In South and Southeast Asia alone, over 15% of the total maize growing areas are intermittently affected by floods and water-logging condition (Kumawat *et al.,*2020a). In India, waterlogging is the second most serious constraint, after drought, where about 8.5 Mha of arable soil is affected by water logging problem. The maize growing area of U.P. and Bihar are highly prone to floods and waterlogging during the monsoon season. Out of the total 6.55 Mha area of maize, about 2.5 Mha are affected by excess soil moisture problems that cause, on average, 25-30% loss of national maize production almost every year (Kumawat *et al.*, 2020b).

In India, research work on excess water tolerance in maize was initiated since 1991 under the ICAR-CIMMYT collaborative programme keeping in view the extent of an excess soil water problem. However, considerable genetic variability has been observed in maize for tolerance to excess moisture (Choudhary *et al.*, 2020) which could be exploited to identification and development of genotypes capable tolerant to intermittent water-logging stress during the summer-rainy season in the tropics. Heritability and genetic advance are important parameters for selecting a genotype (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 (Johnson *et al.*, 1955). 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 yield. The standardized partial regression coefficient *i.e.* path coefficient provides

information, whether the association of these characters with yield is due to their direct effect on yield or a consequence of their indirect effects via other component characters (Kumawat *et al.*, 2020c). Keeping these aspects in view, the proposed study was undertaken to assess the nature and magnitude of genetic variability and association of growth, earliness and yield parameters in maize.

MATERIALS AND METHODS

The field experiment of the present study, consisting of 70 maize hybrids (Table 1) (including five checks), was conducted at Agricultural Research farm of Institute of Agricultural Sciences, Banaras Hindu University during *kharif*-2017. Geographically, the field experimental site is located on 25° 10' North latitude, 83° 03' East longitudes and altitude of location is 123.23 meters above the mean sea level. It falls in the center of North-Gangetic alluvial plain, on the left bank of river Ganga. The primary concern of this research is this to evaluate 70 maize hybrids developed from CIMMYT (International Maize and Wheat Improvement centers) projects, "Climate Resilient Maize for Asia (CRMA)" along with five checks. The experimental material was laid out in alpha lattice design with two replications. The sowing was taken up on 25th June 2017 and the ears were harvested on 12th October 2017. Each genotype was sown in a single line of 3.6 m. row length. Spacing of 70 cm x 25 cm was adopted after thinning. Waterlogging stress was enforced for one week at the 'Knee height stage' (V_6-V_7 growth stage). The depth of water level maintained at the level of 2.0-3.0 inches above the ground surface in the field (water stagnation). Proper bunding was done so that water remains within, and after one week, the plots were drained completely through surface drainage (Kumawat *et al.*,2020b). The observations were recorded for sixteen characters like (pre-harvest) number of surface roots (SR), number of nodes bearing brace roots (BR), days to 50% anthesis (DA), days to 50% silking (DS), anthesis-silking interval (ASI), number of plants per plot (PP), number of ears per plot (EPP),field weight (t/ha) (FW),plant height (cm) (PH), ear height(cm) (EH) and (post-harvest) ear length(cm) (EL), ear diameter (cm) (ED), number of kernel rows per ear (NKRE), number of kernels per row (NKR), 100 seed weight (g) (SW) and yield per plant(g) (YPP). Statistical analysis 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; Dewey and Lu (1959) for path analysis.

RESULTS AND DISCUSSION

Analysis of variance :The success of plant breeding depends on the magnitude of genetic variability present in available germplasm. Knowledge about the nature and extent of genetic variation that governing the inheritance of quantitative characters like yield and yield attributing traits is important for genetic improvement as well as for adopting appropriate breeding techniques. It is very difficult to decide whether observed variability is heritable or not. Heritability measures the extent of transmissibility of a trait into next generations which is important for the

TABLE 1
Details of 70 genotypes of maize (*Zea mays* L.) studied during investigation

S. No.	Name	S. No.	Name	S. No.	Name	S. No	Name	S. No	Name
1	ZH17360	15	ZH17344	29	ZH17363	43	ZH17370	57	ZH17388
2	ZH14595	16	ZH17394	30	ZH17372	44	ZH17389	58	ZH17192
3	ZH17364	17	ZH12112	31	ZH17382	45	ZH17393	59	ZH17392
4	ZH17348	18	VH11128	32	ZH138025	46	ZH17358	60	ZH17352
5	ZH17381	19	ZH17366	33	ZH17396	47	ZH17367	61	ZH17384
6	ZH17383	20	ZH17345	34	ZH17387	48	ZH17378	62	ZH17368
7	ZH17379	21	ZH17350	35	VH112976	49	ZH17397	63	ZH17346
8	ZH17353	22	ZH17362	36	ZH17398	50	ZH17385	64	ZH17391
9	ZH17359	23	ZH17399	37	VH142037	51	ZH17361	65	ZH17376
10	ZH17347	24	ZH17371	38	ZH17351	52	ZH17357	66	900MG
11	ZH17373	25	ZH17355	39	ZH17369	53	ZH17374	67	P3502
12	ZH17223	26	ZH17390	40	ZH17349	54	ZH17354	68	HT5106
13	ZH17356	27	ZH17365	41	ZH17375	55	ZH17377	69	NK6240
14	ZH17380	28	ZH138256	42	ZH17386	56	ZH17395	70	GM6

selection of component characters for yield improvement. Grain yield, being the major and complex character governed by many quantitative genes and it is much more affected by the environment. Therefore, selection based on only grain yield performance may create confusion. A study on the nature and amount of association of yield contributing traits with yield and relationship among yield and other characters assumes more importance for fixing up characters that are likely to contribute an important role in influencing yield (Shanti *et al.*, 2012).

In 70 maize hybrids, Analysis of variance was studied under waterlogging condition for 16 agro-economic traits. for characters *viz*, surface root, anthesis-silking interval, plant height, ear height, number of plants per plot, number of ears per plant, ear length and number of kernels per row showed, significant variation among the hybrids and this might be due to their diverse base populations from which the hybrids have been developed. Similar findings were reported by Begum *et al*, 2016; Pandey *et al.*, 2017; Arya *et al.*, 2020.With respect to these traits, the hybrids exhibited a large amount of genetic variability. So, this population could be used as a base population for growing the next generation in the breeding programme for further improvement.

***Genetic Parameters*:**The phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) indicating the influence of the environment in the expression of the characters and presented in Table 2. The similar result was observed by Ferdoush *et al.*, (2017). Most of the characters showed a small difference between PCV and GCV exhibiting lesser effect of the environment. The similar finding was reported by. Selecting the hybrids on the anthesis-silking interval s of phenotypic values for most of the traits was expected to be effective. The PCV and GCV were highest for anthesis-silking interval followed by field weight, number of plants per plot, number of ears per plot, yield per plant and surface root suggesting that these characters are under the influence of genetic control. Hence, simple selections like mass selection and pedigree selection can be effective for further improvement of these characters. These results are in consonance with Mohan *et al.*, (2014). Moderate PCV and GCV were observed for characters *viz*, plant height, ear height and 100-seed weight. These results were confirmed by earlier reports of Begum *et al.*, (2016). Low PCV and GCV observed in days to 50%

anthesis, days to 50% silking, number of nodes bearing brace roots, ear length, ear diameter, number of kernel rows per ear and number of kernels per row indicating that these characters with low extent of genetic variability and here limited utility in a programme of selection for further improvement. These similar results were noticed by Kandel *et al.*, 2017.

Heritability is a useful measure for identifying the relative importance of variability present in different characters. It provides an index to measure the magnitude of transmission of a character from parents to offspring. High heritability (broad sense) coupled with high genetic advance as percent of mean (GAM) was observed for yield per plant followed by field weight, ear height, number of ears per plot and surface root. Thus, this indicates that the studied characters are anthesis-silking interval under the control of additive gene action and hence the greater effectiveness of selection and improvement for these characters in future breeding programmes can be possible. This finding similar to Ferdoush *et al.*, 2017; Kandel *et al.*, 2017. High heritability with moderate genetics advancement was noticed for plant height and 100 seed weight. This result indicated that both additive and non-additive gene action prevails so desired results may not be obtained by simple selection. This result similar to Hosamani *et al.*, 2018. High heritability with low GAM was revealed for day to days to 50% anthesis and days to 50% silking. This result indicated the operation of non-additive gene actions and desired results would not be obtained by simple selection. Similar result was reported by Mohan *et al.*, 2014.Moderate heritability with high GAM was revealed for Number of plants per plot and Low heritability with high GAM observed for anthesis-silking interval, indicated that operation of additive gene actions. The heritability is being exhibited due to influence of genotype rather than environment indicating the possibility of improvement of these traits through simple selection. Moderate heritability with low GAM was revealed for ear length and ear diameter indicated the operation of non-additive gene actions. It shows that the character is highly influenced by environment and selection would be ineffective. Low heritability with low GAM revealed for number of nodes bearing brace roots, number of kernel rows per ear and number of kernels per row, these indicated more influence of environment on this character.

***Character association* :** A study on the nature and degree of interrelation of yield contributing traits

TABLE 2

Mean, variability, heritability and genetic advance as per cent of mean in 70 maize (*Zea mays* L.) hybrids

S. No.	Characters	Range		PCV (%)	GCV (%)	h²bs (%)	Genetic advance as % percent of Mean (GAM)
		Minimum	Maximum				
1	SURFACE ROOT	3.83	17.50	28.00	22.68	66.00	37.84
2	BR	1.33	6.00	29.01	4.36	2.00	1.35
3	D A	49.50	68.00	5.15	4.31	70.00	7.42
4	DS	55.50	71.00	4.78	4.07	72.00	7.13
5	ASI	1.00	7.00	60.48	26.82	20.00	24.50
6	PH	82.50	150.00	13.51	11.25	69.00	19.29
7	EH	35.00	80.00	21.41	17.49	67.00	29.44
8	PP	1.00	17.00	28.99	22.13	58.00	34.81
9	EPP	1.00	18.00	32.54	26.42	66.00	44.20
10	FW	0.10	1.63	46.34	39.53	73.00	69.46
11	EL	8.59	15.24	9.52	5.82	37.00	7.32
12	ED	3.10	6.48	5.65	3.39	36.00	4.20
13	NKRE	10.20	18.20	6.27	3.33	28.00	3.65
14	NKR	13.70	24.10	10.63	2.87	7.00	1.60
15	YPP	24.50	91.40	23.97	23.07	93.00	45.75
16	SW	17.00	33.05	12.19	10.28	71.00	17.85

with yield assumes greater importance for fixing up characters that are likely to play an important role in influencing yield. The knowledge on genotypic and phenotypic correlation coefficients among various plant characters help to ascertain the degree to which these are correlated with economic productivity. The correlation between two characters can directly be observed as phenotypic correlation while genotypic correlation expresses the extent to which two traits are genetically correlated. Both genotypic and phenotypic association among and between pairs of agronomic characters provide scope for indirect selection in a plant breeding programme. Thus, the correlation studies revealed the direction and extent of association among a pair of variables, when more than two variables are involved.

According to characters association studies, genotypic correlation coefficients were greater than phenotypic correlation coefficients for most of the traits under study. The result showed strong inherent correlation between the characters which governed largely by genetic causes and generally less influenced by environmental factors. These were in agreement with findings of Begum *et al.*, (2016). Grain yield per plant displayed high significant positive association at phenotypic level with field weight followed by number of ears per plot, ear diameter, number of kernels per row, ear length, 100-seed weight, number of plants per plot, number of kernel rows per ear and plant height indicating the importance of these characters

in selection for high yield. Similar results were revealed by many workers *viz*., Kandel *et al.*,2017; Gazal *et al.*,2018.

At genotypic level, yield per plant showed high positive significant correlation with number of kernels per row, followed by year diameter, field weight, number of ears per plot, number of plants per plot, ear length, 100 seed weight, ear height, number of kernel rows per ear and plant height (Table 3). The direct selection for this character would be more effective for improving yield. The findings were in accordance with Begum *et al.*, 2016. Grain yield per plant exhibited significant negative association at phenotypic and genotypic level with days to 50% silking, days to 50% anthesis and anthesis-silking interval. A similar trend was observed by several scientists *viz*- Kandel *et al.*, 2017; Nagrajan and Nallathambi 2017.

Path coefficient analysis : The correlation studies revealed only the nature and magnitude of the association between yield and its component traits but does not show the direct and indirect effects of different yield attributes on yield *per se*. yield per plant is dependent on several traits which are mutually correlated these will in turn, impair the true correlation existing between a component and grain yield. A change in any one component is likely to change the whole network of cause and effect. Thus, each component has two paths of action *viz*., the direct effect on grain

yield, indirect effect through components which are not observed from the correlation studies.

The results on phenotypic path coefficient analysis showed that 100 seed weight had highest positive direct effect followed by field weight, number of kernels per row, ear height, ear length, ear diameter, days to 50% silking, number of ears per plot, number of kernel rows per ear and number of plants per plot at the phenotypic level (Table 4). These traits were contributed directly to yield per plant. Similar conclusions were drawn by another worker *viz-* Gazal *et al.*, 2018. Hence, the above traits were found to be most desirable characters for maximum contribution towards yield per plant; these results concluded that importance of these above traits may be considered during course of selection to improve the grain yield per plant.

The results on genotypic path coefficient showed that the number of ears per plot had highest positive genotypic direct effect followed by days to days to 50% silking, ear diameter, ear height, ear length and anthesis-silking interval (Table 4). These findings

were in consonance with earlier reports *viz-* Kandel *et al.*, 2017. The high direct effect of above traits appeared to be the main factor for their strong association with grain yield. Hence, direct selection for these traits would be more effective. These characters contributed directly to grain yield per plant at the genotypic level as these were also observed to have a positive association with yield per plant except days to 50% silking and anthesis-silking interval which has negative correlation.

High negative direct effects were observed for surface root followed by days to 50% anthesis, number of nodes bearing brace roots, field weight, number of kernel rows per ear and number of plants per plot. At the genotypic level negative direct effect of plant height was negligible. These characters were found to contribute to yield per plant indirectly through days to 50% silking (for days to 50% anthesis, number of nodes bearing brace roots and number of kernel rows per ear), number of ears per plot (field weight), ear height (number of plants per plot and ear height) as they recorded maximum positive indirect effects.

TABLE 3

Phenotypic and Genotypic correlation coefficient of sixteen characters in 70 maize (*Zea mays* L.) genotypes

Characters		BR	DA	DS	ASI	PH	EH	PP	EPP	FW	EL	ED	NKRE	NKR	SW
SR	P	-0.168*	-0.144	-0.118	0.067	0.014	0.216**	0.163	0.130	0.003	0.163	0.057	0.039	0.082	0.131
	G	0.517**	-0.310**	-0.189*	0.578**	0.113	0.240**	0.457**	0.457**	0.226**	0.689**	0.398**	0.389**	0.941**	0.132
BR	P		0.047	-0.055	-0.206*	0.030	-0.025	-0.021	-0.112	-0.118	-0.224**	-0.061	-0.092	-0.137	0.131
	G		0.720**	0.171*	-2.559**	0.782**	-0.642**	-0.372**	0.063	-0.167*	0.798**	0.662**	0.898**	0.404**	-0.221
DA	P			0.880**	-0.340**	-0.219**	-0.439**	-0.354**	-0.433**	-0.385**	-0.139	-0.1749*	-0.135	-0.133	-0.017
	G			0.976**	-0.212*	-0.129	-0.744**	-0.446**	-0.780**	-0.608**	0.059	-0.366**	-0.131	-0.370**	-0.101
DS	P				0.147	-0.152	-0.382**	-0.319**	-0.437**	-0.430**	-0.134	-0.207*	-0.142	-0.171*	-0.050
	G				0.004	-0.088	-0.655**	-0.362**	-0.739**	-0.586**	0.116	-0.195*	0.128	-0.536**	0.007
ASI	P					0.156	0.158	0.106	0.036	-0.048	0.023	-0.048	0.001	-0.063	-0.064
	G					0.196*	0.477**	0.426**	0.268**	0.162	0.254**	0.814**	0.851**	-0.712**	0.498**
PH	P						0.541**	0.240**	0.411**	0.415**	0.170*	0.214*	0.140	0.046	0.171 *
	G						0.805**	0.316**	0.549**	0.593**	0.402**	0.690**	0.407**	0.492**	0.428**
EH	P							0.283**	0.447***	0.409**	0.201*	0.254**	0.191*	0.221**	0.165
	G							0.706**	0.975**	0.917**	0.378**	0.660**	0.913**	0.768**	0.219**
PP	P								0.713**	0.499**	0.268**	0.242**	0.083	0.236**	0.131
	G								0.919**	0.769**	0.442**	0.718**	0.210*	0.473**	0.322**
EPP	P									0.7905**	0.2365**	0.3841***	0.1912*	0.1961*	0.166
	G									0.946**	0.459**	0.883**	0.058	0.685**	0.200*
FW	P										0.233**	0.467**	0.219**	0.247**	0.226**
	G										0.440**	0.900**	0.200*	0.785**	0.238**
EL	P											0.268**	0.098	0.551**	0.057
	G											0.010	-0.201*	0.760**	0.303**
ED	P												0.463**	0.232**	0.326**
	G												0.231**	-0.219**	0.610**
NKRE	P													0.069	0.107
	G													-0.556**	-0.135
NKR	P														-0.128
	G														-0.428**
YPP	P	-0.109	-0.324**	-0.370**	-0.056	0.197*	0.356**	0.320**	0.446**	0.529**	0.337**	0.404**	0.205*	0.343**	0.328**
	G	-0.662**	-0.362**	-0.417**	-0.209*	0.228**	0.410**	0.526**	0.536**	0.654**	0.466**	0.706**	0.240**	0.919**	0.437*

r≥ 0.165 *significance at 5% level,   r ≥ 0.217 **significance at 1% level.

TABLE 4

Phenotypic Path: Direct (diagonal) and indirect effect of sixteen component characters attributing to yield per plant in 70 maize (*Zea mays* L.) genotypes

Characters		SR	BR	DA	DS	ASI	PH	EH	PP	EPP	FW	EL	ED	NKRE	NKR	SW
SR	P	-0.129	0.022	0.019	0.015	-0.009	-0.002	-0.028	-0.021	-0.017	0.000	-0.021	-0.007	-0.005	-0.011	-0.017
	G	-0.926	0.541	0.081	0.706	-0.405	-0.419	0.020	-0.062	-0.055	-0.521	-0.370	-0.019	-0.202	-0.268	-0.698
BR	P	0.014	-0.082	-0.004	0.005	0.017	-0.003	0.002	0.002	0.009	0.010	0.019	0.005	0.008	0.011	-0.011
	G	0.223	-0.690	-0.450	-0.214	-0.013	-0.355	0.737	0.338	0.107	0.359	-0.748	-0.392	-0.107	0.259	0.001
DA	P	0.030	-0.010	-0.207	-0.183	0.071	0.046	0.091	0.073	0.090	0.080	0.029	0.036	0.028	0.028	0.004
	G	0.330	-0.766	-0.922	-0.990	0.031	0.485	0.819	0.500	0.805	0.837	-0.568	0.497	0.133	0.448	0.758
DS	P	-0.005	-0.002	0.037	0.042	0.006	-0.006	-0.016	-0.014	-0.019	-0.018	-0.006	-0.009	-0.006	-0.007	-0.002
	G	0.011	0.665	0.800	0.702	-0.109	-0.890	-0.588	-0.217	-0.725	-0.334	0.107	-0.107	0.498	-0.415	-0.049
ASI	P	-0.007	0.022	0.037	-0.016	-0.108	-0.017	-0.017	-0.011	-0.004	0.005	-0.003	0.005	0.000	0.007	0.007
	G	0.054	-0.351	-0.643	0.091	0.120	0.616	0.292	0.316	0.885	0.715	0.644	0.377	0.384	-0.035	0.061
PH	P	-0.001	-0.003	0.022	0.015	-0.016	-0.100	-0.054	-0.024	-0.041	-0.042	-0.017	-0.022	-0.014	-0.005	-0.017
	G	0.001	-0.209	0.105	0.070	-0.395	-0.065	-0.529	-0.257	-0.538	-0.467	-0.559	-0.735	-0.507	-0.470	-0.650
EH	P	0.029	-0.003	-0.058	-0.051	0.021	0.072	0.132	0.038	0.059	0.054	0.027	0.034	0.025	0.029	0.022
	G	0.115	-0.465	-0.201	-0.330	0.589	0.664	0.344	0.839	0.267	0.378	0.687	0.623	0.101	0.365	0.311
PP	P	0.001	0.000	-0.002	-0.001	0.001	0.001	0.001	0.004	0.003	0.002	0.001	0.001	0.000	0.001	0.001
	G	-0.071	0.659	0.165	0.065	-0.257	-0.484	-0.217	-0.302	-0.292	-0.130	-0.341	-0.222	-0.138	-0.093	-0.310
EPP	P	0.005	-0.004	-0.017	-0.017	0.001	0.016	0.018	0.028	0.040	0.031	0.009	0.015	0.008	0.008	0.007
	G	0.239	-0.099	-0.577	-0.526	0.042	0.650	0.798	0.784	0.811	0.901	3.012	0.631	0.383	0.625	0.015
F W	P	0.001	-0.028	-0.093	-0.104	-0.012	0.100	0.099	0.120	0.190	0.241	0.056	0.111	0.053	0.060	0.055
	G	0.031	0.005	0.477	0.393	-0.294	-0.245	-0.635	-0.540	-0.687	-0.609	-0.446	-0.368	-0.177	0.008	-0.329
EL	P	0.018	-0.024	-0.015	-0.015	0.003	0.018	0.022	0.029	0.026	0.025	0.108	0.029	0.011	0.060	0.006
	G	0.115	0.437	0.133	0.253	0.663	0.366	0.285	0.334	0.317	0.380	0.261	0.150	-0.649	0.446	0.854
ED	P	0.003	-0.004	-0.010	-0.012	-0.003	0.013	0.015	0.014	0.023	0.027	0.016	0.059	0.027	0.014	0.019
	G	0.058	-0.068	-0.216	-0.206	0.205	0.377	0.459	0.449	0.530	0.662	-0.056	0.559	0.099	0.043	0.147
NKRE	P	0.001	-0.003	-0.004	-0.004	0.000	0.004	0.006	0.002	0.006	0.006	0.003	0.014	0.029	0.002	0.003
	G	-0.125	-0.823	0.415	-0.581	-0.607	-0.089	-0.209	-0.619	-0.065	-0.450	0.661	-0.508	-0.392	0.334	0.362
NKR	P	0.015	-0.025	-0.024	-0.031	-0.012	0.008	0.041	0.043	0.036	0.045	0.101	0.042	0.013	0.183	-0.023
	G	0.028	-0.005	0.228	0.289	0.391	-0.302	-0.692	-0.227	-0.381	-0.634	-0.870	0.288	0.422	-0.624	0.317
S W	P	0.036	0.036	-0.005	-0.014	-0.018	0.047	0.046	0.036	0.046	0.063	0.016	0.090	0.030	-0.035	0.276
	G	-0.014	0.508	0.242	-0.140	-0.169	-0.080	-0.473	-0.810	-0.443	-0.432	-0.950	-0.068	0.392	0.295	-0.353
YPP	P	0.009	-0.109	-0.325	-0.370	-0.056	0.198	0.356	0.321	0.446	0.530	0.337	0.404	0.206	0.343	0.328
	G	0.069	-0.662	-0.362	-0.417	-0.209	0.228	0.410	0.526	0.536	0.654	0.466	0.706	0.240	0.919	0.437

R SQUARE = 0.458 RESIDUAL EFFECT = 0.735

CONCLUSION

The results were revealed the existence of moderate to high GCV, PCV coupled with high heritability and high GAM for a surface root, ear height, number of plants per plot, number of ears per plot, field weight and yield per plant suggesting the predominance of additive type of gene action in controlling these traits. Hence, good response to selection can be attained in early generations in improving these traits. The remaining characters under study *viz*., plant height and 100 seed weight had high heritability coupled with moderate GAM indicating the prevalence of both additive and non-additive gene effects in the inheritance of these traits. Hence, for improvement of these characters mass selection, progeny selection or any other suitable modified selection procedure would be effective for exploitation of the mixed effects of both non-additive and additive gene actions. Path coefficient analysis revealed that selection based on characters showing direct positive effect toward yield per plant *viz*., 100 seed weight, field weight, number of kernels per row, number pf kernel per row, ear height, ear length, ear diameter, days to 50% silking, number of ears per plot, number of kernel rows per ear and number of plants per plot might results in higher yield in maize genotypes under water logging conditions.
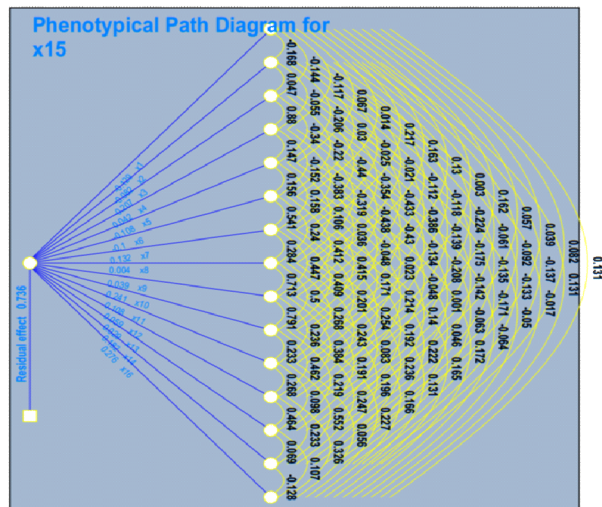
ACKNOWLEDGEMENTS

Fig. 1. Phenotypic path diagram showing cause-effect relationship in maize (*Zea mays* L.).

X1 = Number of surface roots, X2 = Number of nodes bearing brace roots, X3 = Days to 50% anthesis, X4 = Days to 50% silking, X5 = Anthesis-silking interval, X6 = Plant height, X7 = Ear height, X8 = Number of plants per plot, X9 = Number of ears per plot, X10 = Field weight, X11 = Ear length, X12 = Ear diameter, X13 = Number of kernel rows per ear, X14 = Number of kernels per row, X15 = Yield per plant, X16 = 100 Seed weight.

REFERENCES

Al-Jibouri, H. A., P. A. Miller and H. F. Robinson, 1958 : Genotype and environmental variance in an upland cotton cross of interspecific origin. *Agronomy Journal,* **50** : 663-667.

Arya, R. K., M. C. Kamboj and S. Kumar, 2020 : Evaluation of new extra-early maturing hybrids of maize (*Zea mays* L.) for grain yield and its contributing traits under humid and semi-arid conditions of Haryana. *Ekin J.* **6**(2): 23-27.

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

Burton, G. W., 1952 : Quantitative inheritance in grasses. In: Proceedings of 6th International Grassland Congress, **1** : 227-283.

Choudhary, M. K., J. P. Shahi, G. Kumawat, K. Shikha, and G. K. Koli, 2020 : Diversity analysis of maize (*Zea mays* L.) genotypes under excess soil moisture condition. *Journal of Pharmacognosy and Phytochemistry*, **9** : 3407-3413.

Dewey, D. R. and K. Lu., 1959 : A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production. *Agronomy Journal*, **51** : 515-518.

Falconer, D. S. 1996 : Introduction to quantitative genetics. *Pearson Education India.*

Ferdoush, A., M. A. Haque, M. M. Rashid and M. A. A.

Bari, 2017 : Variability and traits association in maize (*Zea mays* L.) for yield and yield associated characters. *Journal of the Bangladesh Agricultural University*, **15** : 193-198.

Gazal, A., Z. A. Dar, A. A. Lone, N. Yousuf and S. Gulzar, 2018 : studies on maize yield under drought using correlation and path coefficient analysis. *International Journal of Current Microbiology and Applied Sciences*, **7** : 516-521.

Hosamani, M., P. H. Kuchanur, M. Mahiboobsa, R. Siddhesh, Nadakarni and Honnappa, 2018 : Genetic variability for yield and yield attributing traits in maize (*Zea mays*. L). *Journal of Pharmacognosy and Phytochemistry*, **7** : 1964-1966.

Johnson, H. W., H. F. Robinson, and R. E. Comstock, 1955 : Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47: 314-318.

Kandel, B. P., A. Poudel, S. Sharma and M. Subedi, 2017 : Correlation and path coefficient analysis of early maize genotype in Western Hill of Nepal. *Nepalese Journal of Agricultural Sciences*, **15** : 119-124.

Kumawat, G., J. P. Shahi, and M. K. Choudhary, 2020b : Studies on genetic parameters, correlation and path coefficient analysis in maize (*Zea mays* L.) hybrids under waterlogging condition. *Range Management and Agroforestry*, **41** : 227-234.

Kumawat, G., J. P. Shahi, and M. Kumar, 2020a : Assessment of genetic diversity of maize (*Zea mays* L.) hybrids under water logging condition. *Electronic J. Pl. Breed*, **11** : 252-258.

Kumawat, G., J. P. Shahi, M. Kumar, A. Singamsetti, M. K. Choudhary, and K Shikha, 2020c : Standard heterosis analysis in maize hybrids under water logging condition. *Journal of Experimental Biology and Agricultural Sciences*, **8** : 90-97.

Mohan L. and S. Dhirendra, 2014 : Studies of variability using morphological and quality traits in quality protein maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **3** : 12-16.

Nagarajan D. and G. Nallathambi, 2017: Correlation studies for grain yield and yield attributes in maize (*Zea mays* L.) *Bulletin of Environment, Pharmacology and Life Sciences*, **6** : 65-68.

Pandey, Yogesh, R. P. Vyas, H. C. Singh, Singh, Lokendra, C. B. Singh, P. C. Yadav, and Vishwanath, 2017 : Genetic variability and selection parameters for yield and quality traits in maize. *Asian Journal of Science and Technology*, **8** : 4348-4351.

Paterson, L. J. and H. D. Patterson, 1984 : An algorithm for generating alpha-lattice designs. *ARS Combinatoria* A, **16** : 87-98.

Shanti, M., D. Nagalakshmi, R. B. Naik, V. Chandrika and H. Chiranjeevi, 2012 : Study on forage quality of various maize cultivars produced under different use patterns. *Forage Res.*, **37**(4): 234-237.