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Genetic variability of quantitative characters over diverse environments in maize inbred lines

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Abstract
Twenty maize inbred lines procured from Maize Research Station, Bhiloda were evaluated during *Kharif*, 2019 over three diverse environments. Variability studies results from pooled environment revealed that PCV was higher in magnitude than GCV for all the characters studied. Grain yield per plant manifested a higher magnitude of GCV and PCV (34.07 and 47.76 %). Heritability estimates ranged from 21.18 per cent for harvest index to 99.04 per cent for protein content. Grain yield and biological yield per plant manifested moderate heritability estimates united with a high genetic gain of 50.06 and 45.03 per cent, respectively. At both genotypic and phenotypic levels, grain yield per plant showed a strong and positive association with plant height, ear height, cob length, cob girth, hundred grain weight, biological yield per plant and harvest index. Genotypic path studies showed the biological yield per plant had the highest and direct positive effect on grain yield per plant followed by harvest index, ear height, cob length and cob girth.

Key words: Maize**,** Correlation, genetic advance, genetic variability, heritability and path analysis.

INTRODUCTION

On the basis of cultivated area, production and grain yield, maize [*Zea mays* (L.)] is considered as the third important cereal crop in the world, after wheat and rice. It is a tall, robust crop and annual in nature. It is versatile in nature and can easily adapt to a wide range of production environments. It is also referred as a “Miracle Crop” and is native to South America. In the genus *Zea,* the only crop which is having chromosome number 2n=20 is a *Zea mays.* In the United States, an agricultural revolution has been brought up by the maize crop and it is the first ever crop that had high yielding varieties within a decade of the rediscovery of Mendelian theory in 1900 (Dasgupta, 2014).

Genetic variability estimation in the available germplasm is an important task in any crop improvement programme. Hence, it is essential to estimate the genotypic and phenotypic coefficient of variation, broad sense heritability and genetic advance as per cent of mean. The study of various traits and their association with each other is an important strategy designed to break the genetic barriers of yield. Whereas, correlation studies are supportive in determining the component of a complex trait *i.e.* grain yield. However, it is not possible to get an exact magnitude of direct and indirect effect towards the yield. Therefore, path analysis is an important tool to screen the correlation coefficient into the direct and indirect effect of the

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independent variables on the dependent variables. This information may be useful to breeders in selecting high yielding genotypes in a particular crop. Hence, the present study was proposed to evaluate the inbreds of maize for genetic parameters that governing character inheritance and association with direct and indirect effects towards grain yields and thereby suggesting better ideotype for rapid improvement in the genetic constitution in a crop.

MATERIALS AND METHODS

The trial with 20 inbred lines was raised in a randomized block design of 12 × 9 m net plot area with three replications and evaluated at three different locations *viz.,* Maize Research Station, Bhiloda, Agricultural Research Station, Ladol and Agronomy Instructional Farm and C. P. College of Agriculture, Sardarkrushinagar, Gujarat, during *Kharif*, 2019. The spacing of 60 × 20 cm with all the recommended cultural practices in the field was adopted during the course of the study. The observations on different agronomic traits were recorded from randomly selected five competitive plants in a genotype and replication on a mean basis except for the days to 50 per cent tasseling and days to 50 per cent silking. The average of five plants for each inbred line in each replication has been worked out for each metic trait *viz.,* plant height (cm), ear height, (cm), cob length (cm), cob girth (cm), hundred grain weight (g), grain yield per plant (g), biological yield per plant (g), protein content (%) and harvest index (%) at each location. Combined data from all the traits across the location were subjected to analysis of variance to test the significant interection of genotype and environment. Here, ANOVA model used for combined analysis was, $Y_{ijk} = \mu + G_i + E_j + R_{kj} + GE_{ij} + e_{ijk,}$ where, Y_{ijk} = response of the i^{th} genotype in j^{th} environment and k^{th} replication within environment, μ = grand mean, G_i = genotype effect, E_j = environment effect, $R_{k(j)}$ = replication within environment effect, GE_{ij} = genotype x environment interaction effect and e_{ijk} = random error (Musvosvi *et al.,* 2016). Statistical analysis such as analysis of variance (Panse and Sukhatme, 1978), genotypic and phenotypic coefficient of variation (Burton, 1952), heritability (Hanson *et al.,* 1956), genetic advance (Johnson *et al.,* 1955), association studies (Al-Jibouri *et al.,* 1958) and path coefficient analysis (Dewey and Lu, 1959) was carried out by the final pooled data over all the environment that included for study.

RESULTS AND DISCUSSION

The prerequisite of any investigation is the existence of variation for the studied characters in the analysed population. The pooled analyses of variance for different quantitative parameters studied across different locations are offered in **Table** 1. Each genotype was studied for all the eleven characters in all the locations and the data were pooled and tested against pooled error. The results revealed that the substantial divergence among genotypes that existed for all the studied characters at 1 per cent probability level indicates highly significant variation except cob length which was significant only at 5 per cent level, whereas cob girth was not significant at both the level of significance. **Table 2** is presented with the variability parameters for the studied characters. The environment in which observations were recorded was tested against pooled error. The results showed that all the characters tested showed the significant difference in the environment for 1 per cent probability level indicated the highly significant except protein content.

The variances by Genotype × Environment interaction were tested against pooled error. The results indicated that days to 50 per cent tasseling, days to 50 per cent silking, ear height, hundred grain weight, grain yield and biological yield per plant and harvest index had significant differences at 1 per cent probability levels indicated the highly significant levels. The range of PCV from the pooled analysis revealed the highest for grain yield tailed by biological yield per plant, harvest index, protein content, hundred grain weight, ear height, cob length, plant height, cob girth, days to 50 per cent tasselling and days to 50 per cent silking. The results obtained in the individual environments were also found to be similar. Finally, it was concluded that the studied traits had a greater chance of genetic improvement because of the broader PCV range.

Table 1. Pooled analysis of variance over environments for different traits in maize

Source of variation	d.f.	Days to 50 % tasselling	Days to 50 % silking	Plant height	Ear height	Cob length	Cob girth	Hundred grain weight	Grain yield per plant	Biological yield per plant	Protein content	Harvest index
Genotype	19	19.217**	19.239**	766.257**	162.902**	5.175*	1.560	26.423**	1989.642**	11760.599**	9.956**	73.912**
Environment	2	278.846**	258.106**	4180.580**	2,611.655**	43.204**	24.519**	368.689**	5457.828**	21709.634**	0.041	274.319**
G × E	38	6.221**	5.505**	180.191	65.932**	2.612	0.510	10.678**	484.333**	2321.897**	0.032	40.922**
Pooled error	114	0.310	0.391	230.741	5.026	2.665	0.995	1.460	69.865	636.380	0.031	14.959
Total	179	6.476	6.095	166.30	60.47	1.59	0.55	9.19	374.99	1983.81	1.06	19.60

* Significant at 5 % probability level, when tested against pooled error.

** Significant at 1 % probability level, when tested against pooled error.

In the present study, the scale of PCV was comparatively higher than that of the GCV suggesting the impact of environmental factors on the phenotypic expression of all the characters. The same result was also testified by Sumathi *et al.*(2005). However, close affinity amid GCV and PCV values were noted for days to 50 per cent silking and tasseling, plant height, cob girth and protein content indicating limited control of the environment in the manifestation of these characters. Grain yield and biological yield per plant were recorded with high GCV and PCV indicating that these characters are highly influenced by genetic control. Hence, simple and effective selection could be practised for further improvement of these traits. These results were in accordance with Bhiusal *et al.*(2017) and Jilo *et al.*(2018). Hundred grain weight and protein content showed moderate GCV and PCV, which allowed for the average chances for selection. Similar results were reported by Sumathi *et al.*(2005) and Gazal *et al.*(2017). Low GCV and PCV were noted for days to 50 per cent tasseling (3.86% and 6.03%), days to 50 per cent silking (3.80% and 5.65%) and cob girth (4.99% and 7.83%) suggesting need of creation of variability either by mutation or hybridization followed by selection. Begum *et al.*(2016) and Sravanti *et al.*(2017) also reported similar findings. Besides, plant height, ear height, cob length and harvest index exerted high differences among GCV and PCV and hence these traits provide practically, less chances of selection, due to the higher influence of environmental factors. Grace beulah *et al.*(2018), Hassan *et al.*(2018), Neelam *et al.*(2018) also observed the high differences among GCV and PCV for these characters.

The heritability estimations were moderate for all the traits studied except cob length, protein content and harvest index. The estimate of broad sense heritability ranged from 21.18 (harvest index) to 99.04 per cent (protein content) (**Table 2**). The protein content is the only trait that exerted a high heritability estimate, whereas moderate estimates of heritability were recorded for days to 50 per cent tasseling and silking, plant height, ear height, cob girth, hundred grain weight, grain yield and biological yield per plant. Moderate heritability values for these characters suggest that the variation noted was partly under genetic control and more influenced by the environment. Cob length and harvest index exerted low heritability estimates. The GAM values ranged from 5.10 (days to 50 % tasseling) to 50.06 per cent (grain yield per plant) (**Table 2**). The GAM for grain yield and biological yield per plant and protein content was high. While, moderate GAM was recorded for plant height, ear height and hundred grain weight. Days to 50 per cent tasseling and silking, cob length, cob girth and harvest index showed the low magnitude of GAM. Characters exhibiting high heritability united with high genetic advances are mainly controlled by additive genes (Panse, 1957). Hence, protein content manifested high heritability united with high GAM suggested the predominance of additive genes in the expression of the character. Gazal *et al.*(2017) also noticed high heritability united with high GAM for this character. Besides, grain yield and biological yield per plant showed moderate heritability associated with high genetic gain, indicating that the character was governed by additive genes and the moderate heritability was exerted due to environmental effects. In such conditions, the selection of these characters may be efficient. These findings were in accordance with the reports of Ferdoush

Table 2. Genetic parameters of eleven quanitative traits of twenty inbred lines of maize evaluated across locations

S. No.	Character	Mean	Range	GCV (%)	PCV (%)	Heritability (%)	GA	GAM (%)
1	Days to 50 per cent tasselling	53.85	48-68	3.86	6.03	41.04	2.75	5.10
2	Days to 50 per cent silking	56.23	50-70	3.80	5.65	45.37	2.97	5.28
3	Plant height (cm)	158.63	78.6-206.2	8.81	12.22	52.02	20.76	13.09
4	Ear height (cm)	59.93	24.6-86.8	9.49	16.54	32.88	6.71	11.21
5	Cob length (cm)	13.05	7.9-18.4	7.08	14.26	24.62	0.94	7.24
6	Cob girth (cm)	11.86	8.0-16.1	4.99	7.83	40.64	0.77	6.55
7	Hundred grain weight (g)	22.20	12.18-33.41	10.32	17.98	32.95	2.71	12.20
8	Grain yield per plant (g)	65.74	21.12-180.58	34.07	47.76	50.88	87.65	50.06
9	Biological yield per plant (g)	194.66	59.6-455.2	28.82	37.99	57.54	3.73	45.03
10	Protein content (%)	10.12	6.55-13.27	17.97	18.06	99.04	3.14	36.85
11	Harvest Index (%)	33.46	21.14-58.10	9.91	21.53	21.18	32.91	9.39

PCV (%) and GCV (%) are phenotypic and genotypic co-efficient of variance, respectively.
GAM (%) and GA are genetic advance as per cent of mean and genetic advance, respectively.

et al.(2017), Jilo *et al.*(2018) and Ilyas *et al.*(2019). Plant height, ear height and hundred grain weight showed moderate heritability associated with moderate genetic gain, indicating the scope of improvement of these traits by direct selection would be limited but delayed selection might be effective for these traits. These findings were similar to the results of Jilo *et al.*(2018) and Sravanti *et al.*(2017). Moderate values of heritability estimate along with low GAM was observed for days to 50 per cent tasseling and silking and cob girth. Sravanti *et al.*(2017), Grace beulah *et al.*(2018) also assessed the moderate values of heritability coupled with low GAM. This variation might be due to the high macro environmental influence in the development of these traits in maize. Cob length and harvest index exerted low heritability estimates associated with low genetic gain, suggesting that the character was highly controlled by environmental factors which results in ineffective selection for crop improvement. These findings were in agreement with Hassan *et al.*(2018) and Neelam *et al.*(2018). However, this is discordant with those obtained by Patil *et al.*(2016) for cob length who reported moderate estimates of heritability for cob length.

Genotypic correlation coefficients (GCV) were higher in scale than their corresponding phenotypic correlation coefficients (PCV) for almost all the traits studied, which clearly indicated the presence of inherent association among the different traits (**Table 3**). When two characters are highly genotypically correlated, the genes responsible for these traits are inherited together. In some cases, however, phenotypic correlations were to some extent higher than their corresponding genotypic coefficients that implied the non-genetic causes inflated the genotypic correlation because of the environmental influence. Similar findings were also reported by Varalakshmi *et al.*(2018). A study was conducted at three locations, the sign and magnitude between genotypic and phenotypic correlations were the same for almost all pairs of traits.

Table 3. Genotypic and phenotypic correlation coefficients among eleven traits in twenty inbreds of maize.

Characters		Days to 50 per cent tasselling	Days to 50 per cent silking	Plant height	Ear height	Cob length	Cob girth	Hundred grain weight	Biological yield per plant	Protein content	Harvest index	Grain yield per plant
Days to 50 per cent tasselling	G	1.000	1.000**	-0.373**	-0.144	-0.624**	-0.260*	0.318*	-0.145	-0.122	0.210	-0.091
	P	1.000	0.988**	-0.415**	-0.268*	-0.365**	-0.410**	0.009	-0.298*	-0.071	-0.090	-0.278*
Days to 50 per cent silking	G		1.000	-0.375**	-0.167	-0.603**	-0.258*	0.301*	-0.157	-0.141	0.153	-0.106
	P		1.000	-0.398**	-0.244	-0.370**	-0.397**	0.037	-0.305*	-0.083	-0.104	-0.291*
Plant height	G			1.000	0.883**	0.915**	1.051**	0.341**	0.539**	-0.103	-0.675**	0.274*
	P			1.000	0.827**	0.645**	0.699**	0.330*	0.580**	-0.063	-0.084	0.438**
Ear height	G				1.000	0.834**	1.024**	0.634**	0.586**	-0.193	-0.749**	0.331**
	P				1.000	0.516**	0.648**	0.474**	0.464**	-0.096	0.094	0.422**
Cob length	G					1.000	0.930**	0.860**	0.754**	0.008	0.058	0.644**
	P					1.000	0.706**	0.516**	0.595**	0.006	0.074	0.531**
Cob girth	G						1.000	0.617**	0.740**	-0.291*	-0.529**	0.493**
	P						1.000	0.457**	0.569**	-0.181	-0.080	0.448**
Hundred grain weight	G							1.000	0.409**	0.133	-0.120	0.347**
	P							1.000	0.262*	0.084	0.205	0.296*
Biological yield per plant	G								1.000	-0.471**	0.336**	0.975**
	P								1.000	-0.354**	0.137	0.892**
Protein content	G									1.000	0.095	-0.427**
	P									1.000	0.052	-0.297*
Harvest Index	G										1.000	0.556**
	P										1.000	0.527**
Grain yield per plant	G											1.000
	P											1.000

* Significantat 5 % probability level.

** Significant at 1 % probability level.

In the present analysis, an economically important trait grain yield per plant recorded a positive and significant correlation with ear height, cob length, cob girth, biological yield per plant and harvest index at both genotypic and phenotypic levels. Hence, direct selection for these characters could bring enhancement in yield and yield attributes in maize. Pavan *et al.*(2011), Ramesh Kumar *et al.*(2017) and Varalakshmi *et al.*(2018) also reported similar findings, whereas grain yield per plant was positively and significantly correlated at the genotypic level and highly significantly correlated at phenotypic level with plant height and with hundred grain weight positively and highly significantly correlated at the genotypic level and significantly correlated at the phenotypic level, respectively. Pavan *et al.*(2011), Ramesh Kumar *et al.*(2017), Vara Prasad *et al.*(2017) and Varalakshmi *et al.*(2018) also recorded similar findings. Hence, to improve the grain yield in maize the above mentioned components may be given prime importance in the selection program. Days to 50 per cent tasseling showed positive and highly significant correlation with days to 50 per cent silking at both genotypic and phenotypic levels, while the significant correlation with hundred grain weight at the genotypic level, only. Ramesh Kumar *et al.*(2017), Vara Prasad *et al.*(2017) and Rajwade *et al.*(2018) also reported similar findings. Days to 50 per cent silking was significant and positively correlated with hundred grain weight at the genotypic level. Plant height had a strong positive association at genotypic and phenotypic levels with ear height, cob length, cob girth,hundred grain weight, biological yield per plant and grain yield per plant. These results are in agreement with Pavan *et al.*(2011), Ramesh Kumar *et al.*(2017) and Vara Prasad *et al.*(2017). A highly significant and positive correlation for ear height was noted with cob length, cob girth, hundred grain weight, biological yield per plant and grain yield per plant at both genotypic and phenotypic levels, respectively. Ramesh Kumar *et al.*(2017) and Belay (2018) also obtained similar recordings. Nagarajan and Nallathambi (2017) also reported similar findings for the association between ear height and grain yield per plant. The trait cob length was highly significant and positively correlated with cob girth, hundred grain weight, biological yield per plant and grain yield per plant at genotypic and phenotypic levels, respectively. These results were in affirmation with the findings of Pavan *et al.*(2011), Vijay kumar *et al.*(2015), Nagarajan and Nallathambi (2017) and Varalakshmi *et al.*(2018). A strong and positive association for cob girth was observed with hundred grain weight, biological yield per plant and grain yield per plant. Pavan *et al.*(2011) and Varalakshmi *et al.*(2018) also observed that cob girth had a strong positive association with hundred grain weight and biological yield per plant. The trait hundred grain weight showed a positive correlation with biological yield per plant and grain yield per plant. Mesenbet *et al.*(2017) and Varalakshmi *et al.*(2018) also recorded similar observations. Biological yield per plant recorded a strong positive correlation with harvest index at the genotypic level and grain yield per plant at both genotypic and phenotypic levels, respectively. Ramesh Kumar *et al.*(2017) also testified the similar findings. Protein content presented as negative and significant association with grain yield per plant at the genotypic level and phenotypic level. Chinnadurai *et al.*(2011) also obtained the negative association of protein content with grain yield per plant. A strong and positive association was noted between harvest index and grain yield per plant at both genotypic and phenotypic levels. A similar association was also reported by Ramesh Kumar *et al.*(2017).

Grain yield per plant was measured as a resultant variable, whereas the remaining ten yield contributing characters were measured as casual variables. Genotypic path coefficients were mainly worked out to facilitate the identification of main grain yield components (**Table 4**). It was further partitioned to study the direct and indirect effect of these traits on grain yield per plant. **Fig. 1** showed the direct and indirect effects of these component traits on grain yield per plant. Path studies result at the genotypic level exposed that among the characters, biological yield per plant had the significant and highest positive direct effect on grain yield per plant followed by harvest index, ear height, cob length and cob girth, while protein content had the significant and highest direct negative effect on grain yield per plant followed by plant height and hundred grain weight. In general, component traits that showing high association with yield also had a high direct effect on yield. In contrast, for the present analysis days to 50 per cent tasseling had positive and days to 50 per cent silking had the negative direct effect on grain yield per plant but a non-significant correlation with grain yield per plant was observed at both 5 per cent and 1 per cent level, respectively. These findings are supported by Manal hefny, (2011) who stated that correlation studies identifies mutual association between the different traits irrespective of causation. Whereas, path analysis specifies the causes and measures their relative importance (Dewey and Lu, 1959). In some instances, path studies give slightly different picture of a net effect than does association studies. That was the case here, though a positive significant association was existed between days to 50 per cent tasseling and days to 50 per cent silking, they exhibited a positive and negative direct effect on grain yield per plant, respectively. Manal hefny, (2011), Pavan *et al.(*2011), Ramesh Kumar *et al.*(2017), Rajwade *et al.*(2018), Varalakshmi *et al.*(2018) and Devasree *et al.*(2020) also obtained similar recordings.

From the present study, the low residual effect (-0. 057) suggested the characters selected for the study of correlation with grain yield per plant had maximum contributions and validate the traits chosen for the study in the present investigation. By considering both path studies and correlation studies together, the grain yield per plant had the significant positive correlation and highest positive direct effect on biological yield per plant

Table 4. Direct and indirect effects on grain yield per plant at genotypic level.

Characters	Days to 50 per cent tasselling	Days to 50 per cent silking	Plant height	Ear height	Cob length	Cob girth	Hundred grain weight	Biological yield per plant	Protein content	Harvest index	Grain yield per plant (g)
Days to 50 per cent tasselling	**1.193**	-1.245	0.039	-0.026	-0.046	-0.005	-0.004	-0.092	0.019	0.077	-0.091
Days to 50 per cent silking	1.199	**-1.240**	0.039	-0.031	-0.044	-0.005	-0.003	-0.100	0.022	0.056	-0.106
Plant height	-0.445	0.465	**-0.106**	0.164	0.068	0.020	-0.004	0.343	0.016	-0.248	0.274*
Ear height	-0.171	0.207	-0.093	**0.186**	0.061	0.019	-0.008	0.373	0.030	-0.276	0.330**
Cob length	-0.744	0.747	-0.096	0.155	**0.074**	0.017	-0.010	0.481	-0.001	0.021	0.643**
Cob girth	-0.310	0.319	-0.111	0.190	0.069	**0.019**	-0.007	0.472	0.046	-0.194	0.492**
Hundred grain weight	0.379	-0.373	-0.036	0.118	0.063	0.011	**-0.013**	0.260	-0.021	-0.044	0.347**
Biological yield per plant	-0.173	0.194	-0.056	0.109	0.056	0.014	-0.005	**0.638**	0.075	0.123	0.975**
Protein content	-0.146	0.175	0.010	-0.035	0.001	-0.005	-0.001	-0.300	**-0.159**	0.035	-0.427**
Harvest index	0.250	-0.189	0.071	-0.139	0.004	-0.010	0.001	0.214	-0.015	**0.368**	0.555**

Residual effect = -0.057
Values mentioned as bold are denoting direct effect.
* Significant at 5 per cent probability level.
** Significant at 1 per cent probability level.

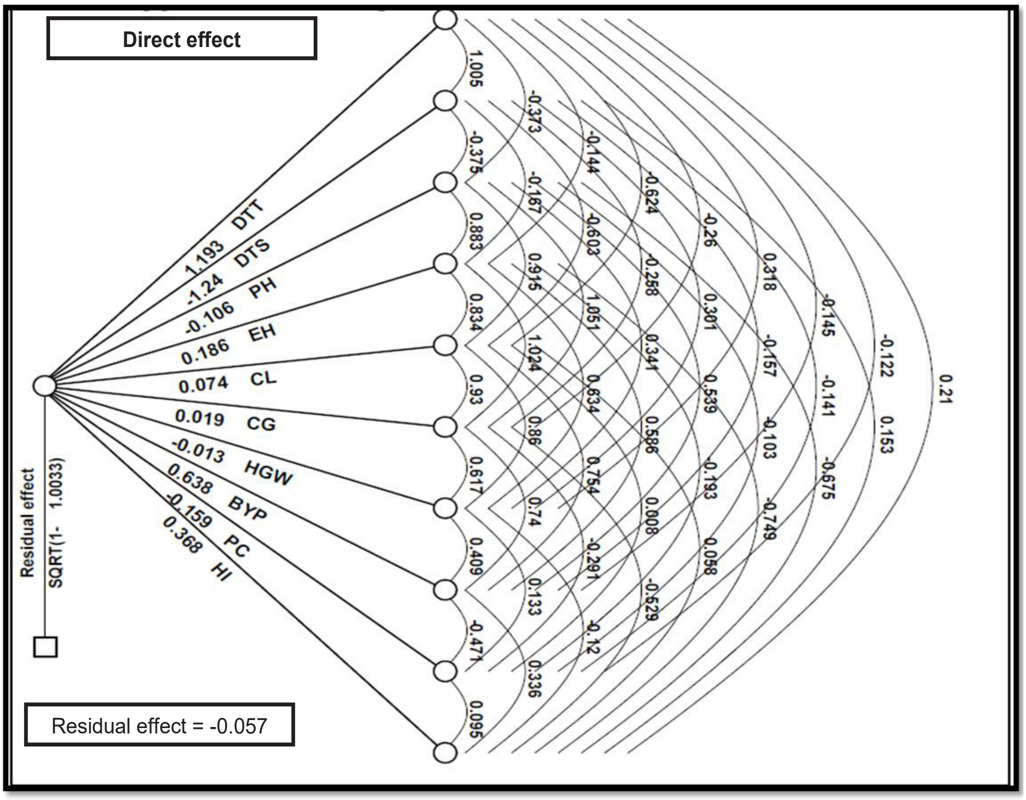

Fig. 1. Path analysis diagram for grain yield per plant in maize at genotypic level

DTT- Days to 50% tasseling, DTS- Days ot 50 % silking, PH- Plant height, EH- Ear height, CL- Cob length, CG-Cob girth, HGW- Hundred grain weight, BYP- Biological yield per plant, PC- Protein content, HI- Harvest index, GYP- Grain yield per plant followed by harvest index, ear height, cob length and cob girth. Hence, to improve the grain yield in maize the above mentioned components may be given prime importance in the selection program.

The above findings revealed that higher estimates of GCV were noticed for grain yield and biological yield per plant, whereas, higher estimates of PCV were noticed for grain yield and biological yield per plant and harvest index indicated that the isolation of desirable genotypes could be possible by the succession exploitation of this variability. Moderate to high heritability along with high genetic gain for grain yield per plant, biological yield per plant and protein content indicated the role of additive gene action and scope of improvement in these characters through selection. The association studies and path analysis revealed that the characters *viz.,* biological yield per plant, harvest index, ear height, cob length and cob girth was considered as the chief yield contributing traits in maize and hence, to improve the grain yield in maize the above mentioned components may be given prime importance in the selection program.

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