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Research Note

Assessment of association between yield and quality traits in Quality Protein Maize (QPM)

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Abstract
An investigation was carried out with 61 genotypes (42 crosses, 14 lines, 3 testers and 2 checks) to assess trait association, Experiments were laid out in Randomized Block Design with three replications during 2021, in three environments namely*, pre-kharif* (date of sowing: 15th May) - E_1, *kharif* (date of sowing: 30th June) - E_2 and *post-kharif* (date of sowing: 15th August)- E_3. Analysis of character association based on the observations recorded on yield, yield contributing and biochemical traits in the three environments revealed that ear height, kernel rows per ear, kernels per row, 1000- grain weight, cob length, cob girth and kernel vitreosity displayed a positive and highly significant correlation with grain yield at both genotypic and phenotypic levels. High direct effect on grain yield was exerted by ear height, kernel rows per ear, kernels per row, 1000- grain weight and cob length. The selection of these traits could improve the crop yield.

Keyword: Maize, QPM, Correlation, Path

Maize (*Zea mays* L.) is an important staple crop of the world next to wheat and rice (Singh *et al.* (2021). It is known as the “Queen of cereal crops” and is used as a model crop owing to its high production potential (Singh *et al.,* 2023). The world population is expected to continue to grow as the estimated population of 7.2 billion in 2014 (Behulah *et al.,* 2018) is expected to grow to nine billion by 2050. Increased production of Maize and its alternate utilization in food channels can reduce the pressure on wheat, rice and its imports. Maize crop serves as a source of basic raw material for a number of industries *viz*., starch, protein, oil, alcoholic beverages, food, sweeteners, cosmetics and biofuels. Maize being a C_4 plant is physiologically more efficient, has higher grain yield and has wider adaptation over a wide range of environmental conditions. Morphologically maize exhibits greater diversity of phenotypes than any other grain crop and is extensively grown in temperate, subtropical and tropical regions of the world. Grain yield, without doubt, is the most economically important character of maize; the major reason for its improvement is the focus of maize breeding programs. However, grain yield is a complex trait; a product of many components which subjects it to high environmental influence. Direct selection for

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yield *per se* may not be the most efficient method for its improvement, but indirect selection for other yield-related characters, which are closely associated with yield and high heritability estimates will be more effective (Mahmood *et al.,* 2004). For developing suitable selection strategies, knowledge of the presence of genetic variability on available germplasm for yield and its related components and heritable difference among cultivars, within a population is always desirable in plant breeding programs (Swapnil *et al.,* 2021). Also, a study on the association of various attributing characters to yield is essential, for accumulating the optimum contribution of such traits to yield. Genetic correlation analysis is a handy technique that elaborates the degree of association among important quantitative traits. Association studies could lead plant breeders in the selection of traits contributing toward the character(s) of concern, and ultimately their improvement through hybridization. For formulating selection indices for genetic improvement of yield, the cause and effect of the trait are very essential and can be done by path analysis. Path analysis shows direct and indirect effects of cause variables on effect variables. In this method, the correlation coefficient between two traits is separated into the components which measure the direct and indirect effects. Generally, this method provides more information among variables than do correlation coefficients since this analysis provides the direct effects of specific yield components on yield, and indirect effects via other yield components. In order to develop promising maize genotypes with higher yield potential, it is essential to know the correlation among different traits, especially with grain yield, which is the most important ultimate objective in any breeding program. It is necessary to have a good knowledge of those characters that have a significant correlation with yield because those characters can be used as indirect selection criteria to enhance the mean performance of varieties in a new plant population. Keeping this in view, the present study was, therefore, designed to identify suitable selection criteria for future maize breeding programs.

The present research was carried out in the Maize section of the Department of Plant Breeding and Genetics at Bihar Agricultural College, Sabour during *rabi,* 2020-21 and *kharif,* 2021. Fifty genotypes of Quality Protein Maize (QPM) were grown during *rabi* 2019-20 at Maize section farm, Bihar Agricultural College, Sabour and they were studied for diverse morphological traits. The seventeen genotypes that performed well were selected and crossed in line x tester fashion. The 42 F_1s (crosses) were evaluated along with 14 lines, 3 testers and two standard checks in randomized block design with three replications in three different environments *viz., pre-kharif* (date of sowing: 15th May) - E_1, *kharif* (date of sowing: 30th June) - E_2 and *post-kharif* (date of sowing: 15th August)- E_3. The association among yield and yield attributing traits was studied using *Windowstat 9.3* version software. The complete information of genotypes are provided in **Table 1**.

Table 1. Details of lines, testers and checks used in experiment

Code	Genotypes	Pedigree
L_1	VL109404	Pop6934(Temp YFQPM)-B-42-B*7
L_2	VL109353	G34QC24-BBB-42-B*9
L_3	VL1017524	P69(58969Q)-BBB-25-B*6
L_4	VL109359	P61C1-BBB-41-B*9
L_5	VL109584	CLQ-RCYQ41-BB-2-B*7
L_6	VL1016010	(CLQ-RCWQ01 xP73TLC3# -153-1-1-##-B)-1-69-2-B*5
L_7	VL1016951	(CML 161 x165)-F2-52-2-1-B-1-1-BB-B1
L_8	VL109282	(CML 161 x CLQ-RCY Q31)-B-3-6-BB-3-B*9
L_9	VL1016416	(CLQ-RCY Q31 xCLQ-RCYQ35)-B-3-1-BBB-B1
L_{10}	VL1016422	(CMQ-RCYQ31 x CLQ-RCYQ49) = (CML 176xCL- G2501)-B-55-2-1-B)-B-10-3-B*5
L_{11}	VL111366	(CML 150 x CLG2501)-B-31-1-B-1-BBB/CML 193-BB)-B-2-BB(Q)-B*4
L_{12}	VL192367	(QPM Syn 2016)-18-1-2-B1
L_{13}	VL121100	([CL-G2501 x CML-170]-B-24-1-1-2-BBB/CML 150 x CL-03618)-B-16-1-1-1-B*5)-B-4-BB(Q)-BB-B1-B1-BBB
L_{14}	VL109378	Pool 17C8(TEYFQPM)-B-117-B*10
T_1	VL192366	(QPM Syn 2016)-16-2-3-B
T_2	VP-191	QPM Het Syn 171-#1
T_3	VQL-1	CM 212 x CML180
C_1	HQPM-5	HKI 163 x HKI 161
C_2	VQPM-9	VQL-1 x VQL-2

Pooled character association through correlation coefficient analysis: Genotypic correlations reveal the existence of real associations, whereas phenotypic correlations may occur by chance. Significant phenotypic correlations without significant genotypic associations are of no value. If the genotypic correlation is significant and phenotypic is not, it means that the existing real association is masked by environmental effects. The genotypic and phenotypic correlation coefficients for all the eighteen characters are presented in **Table 2**.

The results indicated that days to 50% tasselling revealed a positive and significant genotypic as well as phenotypic correlation with the characters *viz.,* days to 50% silking (0.938) and days to 75% brown husk (0.531). This clearly indicates that as the number of days taken for tasselling and silking increases, the number of days for brown husk also increases. However, it displayed a significantly negative correlation with characters like anthesis silking interval (-0.693) and kernel starch content (-0.482). The phenotypic correlation study revealed a positive and significant correlation of days to 50% tasselling with plant height (0.463), cob girth (0.435), kernel protein content (0.734), tryptophan content (0.484), lysine content (0.483) and kernel vitreosity (0.447). Similar observation was reported by several researchers Amegbor *et al.* (2022), Subba *et al.* (2022), Khan and Mahmud, (2021), Singh *et al.* (2020), Verma *et al.* (2020) **and** Prakash *et al.* (2019)**.** These observations indicate that improvements in each of the traits would lead to overall improvements of the genotypes. Such correlations help in making reasonable decisions in selecting traits controlled by multiple genes. A positive and significant association of days to 50% silking with days to 75% brown husk (1.052) and a significantly negative correlation with kernel starch content (-0.595) and kernel oil content (-0.460) at the genotypic level was observed. With the increasing tasselling and silking days, there is a decrease in the starch and oil content which may be due to prolonged vegetative growth and hence lesser starch and oil accumulation in the kernels during the reproductive stages. The phenotypic correlation study showed significant and positive association with days to 75% brown husk (0.829), plant height (0.491), cob girth (0.428), kernel starch content (0.511), kernel protein content (0.764), tryptophan content (0.488), lysine content (0.487) and kernel vitreosity (0.463). The genotypic correlation study revealed a positive and significant association of anthesis silking interval with days to 75% brown husk (0.780). Days to 75% brown husk displayed a positive and significant phenotypic correlation with plant height (0.525), cob girth (0.413), kernel starch content (0.578), kernel protein content (0.709), tryptophan content (0.486), lysine content (0.486) and kernel vitreosity (0.520). Similar findings were reported elsewhere **Izzam** *et al.* **(2017)**, Matin *et al.* (2017), Patil *et al.* (2016), Kinfe and Tsehaye, (2015), Kumar *et al.* (2014), Chukwu *et al.* (2013), Reddy *et al.* (2013), *Pinnisch et al.* (2012), Amegbor *et al.* (2022), Subba *et al.* (2022), Khan and Mahmud, (2021) and Singh *et al.* (2020).

Plant height depicted a positive and significant correlation with ear height (0.402). On the other hand, the phenotypic correlation study revealed a positive and significant correlation with ear height (0.470), kernel protein content (0.524), tryptophan content (0.468) and lysine content (0.466). The increased plant height contributed for increase in the ear height thereby accommodating more protein, lysine and tryptophan content ultimately resulting in improved seed quality.

Ear height depicted a positive and significant correlation with characters *viz.,* kernels row per ear (0.628), kernels per row (0.582), 1000-grain weight (0.652), cob length (0.489), cob girth (0.526) and grain yield (0.645). In the present material under study, increased plant height contributed to an increase in the length of ear thus accommodating more kernel rows and more number of kernels per row ultimately resulting in more kernel yield. The significant correlation indicates that there is a strong association between above traits and grain yield. Therefore, selection for these characters will be rewarding in yield improvement (Pranay *et al.,* 2022). However, it displayed a non-significant correlation for the rest of the characters at the genotypic level. The genotypic and phenotypic correlation study depicted a positive and significant association of kernel rows per ear with characters *viz.,* kernels per row (0.899, 0.881), 1000-grain weight (0.869, 0.845), cob length (0.880, 0.854), cob girth (0.816, 0.792), kernel vitreosity (0.551, 0.872) and grain yield (0.918, 0.872).

Kernels per row depicted a positive and significant correlation with characters *viz.,*1000 grain weight (0.918, 0.897), cob length (0.968, 0.952), cob girth (0.634, 0.754), kernel vitreosity (0.634, 0.616) and grain yield (0.919, 0.896) at the genotypic and phenotypic level, respectively. The overall grain yield is expected to increase with the increase in number of kernels per row. To accommodate more kernels in a row, cob length as well as cob girth is expected to increase.

Similarly, the study depicted a positive and significant association of 1000-grain weight with characters *viz.,* cob length (0.863, 0.828), cob girth (0.773, 0.737) and grain yield (0.858, 0.844) at genotypic and phenotypic level, respectively. Heavy-weighted kernels will positively increase the grain yield.

A positive and significant association of cob length with characters *viz.,* cob girth (0.747, 0.749), kernel vitreosity (0.645, 0.651) and grain yield (0.902, 0.858) at the genotypic level and phenotypic level, respectively. Longer and vitreous cob will certainly increase the grain yield as it will accommodate more grains in the cob.

Table 3. Pooled character association through correlation coefficients analysis for eighteen characters of QPM

	DTS	ASI	DBH	PHT	EHT	KRE	KPR	GWT	COL	COG	KSP	KOP	KPP	KTP	KLP	KVT	GRY
DTT	0.979** 0.938 **	0.102 -0.693**	0.815** 0.531**	0.463* -0.260	0.271 0.014	0.259 -0.01	0.231 0.036	0.204 0.108	0.274 0.01	0.435* 0.159	0.486* -0.482*	0.296 -0.262	0.734** -0.126	0.484* 0.02	0.483* 0.017	0.447* -0.300	0.154 0.159
DTS		0.301 -0.397	0.829** 1.052**	0.491* -0.293	0.281 0.027	0.267 -0.01	0.241 0.069	0.218 0.167	0.295 0.051	0.428* 0.118	0.511** -0.595**	0.283 -0.460*	0.764** -0.119	0.488* -0.018	0.487* -0.022	0.463* -0.366	0.154 0.187
ASI			0.234 0.780**	0.229 0.081	0.102 0.02	0.093 0.018	0.095 0.049	0.109 0.062	0.158 0.08	0.052 -0.175	0.222 0.038	-0.005 -0.262	0.296 0.084	0.116 -0.091	0.118 -0.090	0.201 0.033	0.028 -0.03
DBH				0.525** 0.503**	0.261 0.211	0.278 0.068	0.213 0.155	0.166 0.096	0.281 0.158	0.413* -0.01	0.578** 0.842**	0.378 0.265	0.709** 1.632**	0.486* 0.310	0.486* 0.310	0.520** 0.533**	0.105 -0.066
PHT					0.470* 0.402*	0.162 -0.033	0.06 -0.134	0.078 -0.055	0.081 -0.165	0.205 -0.097	0.345 -0.139	0.130 -0.199	0.524** 0.01	0.468* 0.217	0.466* 0.214	0.292 -0.117	0.017 -0.068
EHT						0.629** 0.628**	0.618** 0.582 **	0.635** 0.652**	0.532** 0.489*	0.590** 0.526**	0.204 -0.003	0.126 -0.002	0.224 -0.067	0.151 -0.01	0.150 -0.009	0.347 0.247	0.607** 0.645**
KRE							0.881** 0.899**	0.845** 0.869**	0.854** 0.880**	0.792** 0.816**	0.221 0.007	0.338 0.246	0.206 -0.102	0.177 0.012	0.181 0.017	0.581** 0.551**	0.872** 0.918**
KPR								0.897** 0.918**	0.952** 0.968**	0.754** 0.757**	0.218 0.066	0.226 0.132	0.192 -0.038	0.151 0.027	0.154 0.031	0.616** 0.634**	0.896** 0.919**
GWT									0.828** 0.863**	0.737** 0.773**	0.109 -0.046	0.142 0.059	0.145 -0.044	0.141 0.043	0.144 0.047	0.577** 0.609**	0.844** 0.858**
COL										0.749** 0.747**	0.249 0.037	0.283 0.172	0.262 -0.015	0.202 0.051	0.205 0.055	0.651** 0.645**	0.858** 0.902**
COG											0.290 -0.003	0.398 0.287	0.314 -0.114	0.189 -0.059	0.191 -0.056	0.541** 0.423*	0.751** 0.817**
KSP												0.364 0.095	0.479* -0.347	0.199 -0.327	0.197 -0.328	0.360 -0.105	0.147 0.105
KOP													0.223 -0.355	0.149 -0.142	0.152 -0.139	0.187 -0.115	0.271 0.250
KPP														0.632** 0.397	0.630** 0.394	0.446* -0.189	0.066 -0.06
KTP															0.999** 0.999**	0.288 -0.065	0.027 -0.045
KLP																0.297 -0.06	0.031 -0.04
KVT																	0.462* 0.513**

*, ** significance at 5 % and 1 % level of probability, respectively

For each character the upper rows and lower rows are the phenotypic and genotypic correlation coefficients, respectively

DTT: Days to 50% tasseling, DTS: Days to 50% silking, ASI: Anthesis Silking Interval, DBH: Days to 75 % brown husk, PHT: Plant height, EHT: Ear height, KRE: Kernel row per ear, KPR: Kernels per row, GWT: 1000 grain weight, COL: Cob length, COG: Cob girth, GRY: Grain yield, KSP: Kernel starch content, KOP: Kernel oil content, KPP: Kernel protein content, KTP: Tryptophan content, KLP: Lysine content, KVT: Kernel vitreosity

Cob girth revealed a non-significant genotypic correlation with all the characters studied. The correlation study depicted a positive and highly significant genotypic and phenotypic association of grain yield with characters *viz.,* ear height (0.607, 0.645), kernels row per ear (0.872, 0.918), kernels per row (0.896, 0.919), 1000 grain weight (0.844, 0.858), cob length (0.858, 0.902), cob girth (0.751, 0.817) and kernel vitreosity (0.462, 0.513). Higher number of kernels rows with a greater number of heavier kernels, longer and broader cobs directly increases the grain yield. These are the important yield attributing traits which can be aimed for simultaneous improvement in yield. Similar results were reported by earlier workers *viz.,* Muneeb *et al.,* (2013), Selvaraj and Nagarajan (2011) and Jaghav *et al.,* (2009).

Kernel starch content revealed a non-significant genotypic correlation with all the characters studied. However, a phenotypic correlation study revealed a positive and significant correlation with kernel protein content (0.479). Kernel oil content revealed a non-significant genotypic as well as phenotypic correlation with all the characters studied. Kernel protein content revealed a non-significant genotypic correlation with all the characters studied. However, phenotypic correlation displayed a positive and significant correlation with tryptophan content (0.632), lysine content (0.630) and kernel vitreosity (0.446). The correlation study depicted a positive and significant association of tryptophan content with lysine content (0.999, 0.630) at both the genotypic and phenotypic levels. This is in agreement with the fact that the lysine content is approximately four times more than the tryptophan content. Lysine content revealed a non-significant genotypic as well as phenotypic correlation coefficient with all the characters studied. Kernel vitreosity depicted a positive and significant correlation with grain yield (0.513, 0.462) at both the genotypic and phenotypic levels, respectively. Similar finding was reported earlier by Amegbor *et al.* (2022), Subba *et al.* (2022), Khan and Mahmud, (2021), Singh *et al.* (2020), Verma *et al.* (2020), Prakash *et al.* (2019), Roy *et al.* (2018), Barman *et al.* (2018), Izzam *et al.* (2017), Matin *et al.* (2017), Patil *et al.* (2016), Kinfe and Tsehaye, (2015), Kumar *et al.* (2014), Chukwu *et al.* (2013), Reddy *et al.* (2013) and *Pinnisch et al.* (2012).

Pooled path coefficient analysis: The correlation study revealed that the traits *viz.,* ear height, kernel rows per ear, kernels per row, 1000 grain weight, cob length, cob girth and kernel vitreosity displayed a positive and highly significant correlation with grain yield at both genotypic and phenotypic levels. The pooled genotypic and phenotypic path coefficient for all the traits has been depicted in **table 3 and 4**, **Fig. 1 and 2** respectively.

Ear height (0.168, 0.062) displayed a positive direct effect on grain yield at genotypic and phenotypic levels respectively. The indirect effect of ear height on grain yield was positive via all the traits studied at both genotypic and phenotypic levels except for some of the characters which displayed negative indirect effects at the genotypic level for traits like kernel starch content, kernel protein content, tryptophan content and lysine content. This implies that higher ear height leads to increased grain yield; the genotypic correlation between ear height and grain yield is predominately attributed to the direct effect of ear height on the grain yield per hectare. The results were in agreement with Hasan *et al.* (2021), Verma *et al.* (2020), Singh *et al.* (2020) and Jilo and Tulu, (2019). Kernel rows per ear (0.200, 0.296) showed a positive direct effect on grain yield at genotypic and phenotypic levels, respectively. The indirect effect of kernel rows per ear on grain yield was positive via all the characters at both genotypic and phenotypic levels except for some of the characters which displayed a negative indirect effect at the genotypic level via days to 50% tasseling, days to 50% silking, plant height and kernel protein content. Kernels per row (-0.014, 0.265) displayed a negative direct effect at the genotypic level and a positive direct effect on grain yield at the phenotypic level. The indirect effect of kernels per row on grain yield was negative via all the characters at the genotypic level except for some of the characters which displayed a positive indirect effect via plant height, kernel protein content, tryptophan content and lysine content. However, the indirect effect on grain yield was positive via all the characters studied at the phenotypic level. 1000- grain weight (0.013, 0.120) showed a positive direct effect on grain yield at genotypic and phenotypic levels, respectively. The indirect effect on grain yield was positive via all the characters at the genotypic level except for some of the characters which displayed negative indirect effects via plant height, kernel starch protein and kernel protein content. However, the indirect effect on grain yield was positive via all the characters studied at the phenotypic level. Cob length (0.680, 0.256) showed a positive direct effect on grain yield at genotypic and phenotypic levels, respectively. The indirect effect on grain yield was positive via all the characters at both genotypic and phenotypic levels except for some of the characters which displayed a negative indirect effect at the genotypic level via plant height and kernel protein content. Cob girth (0.076, 0.091) showed a positive direct effect on grain yield at genotypic and phenotypic levels, respectively. The indirect effect on grain yield was positive via all the characters at both genotypic and phenotypic levels except for some of the characters which displayed negative indirect effect at the genotypic level via anthesis silking interval, days to 75% brown husk, plant height, kernel protein content, tryptophan content and lysine content. Kernel vitreosity (-0.182, -0.113) displayed a negative direct effect at the genotypic and positive direct effect on grain yield at both genotypic and phenotypic levels, respectively. The indirect effect on grain yield was positive via all the characters at genotypic level except for some of the characters which displayed negative indirect effect via anthesis-silking interval, days to 75% brown

Table 3. Partitioning of genotypic correlation into direct and indirect effects by path analysis in Quality Protein Maize (QPM) for grain yield

	DTT	DTS	ASI	DBH	PHT	EHT	KRE	KPR	GWT	COL	COG	KSP	KOP	KPP	KTP	KLP	KVT
DTT	**65.594**	61.500	-45.435	34.822	-17.154	0.899	-0.674	2.336	7.083	0.658	10.476	-31.613	-17.204	-8.246	1.338	1.118	-19.696
DTS	-48.350	**-51.569**	20.556	-54.244	15.130	-1.399	0.258	-3.548	-8.616	-2.640	-6.092	30.673	23.737	6.156	0.948	1.133	18.882
ASI	-17.140	-9.863	**24.745**	19.312	2.009	0.508	0.435	1.220	1.541	1.983	-4.339	0.943	-6.492	2.071	-2.263	-2.228	0.810
DBH	0.015	0.029	0.021	**0.027**	0.014	0.006	0.002	0.004	0.003	0.004	0.000	0.023	0.007	0.045	0.009	0.009	0.015
PHT	-0.004	-0.005	0.001	0.008	**0.016**	0.006	-0.001	-0.002	-0.001	-0.003	-0.002	-0.002	-0.003	0.000	0.003	0.003	-0.002
EHT	0.002	0.005	0.003	0.037	0.067	**0.168**	0.105	0.098	0.109	0.082	0.088	-0.001	0.000	-0.011	-0.002	-0.002	0.041
KRE	-0.002	-0.001	0.004	0.014	-0.007	0.126	**0.200**	0.180	0.174	0.176	0.163	0.001	0.049	-0.021	0.003	0.004	0.110
KPR	-0.001	-0.001	-0.001	-0.002	0.002	-0.008	-0.012	**-0.014**	-0.013	-0.013	-0.010	-0.001	-0.002	0.001	0.000	0.000	-0.009
GWT	0.001	0.002	0.001	0.001	-0.001	0.008	0.011	0.012	**0.013**	0.011	0.010	-0.001	0.001	-0.001	0.001	0.001	0.008
COL	0.007	0.035	0.054	0.108	-0.112	0.332	0.598	0.658	0.587	**0.680**	0.508	0.025	0.117	-0.011	0.035	0.038	0.439
COG	0.012	0.009	-0.013	-0.001	-0.007	0.040	0.062	0.058	0.059	0.057	**0.076**	0.000	0.022	-0.009	-0.005	-0.004	0.032
KSP	-0.012	-0.015	0.001	0.021	-0.004	0.000	0.000	0.002	-0.001	0.001	0.000	**0.025**	0.002	-0.009	-0.008	-0.008	-0.003
KOP	0.015	0.026	0.015	-0.015	0.011	0.000	-0.014	-0.008	-0.003	-0.010	-0.016	-0.005	**-0.057**	0.020	0.008	0.008	0.007
KPP	0.002	0.001	-0.001	-0.020	0.000	0.001	0.001	0.001	0.001	0.000	0.001	0.004	0.004	**-0.012**	-0.005	-0.005	0.002
KTP	-0.201	0.181	0.901	-3.060	-2.137	0.089	-0.122	-0.264	-0.422	-0.503	0.578	3.224	1.403	-3.908	**-9.854**	-9.853	0.643
KLP	0.166	-0.214	-0.877	3.023	2.083	-0.086	0.170	0.304	0.456	0.538	-0.547	-3.211	-1.356	3.838	9.735	**9.736**	-0.585
KVT	0.055	0.067	-0.006	-0.097	0.021	-0.045	-0.101	-0.116	-0.111	-0.118	-0.077	0.019	0.021	0.034	0.012	0.011	**-0.182**
GRY	0.159	0.187	-0.030	-0.067	-0.068	0.646	0.919	0.920	0.858	0.903	0.817	0.105	0.251	-0.060	-0.045	-0.040	0.513
Partial R²	10.425	-9.654	-0.748	-0.002	-0.001	0.108	0.184	-0.013	0.011	0.614	0.062	0.003	-0.014	0.001	0.446	-0.393	-0.094

DTT: Days to 50% tasseling, DTS: Days to 50% silking, ASI: Anthesis Silking Interval, DBH: Days to 75 % brown husk, PHT: Plant height, EHT: Ear height, KRE: Kernel row per ear, KPR: Kernels per row, GWT: 1000 grain weight, COL: Cob length, COG: Cob girth, GRY: Grain yield, KSP: Kernel starch content, KOP: Kernel oil content, KPP: Kernel protein content, KTP: Tryptophan content, KLP: Lysine content, KVT: Kernel vitreosity

Table 4. Partitioning of phenotypic correlation into direct and indirect effects by path analysis in Quality Protein Maize (QPM) for grain yield

	DTT	DTS	ASI	DBH	PHT	EHT	KRE	KPR	GWT	COL	COG	KSP	KOP	KPP	KTP	KLP	KVT
DTT	**-0.649**	-0.636	-0.067	-0.529	-0.301	-0.176	-0.168	-0.150	-0.132	-0.178	-0.283	-0.315	-0.192	-0.477	-0.314	-0.313	-0.286
DTS	0.740	**0.755**	0.227	0.626	0.371	0.212	0.202	0.182	0.165	0.223	0.323	0.386	0.214	0.577	0.369	0.368	0.350
ASI	-0.018	-0.054	**-0.179**	-0.042	-0.041	-0.018	-0.017	-0.017	-0.020	-0.028	-0.009	-0.040	0.001	-0.053	-0.021	-0.021	-0.036
DBH	-0.104	-0.106	-0.030	**-0.128**	-0.067	-0.033	-0.035	-0.027	-0.021	-0.036	-0.053	-0.074	-0.048	-0.091	-0.062	-0.062	-0.066
PHT	-0.002	-0.002	-0.001	-0.002	**-0.004**	-0.002	-0.001	0.000	0.000	0.000	-0.001	-0.001	-0.001	-0.002	-0.002	-0.002	-0.001
EHT	0.017	0.017	0.006	0.016	0.029	**0.062**	0.039	0.038	0.039	0.033	0.037	0.013	0.008	0.014	0.009	0.009	0.021
KRE	0.077	0.079	0.028	0.082	0.048	0.186	**0.296**	0.260	0.250	0.253	0.234	0.065	0.100	0.061	0.052	0.054	0.172
KPR	0.061	0.064	0.025	0.057	0.016	0.164	0.234	**0.265**	0.238	0.253	0.200	0.058	0.060	0.051	0.040	0.041	0.164
GWT	0.025	0.026	0.013	0.020	0.009	0.076	0.101	0.108	**0.120**	0.099	0.088	0.013	0.017	0.017	0.017	0.017	0.069
COL	0.070	0.075	0.041	0.072	0.021	0.136	0.219	0.244	0.212	**0.256**	0.192	0.064	0.073	0.067	0.052	0.053	0.167
COG	0.040	0.039	0.005	0.038	0.019	0.054	0.072	0.069	0.067	0.068	**0.091**	0.026	0.036	0.029	0.017	0.017	0.049
KSP	0.008	0.008	0.004	0.009	0.005	0.003	0.004	0.003	0.002	0.004	0.005	**0.016**	0.006	0.008	0.003	0.003	0.006
KOP	0.011	0.011	0.000	0.015	0.005	0.005	0.013	0.009	0.006	0.011	0.015	0.014	**0.039**	0.009	0.006	0.006	0.007
KPP	-0.031	-0.032	-0.013	-0.030	-0.022	-0.010	-0.009	-0.008	-0.006	-0.011	-0.013	-0.020	-0.009	**-0.042**	-0.027	-0.027	-0.019
KTP	-0.381	-0.384	-0.092	-0.382	-0.368	-0.119	-0.139	-0.119	-0.111	-0.159	-0.149	-0.156	-0.117	-0.496	**-0.786**	-0.786	-0.226
KLP	0.341	0.344	0.083	0.343	0.329	0.106	0.128	0.109	0.102	0.145	0.135	0.139	0.107	0.445	0.706	**0.706**	0.206
KVT	-0.050	-0.053	-0.023	-0.059	-0.033	-0.039	-0.066	-0.070	-0.066	-0.074	-0.061	-0.041	-0.021	-0.051	-0.033	-0.033	**-0.113**
GRY	0.154	0.153	0.028	0.105	0.016	0.606	0.872	0.895	0.843	0.858	0.750	0.146	0.270	0.065	0.026	0.030	0.462
Partial R²	-0.100	0.116	-0.005	-0.013	0.000	0.037	0.258	0.238	0.101	0.220	0.068	0.002	0.010	-0.003	-0.021	0.021	-0.052

DTT: Days to 50% tasseling, DTS: Days to 50% silking, ASI: Anthesis Silking Interval, DBH: Days to 75 % brown husk, PHT: Plant height, EHT: Ear height, KRE: Kernel row per ear, KPR: Kernels per row, GWT: 1000 grain weight, COL: Cob length, COG: Cob girth, GRY: Grain yield, KSP: Kernel starch content, KOP: Kernel oil content, KPP: Kernel protein content, KTP: Tryptophan content, KLP: Lysine content, KVT: Kernel vitreosity

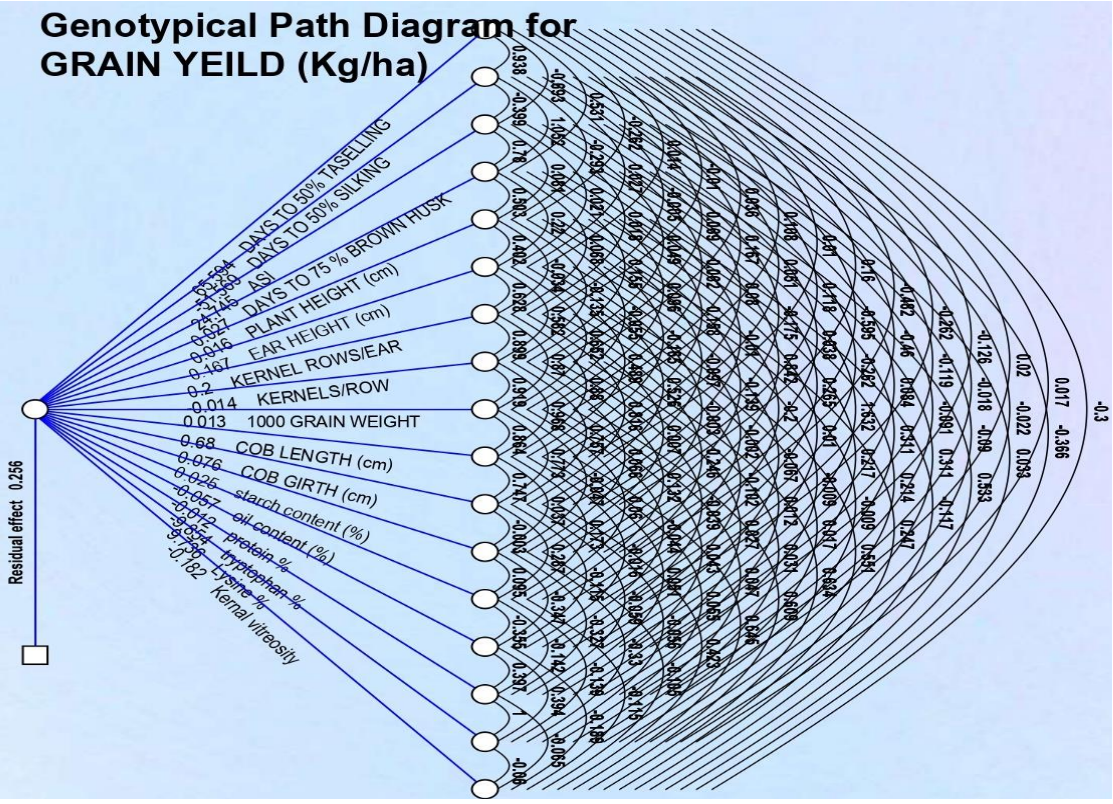

Fig. 1. Phenotypic path diagram for grain yield

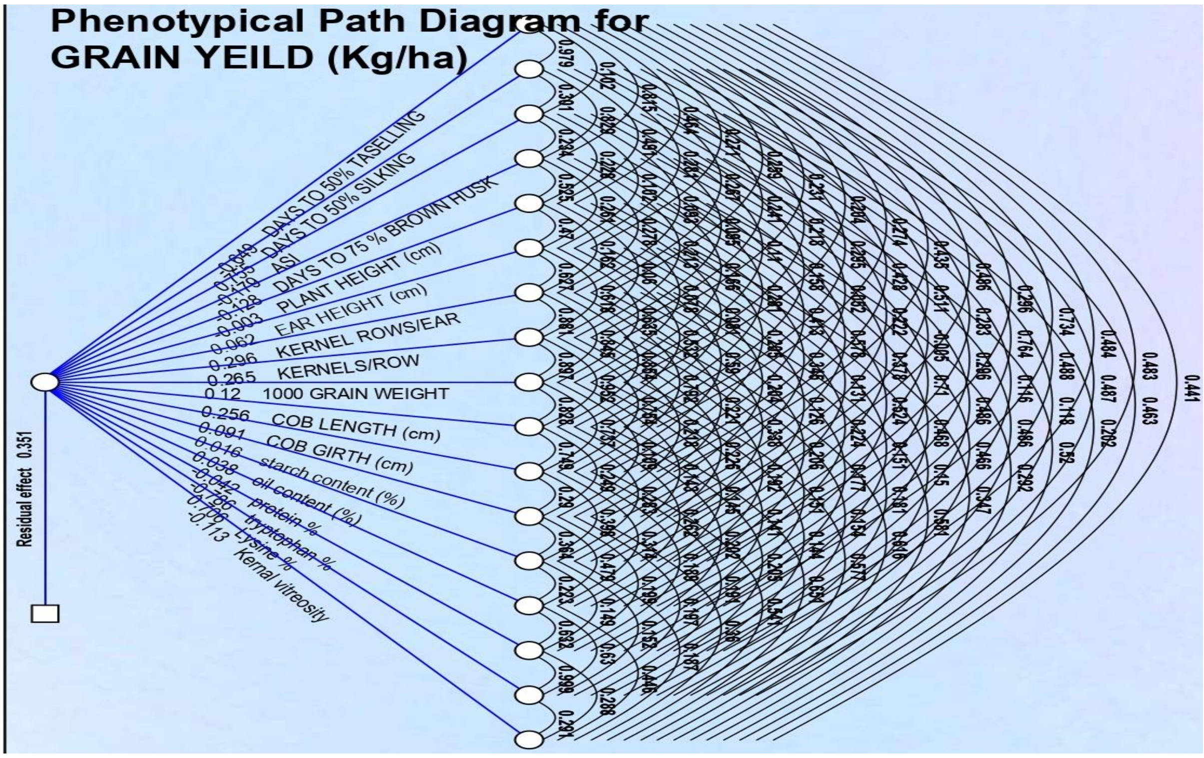

Fig. 2. Genotypic path diagram for grain yield

husk, ear height, kernel rows per ear, kernels per row, 1000- grain weight, cob length and cob girth. However, the indirect effect on grain yield was negative via all the characters studied at the phenotypic level. Similar findings were reported earlier by Hasan *et al.* (2021), Verma *et al.* (2020), Singh *et al.* (2020), Jilo *et al.* (2019), Beulah *et al.* (2018), Prasad *et al.* (2017), Pandey *et al.* (2017), Huda *et al.* (2016), Begum *et al.* (2016), Nataraj *et al.* (2014), Reddy *et al.* (2013) and Zarei *et al.* (2012).

Correlation coefficient analysis revealed that the traits *viz.,* ear height, kernel rows per ear, kernels per row, 1000 grain weight, cob length, cob girth and kernel vitreosity displayed a positive and highly significant correlation with grain yield at both genotypic and phenotypic levels. The positive correlation between the desirable characters leads to simultaneous improvement of both the characters. Path coefficient study depicts a high direct effect on grain yield for traits *viz.,* ear height, kernel rows per ear, kernels per row, 1000 grain weight and cob length. This means that the direct selection of these traits will be rewarding for yield improvement. The full potential of QPM hybrids could be realized if all these traits were incorporated into the genotype.

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