Pak. J. Bot., 40(6): 2361-2367, 2008.

COMPARATIVE EVALUATION AND CORRELATION ESTIMATES FOR GRAIN YIELD AND QUALITY ATTRIBUTES IN MAIZE

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Abstract

A set of 10 elite maize genotypes/populations was evaluated for grain yield and quality attributes. Analysis of variance for the characters under study revealed highly significant differences among the genotypes. The fatty acids detected from grain oil showed significant variability among the genotypes. The quality attributes in most of the cases showed negative genotypic and phenotypic correlation except grain oil contents which was positively correlated at the genotypic level while grain starch contents and lauric acid were positively correlated with grain yield per plant both at the genotypic and phenotypic levels. DP 3062 was found high yielding while Waxy had more oil, protein, sugar, lauric and linoleic acid as compared to other genotypes. It is inferred that DP 3062 and Waxy may be exploited in maize breeding for quality improvement.

Introduction

Maize (*Zea mays* L.), with a remarkable productive potential among the cereals, is the third important grain crop after wheat and rice and accounts for 4.8% of the total cropped area and 3.5% of the value of the agricultural output. In Pakistan it is planted on 0.947 million hectares with an annual production of 1.897 million tons (Anon., 2004). Maize crop is an integral part of our agriculture and has a potential to compete with its multi-products. In order to have access to global market, there is need to improve the quality of crop with judicious use of inputs. International demand for quality parameters such as oil, starch, carbohydrates and protein is increasing. To meet such requirements within and out side country, it is desired to tailor varieties with a favorable comprise of yield and quality components. To this end, it is necessary to explore germplasm to explore genetic variability for such quality traits and their association with grain yield and other yield attributes. The present project is a preliminary study for this purpose to estimate the extent of genetic variability, heritability and correlation for various yield and quality components to formulate a selection criterion.

Materials and Methods

The experimental material comprised 10 viz., Monst-707, Monst-922, Monst-919, Monst-5219, DP-3062, Comp-20, Shl-2002, Ag-2002 DTC and Waxy elite maize hybrids/populations which were sown in the experimental area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, during spring 2002 in a triplicated randomized complete block design. Two seeds per hill were sown by keeping plant-to-plant and row-to-row distances of 30cm and 60cm, respectively and thinned to one seedling few days after germination.

Biochemical analysis: Biochemical analyses for quality attributes were performed in the Central Hi Tech Laboratory, University of Agriculture, Faisalabad and Oil Technology Laboratory, Ayub Agricultural Research Institute, Faisalabad. Oil contents were determined through Nuclear Magnetic Research (NMR), model Oxford MQA-7005. Fatty acid composition was determined through oil chromatography (Variance-3900, US made). Phase was separated for ester on a saturated solution of the Sodium chloride (Bannon *et al.*, 1982). The nitrogen present in each sample was determined through Kjedhal's method as described by Kirk & Sawyer (1991) and Anon., (1990). Protein percentage was calculated by multiplying nitrogen percentage with 6.25. Ash contents of each sample was determined by the interaction of dried sample in muffle furnace at 550°C until the residue obtained was of dusty grey colour and calculated (Anon., 1990.) Grain sugar was determined by using UV-Visible Spectrophotometer (Model Hitachi U-2001). Sugar was extracted and total sugars were determined by the method of Miller (1959). Starch contents was determined by titration method.

Statistical analysis: Analysis of variance and co-variance for all the characters and comparisons of treatment means were made following Duncan' new multiple range test (Steel *et al.*, 1996). Heritability estimate (Burton & DeVane, 1953) and correlations were computed (Kwon & Torrie, 1964).

Results and Discussion

Significant differences among the genotypes for grain yield and quality attributes such as oil, protein, starch, sugar, ash and fatty acids were determined from grain oil chromatography (Table 1). Significant variation found in the present studies could be attributed to the genetic cause. The impact of genetic background of various types has been different for yield and quality parameters. Genetic variability for grain yield components has been reported by Tusuz & Balabanli (1997), Singh *et al.*, (1998) and the same for oil contents (Dudley *et al.*, 1974), fatty acids composition (Dunlap *et al.*, 1995), protein content (Spanner *et al.*, (1992) and total carbohydrates by Korniewicz *et al.*, (2002) and Mazur *et al.*, (2001).

Mean values for grain yield per plant ranged from 84.89g to 157.70g (Table 2). It is evident that DP-3062 had maximum grain yield per plant and Ag-2002 had the lowest grain yield of all the genotypes. DP-3062 showed non-significant variation in comparison with Monst-919 and DTC for this trait whereas it significantly differed with rest of the genotypes. Ag-2002 exhibited non-significant difference with Shl-2002 and Waxy for grain yield per plant, while significantly differed from the remaining genotypes DP-3062 surpassed all in grain yield per plant, DTC appeared second highest yielding in the breeding material. DTC was statistically at par with highest yielding single cross DP-3062 and higher yielder than the average of four single crosses (Monst-919, Monst-922, Monst-5219 and Dp-3062). In a single cross all the plants are necessarily of the same genotype and have maximum possible heterozygosity in their genetic background for the expression of heterosis. DTC is a progeny of top cross, constituting a mixture of hybrids, selfs in their genetic background. Theoretically it should not be better than single cross, but due to accumulation of more favorable genes and presence of heterozygosity might have enabled it to produce higher yield. This solicits clearly that a double top cross could be practically higher yielder than the single crosses.

Mean values for grain oil content ranged from 2.13 to 8.38% (Table 2). Monst-707 had maximum grain oil percentage followed by DP-3062 and Shl-2002. Monst-707 was significantly different in grain oil content compared with all the genotypes under study. It may be used as high oil maize parent in a breeding programme. The range for grain protein content was 8.75 to 13.99% (Table 2). Waxy was recorded as high grain protein containing genotype, while Shl-2002 and Monst-5219 also gave grain protein contents of 13.71% and 13.26%, respectively. DP-3062 was found as having low grain protein (8.92%) genotype. Waxy was significantly different from all other genotypes except Shl-2002, Monst-5219 and Monst-919.

Monst-922 exhibited maximum grain starch contents followed by Monst-707 and Monst-5219. Monst-922 showed significant differences for grain starch contents among all the genotypes. The data showed a range among the genotypes for this trait (38.83 to 61.65 %). Ag-202 had the lowest starch percentage among the genotypes and is non-significantly varied from Dp-3062, Composite-20 and DTC. Mean values for grain sugar contents ranged from 0.65% to 1.93%. The maximum sugar contents were found in the grain of Waxy significantly differing from all other genotypes in this study. Minimum grain sugar was recorded for Ag-2002 (0.65%) and Monst-919 (0.66%) was found significantly different to Composite-20 and Waxy, while it showed non-significant differences with other genotypes. The mean values recorded for ash content were found in the range of 1.13 to 2.50%. Shl-2002 exhibited maximum grain ash contents while Monst-919 recorded lowest ash contents. Shl-2002 was significantly different from all other genotypes and Monst-919 also showed significant differences with the remaining genotypes, whereas rest of the genotypes was at par (Table 2).

Among the saturated fatty acids, maximum lauric acid (4.45%) was found in Composit-20 followed by Monst-707 (3.26%) and DTC (2.32%), the least in Monst-922 (1.03%). Oleic acid percentage ranged from 12.06% (Monst-922) to 37.26% (Composit-20). Significant differences were observed between all the genotypes except between Monst-5291 and AG-2002, DP-3062 and Shl-2002. Linoleic acid ranged from 65.30% to 20.96%. Waxy possessed maximum percentage followed by Monst-919, whereas Monst-922 contained the lowest. Palmatic acid value was highest in case of DTC (21.26%) and Monst-707 (21.21) and lowest in case of Waxy (10.37%). DTC and Monst-707 were significantly different from other genotypes. Thus for the evaluation of attributes of high yielding maize genotypes alongwith high protein, starch and sugar contents to meet the international demand, sufficient genetic variability available in the material under study may be exploited.

Genotypic and phenotypic correlation: Oil content was positively and significantly correlated with grain yield per plant at the genic level (0.096), it was negatively and non-significantly correlated at the phenotypic level (Table 3). The results indicated that although there was significant correlation at the genic level for these trait but increase in oil content could not exhibit great deal of increase in grain yield per plant because these two traits are not responding each other accordingly at phenotypic level. Khakim *et al*., (1998) reported similar results at genic level but different at phenotypic level in maize. The present results are partially in agreement with Lambert *et al*., (1998). A critical review of the results revealed that grain protein contents and grain yield per plant were negatively and significantly correlated at genic and phenotypic level, the correlation coefficients being 0.410 and 0.393, respectively. The results showed that an increase in protein contents may decrease grain yield ultimately, so breeding for high protein genotypes require moderate balance between these two characters. The results are in line

with the finding of Pasztor *et al*., (1998) and Khakim *et al*., (1998). Grain starch content and grain yield per plant were found positively and non-significantly correlated at the genic (0.125) and phenotypic level (0.127). The result indicated that any increase in grain starch would correspond to a positive increase in grain yield per plant. The results are in accord with Li (1997).

The data presented in Table 3 exhibited that grain sugar contents were negatively and significantly correlated at the genotypic and phenotypic levels with grain yield per plant. It was observed that an increase in sugar contents may decrease starch level of grain that ultimately reduces the grain yield (Li, 1997). Negative and significant correlation was found between ash contents and grain yield at the genotypic level (5.89) and the phenotypic level (0.568). The results showed that breeding for high ash contents level may cause significant decrease in grain yield. The results presented in Table 3 revealed that lauric acid and grain yield per plant were positively and non-significantly correlated at both genic and phenotypic level. So it is possible that high yielding genotypes may exhibit high amount of lauric acid.

Oleic acid and yield were negatively and non-significantly correlated at the genotypic (0.004) and phenotypic (0.059) levels. The results demonstrated that an increase in oleic acid concentration inversely affected grain yield per plant. High oleic acid is desired for good quality of grain oil (unsaturated short chained fatty acid). So a moderate selection compromise is needed to produce high yielding genotypes with superior quality oil.

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(Received for publication 5 February 2006)