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Association Analysis for Nutritional Traits in Quality Protein Maize

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Abstract

Identification of elite Quality Protein Maize (QPM) inbreds is a pre-requisite for development of potential QPM hybrids. In the present investigation a set of 49 maize inbred lines were assessed for agro-economic and nutritional traits (total seed protein, lysine and tryptophan content). BQPM 3-4 had significantly highest yield potential (153.4g/Plant) followed by CLQRCY Q 40 (151.3g/plant) and BQPM 5-19(139.5g/plant) and HK1-191-1-2-5(131.2g/plant). While, BQPM 7-4 had shown tremendously high tryptophan and lysine content (0.96% and 3.82% respectively) followed by BQPM 10-9, BQPM 9-6 and BQPM 5-2. Inbreds rich in protein quantity are, in general, not superior in protein quality with regard to above essential amino acids owing to their inverse relationship. Plant height, cob length and number of grains per row maintained strong positive association with grain yield indicating their importance for genetic improvement of productivity in maize. However, seed yield had feeble positive association with protein content, and it negatively correlated with both tryptophan and lysine content indicating major limitation for development of nutritionally rich high yielding elite QPM inbreds for use in QPM hybrid development.

Introduction

Maize (*Zea mays* L.) is consumed by more than a billion people in many countries [1]. Globally, it has great yield potential and attained the leading position among cereals based on production as well as productivity. In India 77% of maize produced is used for human consumption, while only 2% is used as feed for animals. This indicates the importance of maize in India, and the role it plays in meeting the ever-increasing demand for food. Seed protein in maize serves as the important nutrient source for human and livestock. But, it is deficient in lysine and tryptophan [2]. Several spontaneous and induced mutations that affect amino acid composition in maize have been discovered. Among these, Quality Protein Maize (QPM) open up a vistas of research interests owing to its characteristic high lysine and tryptophan content. In recent years, conversion of elite maize inbred lines to QPM status is the main focus for development of parental inbreds to constitute potential QPM hybrids. In this context, study of genetic variation and nature of inter-relationship among agro-economic and nutritional traits would help to

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formulate appropriate selection strategy for identification of potential inbreds. Therefore, in the present investigation, an attempt was undertaken to gauge the extent of genetic variability and character association in a set of 49 inbreds of maize for agro-economic and important nutritional traits.

Materials and methods

The experimental materials used in the present investigation comprised of 49 inbreds developed from 41 maize populations received from Directorate of Maize Research, New Delhi; five populations from Agril. Research Station, Karnal, Haryana and three inbreds from CIMMYT, Mexico, USA. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Each inbred line was sown in two rows of 4 meter length with a spacing of 60cm x 25cm. Fertilizers were applied @ 120 kg N, 60 kg P_2O_5 and 60 kg K_2O / hectare in the form of Urea, SSP and MOP respectively along with FYM @12 cartloads/ha and Zinc Sulphate 25kg/ha. In order to ensure uniform plant stand, 2 seeds were dibbled per hill and later thinned to one seedling per hill. Normal agronomic practices and plant protection measures were applied to raise a successful crop. Need based irrigation was given to avoid problems due to moisture stress.

Three random seed samples of each inbred line were considered for biochemical analysis separately in duplicate with respective standard checks to minimize experimental error. Protein percentage and tryptophan content were estimated as per Bailey [3] and Vivek *et al.* [4] respectively, while lysine content in seed was estimated as per Tsai *et al*. [5]. Amount of these two essential amino acids were expressed as percentage of total crude protein in seed.

The analysis of variance was carried out separately for each agro-economic traits e.g., days to 50% tasselling (DT), days to 50% silking (DS), days to 50% dry husk (DH), plant height (PHT), height to the ear or cob (EHT), cob length (CL), cob diameter (CD), number of rows per cob (RC), number of grains per row (GR), tryptophan (Trp%), Lysine (Lys%) and protein (P%) and seed yield/plant (SY/P) following the procedures of Panse and Sukhatme [6]. The test of significance of difference between replications and among the genotypes for any character was done by F-test. The significance of difference between means of any two genotypes was tested by 't'- test through computation of critical difference ($CD_{0.05}$).

Results & discussion

Mean performance of agro-economic traits

Wide genetic variability among 49 test inbred lines was observed for ten morpho-economic traits including grain yield/plant (Table 1 & Figure 1). Genotypic difference among these inbred lines was found to be statistically significant at even 1% level of significance for all the characters. Homayoun [7] also reported significant differences among the genotypes in majority of traits based on analysis of variance.

Days to 50% tasselling and days to 50% silking are stable agro-economic traits as these are less liable to have minimum environmental influence. Usually silking appears 1-3 days later to tasselling. Days to 50% tasselling and days to 50% silking ranged from 58.3-76.3days and 59.3 -77.6days (Table 7). Days to 50% tasselling and days to 50% silking attained as early as around 58-60days in BQPM 3-7 and BQPM 8-15, while some of the inbreds i.e., BQPM-5-20, HK1-193-1, BQPM-1-8 , HK1-164-4(1-3)-2 , CML-195 and CML-163-B came to tasselling and silking at around 75-77days after sowing (Table 1).

Days to 75% dry husk is in principle attained at physiological maturity. The time gap between days to silking and days to harvest is important consideration for translocation of assimilate to the sink. These two phenomena do exist simultaneously, but their rate is genotype dependent which ultimately affect productivity. Some of the inbreds attained significantly early maturity as early as 84.6 days after sowing which is just after 19.6days from days to silking as in the case of BQPM 10-1. Similarly, seven other inbreds i.e., BQPM 3-7, BQPM 10-9, BQPM 1-2, BQPM 5-20, BQPM 8-15, BQPM 9-4 and CML 195 took 27 days from days to silking to days to harvest. Rest of the inbreds came to physiological maturity (days to 75 % dry husk) much later. In QPM 10-1; the ethylene.

Table 1: Mean performance of agro-economic and nutritional traits of a set of 49 QPM inbred lines.

Sl. No	GENOTYPES	DT	DS	DH	PHT	EHT	CL	CD	RC	GR	Trp (%)	Lys (%)	P (%)	SY/P
01.	BQPM-3-7	58.3	59.3	87.6*	124.8	63.7	11.3	13.0	14.0	15.4	0.71*	2.83*	7.41	76.0
02.	BQPM-5-2	66.3	69.3	100.0	122.8	54.7	09.8	11.6	14.0	20.1	0.84*	3.37*	8.50	62.0
03.	BQPM-7-4	63.3	65.6	96.6	146.2	74.4	13.7	11.9	12.0	23.8	0.96*	3.82*	9.89	92.3
04.	BQPM-9-2	63.3	64.3	94.6	141.0	73.9	12.6	11.8	14.0	23.3	0.65	2.72*	10.08	77.4
05.	BQPM-9-16	60.3	62.0	91.6*	150.7	74.4	15.6*	11.7	12.0	26.3	0.85*	3.38*	8.42	74.6
06.	BQPM-10-9	66.6	69.6	96.6	157.9*	76.6	15.3*	13.2*	14.0	31.5*	0.90*	3.63*	7.75	109.4*
07.	BQPM-1-15	65.3	66.6	97.3	167.2*	80.2	13.5	13.3*	14.0	29.0*	0.39	1.55	9.53	87.5
08.	B1110-7-2	65.6	66.6	96.3	128.1	62.4	11.4	11.2	12.0	16.3	0.48	1.98	10.85*	86.6
09.	BQPM-3-10	63.3	65.3	95.6	146.2	75.0	13.4	11.1	14.0	21.2	0.38	1.54	8.53	92.3
10.	BQPM-6-8	64.6	66.6	97.0	139.4	80.2	10.3	11.7	16.0*	13.9	0.40	1.71	11.84*	58.7
11.	BQPM-1-8	72.3	71.3	101.0*	104.7	45.4	10.0	8.7	8.6	18.3	0.34	1.41	10.04	74.2
12.	BQPM-1-14	66.3	66.6	96.6	132.2	62.2	13.1	13.5*	14.0	32.0*	0.48	1.96	8.49	102.4*

13.	B1130-7	69.6	70.6	100.6*	105.1	85.2	11.2	11.8	12.0	18.7	0.40	1.64	10.67*	61.5
14.	B1131-8	67.6	69.3	97.3	157.0*	72.2	13.8	14.2*	13.3	28.2*	0.34	1.41	7.16	103.9*
15.	BQPM-1-2	66.6	68.0	95.0	187.0*	45.2	12.5	9.0	11.3	12.3	0.33	1.39	12.08*	119.7*
16.	BQPM-1-3	68.6	70.3	99.6	117.0	50.3	07.6	7.7	13.3	19.9	0.72*	2.91*	10.09	88.9
17.	BQPM-1-6	65.0	67.0	97.0	113.1	41.0	12.4	10.5	12.0	20.2	0.35	1.42	9.02	87.4
18.	BQPM-1-7	67.6	68.3	100.3*	116.4	70.6	13.9	11.8	12.6	24.0	0.36	1.43	11.43*	58.0
19.	BQPM-2-4	68.6	70.3	100.7*	103.8	41.3	15.8*	13.5*	14.0	32.6*	0.41	1.62	11.42*	112.0*
20.	BQPM-2-10	67.6	70.6	98.0	132.1	68.4	09.6	8.5	11.3	11.0	0.42	1.70	11.47*	58.3
21.	BQPM-215	65.0	67.0	96.6	158.7*	77.3	12.6	12.6	14.0	24.7	0.31	1.26	9.03	112.7*
22.	BQPM-2-18	65.0	66.6	97.3	147.8	71.3	14.8*	11.4	13.3	19.3	0.75*	3.06*	9.30	73.7
23.	BQPM-3-4	64.3	67.6	96.6	182.8*	95.0	17.8*	15.5*	15.3*	34.2*	0.42	1.66	11.30*	153.4*
24.	BQPM-5-9	64.6	66.0	96.0	159.7*	71.4	15.5*	14.6*	15.3*	24.9	0.32	1.30	11.25*	124.3*
25.	BQPM-5-19	64.6	67.3	97.3	152.2	71.7	10.6	10.9	14.0	13.5	0.45	1.85	9.73	139.5*
26.	BQPM-5-20	76.3	77.6	104.6*	131.5	72.9	10.6	11.9	13.3	21.3	0.32	1.28	9.04	57.2
27.	BQPM-6-4	65.6	67.3	98.3	168.7*	81.1	14.2	13.0	13.3	28.3*	0.35	1.50	11.71*	101.2*
28.	BQPM-7-8	63.0	63.8	91.0*	133.6	70.4	10.1	11.6	13.3	22.5	0.30	1.22	8.44	51.3
29.	BQPM-7-14	66.0	68.3	96.7	174.0*	87.5	13.3	12.0	15.3*	24.1	0.36	1.48	9.75	76.5
30.	BQPM-8-1	63.6	65.0	95.3	151.5	72.9	14.5*	12.5	14.0	32.2*	0.34	1.41	10.85*	100.3*
31.	BQPM-8-5	64.6	66.0	94.6	101.2	47.3	10.8	12.3	14.0	18.4	0.54	2.51	9.96	54.673
32.	BQPM-8-7	63.3	64.6	94.0	139.5	64.5	13.9	13.7*	15.3*	23.5	0.72*	2.91*	7.26	100.1*
33.	BQPM-8-11	66.3	67.3	96.3	161.1*	85.4	15.3*	13.3*	14.0	27.1*	0.48	1.98	9.09	99.6*
34.	BQPM-8-12	68.0	69.3	97.0	168.9*	79.8	16.0*	13.1*	15.3*	35.3*	0.32	1.31	10.62*	119.4*
35.	BQPM-8-15	58.3	61.0	88.6*	151.1	67.3	16.8*	12.7	13.3	26.2	0.60	2.52	9.32	100.4*
36.	BQPM-9-4	64.3	66.6	92.0*	131.4	58.6	15.1*	12.6	12.6	27.2*	0.62	2.50	8.63	81.1
37.	BQPM-9-19	66.3	67.0	96.3	183.6*	89.8	15.2*	11.8	12.0	27.7*	0.42	1.67	10.48	58.5
38.	BQPM-10-1	63.0	65.0	84.6*	153.0	74.5	13.6	13.0	12.0	22.7	0.63*	2.55	8.26	80.0
39.	BQPM-10-4	61.6	62.3	93.0	139.4	64.0	11.0	13.0	12.6	18.8	0.31	1.25	8.96	75.4
40.	BQPM-10-13	62.3	63.6	91.3*	119.9	47.5	11.8	11.3	12.0	22.2	0.64*	2.70*	8.94	61.1
41.	HK1-164-4(1-3)-2	70.6	71.3	100.3*	118.9	89.5	16.6*	12.1	14.0	34.2*	0.38	1.57	8.60	113.2*
42.	HK1-164-7-6*161-2	68.6	72.0	99.0	155.4*	79.1	13.6	13.3*	13.3	25.3	0.44	1.80	9.37	104.0*
43.	HK1-191-1-2-5	66.6	68.3	97.3	217.6*	110.8	15.3*	14.3*	14.6*	28.2*	0.34	1.37	8.24	131.2*
44.	HK1-193-1	75.6	76.6	104.3*	117.1	83.4	11.4	13.8*	14.0	21.5	0.45	1.78	7.78	90.6
45.	HKI 193-2	65.3	65.0	96.3	180.1*	86.9	14.4*	12.5	12.6	26.4	0.62	2.52	8.53	71.8
46.	CLQ RCY Q 40	64.3	65.3	94.3	182.6*	90.6	17.2*	14.4*	12.6	38.0*	0.40	1.59	10.86*	151.3*
47.	BQPM-3-124	68.6	71.0	98.3	179.8*	88.9	10.1	13.3*	13.3	22.2	0.42	1.70	9.26	119.8*
48.	CML-163-B	70.6	70.7	100.3*	183.0*	87.3	15.8*	11.6	14.0	31.6*	0.37	1.51	8.00	122.3*
49.	CML-195	71.6	74.0	100.0	179.4*	95.6	15.8*	13.0	12.6	34.6*	0.32	1.30	10.70*	124.4*
GRAND MEAN		66.0	67.6	96.49	147.3	72.07	13.30	12.29	13.3	24.3	0.48	1.97	9.55	92.52
$CD_{0.05}$		1.63	1.22	3.79	5.80	2.07	0.936	0.730	1.32	2.19	0.15	0.67	1.03	14.81

production might have been tremendously higher rate leading to attain earlier for 75% dry husking. Atta *et al.* [8] also evaluated a set of high lysine rich Recombinant Inbred Lines (RILs) of maize derived from a cross between inbreds CM L161(Tropical QPM inbred line released by CIMMYT) and B73o2(a floury B73 inbred line carrying *opaque-2* recessive allele). The RILs had shown significant differences for maturity measured as days from planting to flowering, grain yield, and grain texture.

Medium height plant type with strong and stout stem is desirable for maize hybrids. Therefore, in the present investigation, preference should be given for selection of dwarf and tall plant types with sturdy stem to realize high heterotic performance and medium height. But, for ease in crossing point of view, plant height should be restricted to moderately tall inbreds. In the present investigation, there was wide variability in plant height ranging from 101.2-217.6cm. BQPM 8-5, BQPM 2-4, BQPM 1-8 and inbred line B1130-7 exhibited significantly dwarf plant type while HKI -191-1-2-5 was the tallest and its height was even more than 2m (217.6cm).

In general, maize is monostem in habit with a single cob at about the middle of the stem although there is exception in some inbreds which produce two cobs per plant. Appearance of ear at comparatively lower height is desirable as it will have enough time to store mobilized food in grains through translocation. In the present pursuit, Ear Height (EHT) ranged from 41.0cm (BQPM 1-6) to 110.8 cm (HKI 191-1-2-5). A few of the inbred lines i.e., BQPM 1-6, BQPM 2-4, BQPM 1-2 and BQPM 1-8 exhibited emergence of cob at a height significantly as low as 40-45cm while HKI 191-1-2-5, CML 195 and BQPM 3-4 showed position of cob at a height of 110.8cm., 95.6 cm and 95.0cm. respectively. Rest of the inbreds bore cob at about middle of the plant stalk.

Cob being the single important economic plant part in maize; the cob characteristics i.e., Cob Length (CL), Cob Diameter (CD), number of rows per cob (R/C) and number of grains per row (G/R) are more or less considered principal components contributing to productivity. There was wide range of variation in each of these component traits. It was 7.6-17.8cm in case of cob length, 7.7-15.5cm in case of cob diameter, 8.6-16.0 in case of number of rows per cob and 11.0-38.0 in case of number of grains per row. BQPM 3-4 exhibited significantly highest cob length (17.8cm) and cob diameter (15.5cm) and higher value of number of rows per cob (15.3) and grains per row (34.2). While, BQPM 6-8 revealed significant highest number of rows per cob (16.0) and the inbred line CLQRCYQ 40 exhibited high cob length (17.2 cm) as well as the highest number of grains per row (38.0). In this context, a inbred line BQPM 5-9 was found to have significantly high cob length (15.5cm), cob diameter (14.6cm) and higher number of rows per cob (15.3). BQPM 8-12 and BQPM 8-15 had high cob length and particularly the former being high in number of rows per cob and number of grains per row. These inbreds are of immense value for QPM hybrid production.

Seed yield is an artifact which resulted from favourable and unfavourable combination of component traits. Therefore, the *per se* performance is often considered as an important economic criterion for selection of maize inbreds. In the present investigation, 20 inbred lines yielded higher than 100g per plant. Among these better performing inbred lines, BQPM 3-4 had significantly highest yield potential (153.4g/Plant) followed by CLQRCY Q 40 (151.3g/plant) and BQPM 5-19(139.5g/plant). Besides, BQPM 5-9, CML 163-B and CML 195 also performed well so far as productivity is concerned. Similarly, Bello *et al*. [9] identified three promising QPM inbred lines (CML 437, CML 490 and CML 178) that showed superior performance for grain yield, other yield attributes and nutritional qualities over the standard and local checks.

Figure 1: Field trial of 49 selected inbreds for evaluation of agro-economic traits.

Biochemical characterization

Protein being the primary structural and functional component of every living cell, hence it serves as the most important ingredients that determine the quality of food and feed. The normal maize grain under Indian conditions on an average contains 9.0 % protein [10]. In general, cereals including the normal maize are deficient in two important essential amino acids i.e., lysine and tryptophan. In normal maize first limiting amino acid is lysine and second limiting amino acid is tryptophan. For this purpose, lysine is added from inorganic source for preparation of poultry and cattle feed. Feeding QPM to rabbits without lysine supplementation had shown sustenance of their normal health and growth performance [11]. General public including tribals also consume normal maize as food mixture and green cobs. So, there is every possibility of protein energy malnutrition. In contrast, the Quality protein maize harbour sufficiently high seed protein bound lysine and tryptophan owing to the presence of *opaque 2* mutation. After intervention of QPM maize, a good number of value added products for children and adult are now available in varied forms.

The *opaque -2* (*o2*)-a natural recessive mutation in maize led to nearly double the lysine and tryptophan content in endosperm [12,13]. Therefore, a major emphasis was laid on conversion of normal genotypes to *opaque-2* versions. But, subsequently, the pleiotropic effects of *opaque-2* mutation was realized which made the endosperm soft resulting damaged kernel while harvesting, increased susceptibility to pest and diseases, inferior for food processing and in general reduced yield. However, subsequently remedial strategies were adopted for improving the hardness of the kernel by modified backcross and recurrent selection.

Cereal grains harbour major fraction of prolamin seed protein [14]. The prolamins of maize (called zeins) and of other panicoid cereals (sorghum and many millets) are comprised of one major group of proteins (α- zeins) and several minor groups (β, γ and σ -zeins) [15,16]. The α- zeins consist of two major subclasses e.g., 19kD and 22kD zeins based on SDS-PAGE. Zeins are normally alcohol-soluble and are located within protein bodies on the rough endoplasmic reticulum; and these are products of multigene families [17]. Zein is particularly rich in glutamic acid (21-26%), leucine (20%), proline (10%) and alanine (10%), but deficient in basic and acidic amino acids. The notable absence of tryptophan and lysine in zein accounts for its negative dietary nitrogen balance.

In the present pursuit, 49 inbred lines were analysed for total crude protein content in seed and amount of two important essential amino acids i.e., tryptophan and lysine (Table 1). Total seed storage protein content had shown wide range of variability which ranged from 7.16% in B 1131-8 to as high as 12.08% in BQPM 1-2 followed by BQPM 6-8(11.84%) and BQPM 6-4(11.71%). While Bantte and Prasanna [18] reported a range of 6.9% to 11.3% for seed protein content in a set of 89 maize inbred lines. Altogether 17 inbred lines exceeded protein content more than 10%. Barring three above protein rich genotypes, some of the inbred lines i.e., BQPM 1-7, BQPM 2-4, BQPM 2-10, BQPM 3-4 and BQPM 5-9 also revealed more than 11% seed protein content. It is worth to note that maize inbred lines having tryptophan content on an average more than 0.50% and lysine more than 2.50% regarded as QPM maize. 15 inbred lines(BQPM-3-7, BQPM-5-2, BQPM-7-4, BQPM-9-2, BQPM-9-16, BQPM-10-9, BQPM-1-3, BQPM-2-18, BQPM-8-5, BQPM-8-7, BQPM-8-15, BQPM-9-4, BQPM-10-1, BQPM-10-13 and HKI-193-2) qualified the above standard fixed for QPM maize. Among these, BQPM 7-4 had shown tremendously high tryptophan and lysine content (0.96% and 3.82% respectively) followed by BQPM 10-9, BQPM 9-6 and BQPM 5-2 while, BQPM 7-8 recorded lowest estimated values (0.30% and 1.22%) for both the amino acids. The result shows that inbreds rich in protein quantity are, in general, not superior in protein quality with regard to the two essential amino acids. For instance, BQPM 10-9, BQPM 5-2 and BQPM 9-6 harbour low seed protein content (7.75-8.50%), but are excellent in protein quality. In contrast, the highly protein rich inbreds (BQPM 1-2, BQPM 6-8and BQPM 6-4) were shown to have low tryptophan and lysine content. However, a few inbred lines i.e., BQPM 7-4 and BQPM 1-3 may be sorted out for moderately high protein content with superior protein quality. A inbred line BQPM 9-2 could be also selected for inclusion in the single cross hybrid production owing to its high protein content along with high lysine content. Tripathy *et al*. [19] reported 0.4% tryptophan and 1.66% lysine content in seed of normal maize as against 0.77% and 3.11% in QPM test entries which was nearly double. Similarly, a promising QPM inbred line DMRQPM-66 was reported to harbor high tryptophan (1.09) content [18]. Scott *et al*. [20] developed a series of QPM inbred lines (*o_2/o_2 lines*) among which eight QPM inbreds had shown increase in lysine and tryptophan content up to the extent of 40% and 46% respectively over two non-QPM inbreds B110 and B 97.

Association of agro-economic traits

Grain yield in maize is a complex character and is the result of correlation between yield and yield components and between yield components themselves. Therefore, it is very imperative to examine the inter-relationship among agro-economic traits to formulate selection strategy to improve grain yield.

Table 1: Association of nutritional traits with Seed yield and yield contributing traits in a set of 49 QPM inbred lines.

Traits	DT	DS	DH	PHT	EHT	CL	CD	RC	GR	Trp	Lys	P%
DS	0.996**											
DH	0.982**	0.983**										
PHT	0.538**	0.554**	0.559**									
EHT	0.559**	0.567**	0.562**	0.786**								
CL	0.515**	0.523**	0.546**	0.683**	0.626**							
CD	0.649**	0.661**	0.676**	0.644**	0.687**	0.763**						
RC	0.714**	0.734**	0.769**	0.593**	0.612**	0.592**	0.805**					
GR	0.438**	0.436**	0.440**	0.536**	0.576**	0.822**	0.674**	0.505**				
Trp	0.110	0.135	0.167	0.014	-0.026	0.133	0.131	0.178	0.041			
Lys	0.099	0.123	0.156	-0.003	-0.047	0.120	0.118	0.175	0.022	0.996**		
P%	0.657**	0.666**	0.700**	0.438**	0.341*	0.420**	0.387**	0.493**	0.293*	-0.074	-0.070	
SY/P	0.385**	0.406**	0.399**	0.646**	0.484**	0.632**	0.563**	0.481**	0.59**	-0.095	-0.113	0.314*

Estimation of correlation coefficients between grain yield and component characters as well as *inter se* association provides information for choice of characters in selection programme. The strength of character association as measured by estimates of co-efficient of correlation depends upon the composition of the test materials, characters studied, previous selection history and the environment under which the breeding materials are tested. In the present investigation, all agro-economic ancillary traits exhibited significant positive correlation with grain yield. Among these, the strength of positive association of plant height (r = 0.646), cob length(r=0.632) and number of grains per row (r=0.589) with grain yield were very high indicating their importance for genetic improvement of productivity in maize. A highly significant and positive correlation between grain yield and cob length was also noticed by Rafiq, *et al.* [21]. Ei-Shouny *et al.* [22] showed that grain yield per plant correlated positively and significantly with ear diameter, ear length, number of kernels per row, 100-kernel weight, number of rows per ear, ear height, plant height and days to silking under normal planting date and with number of kernels per row, ear diameter, 100-kernel weight, ear length, number of rows per ear, ear height under late planting date. Other researchers noticed significant positive correlation of grain yield with 100-kernel weight [23,24,25,26]. While, Bello *et al.* [27] reported kernel number per cob to have most positive correlation (r=0.671**) with grain yield followed by kernel rows per cob (r =0.556**), cob diameter (r=0.543**) and cob weight (r=0.452**). Besides, Venugopal *et al.* [28] indicated that plant weight and number of seeds per row were positively associated with grain yield. On the other hand, Mohammadi *et al.* [29] had shown high correlation of grain yield with the number of rows per cob.

In our study, a strong positive association was noticed among days to tasselling (DT), Days to Silking (DS) and days to 50% Dry Husk (DH). In maize, cob length, cob diameter, rows per cob and grains per row determines the grain yield per plant [30]. Among these, rows per cob maintained higher strength of significant positive correlation with flowering and maturity traits (DT, DS and DH). As expected, very strong positive association was realized between cob length and grains per row; and similarly between cob diameter and number of rows per cob. Besides, cob diameter was shown to increase concurrently with cob length; and both being important for significant improvement in grain yield. Such, above desirable significant *inter se* associations indicates that selection for any one of these characters automatically selects the other trait and thus, together could result recovery of high grain yield.

Association of nutritional traits with agro-economic traits

Among three nutritional traits, protein content feebly correlated in positive direction (0.314) with seed yield and also other yield contributing traits except having strong association with days to tasseling, days to silking and days to 50% dry husk (Table 2). This envisaged that delayed flowering and maturity may have positive role in improving seed protein content. But, both the most limiting amino acids e.g., tryptophan as well as lysine revealed negative correlation with seed yield. Improvement in protein content was shown to have negative impact on enrichment of either of the amino acids as revealed from their inverse relationship with protein content (-0.074 and -0.070). However, both such amino acids had shown strong *inter se* correlation (0.996) indicating scope of their simultaneous improvement in maize.

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References

1. Gupta HS, Agrawal PK, Mahajan V, Bisht GS, Kumar A, et al, Quality protein maize for nutritional security: Rapid development of short duration hybrids through molecularmarker assisted breeding, Current Science. 2009; 96: 230-237.

2. Tripathy Swapan K, Lenka D, Ithape DM, Maharana M. Development of opaque-2 introgression line in maize using marker assisted backcross breeding. Plant Gene. 2017; 10: 26-30.

3. Bailey JL. Techniques in Protein Chemistry. Elsevier Publishing Co. Amsterdam. New York. 1967; 346.

4. Vivek BS, Krivanek AF, Palacios-Rojas N, Twumasi-Afriyie S, Diallo AO. Breeding Quality Protein Maize (QPM): Protocols for developing QPM cultivars. CIMMYT. Mexico. DF. 2008; 5: 978-970-648-160-3.

5. Tsai CY, Hansel LW, Nelson OE. A colorimetric method of screening maize seeds for lysine content. Cereal Chemistry. 1972; 49: 572–579.

6. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. Fourth Edition. 1985; 48-117.

7. Homayoun H. Study of some Morphological Traits of Corn Hybrids. American-Eurasian Journal of Agriculture and Environmental Science. 2011; 10: 810-813.

8. Atta H, Isakeit T, Mayfield K, Betran J. Phenotypic evaluation of a high lysine maize recombinant inbred line population. Bulletin, TEXAS A and M University. College Station. TX. 2005 77840. 2005; pp.-50-55.

9. Bello OB, Olawuyi OJ, Ige SA, Mahamood J, Afolabi MS, et al. Agro-nutritional variations of quality protein maize (Zea mays L.) in Nigeria. Journal of Agricultural Sciences. 2014; 59: 101-116.

10. Lenka D, Tripathy Swapan K. Development of high yielding Quality Protein Maize (QPM) hybrids and their molecular detection. Research Journal of Biotechnology. 2017; 12: 72-78.

11. Omage JJ, Agubosi OCP, Bawa GS, Onimisi PA. Evaluation of the nutritive value of quality protein maize on the growth performance and carcass characteristics of weaner rabbits. Pakistan Journal of Nutrition. 2009; 8: 106-111.

12. Vasal SK. High quality protein corn. In: Hallauer AR. (Ed.), Specialty Corns. CRC Press, Boca Raton, Florida. 1994; 79–121.

13. Krivanek A, Groote H, Gunaratna N, Diallo A, Freisen D. Breeding and disseminating quality protein maize for Africa. African Journal of Biotechnology. 2007; 6: 312-324.

14. Tripathy Swapan K. Quality protein maize: A way forward for food and nutritional security. Genomics and Applied Biology. 2019; 10: 10-19.

15. Coleman CE, Larkins BA. The prolamins of maize. In: Shewry PR, Casey R, eds. Seed proteins. Dordrecht: Kluwer Academic Publishers. 1999; 109-139.

16. Leite A, Neto GC, Vettore AL, Yunes JA, Arruda P. The prolamins of sorghum, coix and millets. In: Shewry PR, Casey R. (Eds.), Seed Proteins. Kluwer Academic Publishers, Dordrecht. 1999; 141-157.

17. Lending CR, Larkins BA. Changes in the zein composition of protein bodies during maize endosperm development. Plant Cell. 1989; 1: 1011-1023.

18. Bantte K, Prasanna BM. Analysis of grain protein, tryptophan and lysine contents of Quality Protein Maize (QPM) lines. Ethiopean Journal of Health Science. 2004; 14: 31-41.

19. Tripathy Swapan K, Lenka D, Maharana M, Ithape DM. Biochemical analysis and validation of molecular markers for identification of quality protein maize. Plant Gene. 2018; 14: 69-73.

20. Scott MP, Peterson JM, Hallauer AR. Evaluation of combining ability of quality protein maize derived from U.S. public inbred lines. Maydica. 2009; 54: 449-456.

21. Rafiq M, Rafique M, Hussain A, Altaf M. Studies on heritability, correlation and path analysis in maize (Zea mays L.) Journal of Agricultural Research. 2010; 48: 35-38.

22. Ei-Shouny KA, Ei-Bagoury OH, Ibrahim KIM, Al-Ahmed SA. Correlation and path coefficient analysis in four yellow maize crosses under two planting dates. Arab University Journal of Agricultural Sciences. 2005; 13: 327-339.

23. Guang C, Yan X, Shongue G. Path analysis of eight yield components of maize. Journal of Maize Science. 2002; 10: 33-35.

24. Khayatnezhad M, Gholamin R, Jamaati-e-Somarin SH. Study of genetic diversity and path analysis for yield in maize (Zea mays L.) genotypes under water and dry conditions. World Applied Science Journal. 2010; 11: 96-99.

25. Prakash O, Shanthi P, Satyanarayana E, Kumar RS. Studies on inter relationship and path analysis for yield improvement in sweet corn genotypes (Zea mays L.). New Botany. 2006; 33: 91-98.

26. Golam F, Farhana N, Zain MF, Majid NA, Rahman MM, Kadir MA. Grain yield and associated traits of maize (Zea mays L.) genotypes in Malaysian tropical environment. African Journal of Agricultural Research. 2011; 6: 6147-6154.

27. Bello OB, Mahamood J, Afolabi MS, Azeez MA, Ige SA, et al. Biochemical analysis and grain yield characteristics of quality protein maize (zea mays Linnaeus) in the southern guinea savanna of Nigeria. World Research Journal of Biochemistry. 2012; 1: 11-19.

28. Venugopal M, Ansari NA, Rajanikanth T. Correlation and path analysis in maize (Zea mays L.). Crop Research. 2003; 25: 525-529.

29. Mohammadi SA, Prasanna BM, Singh NN. Sequential path for determining interrelationships among grain yield and related characters in maize. Crop Science. 2003; 43: 1690-1697.

30. Pinnisch R, Mowers R, Trumpy H, Walejko R, Bush D. Evaluation of maize (Zea mays L) inbred lines for yield component traits and kernel morphology. Maydica. 2012; 57: 1-5.