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Genetic variability, inter-relationship and path analysis studies in single cross quality protein maize (*Zea mays* L.) hybrids

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Abstract: The present study was undertaken with the objective to determine the nature and magnitude of variability, degree of inter-relationship between yield and its component traits and their direct, indirect effects on grain yield in 45 single cross Quality Protein Maize hybrids (*Zea mays* L.). The results indicated that the hybrids showed significant variability for most of the traits studied. The range of PCV was observed from 2.56 to 30.63% for the traits under study which provides a picture to the extent of phenotypic variability in the hybrids. The PCV was noted high for the grain yield per plant (30.63%) and moderate for grains per row (16.25%). Genotypic coefficient of variation ranged from 2.35 to 30.12%. Maximum GCV was observed for grain yield per plant (30.12%). Grain yield per plant was found to be significant positively associated with plant height, cob placement height, 100-seed weight, cob length, cob girth, grains per row and protein content at genotypic level. Days to 50% silking exhibited the highest magnitude of direct effects on grain yield followed by 100-seed weight, grains per row and plant height. The component traits *viz.,* plant height, 100-seed weight and grains per row with grain yield per plant showed positive and significant correlation (0.6647, 0.8182 and 0.8314) and also exhibited positive and strong direct effects (0.3244, 1.0809 and 0.9167) on grain yield per plant.

Key words: QPM, Hybrids, Genetic parameter of variability, Correlation, Path analysis, *Zea mays* L.

Introduction

Maize (*Zea mays* L. 2n=20) assumes worldwide significance owing to its utilization as a major cereal crop for livestock feed, human consumption and several industrial uses as well (Prasanna *et al.,* 2001). It occupies third place in terms of calorie requirement after rice and wheat. It is one of the most important livestock feed sources. With the rapid growth of animal husbandry and bio-energy industry, maize will be more important in the development of agriculture economy and identification of food security (Yue, 2006). Globally, maize occupies an area of 181.44 mha with production of 990.64 mt and productivity 54.60 q/ha. India is the second most important maize growing country in Asia and world's sixth largest producer and the fifth largest consumer. In India maize is cultivated in an area of 9.42 mha with production of 24.35 mt and productivity of 25.83 q/ha (Anonymous, 2015). The maize grain accounts for about 15 to 56% of the total daily calories in the diets of people in about 25 different developing countries. In India more than 25% of maize produced is consumed as human food (Prasanna *et al.,* 2001). However, in spite of several important uses, maize has an inbuilt drawback of being deficient in two essential amino acids *viz.*, lysine and tryptophan (Osborne and Mendel, 1914). This leads to poor net protein utilization and low biological value. The tragedy of hunger is still a reality in today's world. Globally, an estimated 805.3 million people were chronically undernourished in 2012-14, with insufficient food for an active and healthy life (Anonymous, 2014). India remains home to the largest numbers of undernourished people in the world; 217 million as of 2012 (Anonymous, 2012). Thus quality protein maize developed by maize breeders, emerged as a viable option to mitigate this problem.

Quality protein maize (*Zea mays* L.) is found to be having protein equivalent to skimmed milk, therefore giving an opportunity to deal with the issue of malnutrition and hunger. The maize breeders initially developed *opaque2* maize by incorporating *opaque2* mutant gene, which is responsible for enhancing lysine and tryptophan content of maize endosperm protein (Crow and Kermicle, 2002). However, pleiotropic effects of the *opaque2* allele make the maize endosperm soft and susceptible to cracking, ear rot, and weevils. Such negative secondary effects are obviously undesirable (Mertz, 1994; Villegas, 1994). These defects were overcome by selection based on a third, distinct genetic system, comprising of minor modifying loci that convert the mutant endosperm of the soft phenotype to a hard phenotype similar to normal maize. This upgraded version of *opaque2* maize was termed as quality protein maize (QPM) by CIMMYT's maize breeders (Vasal, 2002). In general, QPM maize contains about 55% more tryptophan, 30% more lysine and 38% less leucine than the normal maize. It was demonstrated that *opaque2* maize has 90% of the nutritive value of milk protein for young children (FAO, 1992). This emphasizes an urgent need to enhance the normal maize quality by incorporating the QPM gene to meet the increasing demand for maize grain and its products. India is one of the first countries who released QPM composites and hybrids, though these were introduction from CIMMYT, hence there is a need to introgress QPM traits into local land races for the development of better adapted QPM genotypes. In order to meet the nutritional security among resource poor people on a global front, it is important to develop quality protein maize hybrids to provide a better nutrition.

The assessment of genetic parameters like genotypic variability, phenotypic variability, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful for the effective selection and improvement of breeding population. The study of correlation and path analysis for yield and its attributing traits will be helpful in improving the grain yield. In view of this the investigation was undertaken to assess the magnitude of phenotypic and genotypic variability, PCV, GCV, correlation coefficient and path analysis so that these information may be utilized in development of superior QPM hybrids.

Materials and Methods

The experiments comprising 42 single cross F_1 hybrids along with two single cross QPM checks *viz*., HQPM 1 and Vivek QPM 9 and non-QPM check EHL161708. The trial was conducted in α-randomized block design with two replications, fifteen blocks per replication and three entries per block with 60 cm and 20 cm spacing between rows and plants, respectively during *kharif* 2014 at Experimental Farm, Department of Crop Improvement, CSK HPKV, Palampur, Himachal Pradesh. All recommended agronomical practices were followed for raising the good crop. Ten plants were randomly selected for recording the data on days to 50% pollen shed, 50% silking, 75% maturity, plant height (cm), cob placement height (cm), cob length (cm), cob girth (cm), kernel rows per ear, grains per row, grain yield per plant (g), 100-seed weight (g), protein content (%) and tryptophan content (%). The crude protein content for each entry was calculated by Micro-Kjeldhal Method (AOAC, 1965) and expressed as per cent of protein in endosperm. Tryptophan content was estimated by method given by Mertz *et al.* (1975) and expressed as % tryptophan in endosperm protein. The mean data was analyzed for genetic variability as per Parsad *et al.* (2007), genotypic and phenotypic variance; GCV and PCV were estimated as suggested by Burton and De Vane (1953). The data were also analyzed for estimating the correlation coefficient (Al-Jibouri *et al.* 1958) and path analysis as per Dewey and Lu (1959) for grain yield and its components. Morphological traits were measured based on maize descriptors developed by the Bioversity International. The analysis was performed using the software PROC GLM SAS.

Results and Discussion

Analysis of variance revealed significant differences among hybrids at 5% level of significance for all the characters studied except cob girth and kernel row per ear indicating presence of sufficient genetic variability in the material under study (Table 1).

Estimates of genetic parameters, *viz*., genotypic and phenotypic variability, PCV and GCV are presented in Table 2. A considerable range of variation was observed for all the characters under study. The range of PCV was observed from 2.56 to 30.63% whereas the GCV ranged from 2.35 to 30.12%. The PCV and GCV values were high for grain yield per plant followed by grains per row indicating the considerable level of observable variations among the tested hybrid for these traits. Although, remaining traits revealed low values of PCV and GCV. In general, genotypic correlations were of higher magnitude than the corresponding phenotypic correlations for all the traits indicated the genetic reason of association (Table 3). Grain yield per plant was found to be significant positively correlated with plant height, cob placement height, 100-seed weight, cob length, cob girth, grains per row and protein content. Days to 50% pollen shed and silking were negatively correlated with grain yield per plant. Correlations among maturity traits were positive and significant. Days to 75% maturity was negatively correlated with all the traits, while the plant and ear height were positively correlated with grain yield plant, 100-seed weight, cob length, cob girth, kernel rows per ear, grains per row and protein content. Significant positive correlation was observed for 100-seed weight with grain yield per plant, cob length, cob girth, grains per row and protein content. Cob length showed significant positive correlation with cob girth and grains per row and protein content. Cob girth also showed significant positive correlation with kernel rows per ear, grains per row and protein content. Positive correlation was observed for kernel rows per ear with grains per row. Grains per row showed significant positive correlation with protein content, whereas protein content exhibited positive correlation with tryptophan content.

The direct and indirect effects of yield components on grain yield at phenotypic and genotypic levels are depicted in Table 4, Fig. 1 and 2. The grains per row (0.3538) exhibited the highest magnitude of direct effects on grain yield at phenotypic level, while at genotypic level days to 50% silking (1.3161) followed by 100-seed weight (1.0809), grains per row (0.9167) and plant height (0.3244) exhibited the largest direct effect on grain yield per plant. The negative associations of days to 50% pollen shed and 75% maturity with grain yield was attributed to the negative indirect effects of these traits through days to 75% maturity, plant height, 100-seed weight, cob girth and grains per row. Whereas, direct effect of days to 50% silking was positive and of high in magnitude (1.3161). This character also showed positive indirect effect via cob placement height, cob length, kernel rows per ear protein and tryptophan content.

Plant height also revealed positive direct effect (0.3244) and indirectly contributed to the grain yield per plant via positive indirect effect of days to 50% pollen shed (0.2799), 75% maturity (0.0567), 100-seed weight (0.7957), cob girth (0.1069) and grains per row (0.6320). Direct effect of cob placement height was registered high negative path value (-0.6828). Positive path values of indirect effect were noticed for days to 50% pollen shed (0.1980), 75% maturity (0.0481), plant height (0.2917), 100-seed weight (0.8484), cob girth (0.1132) and grains per row (0.6031) via cob placement height. 100-seed weight revealed high direct effect (1.0809) on grain yield per plant. This trait indirectly contributed to grain yield per plant via positive path values of days to 50% pollen shed (0.3646), 75% maturity (0.0198), plant height (0.2388), cob girth (0.1450) and grains per row (0.7091). Cob length revealed significant positive correlation (0.8463) with grain yield per plant. However, it had negative direct effect (-0.2477) on grain yield per plant. This character indirectly influenced to the grain yield per plant via days to 50% pollen shed (0.2139), 75% maturity (0.1241),

Table-1: Analysis of variance of Quality Protein Maize (QPM) hybrids for different traits

Source of variation	Replication	Blocks within replication	Lines	Error
Days to 50% pollen shed	13.611*	0.914*	8.478*	0.393
Days to 50% silking	19.600*	1.059	7.089*	0.672
Days to 75% maturity	0.711	1.081	8.091*	1.001
Plant height (cm)	56.803*	21.756	493.126*	12.116
Cob placement height (cm)	87.419	23.280	187.252*	26.064
Grain yield/plant (g)	101.518*	45.127	1513.377*	21.295
100-seed weight (g)	279.488*	3.252	17.328*	3.037
Cob length (cm)	72.397*	1.400	3.747*	1.308
Cob girth (cm)	34.250*	0.817	1.547	0.760
Kernel rows/ear	0.114	0.473	0.582	0.492
Grains per row	72.003*	5.261*	27.192*	1.998
Protein content (%)	1.942*	0.109	1.679*	0.186
Tryptophan content (%)	0.0008	0.0002	0.0080*	0.0005

Table-2: Estimates of variability parameters for various traits in QPM hybrids

Traits	Variance		Coefficient of variation	
	Phenotypic	Genotypic	Phenotypic	Genotypic
Days to 50% pollen shed	7.02	6.29	4.47	4.24
Days to 50% silking	5.91	4.99	3.99	3.67
Days to 75% maturity	6.79	5.74	2.56	2.35
Plant height (cm)	456.43	438.18	12.31	12.06
Cob placement height (cm)	204.54	180.25	14.84	13.93
Grain yield/plant (g)	1098.23	1061.77	30.63	30.12
100-seed weight (g)	14.53	11.36	13.26	11.72
Cob length (cm)	3.11	1.75	12.28	9.20
Cob girth (cm)	1.52	0.72	9.73	6.72
Kernel rows/ear	0.65	0.17	5.88	3.01
Grains/row	22.71	18.64	16.25	14.72
Protein content (%)	1.33	1.20	13.52	12.81
Tryptophan content (%)	0.005	0.005	9.42	9.13

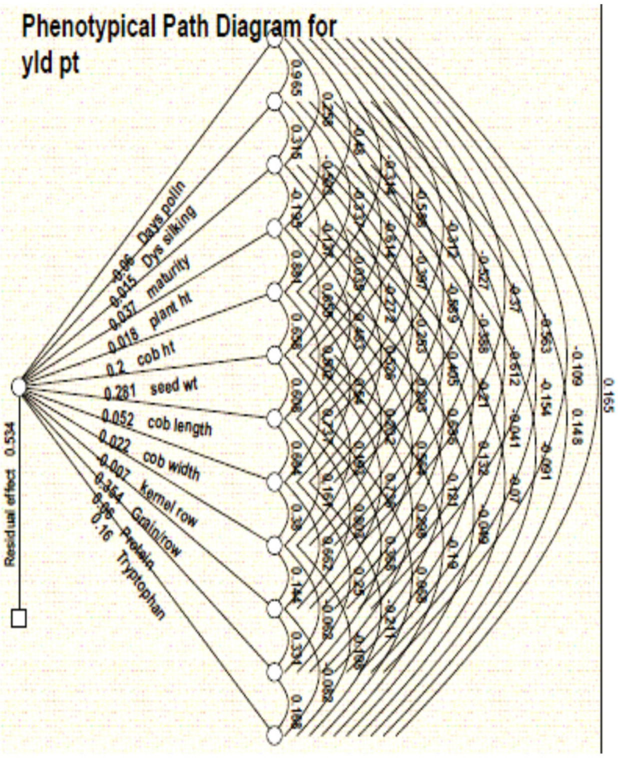

Fig. 1: Phenotypic path diagram of grain yield and its components in Maize

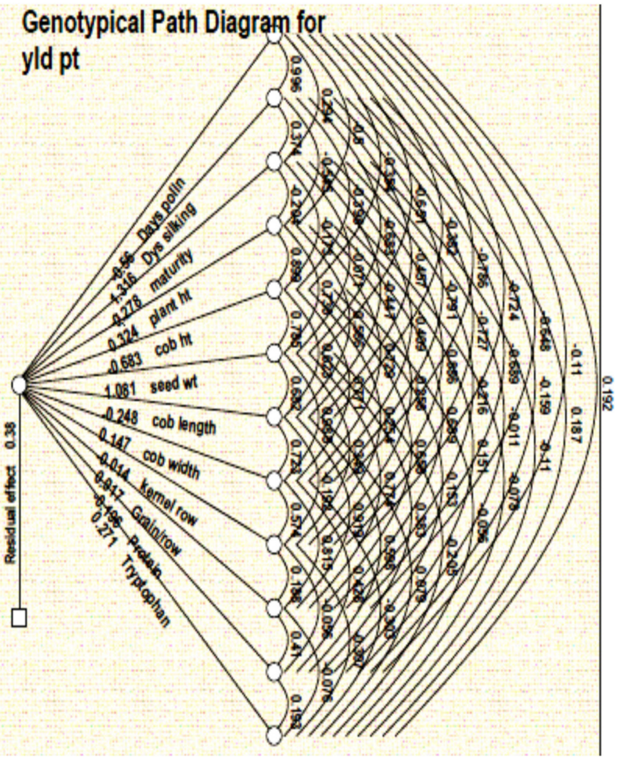

Fig. 2: Genotypic path diagram of grain yield and its components in Maize

Table-3: Estimates of correlation coefficients at phenotypic (P) and genotypic (G) levels among different traits of QPM hybrids

Traits		Days to 50% silking	Days to 75% maturity	Plant height (cm)	Cob placement height (cm)	Grain yield/ plant	100-seed wt. (g)	Cob length (cm)	Cob girth (cm)	Kernel rows/ ear	Grains per row	Protein content (%)	Tryptophan content (%)
Days to 50% pollen shed	P	0.965**	0.258*	-0.480**	-0.314**	-0.477**	-0.588**	-0.312**	-0.527**	-0.370**	-0.563**	-0.109	0.166
	G	0.996**	0.294**	-0.500**	-0.354**	-0.486**	-0.651**	-0.382**	-0.786**	-0.724**	-0.648**	-0.110	0.192
Days to 50% silking	P		0.315*	-0.503**	-0.337**	-0.513**	-0.614**	-0.397**	-0.589**	-0.388**	-0.612**	-0.154	0.148
	G		0.374**	-0.545**	-0.398**	-0.531**	-0.684**	-0.457**	-0.791**	-0.727**	-0.689**	-0.159	0.187
Days to 75% maturity	P			-0.195	-0.137	-0.123	-0.035	-0.272**	-0.253*	-0.405**	-0.210*	-0.041	-0.091
	G			-0.204	-0.173	-0.137	-0.071	-0.447**	-0.409**	-0.886**	-0.216*	-0.011	-0.110
Plant height (cm)	P				0.881**	0.650**	0.655**	0.483**	0.526**	0.203	0.636**	0.132	-0.070
	G				0.899**	0.665**	0.736**	0.586**	0.729**	0.258*	0.690**	0.151	-0.078
Cob placement height (cm)	P					0.646**	0.658**	0.502**	0.540**	0.202	0.564**	0.121	-0.049
	G					0.693**	0.785**	0.623**	0.771**	0.254*	0.658**	0.153	-0.056
Grain yield per plant (g)	P						0.744**	0.666**	0.608**	0.139	0.764**	0.343**	0.065
	G						0.818**	0.846**	0.831**	0.200	0.831**	0.363**	0.065
100-seed weight (g)	P							0.608**	0.738**	0.193	0.736**	0.298**	-0.190
	G							0.682**	0.988**	0.349**	0.774**	0.383**	-0.205
Cob length (cm)	P								0.664**	0.162	0.803**	0.368**	0.068
	G								0.723**	-0.192	0.919**	0.598**	0.079
Cob girth (cm)	P									0.380**	0.662**	0.250*	-0.211*
	G									0.574**	0.815**	0.428**	-0.303**
Kernel rows/ear	P										0.144	-0.062	-0.108
	G										0.188	-0.056	-0.307**
Grains per row	P											0.331**	-0.082
	G											0.410**	-0.076
Protein content (%)	P												0.168
	G												0.193

* Significant at 5% level, ** Significant at 1% level

Table-4: Estimates of direct and indirect phenotypic (P) and genotypic (G) effects of different traits on seed yield

Traits		Days to 50% pollen shed	Days to 50% silking	Days to 75% maturity	Plant height (cm)	Cob placement ht. (cm)	100-seed weight (g)	Cob length (cm)	Cob girth (cm)	Kernel rows/ ear	Grains/ row	Protein content (%)	Tryptophan content (%)	Correlation with yield
Days to 50% pollen shed	P	-0.0596	0.0147	0.0095	-0.0086	-0.0629	-0.1653	-0.0163	-0.0115	0.0025	-0.1993	-0.0066	0.0265	-0.4771**
	G	-0.5598	1.3111	-0.0816	-0.1622	0.2415	-0.7041	0.0947	-0.1154	0.0105	-0.5938	0.0216	0.0519	-0.4855**
Days to 50% silking	P	-0.0575	0.0152	0.0116	-0.0091	-0.0674	-0.1727	-0.0208	-0.0129	0.0026	-0.2167	-0.0093	0.0237	-0.5132**
	G	-0.5576	1.3161	-0.1039	-0.1768	0.2716	-0.7388	0.1131	-0.1161	0.0105	-0.6313	0.0311	0.0507	-0.5313**
Days to 75% maturity	P	-0.0154	0.0048	0.0369	-0.0035	-0.0273	-0.0098	-0.0143	-0.0055	0.0027	-0.0743	-0.0025	-0.0146	-0.1228
	G	-0.1645	0.4925	-0.2776	-0.0663	0.1183	-0.0772	0.1107	-0.0601	0.0128	-0.1976	0.0021	-0.0298	-0.1365
Plant height (cm)	P	0.0286	-0.0076	-0.0072	0.0180	0.1765	0.1842	0.0253	0.0115	-0.0014	0.2249	0.0079	-0.0112	0.6496**
	G	0.2799	-0.7172	0.0567	0.3244	-0.6139	0.7957	-0.1452	0.1069	-0.0037	0.6320	-0.0297	-0.0211	0.6647**
Cob placement height (cm)	P	0.0187	-0.0051	-0.0050	0.0159	0.2002	0.1850	0.0263	0.0118	-0.0014	0.1996	0.0073	-0.0078	0.6456**
	G	0.1980	-0.5236	0.0481	0.2917	-0.6828	0.8484	-0.1544	0.1132	-0.0037	0.6031	-0.0299	-0.0152	0.6928**
100-seed wt. (g)	P	0.0350	-0.0093	-0.0013	0.0118	0.1317	0.2813	0.0319	0.0162	-0.0013	0.2605	0.0180	-0.0305	0.7439**
	G	0.3646	-0.8996	0.0198	0.2388	-0.5359	1.0809	-0.1688	0.1450	-0.0051	0.7091	-0.0751	-0.0556	0.8182**
Cob length (cm)	P	0.0186	-0.0060	-0.0100	0.0087	0.1005	0.1711	0.0524	0.0146	-0.0011	0.2840	0.0222	0.0109	0.6658**
	G	0.2139	-0.6010	0.1241	0.1902	-0.4256	0.7367	-0.2477	0.1061	0.0028	0.8428	-0.1171	0.0213	0.8463**
Cob girth (cm)	P	0.0314	-0.0089	-0.0093	0.0095	0.1081	0.2075	0.0348	0.0219	-0.0026	0.2342	0.0151	-0.0338	0.6078**
	G	0.4402	-1.0412	0.1136	0.2363	-0.5265	1.0684	-0.1791	0.1468	-0.0083	0.7468	-0.0839	-0.0819	0.8312**
Kernel rows/ear	P	0.0221	-0.0059	-0.0149	0.0037	0.0404	0.0543	0.0085	0.0083	-0.0067	0.0508	-0.0038	-0.0173	0.1394
	G	0.4052	-0.9570	0.2459	0.0838	-0.1734	0.3773	0.0475	0.0843	-0.0145	0.1724	0.0110	-0.0830	0.1996
Grains/ row	P	0.0336	-0.0093	-0.0077	0.0115	0.1130	0.2071	0.0421	0.0145	-0.0010	0.3538	0.0200	-0.0132	0.7643**
	G	0.3626	-0.9064	0.0598	0.2236	-0.4493	0.8361	-0.2278	0.1196	-0.0027	0.9167	-0.0804	-0.0204	0.8314**
Protein content (%)	P	0.0065	-0.0023	-0.0015	0.0024	0.0243	0.0837	0.0193	0.0055	0.0004	0.1171	0.0604	0.0269	0.3427**
	G	0.0618	-0.2087	0.0029	0.0491	-0.1043	0.4142	-0.1480	0.0628	0.0008	0.3760	-0.1961	0.0523	0.3630**
Tryptophan content (%)	P	-0.0099	0.0023	-0.0034	-0.0013	-0.0097	-0.0536	0.0036	-0.0046	0.0007	-0.0291	0.0101	0.1602	0.0653
	G	-0.1074	0.2463	0.0306	-0.0253	0.0384	-0.2220	-0.0194	-0.0444	0.0044	-0.0692	-0.0379	**0.2707**	0.0647

Residual effect (P) = 0.5336, (G) = 0.3804, * = Significant at 5% level, ** = Significant at 1% level plant height (0.1902), 100-seed weight (0.7367), cob girth (0.1061), kernel rows per ear (0.0028), grains per row (0.8428) and tryptophan content (0.0213). Cob girth showed significant positive association (0.8312) with grain yield per plant and it also revealed positive direct effect (0.1468). This trait indirectly contributed to grain yield per plant via positive path values of 50% pollen shed (0.4402), 75% maturity (0.1136), plant height (0.2363), 100-seed weight (1.0684) and grains per row (0.7468). Kernel rows per ear revealed positive correlation (0.1996) with grain yield per plant. However, it had negative direct effect (-0.0145) on grain yield per plant. This character indirectly contributed to the grain yield per plant via days to 50% pollen shed (0.4052), 75% maturity (0.2459), plant height (0.0838), 100-seed weight (0.3773), cob length (0.0475), cob girth (0.0843), grains per row (0.1724) and protein content (0.0110).

Significant and positive association was noticed for grains per row (0.8314) with grain yield per plant alomg with positive direct effect (0.9167). This character indirectly contributed to the grain yield per plant via days to 50% pollen shed (0.3626), 75% maturity (0.0598), plant height (0.2236), 100-seed weight (0.8361) and cob girth (0.1196). Negative direct effect was found for protein content (-0.1961), whereas it had positive association (0.3630). Positive path values of indirect effects were noticed for days to 50% pollen shed (0.0618), 75% maturity (0.0029), plant height (0.0491), 100- seed weight (0.4142), cob girth (0.0628), kernel rows per ear (0.0008), grains per row (0.3760) and tryptophan content (0.0523). Tryptophan content showed positive association (0.0647) with grain yield per plant. Its direct effect was also registered positive path value (0.2707). This trait indirectly contributed via days to 50% silking (0.2463), 75% maturity (0.0306), cob placement height (0.0384) and kernel rows per ear (0.0044) towards grain yield per plant. A residual effect was found to be 0.53 and 0.38 at phenotypic and genotypic levels, respectively. This indicated that other attributing traits were also important and may play a crucial role in quality protein maize improvement. Perusal of the analysis of variance revealed significant differences among hybrids for yield and morphological traits. Similar results were reported by Aman *et al*. (2016), Hussain *et al*. (2016), Lal and Singh (2014) and Tullu (2014).

In the present investigation the values of PCV was higher than GCV for all the traits studied indicated the influence of environment to some degrees in the phenotypic expression of traits which was also observed by Nayaka *et al*. (2015) and Rahman *et al*. (2015). The estimates of GCV and PCV were noted high for grain yield per plant which is in consonance with Rahman *et al*. (2015) and Reddy *et al.* (2013). The maize hybrids had sufficient variability with regard to grain yield per plant thus genetic improvement could be achieved through selection for this trait and its critical role in predicting the gains from selection. Low GCV and PCV values were observed for all the traits except grain yield per plant and this could probably due to the presence of both positive and negative alleles leading to low genetic variation. The above findings are in accordance with the findings of Kanagarasu *et al.* (2013) and Alvi *et al.* (2003).

Correlation is also an important measurement indicating traits that should be given importance to increase yield. Ofori *et al.* (2015) showed that grain yield had a highly positive correlation with plant height, cob placement height, cob length, cob girth and grains per row. Similar results were also observed by Khan *et al.* (2015), Kinfe *et al.* (2015), Tullu *et al.* (2014) and Sujirihati *et al.* (2003) which are in conformation with the present study. Aziz *et al.* (1998) observed that 100-seed weight was significantly and positively correlated with grain yield per plant; Singode *et al.* (2014) and Bekele and Rao (2014) reported negative correlation of days to 50% pollen shed and silking with grain yield per plant which are in accordance with the present study. Zeeshan *et al*. (2013) observed that plant height was significantly and positively correlated with 100-seed weight; Rahman *et al*. (2015) observed positive significant correlation of plant height with yield per plant and cob girth with cob length which is in consonance with the present study. The positive relationships observed in this study indicate that favourable genes controlling these traits could be utilized for the improvement of the population sources in maize breeding programs (Sujiprihati *et al*., 2003). Thus, the information on correlations among traits remains crucial in improving the efficiency of breeding programs by employing the appropriate selection indices in cultivar or varietal improvement.

The path analysis provides an effective measure of direct and indirect causes of association and depicts the relative importance of each factor involved in contributing to the final product. It showed that traits like, days to 50% silking, 100-seed weight, grains per row and plant height have high positive direct effect towards grain yield which are in consonance with Kinfe *et al*. (2015), Kumar *et al.* (2011), Palia (2013), Pavan *et al.* (2011) and Geetha and Jayaraman (2000). 100-seed weight revealed high direct effect on grain yield per plant. Similar results were also obtained by Kumar *et al.* (2011), Pavan *et al.* (2011) and Singhal *et al.* (2006). Tullu (2014) observed high direct effect of grains per row on grain yield. The high direct effects of these traits appeared to be the main reason for their strong association with grain yield. Hence, direct selection for days to 50% silking, 100-seed weight, grains per row and plant height can play an important role in increasing the grain yield per plant. Traits having strong relationship with grain yield can be used for indirect selection to improve grain yield because grain yield can be simultaneously improved along with the traits for which it showed strong relationship.

Considering all the parameters together it can be suggested that the characters like days to 50% silking, 100-seed weight, grains per row, plant height and grain yield per plant may be given due importance in selection during QPM breeding programme.

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References

Al-Jobouri, H.A., Miller, P.A. and Robinson, H.F.: Genotypic and environment variances and covariance in upland cotton cross of interspecific origin. *Agron. J.,* **50**: 633-636 (1958).

Aman, J., Bantte, K., Alamerew, S. and Tolera, B.: Evaluation of quality protein maize (*Zea mays* L.) hybrids at Jimma, Western-Ethiopia. *J. Forensic Anthropol*., **1**: 101 (2016).

Anonymous: The State of Food Insecurity in the World 2012. Strengthening the enabling environment for food security and nutrition.Food and Agriculture Organization, Rome (2012).

Anonymous: The State of Food Insecurity in the World 2014. Strengthening the enabling environment for food security and nutrition.Food and Agriculture Organization, Rome (2014).

Anonymous: Annual Progress Report Rabi Maize 2014. All India Coordinated Research Project on Maize. Indian Institute of Maize Research, New Delhi, India (2015).

Anonymous: World agricultural production. Foreign Agricultural Service, USDA (2015).

AOAC: Official methods of analysis of the association of official agricultural chemists, Washington DC, p. 744-745 (1965).

Aziz, K., Rehman, A. and Rauf, A.: Heritability and interrelationship for some plant traits in maize single crosses. *Pak. J. Biol. Sci.,* **1**: 313-314 (1998).

Bekele, A. and Rao, T.N.: Estimates of heritability, genetic advance and correlation study for yield and it's attributes in maize (*Zea mays* L.). *J. Plant Sci*., **2**: 1-4 (2014).

Burton, G.W. and De Vane, E.W.: Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated colonal material. *Agron. J*., **45**: 478-481(1953).

Crow, J.F. and Kermicle, J.: Oliver Nelson and quality protein maize. *Genetics,* **160:** 819-821 (2002).

Dewey, D.R. and Lu, K.H.: A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.,* **51**: 510-515 (1959).

FAO: Maize in human nutrition, Rome, Italy, (1992).

Geetha, K. and Jayaraman, N.: Path analysis in maize (*Zea mays* L.). *Agric. Sci. Dig.,* **20**: 60-61 (2000).

Hussain, N., Rehman, H.B. and Khan F.: Phenotypic and genotypic association between maturity and yield traits in maize hybrids (*Zea mays* L.). *Afr. J. Agric. Food Sci.,* **4:** 157-160 (2016).

Kanagarasu, S., Nallathambi, G., Ganesan, K.N. and Kannan, S.: Genetic variability and association analysis for yield and its components in single cross hybrids of maize (*Zea mays* L.). *Electron. J. Plant Breed.,* **4**: 1319-1324 (2013).

Khan, K.M., Ali, S., Iqbal, M., Khan, A., Hussain, I., Khan, S.A., Khan, S.M. and Ali, I.: Genetic variation and correlation studies in maize testcrosses under the agro climatic condition of Nowshera. *Int. J. Biosci*., **7**: 57-64 (2015).

Kinfe, H., Alemayehu, G., Wolde, L. and Tsehaye, Y.: Correlation and path coefficient analysis of grain yield and yield related traits in maize (*Zea mays* L.) hybrids, at bako, Ethiopia. *J. Biol. Agric. and Healthcare.,* **5**: 44-52 (2015).

Kumar, T.S., Reddy, D.M., Reddy, K.H. and Sudhakar, P.: Targeting of traits through assessment of interrelationship and path analysis between yield and yield components for grain yield improvement in single cross hybrids of maize (*Zea mays* L.). *Int. J. Appl. Biol. Pharm.,* **2**: 123-129 (2011).

Lal, M. and Singh, D.: Studies of variability using morphological and quality traits in quality protein maize (*Zea mays* L.). *Electron. J. Plant Breed.,* **5**: 526-530 (2014).

Mertz, E.T., Bunathan, J.R. and Misra, P.S.: In Protein Quality, Agric Experiment Stn. Bull No. 70 Purdue University, USA: 11 (1975).

Mertz, E.T.: Thirty years of *opaque2* maize. In: Quality Protein Maize 1964-1994. Proceedings of the international symposium on quality protein maize (BA Larkins and ET Mertz, eds.). EMBRAPA/CNPMS, Sete Lagoas, MG, Brazil, p. 1-9 (1994).

Nayaka, M.P., Lambani, N., Sandhya and Marker., S.: genetic variability and heritability studies in the maize genotypes. *Int. J. Tropical Agric.,* **33**: 1987-1990 (2015).

Ofori, A.P., Ofori K., Obeng-Antwi, K., Tengan, K.M.L., Agyeman, A. and Badu-Apraku, B.: Genetic analysis of single cross quality protein maize (QPM) hybrids. *J. Plant Breed. Crop Sci.,* **7**: 251-255 (2015).

Osborne, T.B. and Mendel, L.B.: Nutritive properties of the proteins of the maize kernel. *J. Biol. Chem*., **18**: 1-16 (1914).

Palia, N.: Analysis of genetic diversity in maize germplasm (*Zea mays* L.) using morphological and molecular markers. MSc Thesis. Department of Crop Improvement, CSK HPKV, Palampur, India. p. 136 (2013).

Parsad, R., Gupta, V.K., Batra, P.K., Satpati, S.K. and Biswas, P.: á-Designs. IASRI, New Delhi (2007).

Pavan, R. Lohithaswa, H.C. Wali, M.C. Prakash, G. and Shekara, B.G.: Correlation and path coefficient analysis of grain yield and yield contributing traits in single cross hybrids of maize (*Zea mays* L.). *Electron. J. Plant Breed.,* **2**: 253-257 (2011).

Prasanna, B.M., Vasal, S.K., Kassahun, B. and Singh, N.N.: Quality protein maize. *Curr. Sci.*, **81**: 1308-1319 (2001).

Rahman, S., Mia, M.M., Quddus, T., Hassan, L. and Haque, M.A.: Assessing genetic diversity of maize (*Zea mays* L.) genotypes for agronomic traits. *Res. Agric. Livest. Fish*., **2**: 53-61 (2015).

Reddy, V.R., Jabeen, F., Sudarshan, M.R. and Rao, A.S.: Studies on genetic variability, heritability, correlation and path analysis in maize (*Zea mays* L.) over locations. *Int. J. Appl. Biol. Pharm.,* **5**: 195-199 (2013).

Singhal, N., Verma, S.S., Baskheti, D.C. and Kumar, A.: Heritability, genetic advance, correlation and path-coefficient estimation in high quality protein maize (*Zea mays* L.). *Asian J. Plant Sci*., **1**: 54-56 (2006).

Singode, A., Singh, K.P., Srivastava, E., Guleria, S.K., Devlash, R., Dar, Z.A., Lone, A.A., Ahmad, B. and Mahajan, V.: Heterosis and correlation deviations in maize under different agro ecologies. *J. Genet*., **74**: 438-443 (2014).

Sujiprihati, S. Saleh, G.B. and Ali, E.S.: Heritability, performance and correlation studies on single cross hybrids of tropical maize. *Asian J. Plant Sci*., **2**: 51-57 (2003).

Tullu, B.N.: Correlation and path coefficients analysis studies among yield and yield related traits of quality protein maize (QPM) inbred lines. *Int. J. Plant Breed. Crop Sci*., **1**: 6-17 (2014).

Vasal, S.K.: Quality protein maize: Overcoming the hurdles. *J. Prod. Agric.,* **6**: 193-227 (2002).

Villegas, E.: Factors limiting quality protein maize (QPM) development and utilization. *In*: Quality Protein Maize: 1964-1994. Proceedings of the international symposium on quality protein maize (BA Larkins and ET Mertz eds.). Sete Lagoas, MG, Brazil, p. 79-86 (1994).

Yue, D.R.: Speeding up science and technology innovation to enhance development of maize industry. *J. Maize Sci*., **14**: 1-3 (2006).