RESEARCH PAPER

Evaluation of maize genotypes for some quantitative traits in the agro-climatic conditions of Swat Valley

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Abstract

The present study was carried out at Agriculture Research Institute (North) Mingora (ARI-N) Swat, Khyber Pakhtunkhwa for the evaluation of 20 maize genotypes for ten quantitative traits in the agro-climatic conditions of Swat valley with the aim to reveal information on the nature and degree of genetic variability, the pattern of association between yield and its components characters. The experiment was layout in Randomized Complete Block Design (RCBD) with three replications. Data for ten traits including days to germination, days to 50% tasseling, days to 50% silking, plant height (cm), ear height (cm), ear diameter, kernel rows ear^{-1}, number of kernels row^{-1}, 100 grain weight (g), grain yield (t ha^{-1}) was recorded and analyzed. Analysis of variance revealed significant differences among the genotypes for the all the studied traits which confirm the presence of genetic diversity. Seed yield revealed significant positive phenotypic correlation with Plant height, Ear diameter, Kernel row ear^{-1}, Kernel row^{-1} and 100 grain weight. Similarly days to 50% silking, ear diameter, kernal rows ear^{-1} and kernal row. Among the tested genotypes, BKC-07 was early maturing type which took 111 days to maturity, while the genotype Islamabad Gold out yielded all the tested genotypes including the check cultivars by producing 4.8 t ha^{-1} maize seed. It was followed V2-Jalal-78 (4.63 t ha^{-1}). These genotypes may further studied for yield and maturity to identify better performing lines for site specific and wider adaptations.

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Introduction

Maize (*Zea mays* L) is an important cereal crop grown in irrigated and rainfed areas. It belongs to the family *Poaceae*, genus *Zea* has chromosome number 2n= 20. It is annual and short day highly cross pollinated summer crop. It can be grown on all types of soils ranging from sandy loam to clay loam (Poehlman, 1977). Maize is a multipurpose crop and is mainly grown for human consumption as well as for feed and fodder for livestock. The by-products like gluten feed; maize oil meal and distillers dried grains are used to provide feed for livestock (Gardner and Pandey, 1995). The main objectives of breeding program in maize are to produce varieties/hybrids with high yielding and desirable characters. Several breeding techniques have been established to increase grain yield of maize populations. In order to select the best and high yielding hybrid combinations, a considerable number of best performing inbred lines are crossed to each other (Unay *et al.* 2004) .Evaluation of adaptability and stability of maize genotypes is more advantageous to evaluate genetic materials at several locations than for several years. Besides it, authors obtained data showing a better adaptation from hybrids in relation to cultivars (De Silva *et al.,* 2012). Correlation can serve as a marker of the plant character that has impact on its yield performance. This correlation analysis was embraced to conclude the interrelation between maize grain yield and yield traits and use as choice criteria in maize work (Yohanna. M. K., 2014). The correlation studies basically measure the relation between yield and different characteristics. It gives data that selection for one quality will result about progress for all positively associated characters. Correlation has been measured as a systematic interrelationship between variables (Rangaswamy, 2010). For plant breeders it is one of most essential task to increase the grain yield and quality of maize genotypes. With a specific end goal to improve the production, it is important to grow new, high yielding varieties/hybrids alongside with early maturity, desirable characters and resistance against insects, pests and diseases. The objectives of the present study are to estimate genetic variability, phenotypic correlation and Genotypic correlation among the hybrids for yield and yield components.

Materials and methods

Experimental site and design

The present study was carried out at Agriculture Research Institute (North) Mingora (ARI-N) Swat, Khyber Pakhtunkhwa. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications across during, summer 2013. Rows length was 5 meter, row to row distance with 75 cm and plant to plant distance of 25 cm. Experimental materials comprised of 20 genotypes. Standard agronomic practices were carried out for successful crop production. Ten plants were randomly selected from each plot in each replication to record the data. Data was recorded on the following parameters.

Data observing

The data was recorded on ten traits i.e., days to germination, days to 50% tasseling, days to 50% silking, plant height (cm), ear height (cm), ear diameter, kernel rows ear^{-1}, number of kernels row^{-1}, 100-grain weight (g), grain yield (t ha^{-1}).

Statistical analysis

Averages were calculated for recorded data in each replication. All the data was subjected to analysis of variance (ANOVA) according to Steel and Torrie (1980) by using the following ANOVA.

Results

Analysis of variance

Statistical analysis revealed highly significant differences for the traits studied (Table 1). Data regarding seedling emergence varied among the different genotypes from 7.66 to 5.66 days, days to 50% tasseling from 49.33 to 46.33 days, days to 50% silking from 54.33 to 49.00 days, plant height ranging from 194.67 to 154.50 cm, ear height from 96 to 72.66 cm, ear diameter ranging from 5.18 to 4.03 cm, Kernel rows ear^{-1} ranging from 16.33 to 10.66 rows, Kernel row^{-1} from 41.33 to 33.83 kernals, 100 grain weight ranging from 75.88 to 47.80 (g) and grain yield among the different genotypes ranging from 4.8

to 2.44 tons (Table 2).

Correlation

Genotypic Correlation

Analysis revealed genotypic significant positive correlation for days to germination with plant height, ear height and ear diameter while was positive with days to tasseling, days to silking, ASI, kernel row ear[-1] and 100 grain weigh. Significant negative genotypic correlation was observed with kernel row[-1] while

negative genotypic correlation with grain moisture and grain yield. Kanagarasu *et al.,* (2013) reported significant positive correlation of days to tasseling and kernel row ear[-1] with grain yield. Ahmad and Saleem (2003) reported positive and significant genotypic correlation of days to silking and kernel row[-1] with grain yield. Nastasic *et al.,* (2010) observed positive significant genetic correlation of kernel row[-1] and 100 grain weight with grain yield.

Table 1. Mean squares, F. ratios along with CV (%) for various traits of maize.

SOV	Replication	GMS	EMS	CV
DF	2	19	38	9.43
Days to germination	0.1166	1.3824**	0.3798	1.75
Days to 50% tasseling	1.05	2.8983**	0.6991	3.13
Days to 50% silking	1.2166	7.7403*	2.6377	0.57
Plant height	71.84	305.49	128.26	3.69
Ear height	0.422	108.892**	9.475	5.84
Ear diameter	0.10771	0.26370**	0.03026	3.24
Kernel row per ear	0.81667	5.16754**	0.64123	2.83
Kernels per ears	0.5542	22.1842**	1.4928	13.61
Hundred grain weight	0.866	250.990**	3.133	1.47
Grain yield t hac[-1]	0.0029	1.27154**	0.00323	1.47

Where, **= significant at 1% and *= significant at 5% level of probability.

Table 2. Mean performance of Maize cultivars for various traits.

Genotypes	DTG	DTT	DTS	PH	EH	ED	KRE	KR	HGW	YHa
Pahari	6.33b/d	48.00a/e	53.66ab	177.33a/d	90.00a/c	4.22ij	14.33bc	37.00c/e	47.80h	3.67h
Iqbal	6.00cd	49.00ab	54.33a	193.67ab	82.33d/f	4.72d/g	13.00d/f	34.00gh	63.09de	3.99fg
Azam	6.00cd	48.66a/c	54.00ab	181.80a/d	76.47hi	4.82c/e	14.67b	33.67h	66.40c	4.13ef
MTM-2	6.00cd	47.33c/f	52.33a/e	178.13a/d	95.00a	5.12ab	14.00b/d	36.00e/g	58.00f	3.73h
Agaitti2002	7.00a/c	46.66ef	53.0a/d	181.13a/d	85.00c/e	4.77c/g	13.00d/f	36.67d/f	74.31a	4.49bc
JG	7.00a/c	48.00a/e	53.66ab	178.60a/d	89.27bc	4.38hi	15.00b	39.33b	53.48g	3.11i
Islamabad white	5.68 d	47.66b/f	52.33a/e	172.33c/e	77.33f/i	4.62d/h	12.00f	41.83a	75.89a	4.60b
IL-Jalaj	5.66d	47.00d/f	51.33b/f	176.40b/d	88.47bc	4.50g/i	14.00b/d	39.00bc	60.90ef	4.06e/g
Raka poshi	6.33b/d	46.33f	51.66a/f	166.67de	85.00c/e	4.66d/h	15.00b	40.50ab	53.87g	3.11i
EV-7004	7.33ab	49.33a	51.66a/f	187.47a/c	82.06d/g	5.03a/c	14.66b	38.67b/d	73.00ab	3.02i
EV-1098	7.00a/c	46.66ef	50.66c/f	178.57a/d	77.13g/i	5.03a/c	14.33bc	40.17ab	58.00f	3.10i
EV-1097	5.66d	48.33a/d	52.00a/e	195.67a	86.60b/d	4.73d/g	16.33a	38.00b/d	65.38cd	4.18de
V-9	6.00cd	48.33a/d	50.33d/f	190.67a/c	90.40ab	5.03a/c	12.33ef	41.83a	75.22a	3.56h
Islamabad Gold	6.33b/d	49.33a	53.0a/d	176.73b/d	76.67hi	4.80c/f	13.00d/f	40.50ab	73.11ab	4.80a
V1	7.33ab	47.00d/f	53.33a/c	190.13a/c	86.33b/d	4.52f/h	14.00b/d	35.83e/g	65.00cd	4.33cd
Pahari-V3	7.66a	49.00ab	53.0a/d	176.73b/d	80.27e/h	4.55e/h	14.00b/d	40.00ab	53.18g	2.44j
MKT-1	7.00a/c	47.33c/f	49.66ef	186.73a/c	89.27bc	5.18a	14.67b	34.50gh	70.75b	4.59b
BKC-07	7.66a	48.00a/e	50.00ef	186.73a/c	79.13f/h	4.03j	10.667 g	34.83f/h	58.81f	3.93g
V2-Jalal-78	6.33b/d	46.33f	49.66ef	165.67de	87.00b/d	4.70d/g	12.00f	33.67h	52.99g	4.63ab
V-13	5.66d	48.66 a/c	49.00f	154.60e	72.68i	4.87b/d	13.33c/e	36.83d/f	48.69h	3.62h
LSD	1.01	1.38	2.68	18.72	5.08	0.29	1.32	2.02	2.93	0.18

Phenotypic Correlation

Phenotypic correlation analysis revealed positive association of days to germination with days to tasseling, days to silking, plant height, ear height and ear diameter. Days to germination exhibited negative phenotypic correlation with ASI, kernel rows ear[-1], kernel row[-1], 100 grain weight, grain moisture contents and grain yield. Phenotypic correlation analysis revealed positive association of days to germination with grain yield have also reported Akinwale *et al.,* (2013) and Mitritovic *et al.,* (2012).

Table 3. Genotypic correlation among 10 morphological yield and yield components characters.

Variables	DG	DT	DS	PH	EH	ED	KRE	KR	GW
DT	0.2367								
DS	0.2823	-0.8011**							
PH	0.5265*	1.8791*	1.3454*						
EH	0.6793**	0.302	0.1075	0.6787**					
ED	0.6688**	1.7351**	1.1403**	-0.3544	-0.1802				
KRE	0.1103	0.6478**	1.1315**	0.1707	0.9552**	-3.3501**			
KR	-0.8248**	-0.5029*	-0.553*	-1.1814*	-1.1873*	2.6241**	2.5933**		
GW	0.2027	2.8098	2.0797	0.8455**	-0.0927	-0.1492	-3.1617**	1.1087**	
Yield	-0.1204	1.1406	0.5293*	-0.3943	-0.4125	2.2842**	1.4449**	0.714**	0.1867

Table 4. Phenotypic correlation among 10 morphological yield and yield components characters.

Variables	DG	DT	DS	PH	EH	ED	KRE	KR	GW
DT	0.1864								
DS	0.1054	0.8666**							
PH	0.0199	0.1242	0.1453						
EH	0.0872	0.1665	0.1624	0.3707					
ED	0.0432	-0.2737	-0.2879	0.0517	0.0009				
KRE	-0.0925	-0.1229	-0.1056	0.0958	0.068	0.4573*			
KR	-0.2497	0.0197	0.0343	-0.182	-0.1631	-0.1373	-0.1918		
GW	-0.0366	-0.1252	-0.2229	-0.0374	-0.1643	0.4915*	-0.0632	-0.1463	
Yield	-0.2448	-0.2232	-0.3056	0.0001	-0.1127	0.4804*	0.2354	0.4619*	0.3309

Bekele and Rao (2014) observed negative and non significant association of days to 50% tasseling and days to 50% Silking with grain yield. Kumar *et al.* (2014) concluded similar results of positive and highly significant association of plant height With grain yield. Bocanski *et al.* (2009) finding the conformity close results highly significant positive association of ear height with grain yield. Kumar *et al.* (2014) reported highly significant positive association of ear diameter and kernels row[-1] with grain yield. Nemati *et al.* (2009) conducted corroborating results to the present findings of positive but non-significant relationship with grain yield. Ullah *et al.* (2011) pointed out similar results of highly significant and positive association of 100-grain weight with grain yield.

Conclusion

The tested genotypes confirm the presence of genetic variation. Grain yield revealed significant positive phenotypic and genotypic correlation with Plant height, Ear diameter, Kernel row ear[-1], Kernel row[-1] and 100-grain weight while, days to 50% silking, ear diameter, kernel rows ear, exhibited positive genotypic correlation with yield. These results suggest that these traits may be used as selection criteria during selection procedure to constitute source populations for varietal development. Among the

tested genotypes, BKC-07 was early maturing while the Genotype Islamabad Gold out yielded these genotypes might further be evaluated and studied in breeding programs.

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