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Evaluation of quality protein maize hybrids for agromorphological characters

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Abstract

To measure the extent of genetic variability, an experiment was conducted among twenty hybrids of quality protein maize and two open pollinated local germplasms in RBD with three replications over two seasons viz., *kharif* 2017 and *pre-kharif* 2018. The ANOVA revealed high significant differences among all the genotypes studied for all the characters except shelling percentage. The pooled ANOVA also indicated significant differences among the genotypes as well as among the environments over the two seasons. Highest PCV and GCV were recorded in ear height followed by plant height and ear weight. Highest heritability in broad sense was recorded in grain yield per plant followed by 100 seed weight and ear weight. And genetic advance as per cent of mean was recorded highest in ear height followed by ear weight and number of kernels per ro.

Keywords: PCV, GCV, heritability, genetic advance, quality protein maize

1. Introduction

Maize (*Zea mays* L.) is an important annual cereal crop of the world which contributes about 34.5 per cent of total cereal production of the world. It occupies an important position in the world economy and trade as a food, feed and industrial grain crop (Abebe *et al.*, 2005) [1]. In India, a major part of grain produced is utilized as feed followed by human consumption. At global level, maize accounts for 15 per cent of proteins and 20 per cent of calories in world food diet. But unfortunately, the nutritional profile of normal maize is poor as it is deficient in essential amino acids such as lysine, tryptophan and methionine due to a relatively higher proportion of prolamines in maize storage proteins which are essentially devoid of lysine and tryptophan.

In contrast, with the discovery of opaque-2 (o2) and flourey (fl2) mutant which have enhanced level of lysine and tryptophan in the endosperm protein open up the possibilities of the development of Quality Protein Maize (QPM). This QPM has exactly the same qualities as normal maize in respect of grain texture, taste and colour with the advantage that it possesses almost double the levels of lysine and tryptophan.

Moreover, Quality Protein Maize (QPM) could be a good source of protein for the people who have limited access to other protein sources. Despite its importance, the cultivation and use of QPM in Manipur is very limited. Mostly cultivation of maize is concentrated in the hilly and foot hills where cultivation of rice is not possible. However, people in hilly tracts consumed maize as second most important cereal next to rice. Average production of maize in this region is 2684.58 kg/ha (Directorate of Economics & Statistics, Manipur). Thus, it expands the scope of introducing well adapted varieties of QPM so as to increase the nutritional status of the people in hilly tracts in particular. Therefore, systematic effective breeding methods on the development of well adapted variety of QPM need to be initiated.

However, possibility of achieving improvement in any crop plant depends largely on the magnitude of genetic variability. In many cases, characters are mostly governed by poly genes which are highly influenced by the environment. Therefore, it is difficult to predict whether the existing variability is heritable or not. So, improvement of quantitative characters like yield through selection is conditioned by the nature and magnitude of variability existing in the population. Since, the phenotypic expression of a complex character like yield is a combination of genotype, environment and their interaction, it is necessary to partition overall variability into heritable and non-heritable components with the help of appropriate statistical techniques.

Furthermore, heritability of a genetic trait is very important in determining the response to selection because it implies the extent of transmissibility of that trait into next generations.

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In addition, high genetic advance coupled with high heritability offers the most effective condition for selection for a specific character. Therefore, knowledge of genetic variability, heritability and genetic advance is helpful in selection of suitable genotypes for quick improvement, through appropriate breeding techniques.

2. Material and Methods

The experiment was carried out in a randomized block design with three replications at the experimental field of Genetics and Plant Breeding, College of Agriculture, CAU, Imphal during *Kharif* and *Pre-Kharif* 2017-2018. The experimental site is located at latitude of 24° 45'N and longitude of 93° 56'E with an elevation of 790 meters above the mean sea level. Each genotype was planted in plot consisting of 4 rows in each plot. In both the two seasons, uniform spacing of row to row 65 cm and plant to plant 20 cm was followed. All the recommended package of practices was followed to raise a good crop during the experiment. Various agro-morphological characters were considered for evaluation. The characters include days to 50% tasselling, days to 50% silking, days to maturity, ear height, plant height, ear length, ear girth, number of kernel rows per ear, number of kernels per row, ear weight, 100 seed weight, grain yield per plant and shelling percentage.

The materials for this study comprised of 20 hybrids of QPM germplasms obtained from IIMR, Ludhiana and 2 local open pollinated genotypes.

3. Statistical analysis

3.1 Analysis of variance

The experimental data were analyzed statistically following standard statistical method by the method of analysis of variance following Gomez and Gomez (1987).

3.2 Genotypic and phenotypic variance

Genotypic variance (σ^2g) was estimated according to Burton and Devane (1953).

$$\sigma^2g = (MSG - Mse) / r$$

Where, σ^2g = Genotypic variance
MSG = Mean square due to genotype
MSE = Mean square due to error
r = Number of replication

Phenotypic variance, $\sigma^2p = \sigma^2g + \sigma^2e$

Where, $\sigma^2e = Mse$

3.3 Genotypic and phenotypic co-efficient of variation

Genotypic co-efficient of variation (GCV) was defined as the ratio of the square root of genotypic variance (σ^2g) to the population mean (\bar{X}), expressed in percentage. It was estimated according to formula suggested by Burton (1951).

$$GCV = \sqrt{(\sigma^2g) / (\bar{X})} \times 100$$

Where, \bar{X} = Grand mean

σ^2g = Genotypic standard deviation

σ^2g = Genotypic variance

Phenotypic co-efficient of variation (PCV) is defined as the ratio of the square root of phenotypic variance (σ^2p) to the population mean (\bar{X}) expressed in percentage.

$$PCV = \sqrt{(\sigma^2p) / (\bar{X})} \times 100$$

Where, σ^2p = Phenotypic standard deviation

σ^2p = Phenotypic variance

3.4 Heritability in broad sense and genetic advance

Based on the method of Lush (1940), heritability in broad sense (h^2) is equal to

$$h^2 = (\sigma^2g) / (\sigma^2p) \text{ or } (\sigma^2g) / (\sigma^2g + \sigma^2e)$$

Where, σ^2p = Phenotypic variance

σ^2g = Genotypic variance

σ^2e = Error variance

Genetic advance as suggested by Johnson *et al.* (1955) is

$$G.A. = Kh2\sigma p$$

Where, K = Selection differential at 5% selection intensity, the value of which is 2.06

h^2 = Heritability in broad sense

σ^2p = Phenotypic standard deviation

G.A. was expressed as the percentage of mean as follow:

$$\text{Genetic gain} = (G.A.) / (\bar{X}) \times 100$$

Where, G.A. = Genetic advance, \bar{X} = Grand mean

4. Results and Discussion

4.1 Analysis of variance (ANOVA)

The significant pooled analysis of variance for the twenty-two genotypes over two seasons for all of the characters indicated significant differences among the genotypes as well as among the environments. The genotype x environment mean sum of squares was also significant for most of the characters indicating differential influential effect of environment.

The mean sum of squares for seed yield and their component characters in twenty-two QPM genotypes (20 hybrids and 2 local open pollinated genotypes) over the two seasons are presented in Table 2 and Table 3. Highly significant differences among the genotypes were observed for all the characters in both the seasons indicating presence of sufficient amount of variability in all the characters studied. But the genotypic difference for shelling percentage was not significant in the second season. Similar results were reported by Neha *et al.* (2006), Ali *et al.* (2007) [2] and Bello *et al.* (2012) [5].

4.2 Mean performance of genotypes

Mean performance of genotypes combined over the two seasons in respect of yield and its component characters showed (Table 4) significant differences among all the materials, thus signifies the substantial variability among the experimental materials. Similar result was observed by Ali *et al.* (2007) [2]. The most outstanding genotypes in term of grain yield per plant were IHHQPM 1530 followed by IIMRQPMH 1610 and IIMRQPMH 1603 as compared with commercial hybrid Vivek QPM 9 with yields ranging from 479.369-541.56g. FHQ 106 showed lowest grain yield per plant followed by Pratap QPM Hybrid 1 and HQPM 4. After observing all the characters under study, it was found that genotypes which recorded higher yield showed desirable performance in other characters also. The highest yielding IHHQPM 1530 was found to have high mean performance in plant height, ear girth, ear length, number of kernels per row, ear weight, 100 seed weight and shelling percentage. Similar

pattern was observed in other genotypes as well.

4.3 Phenotypic and genotypic coefficient of variation

The results with regard to mean, overall range, phenotypic coefficients of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2_{bs}) and expected genetic advance as per cent of mean (GA%) for all the thirteen characters for the two seasons are furnished in Table 5 and Table 6. Phenotypic coefficient of variation was found greater than the genotypic coefficient of variation for all the characters in both the two seasons. This indicates that there was environmental influence on the expression of these characters. Found similar results in his experiment. Moderate to high PCV and GCV had been recorded for ear height, plant height, ear weight and number of kernels per row in the first season. And for the second season, ear height, ear length, ear weight, grain yield per plant, number of kernels per row and 100 seed weight had moderate to high PCV as well as GCV. Similar results were also reported by Bello *et al.* (2012) [5] and Aman *et al.* (2016) [3].

4.4 Heritability and genetic advance

Heritability in broad sense was high for all the characters in both the two seasons. In the first season, heritability in broad sense was recorded highest in grain yield per plant (97.92) followed by 100 seed weight (96.62), ear weight (96.56) and

ear height (93.28). Bekele and Rao (2013) [4] reported similar results. In the second season also heritability was high for all the characters except shelling percentage which supports the result given by Sundeep *et al.* (2015). This high heritability indicated that selection based on individual phenotype may be effective.

High heritability with high genetic advance was recorded in ear height, plant height, number of kernel rows per ear, number of kernels per row, ear weight, 100 seed weight and grain yield per plant in both the two seasons. Similar results were reported by Bello *et al.* (2012) [5] and Bekele and Rao (2013) [4]. High heritability along with high genetic advance indicates the presences of predominant additive gene action for a given character are desirable as this indicates the scope for rapid gains in selection. Further selection of these characters will be useful in improving the crop.

Low genetic advance was recorded for days to maturity, ear girth and shelling percentage in both the two seasons. But high heritability was observed for these characters. This means that there is presence of non-additive gene action and expression of high heritability may be due to favorable environmental influence or the influence of environment on the particular character is less. So selection of these characters may not be effective. But these characters can be improved with the use of hybridization and hybrid vigour (Bello *et al.* 2012) [5].

Table 1: Pooled data for 13 character of QPM under two environments

Source of variation	DF	DS	DT	EH(CM)	PH (CM)	EG (CM)	EL (CM)	NKRE	NKR	DM	EW(G)	HSW (G)	SP(G)	GYP (%)
Environment	1	5143.76	3340.12	59699.8	106023.3	25.68	68.20	21.04	42.05	2865.34	4646.99	28.35	0.11	19188.71
Replication/ Environment	4	43.30	15.44	245.59	865.07	1.16	24.21	2.04	16.44	13.81	1280.23	4.69	32.40	4563.90
Genotype	21	66.33**	55.61**	1732.3**	2901.22ns	2.60**	39.1**	14.2**	91.9**	127.64*	7032.65**	97.2**	45.27**	13385.4**
Genotype x Environment	21	23.23**	17.98**	612.45**	1740.55**	0.31**	6.04ns	0.35ns	1.23ns	59.07**	325.23**	1.72ns	19.02**	1111.55**
Error	84	2.23	2.53	33.48	156.15	0.11	4.90	0.204	2.59	6.24	92.54	2.34	7.95	224.19

** : Significant at 0.01 probability level, * : Significant at 0.05 probability level, ns: non-significant at 0.01 and 0.05 probability levels, df: Degrees of freedom, DS: Days to 50% silking, DT: Days to 50% taselling, EH: Ear height, EL: Ear length, NKRE: Number of kernel rows per ear, NKR: Number of kernels per row, DM: Days to maturity, EW: Ear weight, HSW: 100 seed weight, SP: Shelling percentage

Table 2: Analysis of variance for 13 characters of QPM for *Kharif* 2017.

Source of variation	Df	DT	DS	DM	EH (CM)	PH (CM)	EG (CM)	EL (CM)	NKRE	NKR	EW (G)	HSW (G)	GYP(G)	SP (%)
Genotype	21	35.77**	46.18**	81.62**	1160.31**	2856.2**	1.52**	10.707**	6.72**	43.61**	3169.32**	42.42**	4861.89**	51.46**
Replication	2	11.227	24.288	8.424	116.734	950.765	0.535	1.224	0.696	4.564	244.651	2.323	263.631	33.772
Error	42	2.322	1.447	2.361	27.224	284.596	0.098	0.406	0.189	1.264	37.175	0.489	34.225	6.733
S.Ed(±)		1.244	0.982	1.254	4.260	13.774	0.256	0.520	0.354	0.918	4.978	0.571	4.777	2.119
C.D		2.513	1.984	2.534	8.606	27.824	0.517	1.051	0.716	1.854	10.056	1.154	9.649	4.280

** : Significant at 0.01 probability level, ns: not significant at 0.01 and 0.05 probability levels, df: Degrees of freedom, DS: Days to 50% silking, DT: Days to 50% taselling, EH: Ear height, EL: Ear length, NKRE: Number of kernel rows per ear, NKR: Number of kernels per row, DM: Days to maturity, EW: Ear weight, HSW: 100 seed weight, SP: Shelling percentage.

Table 3: Analysis of variance for 13 characters of QPM for Pre- *Kharif* 2018.

Source of variation	df	DT	DS	DM	EH (cm)	PH (cm)	EG (cm)	EL (cm)	NKRE	NKR	EW(g)	HSW (g)	GYP(g)	SP (%)
Genotype	21	37.83**	43.38**	105.09**	1184.50**	1785.58**	1.40**	34.46**	8.38**	49.55**	4188.56**	56.51**	9635.05**	12.83ns
Replication	2	19.65	62.32	19.20	374.44	779.37	1.79	47.19	3.39	28.32	2315.82	7.05	8864.17	31.03
Error	42	2.75	3.02	10.12	39.74	27.70	0.12	9.39	0.22	3.91	147.91	4.18	414.15	9.17
S.Ed(±)		1.35	1.42	2.60	5.15	4.30	0.28	2.50	0.38	1.61	9.93	1.67	16.62	2.47
C.D		2.73	2.86	5.25	10.40	8.68	0.57	5.05	0.77	3.26	20.06	3.37	33.56	4.99

** : Significant at 0.01 probability level, ns: non-significant at 0.01 and 0.05 probability levels, df: Degree of freedom, DS: Days to 50% silking, DT: Days to 50% taselling, EH: Ear height, EL: Ear length, NKRE: Number of kernel rows per ear, NKR: Number of kernels per row, DM: Days to maturity, EW: Ear weight, HSW: 100 seed weight, SP: Shelling percentage

Table 4: Mean performance for agro-morphological traits of twenty-two QPM genotypes evaluated in *Kharif* 2017 and *Pre-kharif* 2018.

Sl. No.	Genotypes	DT	DS	DM	EH (cm)	PH (cm)	EG (cm)	EL (cm)	NKRE	NKR	EW (g)	HSW (g)	GYP(g)	SP (%)
1.	IIMRQPMH 1608	61.66	67.33	112.17	92.16	225.78	15.39	26.15	13.60	28.85	255.50	32.21	417.47	80.21
2.	FQH 106	51.67	55.83	106.00	80.80	224.44	14.90	25.46	14.27	30.83	222.76	34.72	341.14	73.57
3.	IIMRQPMH 1601	53.00	57.50	109.16	98.63	221.07	14.43	27.27	16.27	34.30	262.96	30.34	414.71	77.77
4.	IIMRQPMH 1605	55.16	59.67	110.67	92.10	232.32	15.60	28.33	15.20	33.60	263.90	38.12	445.06	84.91
5.	IIMRQPMH 1606	55.17	60.83	112.00	115.86	266.15	15.66	27.53	15.93	39.73	260.33	29.91	423.57	77.21
6.	VEHQ-16-1	56.00	60.83	109.66	117.67	266.34	16.35	27.80	17.00	36.73	327.00	37.54	487.61	78.15
7.	IIMRQPMH 1607	51.67	57.17	105.5	104.33	256.44	15.60	26.93	17.33	38.10	274.50	33.31	447.94	82.07
8.	IIMRQPMH 1603	59.16	66.50	114.33	107.10	272.55	16.24	28.30	14.87	32.83	317.66	40.54	491.11	75.40
9.	BQPMH 16	54.33	60.00	104.83	105.77	261.32	16.68	27.23	16.07	33.13	275.90	36.35	467.11	80.62
10.	IIMRQPMH 1508	55.00	59.67	103.67	116.27	259.14	14.35	26.73	15.46	28.40	263.83	30.61	432.16	79.61
11.	IMHQPM 1530	52.83	57.83	105.17	97.50	267.88	16.49	29.60	15.93	40.60	344.66	41.37	541.56	80.44
12.	IIMRQPMH 1604	57.00	63.67	108.66	106.00	256.11	16.01	24.73	15.93	28.80	249.16	34.30	423.35	80.48
13.	IIMRQPMH 1610	58.16	61.50	109.50	104.07	250.00	16.01	29.63	14.20	36.50	346.66	46.85	519.48	75.08
14.	IIMRQPMH 1609	56.16	61.67	104.33	97.56	252.07	15.98	26.73	17.07	30.93	284.66	35.27	438.99	76.00
15.	IIMRQPMH 1504	59.50	64.67	111.33	93.00	257.51	15.59	28.10	14.80	29.63	253.66	33.78	395.81	76.22
16.	IIMRQPMH 1501	56.67	59.33	107.66	112.20	260.4	15.80	25.87	15.47	28.97	264.17	31.74	435.08	79.06
17.	Vivek QPM 9	48.83	56.33	98.83	117.80	261.54	16.94	26.07	16.93	29.63	300.50	34.93	479.36	78.16
18.	HQPM 1	57.33	63.00	113.50	113.10	266.21	16.30	27.10	17.13	29.36	264.00	34.44	435.90	80.83
19.	HQPM 4	56.00	61.17	111.50	131.40	277.73	15.37	28.10	14.87	30.06	238.83	37.06	380.62	75.87
20.	Pratap QPM Hybrid 1	53.83	58.50	109.00	108.06	265.54	16.02	29.37	15.13	29.36	246.50	34.90	380.35	79.80
21.	CAULC-1	58.17	65.33	117.5	160.93	315.17	15.90	28.03	13.65	34.60	262.17	32.12	442.29	79.10
22.	CAULC-2	59.33	65.33	118.17	131.93	298.87	15.20	37.73	10.57	27.40	229.50	38.27	390.40	74.73
	Grand Mean	55.76	61.07	109.23	109.28	259.75	15.76	27.85	15.35	32.38	273.13	35.40	437.78	78.42

Table 5: Estimation of variability, heritability and genetic advance as per cent of mean for 13 characters in 22 genotypes of QPM in *Kharif* 2017.

Sl. No.	Characters	Mean	Range	PCV (%)	GCV (%)	h^2_{bs}	GA	GA as % of mean
1	Days to 50% tasselling	50.73	41.33-58.33	7.23	6.58	82.76	6.26	12.33
2	Days to 50% silking	54.83	47.67-65	7.38	7.042	91.16	7.59	13.85
3	Days to maturity	104.57	93.67-114.67	5.13	4.91	91.80	10.14	9.70
4	Ear height (cm)	88.02	58-125.13	22.86	22.08	93.28	38.66	43.93
5	Plant height (cm)	231.41	182.41-283.21	14.60	12.65	75.07	52.26	22.58
6	Ear girth (cm)	15.32	13.77-16.75	4.93	4.49	82.78	1.29	8.41
7	Ear length (cm)	27.14	24.13-33.47	6.83	7.22	89.43	3.61	13.30
8	No. of kernel rows per ear	14.95	10.4-17.2	10.28	9.89	92.02	2.91	19.50
9	No. of kernels per row	31.82	27.2-39.67	12.33	11.81	91.79	7.42	23.31
10	Ear weight (g)	267.20	221-350	12.31	12.09	96.56	65.41	24.48
11	100 seed weight (g)	34.93	29.64-45.49	10.89	10.70	96.62	7.57	21.67
12	Grain yield per plant (g)	430.27	337.32-577.48	9.52	9.42	97.92	81.77	19.21
13	Shelling percentage (%)	78.39	70.65-88.87	5.93	4.92	68.89	6.47	8.26

Table 6: Estimation of variability, heritability and genetic advance as per cent of mean for 13 characters in 22 genotypes of QPM in *Pre-kharif* 2018

Sl. No.	Characters	Mean	Range	PCV (%)	GCV (%)	h^2_{bs}	GA	GA as % of mean
1	Days to 50% tasselling	60.788	53.667-66.33	6.25	5.62	86.97	6.34	10.43
2	Days to 50% silking	67.318	60.33-76.667	6.02	5.44	81.68	6.83	10.14
3	Days to maturity	113.89	103-123	5.67	4.94	75.78	10.09	8.86
4	Ear height (cm)	130.55	95.33-200.27	15.72	14.96	90.57	38.29	29.33
5	Plant height (cm)	288.10	253.13-347.13	8.60	8.40	95.49	48.73	16.91
6	Ear girth (cm)	16.21	14.85-17.31	4.56	4.029	78.20	1.19	7.34
7	Ear length (cm)	28.57	25.33-42	14.74	10.12	47.10	4.09	14.30
8	No. of kernel rows per ear	15.73	10.4-17.87	10.57	10.14	92.05	3.16	20.05
9	No. of kernels per row	32.94	27.6-42.67	13.27	11.84	79.55	7.16	21.75
10	Ear weight (g)	279.06	219.53-377.33	13.85	13.15	90.10	71.76	25.72
11	100 seed weight (g)	35.86	30.18-48.22	12.97	11.65	80.66	7.73	21.55
12	Grain yield per plant (g)	449.83	344.96-605.64	13.13	12.32	88.12	107.21	23.83
13	Shelling percentage (%)	78.45	74.39-81.60	4.11	1.41	11.73	0.78	0.99

5. Conclusion

This study measured the extent of variability, heritability and genetic advance among twenty-two quality protein maize genotypes under two environments. The study revealed that there are different levels of variability, heritability and genetic advance among the all the genotypes in respect of grain yield and yield contributing characters which are the basis for crop

improvement programme. Heritability in broad sense is found useful to measure the importance of additive component of genetic variance which can be transmitted to offspring. Characters which gave both high heritability and genetic advance shows that there is presence of additive gene action, while those characters which are governed by non-additive gene action would give high heritability and low genetic

advance. In the present study, the expected genetic advance values were based on heritability in broad sense, which integrates additive portion of the total phenotypic variance. High heritability with high genetic advance was recorded in ear height, plant height, number of kernel rows per ear, number of kernels per row, ear weight, 100 seed weight and grain yield per plant in both the two seasons. Therefore, these characters can be considered for effective selection of superior genotypes.

Based on the grain yield per plant, IMHQPM 1530 and IIMRQPMH 1610 were the best performing genotypes in both the two seasons. Considering PCV, GCV and heritability in broad sense, conclusion can be made that ear weight, ear girth, 100 seed weight, number of kernels per row and number of kernel rows per ear influenced in grain yield per plant. Therefore, these characters can be considered for selection for future crop improvement programme.

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