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EVALUATION OF BIOCHEMICAL COMPOSITION IN SOME PROMISING NON-QPM INBRED LINES AND QPM HYBRIDS OF MAIZE (*Zea mays* L.)

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ABSTRACT
Present study was conducted to identify overall nutritionally superior/versatile genotypes through evaluation of biochemical constituents in nine genotypes of maize consecutively for three years. In biochemical analysis, significantly higher carbohydrate content was recorded from HQPM-1(70.65%), CM-140(68.78%) and VL-109178(68.59%), the highest starch content was recorded from BLD-233(61.91%), HY-235(61.78%) and GAYMH-1(61.43%), the highest protein content was recorded from HY-235(10.26%), JCS-2-7(10.11%) and VL-109178(10.11%), the highest oil content was recorded from HQPM-1(4.68%), GAYMH-1(4.99%) and JCS-2-7(4.83%). Genotypes VL-109178 (3.85%), CM-140(3.47%) and CM-135(3.43%) recorded highest lysine content whereas JCS-2-7(0.6%), BLD-233(0.61%) and GAYMH-1(0.55%) recorded highest tryptophan content. Significant negative correlation was found between protein and lysine contents ($p < 0.01$). Furthermore, non-significant differences ($p > 0.05$) were observed among maize genotypes for fatty acid composition of oil and micronutrients. High levels of unsaturated fatty acids were recorded in QPM hybrids HQPM-1 (77.86%) and GAYMH-1 (83.09%) whereas BLD-233 (79.4%) and JCS-2-7(78.49%) recorded nearly similar amount of it. On the other end, HQPM-1 had the highest value of iron (49.00ppm) and zinc (37.5ppm) whereas VL-1010090 recorded the maximum Mg content (943.3ppm). Besides, based on varietal rating on the basis of all quality attributes, HQPM-1, BLD-233 and JCS-2-7 were identified to be overall superior multipurpose genotypes in that order to be useful for maize nutritional improvement.

INTRODUCTION

Maize is one of the most important cereal crops of the world and contributes to food security in most of the developing countries. In India, maize is emerging as third most important crop after rice and wheat. With its high content of carbohydrates, proteins, fats, some of the important vitamins and minerals, maize acquired a well-deserved reputation as a poor man's nutria-cereal (Prasanna *et al*., 2001). Its importance lies in the fact that it is not only used for human food and animal feed but at the same time it is also widely used for corn starch industry, corn oil production, baby corns *etc*. The typical maize kernel, on dry weight basis is composed of 61-78% of starch, 6-12% of proteins, 3.1-5.7% of oil, 1.0-3.0% of sugar and 1.1-3.9% of ash (Miller, 1958; Watson, 2003). Corn oil is considered most suitable for human nutrition as it possesses a very high proportion of unsaturated fatty acids *viz*., oleicacid and linoliec acid with a very low content of cholesterol (Singh *et al*., 1998). Among the various mineral elements, iron (Fe) and zinc (Zn) are the most common micronutrients that have been found deficient predominantly in cereal-based human diet (Bouis *et al*., 2011). The iron, which plays an important role as a catalyst in transporting the oxygen to red blood cells varies from 11. 28-83. 35 mg/kg in maize kernel (Agrawal *et al*., 2012, Prasanna *et al*., 2011, Mallikarjuna *et al*., 2014, Chakraborti et al. 2011b). Zinc (Zn), an integral part of different enzymes involved in synthesis and degradation of carbohydrates, protein and lipids, range from 3.81-52.95 mg/kg in maize kernel (Chakraborti *et al*., 2011a, Prasanna *et al*., 2011, Guleria *et al*., 2013, Mallikarjuna et al. 2014). The plant nutrient magnesium (Mg) is involved in various physiological processes and its deficiency can severely reduce the yield and quality of crops. Unfortunately, even though maize kernels supply many macro and micronutrients necessary for human metabolic needs, the amounts of some essential nutrients are imbalanced or inadequate for consumers that rely on maize as a major food source. For instance, maize kernels are deficient in ascorbic acid (vitamin C), B vitamins, iron, and iodine. Maize protein possesses low nutritional significance to humans due to reduced content of essential amino acids like lysine and tryptophan. This leads to poor net protein utilization and low biological value (Bantte and Prasanna, 2003; Huang *et al*., 2006). The problem can be addressed to a considerable extent by shifting to quality protein maize diet. The proportion of lysine and tryptophan in the total portion of protein were found to be almost double in QPM materials (4.1% and 1%, respectively) than in non-QPM (2.7% and 0.6%, respectively) (Vivek *et al*., 2008).

Malnutrition has emerged as one of the most serious health problem worldwide. Deficiency of essential micronutrients in the diet leads to abnormal growth and development of humans. The deficiency of nutrients contributes to global burden of disease, and significant loss in annual domestic

product, thereby posing severe socio-economic loss. It is estimated that alleviating malnutrition is one of the most cost effective steps that offers benefit worth $16 with every $1 worth invested in proven nutrition programme. Though various avenues like food-fortification, medical-supplementation and dietary diversification are in place to all eviatemalnutrition, ' biofortification', a process of enriching crop plants with essential nutrients through breeding is regarded as the most sustainable and cost-effective approach. By considering all these above facts, it is assumed that QPM might possess distinct biochemical composition than non-QPM inbred lines. Keeping this in mind, the present study was planned to identify overall nutritionally superior multipurpose genotypes through evaluation of biochemical composition. Assessment of extent of genetic variance existing in quality traits in the available maize germplasm under this study may be useful in developing nutritionally improved cultivars having industrial value as well.

MATERIALS AND METHODS

Description of Plant Material

The field experiment was conducted for three consecutive years at Maize Research Station, Sardarkrushinagar Dantiwada agricultural University, Bhiloda, Gujarat, India. Bhiloda is in the northern part of Gujarat with latitude 23.76º N and 73.24º E longitude and altitude 190 m above sea level. Seven elite non-QPM inbred lines along with two QPM hybrids were selected from on-station trials based on high grain yield and stability.

For sampling of the grain to be used for chemical analysis central row was selected in which three cobs in selected row were self pollinated to avoid any mixture from other pollen. Grains from self pollinated cobs were harvested manually on canvas, kept in labelled plastic bags and taken to laboratory for chemical analysis. Grain nutritional quality analysis was conducted at biochemistry laboratory, Bioscience Research Centre, Sardarkrushinagar Dantiwada agricultural University, Sardarkrushinagar, Gujarat.

Methods

Moisture, Protein and Starch content

Moisture, protein and starch contents were determined using NIR (Model: Instalab-600; dickey-johns NIR analyzer, USA) and reported in per cent on gram basis. Seeds powder of each replicate of different maize entries was used for NIR analysis. The possibility of doing an analysis in any NIR spectroscopy instrument is dependent on the presence of a "calibration", created for the estimation of the trait of interest within that particular instrument. Organic molecules have specific absorption patterns in the near infrared region that can report the chemical composition of the material being analyzed (Williams and Norris, 2001). In this respect, many studies have been carried out to investigate the usability of NIR instruments in the analyses of maize grain quality traits (e.g., dry matter) (Welle *et al*., 2005), protein, starch, fatty acid composition (Baye *et al*., 2006).

Oil content

The Soxhlet method developed by A.O.A.C.(1965) was used for the estimation of oil content in percentage. Oil was extracted by repeated washing of the crushed seed powder with the organic solvent petroleum ether (40-60ºC) under reflux condenser. The experiment was carried out at 110ºC for 3 hours using fully automated soxtherm instrument (Gerhardt Analytical Systems, Germany). The solvent was recovered and the yield of the oil obtained was computed. Oil percentage was calculated using the following formula:

$$\text{Oil}(\%) = \frac{(\text{Weight of oil} + \text{flask}) - (\text{Weight of flask})X100}{\text{Weight of sample(gm)}}$$

Total carbohydrate content

The total carbohydrate content was determined by anthrone reagent method (Hedge *et al*., 1962). 100 mg of seed powder was taken in capped test tubes in which 5 ml of 2.5N HCL further added. These test tubes were kept in boiling water bath for 3.5 hr. After incubation all test tubes were neutralized with solid sodium carbonate until the effervescence ceases. After neutralization, each sample was filtered through whatmann filter no.1 in to 100ml volumetric flask. After this, volume was made up to 100 ml using distilled water. From this 1 ml test solution (diluted) was used for assay in which freshly prepared 4 ml anthrone reagent was added. After mixing the solution was kept for 10 minute in a boiling water bath. After this read the green to dark green colour at 630 nm.

$$\text{Total carbohyfrate}(\%) = \frac{\text{Sugar value from graph(mg)}}{\text{Aliquot sample used (ml)}} X \frac{\text{Total volume of extract(ml)X100}}{\text{Weight of sample(mg)}}$$

Lysine Content

Lysine content was determined as per method described by Tsai *et al*. (1972). Maize powder of different genotypes was defatted using soxhlet extractor and then the fine powder of defatted sample (100 mg) was used for Lysine estimation. 100 mg of the sample was digested with 5ml of papain solution and incubated at 65º C overnight. Cooled and centrifuged at 3000g for 5 minutes and collected the supernatant. To 1 ml of the supernatant added 0.5ml of carbonate buffer and 0.5 ml of copper phosphate. Centrifuged followed by addition of 0.1 ml of 2-chloro-3,5-dinitropyridine solution and kept in shaker for 2 hrs at room temperature. Added 5 ml of 1.2N HCl and extracted 3 times with 5 ml of ethyl acetate using separating flask and discarded the ethyl acetate layer. Read the OD value at 390nm against reagent blank. Standard lysine solutions were also treated simultaneously and calculated lysine content as follows:

$$\text{Lysine in pertein}(\%) = \frac{(\%)\text{Lysine in sampleX100}}{(\%)\text{Protein in sample}}$$

Tryptophan content

Tryptophan content was estimated using method developed by Mertz *et al*. (1975). The color was developed in the reaction of defatted flour hydrolysate (obtained by overnight digestion with papain solution at 65ºC) with 4 mL of reagent C (Reagent A: $FeCl_3$ $6H_2O$ (135 mg) in distilled water and diluted to 500 ml with glacial acetic acid containing 2% acetic anhydride; Reagent B:30 N sulphuric acid; Make mixture of reagent A and B , 1-2 hours prior to use makes reagent C). After incubation at 65 ºC for 15 min, absorbance was read at 545 nm using a spectrophotometer. The tryptophan content was calculated

using a standard calibration curve, developed with known amounts of tryptophan, ranging from 10 to 50μg mL^{-1}.

$$\text{Tryptophan in protein}(\%) = \frac{(\%)\ \text{Tryptophan in sample}}{(\%)\ \text{protein in sample}} X100$$

Fatty acid composition of oil

Fatty acids present in the oil were converted to their methyl esters as per method described by AOAC, 1970 with . Four to five drops of oil was introduced into a 50 ml screw capped tube. One ml of 4 per cent methanolic potassium hydroxide was added and the mixture heated at 60ºC in water bath until the oil globules dissolved. Then after 5 ml of n-hexane (Spectroscopy grade) was added to the tube for to recover the methyl esters formed. Tubes were shaken vigorously and let them stand for 10 minute to get two separate layers. Upper hexane layer was removed and added to the new tube. Thereafter, hexane layer was washed several times with distilled water for to remove any polar impurities. Once bottom layer in the tube was less turbid then remove the upper top hexane phase in to new tube. Allow the hexane phase containing the methyl esters to be in contact with anhydrous Na_2SO_4 for at least 10 min prior to analysis. Then transfer the hexane phase to a small vial for subsequent GC analysis. The hexane solution was analysed in a gas liquid chromatography (Trace GC Ultra, Thermo fisher Scientific PVT. Ltd) using flame ionization detector with nitrogen as the carrier gas. Oven, injection port and detector temperatures were set at 190, 230 and 240ºC, respectively. The methyl esters were identified and quantified by comparing the retention time and peak area with those of the five major fatty acid methyl ester standards (palmitic, stearic, oleic, linoleic acids and linolenic acid).

Micronutrients content

The flour of maize samples was digested for elemental analysis through following the wet ashing (acid digestion) method (Jones *et al*., 1991 with). One gram flour of maize sample was taken in 250 ml conical flask and than 10 ml of concentrated nitric acid was added to the flask and kept overnight. Next day digestion of samples were carried out with addition of diacid mixture (3HNO_3: 1 $HClO_{4)}$ in a conical flask through heating on hot plate in open space until white fumes are produced. When the residue was white or very light-yellow in colour, remove the flasks from the hot plate and let them cool. Finally dissolve the acid extract using deionised water, filter and the final volume of filtrate was made up to 100 ml in volumetric flask. Thereafter diluted acid extract solution was used for elemental analysis. Iron and Zinc concentration (ppm) was determined by using Atomic Absorption Spectrophotometer whereas magnesium concentration (ppm) computed by using EDTA titrimetric method as described by Pearson (1976).

Varietal grading in search of multipurpose genotypes

In order to identify multipurpose versatile cultivars of maize, rating (ranking) of various germplasm was done based on nutritionally desirable traits *i.e.*, protein, tryptophan, lysine, carbohydrate, starch, oil and its quality, micronutrients such as zinc, iron and magnesium as adopted by Dogra (2010).

Statistical analysis

Analysis of variance (ANOVA) was calculated using online SAS 9.3 Software developed at IASRI, New Delhi. Pearson's simple correlation coefficient between limiting amino acids *i.e.*, Tryptophan and Lysine and protein content was computed using SPSS software. The data analysis of three years data was done separately following completely randomized design. Instead of year-wise data, pooled values were given for discussion and interpretation.

RESULTS AND DISCUSSION

Proximate analysis

Proximate composition was analyzed in nine tested genotypes for three consecutive years and mean value of three year pooled data are presented in (table 1).

Moisture per cent in tested maize germplasm ranged between 8.82-9.56 % with an average of 9.17 per cent (Table 1). The genotype VL-1010090(9.56%) and HY-235(9.4%) recorded higher moisture content (both were statistically significant with each other) and differed significantly from the rest of all the genotypes under study. The lowest moisture content was noted in the genotype JCS-2-7(8.82%) which differed significantly from the remaining all genotypes. The hybrid HQPM-1(8.91%) was statistically *at par* with BLD-233(8.97%) and differed significantly from the others whereas GAYMH-1 (9.05%) differed significantly from all the other entries. Ullah *et al*. (2010) studied on the proximate composition showed moisture content in the range of 9.20-10.91 per cent.

Significant differences were observed for carbohydrate and starch contents in Zea mays genotypes during the course of our present study (Table 1). Carbohydrate content in tested maize germplasm varied from 63.39-70.65% with an average of 67.65% whereas starch content was varied from 59.95-61.91% with an average of 61.09%. The genotypes CM-140(68.78%), VL-109178(68.59%) and HQPM-1(70.65%) were statistically *at par* with each other. The QPM hybrid

Table-2 (A): Pearson correlation coefficients of protein, tryptophan and lysine content of maize genotypes

Particular	% Protein	Lysine in protein (%)	Tryptophan in protein (%)
% Protein	1	-0.388**	-0.035
% Lysine in protein	-0.388**	1	-0.052
% Tryptophan in protein	-0.035	-0.052	1

**Correlation was significant at the 0.01 level (2-tailed).

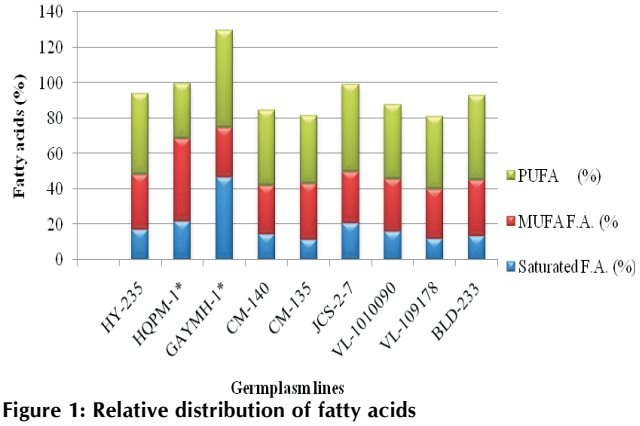

Figure 1: Relative distribution of fatty acids

Table1:Mean values of three year pooled data for moisture, carbohydrate and starch analysis

Genotypes		Moisture (%)			Carbohytrate(%)			Starch (%)		
Treatment Name	Treatment Description	Original Mean Values	Transformed Mean Values	Rank	Original Mean Values	Transformed Mean Values	Rank	Original Mean Values	Transformed Mean Values	Rank
1	HY-235	9.4	138.00^{a}	2	66.95	32.48^{cd}	7	61.78	383.14^{a}	2
2	CM-140	9.29	135.85^{b}	3	68.78	33.53^{ab}	2	60.54	374.07^{f}	8
3	CM-135	9.3	134.74^{c}	4	63.39	30.66^{e}	9	60.77	375.27^{e}	7
4	JCS-2-7	8.82	128.62^{f}	9	66.39	32.66b^{cd}	6	60.97	377.87^{d}	6
5	VL-1010090	9.56	138.28^{a}	1	68.19	32.75b^{cd}	5	61.48	379.39^{c}	4
6	VL-109178	9.24	134.38^{c}	5	68.59	33.39^{abc}	3	59.95	368.95^{g}	9
7	BLD-233	8.97	130.08^{e}	8	68.92	33.03^{bcd}	4	61.91	383.90^{a}	1
8	HQPM-1	8.91	130.09^{e}	7	70.65	34.22^{a}	1	60.99	378.80^{cd}	5
9	GAYMH-1	9.05	132.01^{d}	6	67.02	32.13^{d}	8	61.43	381.59^{b}	3
General Mean		9.17	133.56	.	67.65	32.76	.	61.09	378.11	.
p-Value		.	<0.01	.	.	<0.01	.	.	<0.01	.
CV (%)		.	0.75			3.05			0.26	.
SE(d)		.	0.471			0.584			0.575	.
LSD at 5%		.	0.95			1.177			1.16	.

HQPM-1andGAYMH-1 genotypes were QPM hybrids whereas remaining belongs to non-QPM inbred lines.Error Variances were not same and thus transformed variable was used for Combined Analysis.

Transformed mean in the column with varying superscripts differs significantly at ($p < 0.01$). Means with at least one letter common in superscript are not statistically significant using fisher's least significant difference.

Table2: Mean values of three year pooled data for tryptophan, lysine and protein analysis

Genotype		Original Mean Values	Tryptophan in protein (%)	Rank	Original Mean Values	Lysine in protein (%)	Rank	Original Mean Values	In protein% Mean vlues	
Treatment Name	Treatment Description									
1	HY-235	0.51	17.03^{cd}	7	2.89	13.14^{ef}	7	10.26	194.37^{a}	1
2	CM-140	0.49	16.34^{d}	8	3.47	15.49^{ab}	2	9.54	179.01^{f}	7
3	CM-135	0.37	12.78^{e}	9	3.43	14.94^{abc}	3	9.82	184.51^{e}	5
4	JCS-2-7	0.6	20.41^{a}	1	3.52	14.32^{cd}	5	10.11	191.69^{b}	2
5	VL-1010090	0.52	17.86^{c}	6	2.75	12.50^{f}	9	9.77	183.82^{e}	6
6	VL-109178	0.59	19.22^{b}	5	3.85	15.83^{a}	1	10.11	189.82^{c}	3
7	BLD-233	0.61	19.91^{ab}	2	3.16	14.73^{bcd}	4	9.28	173.01^{g}	9
8	HQPM-1	0.58	19.63^{ab}	4	3	13.85^{de}	6	9.88	185.53^{d}	4
9	GAYMH-1	0.55	19.67^{ab}	3	2.95	12.89^{f}	8	9.55	178.66^{f}	8
General Mean		0.54	18.09	.	3.22	14.19	.	9.81	184.49	.
p-Value		.	<0.01	.	.	<0.01	.	.	<0.01	.
CV (%)		.	5.53	.	.	7.05	.	.	0.54	.
SE(d)		.	0.58	.	.	0.465	.	.	0.92	.
LSD at 5%		.	1.17	.	.	0.938	.	.	1.86	.

HQPM-1andGAYMH-1 genotypes were QPM hybrids whereas remaining belongs to non-QPM inbred lines. Error Variances were not same and thus transformed variable was used for Combined Analysis.

Transformed mean in the column with varying superscripts differs significantly at ($p < 0.01$). Means with at least one letter common in superscript are not statistically significant using fisher's

HQPM-1 was differed significantly from BLD-233(68.92%),VL-1010090(68.19%),JCS-2-7(66.39%), HY-235 (66.95%), GAYMH-1(67.02%) and CM-135(63.39%). The genotypes CM-140 and VL-109178 were statistically *at par* with BLD-233, VL-1010090, JCS-2-7, HQPM-1 and differed significantly from HY-235, GAYMH-1 & CM-135, respectively. Dhaliwal *et al*. (2002) reported carbohydrate content of maize varieties in the range of 66.23 to 76.05 per cent. Awasthi *et al*. (2002) reported that carbohydrate content in maize genotypes varied from 59.00 to 70.20 per cent which was in close proximity with the results of the present study. The genotypes BLD-233(61.91%) and HY-235(61.78%) were statistically *at par* with each other but found significant from the rest of the genotypes. The genotype HQPM-1(60.99%) was statistically *at par* with VL-1010090(61.48%) and JCS-2-7(60.97%) and differed significantly from the remaining all the genotypes under study whereas GAYMH-1(61.43%) differed significantly from the rest of the genotypes under study. The variation in starch and carbohydrate content could be attributed to the variation in genetic makeup of the maize germplasm studied. Zilic *et al*. (2011) reported starch content in the range of 54.59 to 69.92 % in maize cultivars which was in the close proximity with the results of the present study. Khan *et al*. (2015) reported starch content in the range of 61.13% to 66.61% in maize hybrids.

Determination of protein, tryptophan and lysine content

The criteria used in QPM breeding for selection or rejection of breeding lines include protein content which should be $\geq$ 9% protein whereas tryptophan and lysine levels in endosperm protein should be $\geq$ 0.6 per cent tryptophan and $\geq$ 2.5 per cent lysine.

Protein content

A significant variation was observed in the tested entries for protein content ranging from 9.28 (BLD-233) to 10.26 % (HY-235) (Table 2). Significantly higher protein content was

Table 3: Mean value for three year pooled data for oil and its fatty acid composition

Genotype Treatment Name	Treatment Description	Oil (%) Original Mean values	Oil (%) Transformed Mean Values	Rank	Fatty acid Composition Myristic acid (%)	Palmitic acid(%)	Stearic acid(%)	Oleic acid(%)	Linoleic acid(%)	Linolenic acid(%)
1	HY-235	3.79	43.56f	7	Trace	14.35	2.793	31.087	43.947	1.517
2	CM-140	4.15	47.11e	5	Trace	12.26	2.07	27.653	41.637	0.77
3	CM-135	3.67	42.53g	8	0.079	8.34	2.933	31.577	37.867	0.707
4	JCS-2-7	4.83	53.89c	3	0.014	18.32	2.413	29.19	47.937	1.36
5	VL-1010090	3.31	37.61h	9	1.619	12.12	2.74	29.59	41.373	0.85
6	VL-109178	4.17	47.00e	6	Trace	9.66	2.4	27.897	39.843	0.88
7	BLD-233	4.42	51.11d	4	0.121	11.9	1.477	31.53	47.4	0.47
8	HQPM-1	4.68	57.00a	1	0.303	18.71	2.95	46.713	30.34	0.803
9	GAYMH-1	4.99	55.30b	2	0.187	13.12	3.267	28.313	54.233	0.553
General Mean		4.22	48.35	.	0.086	13.2	2.56	31.57	42.731	0.879
p-Value		.	<0.01	.	0.473	0.294	0.5471	0.3073	0.595	0.399
CV (%)		.	2.07	.	16.77	1.832	5.27	1.423	1.146	11.51
SE(d)		.	0.494	.	0.805	5.213	0.906	10.329	12.457	0.53
LSD at 5%		.	0.996	.	NS	NS	NS	NS	NS	NS

HQPM-1andGAYMH-1 genotypes were QPM hybrids whereas remaining belongs to non-QPM inbred lines.Error Variances were not same and thus transformed variable was used for Combined Analysis.

Transformed mean in the column with varying superscripts differs significantly at ($p < 0.01$). Means with at least one letter common in superscript are not statistically significant using fisher's least significant difference

Table 4: Mean value of three year pooled data for mineral content

Treatment Name	Treatment Description	Fe^{2+} Conc. (ppm)	Zn^{2+} Conc. (ppm)	Mg^{2+} Conc. (ppm)
1	HY-235	37.7	27.6	837.5
2	HQPM-1	49	37.5	804.8
3	GAYMH-1	41.2	31.3	812.4
4	CM-140	43.8	28.8	932.2
5	CM-135	43.2	25	940.2
6	JCS-2-7	28.1	31.8	661.4
7	VL-1010090	35.6	22.2	943.3
8	VL-109178	42.9	27.5	786
9	BLD-233	32.1	28.4	881.7
General Mean		39.3	28.9	844.4
p-Value		>0.05	>0.05	>0.05
CV (%)		16.6	15.1	10.9
SE(d)		11.378	8.18	142.07
LSD at 5%		NS	NS	NS

observed in non-QPM inbred lines HY-235 (10.26%), JCS-2-7 (10.11%), VL-109178 (10.11%) than QPM hybrids. All these three genotypes were differed significantly from the rest of all the genotypes. The genotypes GAYMH-1(9.55%) and CM-140(9.54%) were found statistically *at par* with each other whereas CM-135(9.82%) and VL-1010090(9.77%) also found statistically *at par* when compared with each other. The genotype BLD-233 (statistically differed from the rest of the genotypes) scored the lowest value. The considerable variation in protein content could be attributed to the variation in genetic makeup of the maize germplasm studied. Moreover, all the non QPM and QPM genotypes recorded higher protein content than threshold concentration(≥9% protein) required for QPM breeding. This result was in the agreement of the results obtained by Sofi *et al*. (2009). Vasal (2005 and 1993) and Villegas and Mertz (1970) also reported similar protein content in maize ranging from 8 - 11 per cent and 8.9 -10.2 per cent, respectively. This result was in the agreement of the results obtained by Khan *et al*. (2015).

Tryptophan and Lysine content

The major maize seed storage proteins, zeins, are deficient in essential amino acids lysine and tryptophan content, which contribute to the poor nutritional quality of corn (Haung *et al.*, 2006). The Lysine and Tryptophan content of different maize germplasms are depicted in Table 2. The range of lysine content was 2.75 (VL-1010090) to 3.85 (VL-109178) per cent, respectively. It was noted that genotypes CM-140(3.47%), CM-135(3.43%) and VL-109178 (3.85%) were statistically *at par* with each other. The genotype BLD-233(3.16%) was differed significantly from rest of all genotypes except CM-135(3.43%), CM-140(3.47%), JCS-2-7 (3.52%) and HQPM-1(3.0%). The genotype HY-235 (2.89%), GAYMH-1(2.95%) and VL-1010090(2.75%) (statistically *at par*) scored the lowest value in that order. All the tested genotypes and hybrids representing lysine content above the threshold concentration (≥2.50 %) that expressed their suitability for QPM breeding. The trend of variability on this aspect in the present study was in agreement with those reported by Sentaheyu *et al.*, 2008. Significant variation was observed in the tested entries for tryptophan content ranging from 0.37-0.61% with a mean value of 0.54%. The genotype JCS-2-7(0.60%) showed the highest value for tryptophan content followed by the genotype BLD-233 (0.61%). The genotype JCS-2-7 was differed significantly from the rest of the genotypes except the genotypes HQPM-1(0.58%), GAYMH-1(0.55%) and BLD-233(0.61%) whereas the genotype BLD-233 was differed significantly from the remaining all the genotypes except HQPM-1, GAYMH-1, JCS-2-7 and VL-109178(0.59%), respectively. Selvi *et al.*, 2015 also reported the nearly similar range of tryptophan content in maize genotypes.

The correlation matrix showed the relationships among the analyzed values of tryptophan, lysine and protein for the seven non-QPM inbred lines and two QPM maize hybrids (Table 2 (A)). Significant negative correlation between protein and lysine ($r = -0.388^{**}$, $p \leq 0.01$) indicates that maize genotypes high in

Table5 : Varietal grading of maize genotypes/hybrids in search of versatile/multipurpose genotypes

Parameters	HY-235	CM-140	CM-135	JCS-2-7	VL-10 10090	VL-10 9178	BLD-233	HQPM-1	GAY MH-1
Protein (%)	1	7	5	2	6	3	9	4	8
Tryptophan (%)	7	8	9	1	6	5	2	4	3
Lysine (%)	7	2	3	5	9	1	4	6	8
Oil (%)	7	5	8	3	9	6	4	1	2
Carbohydrate (%)	7	2	9	6	5	3	4	1	8
Starch (%)	2	8	7	6	4	9	1	5	3
Unsaturated Fatty acid in oil (%)	5	8	7	3	6	9	2	4	1
Iron concentration (ppm)	6	2	3	9	7	4	8	1	5
Zinc concentration (ppm)	6	4	8	2	9	7	5	1	3
Magnesium concentration (ppm)	5	3	2	9	1	8	4	7	6
Total	53	49	61	46	62	55	43	34	47
Overall grading	6	5	8	3	9	7	2	1	4

Cumulative ranking was done in the ascending order.

protein may likely to be low in lysine. The study did not show any significant correlation (r= -0.052) between lysine and tryptophan. Konsam Sarika *et al*., 2017 had also reported the non significant correlation between tryptophan and lysine content in maize.

Oil content and its fatty acid composition

The total oil per cent in the tested entries varied from 3.31-4.99% with an average of 4.22% (Table 3). The significant differences were found among all tested entries. The hybrid HQPM-1 (4.68%) and GAYMH-1(4.99%) recorded higher oil content and both were found significantly different from rest of all the genotypes under study. The genotypes VL-109178(4.17%) and CM-140(4.15%) were statistically *at par* with each other and differed significantly from rest of the genotypes. The genotype VL-1010090(3.31%) scored lower value and differed significantly from the others. Similar results have been reported by Aliu *et al*. (2012) and Sharma *et al*. (2015). When developing new high-oil breeding lines, the quality of oil and other desirable characteristics are considered. Perusal of the (Table 3) revealed non-significant difference among the tested entries with respect to fatty acid composition of oil. The result indicated that the dominant saturated fatty acids, *viz*., palmitic acid was ranged from 8.34 percent (CM-135) to 18.71 percent (HQPM-1) and stearic acid was ranged from 1.48 percent (BLD-233) to 3.27 per cent (GAYMH-1). Among the polyunsaturated fatty acids, the linoleic acid present in corn seed ranged from 30.34-54.23% with an average value of 42.73%. The data indicated that highest linoleic acid content recorded in GAYMH-1(54.23%) whereas HQPM-1(30.34%) showed lower value. In case of monounsaturated fatty acid *i*.e., oleic acid is most abundant in corn seeds. It was ranged between 27.65-46.71% with a mean value of 31.57%. The data indicated that QPM hybrid HQPM-1(46.71%) recorded high oleic acid content whereas GAYMH-1 (28.31%) recorded the lower value. High levels of unsaturated fatty acids were recorded in QPM hybrids HQPM-1 (77.86%) and GAYMH-1 (83.09%) whereas BLD-233 (79.4%) and JCS-2-7(78.49%) recorded nearly similar amount of it (Figure-1). The high content of unsaturated fatty acid in maize oil is the main factor in its high quality (Ozcan, 2009). The higher proportion of unsaturated fatty acids in corn oil appears to be quite beneficial for human health. From the above discussion, it was concluded that fatty acid profile of maize genotypes under study was better particularly due to high concentration of linoleic acid and oleic acid and a lower concentration of stearic acid. In India, Sanjeev *et al*. (2014) have recorded 12.61-16.22% palmitic acid, 2.63-6.04% stearic acid, 33.54-46.61% oleic acid and 33.00-44.65% linoleic acid contents in the oil obtained from several normal and specialty maize genotypes. Similar results have been reported by (Ignjatovic-Micic *et al*., 2015). Thus, our findings on oil content as well as fatty acid composition in the present study essentially corroborate these reports.

Mineral content

Levels of several nutritionally essential minerals (Fe, Zn and Mg) were determined in tested maize germplasms. Perusal of the (Table 4) reveals non-significant difference among the all treatments with respect to mineral content. The total amount of iron content present in all tested entries ranged from 28.1 to 49.0 ppm with lowest and highest values being exhibited by the genotypes JCS-2-7 and HQPM-1, respectively. Zinc content in all the tested hybrids and inbred lines varied from 22.2 to 37.5 ppm. Genotype HQPM-1 (37.5 ppm) had the highest zinc whereas genotype VL-1010090 (22.2 ppm) exhibit lowest zinc content. Lata *et al*. (2015) also reported the nearly similar range of iron content (22.59-41.03 ppm) and zinc content (19.38-32.59 ppm) in maize genotypes. Queiroz *et al*. (2011) also reported significant variability in the contents of zinc (17.5 to 42 mg kg^{-1}) and iron (12.2 to 36.7 mg kg^{-1}) in 22 tropical maize inbred lines with different genetic backgrounds. The range of magnesium content was 661.4 to 943.3 ppm. Genotype VL-1010090 (943.3ppm) had the highest magnesium while JCS-2-7 (661.4 ppm) exhibit lowest magnesium content. Ali *et al*. (2010) had also reported the nearly similar range of magnesium content (985.2 to 1125.3 ppm) in maize varieties.

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