



STUDIES ON THE PER SE PERFORMANCE OF SINGLE CROSS HYBRIDS FOR GRAIN YIELD AND ITS COMPONENTS

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Abstract

Study was conducted to assess the performance and identified the hybrids in the Line × tester analysis involving 25 best lines selected based on top cross performance and four tester indicated presence of significant variability among the genotypes for yield and yield contributing traits. Among the crosses, ARYP-24 × CM-111 and ARYP-15 × CM-111 were the superior crosses for grain yield over best check hybrid.

Keywords: Heterosis, Zea mays, variability, morphological traits and yield

I. INTRODUCTION

Maize (*Zea mays* L.; $2n = 20$) is an important cereal crop with high yield potential. The total production at world level has surpassed both sorghum and pearl millet gaining a third place after wheat and rice. The demand for maize grain is increasing every year due to its diversified use in poultry, piggery and industry. During the year 2005-06, the total area in the country under maize cultivation was 7.58 m.ha. and the total production was 14.70 mt. as compared to 14.17 mt. during 2004-05. The increased production from Andhra Pradesh, Gujarat, Karnataka, Maharashtra, Orissa and Tamil Nadu was due to the availability and adaptation of recently released hybrids (Anon., 2005).

Karnataka state ranked first in yield realization till 1996-97, but now (2004-05) it is lagging behind compared to Andhra Pradesh. The average productivity of maize in Karnataka state (3110 kg/ha) is much higher than the national productivity (1938 kg/ha). During 2004-05, a total of 8.5 lakh ha in the state was under maize with a production of 25.12 lakh tonnes and productivity of 3110 kg per ha. Area under maize is increasing rapidly in the state because of better environment, high yield and ease with which the crop is cultivated. Hence, there is an enormous scope to increase the productivity in Karnataka to a global level.

Maize has more than 1000 industrial uses and mainly used for production of starch due to its high starch content (66.2 to 77%). Maize seed oil contains highest polyunsaturated fatty acid (PUFA), linoleic acid (61.9%) and it remains as liquid at fairly low temperatures which is helpful in combating heart diseases. Maize seed oil is also low in linolenic acid (0.7%) and contains a high level of natural flavour. Maize is used primarily as food for humans in Africa and Asian sub-continent.

Principal types of maize are dent, flint, pod, pop, soft or flour, sweet and waxy corn. The floury and opaque are nutritional quality types with high tryptophan and lysine content, respectively. Maize is the only cereal, which can be used as food at various stages of its plant development. It is used as baby corn as soon as the plant flowers. Green ears of maize are used on large scale for roasting and boiling and consumed as food at dough stage.

In India, about 50-55 per cent of maize production is consumed directly as food, 30-35 per cent for poultry, piggery and fishmeal and 10 to 12 per cent in wet milling industry viz., in starch and oil and about 3 per cent in dry milling for traditional requirement like Dalia and Sattu.

A number of genotypes viz., single cross, three way cross, double top cross, double cross hybrids, composites, synthetic population are being cultivated by farmers.

Shull, 1908 and 1911) gave the original concept for production and growing of single cross hybrids, but the cost of seed production has limited its utility. Jones (1918) suggested that double cross hybrids can be produced from two single cross hybrids to reduce the cost of seed production. Subsequently, with the improvement in vigour and yield potential of inbred lines and development of better cultural practices, single crosses were adapted for commercial cultivation in the advanced countries. The recent trend even in the developing and underdeveloped countries single cross hybrid are more popular due to their higher yield levels under favorable environments and uniformity in expression and low cost of hybrid seed production. Hence, there is a greater scope for the exploitation of heterosis through single cross hybrids.

Beal (1880) was the first to conduct experiment on various hybridizations in maize. The inbreeding experiments were first reported by Darwin (1877) which continued for only one generation with limited impact on the future of maize breeding. East (1908) and Shull (1908, 1909) were first to report the results of their experiments on inbreeding and restoration of vigour upon crossing. Shull (1909) published “A pure line method of corn breeding”, which outlined the three essential steps a) large scale inbreeding to obtain many homozygous or near homozygous lines, (b) testing the selected pure lines in all possible crosses and (c) utilizing the best cross for practical corn production. In early days when relatively few lines were available, it was common to evaluate inbreds in all possible cross combinations. However, as the number of inbred parents increased, the number of possible single crosses also increased rapidly involving much labour and resource for evaluation. Hence, a simple procedure was required for the preliminary evaluation of inbred lines. Davis (1927) suggested the use of inbred \times variety or top cross test to evaluate the large number of inbred lines.

II. MATERIAL AND METHODS

Line \times tester analysis

Based on the results of top cross evaluation, best 25 S_2 lines were identified. The selected S_2 lines were planted along with four testers, namely CM-111, CI-5, KDMI-10 and NEI-9202B to make design in line \times tester crosses during kharif 2005. The salient features of the above mentioned four testers are mentioned in the Table 2. One hundred hybrids were made by crossing the best 25 S_2 lines with four testers in line \times tester mating design.

The 100 crosses along with 25 S_2 lines, four testers, viz., CM-111, CI-5, KDMI-10 and NEI-9202B and three commercial checks, viz., DMH-2, Cargil 900M and Prabha were evaluated during kharif 2005 at Agricultural Research Station, Arabhavi.

III. RESULTS AND DISCUSSION

PERFORMANCE OF S_2 PROGENIES DERIVED FROM YELLOW POOL:-

Analysis of variance:-

The analysis of variance for 16 quantitative traits in S_2 progenies of yellow pool base population are presented in Table 2. The variance due to genotype for all the 16 characters was highly significant.

Genetic variability studies:-

Genetic variability parameters of S_2 progenies like mean, range and the components of genetic variability viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability, genetic advance (GA) and genetic advance as per cent mean (GAM) were worked out for the 16 quantitative characters. Results obtained in the present investigation for each character is presented in Table 3 and 4.

Plant height at 60 DAS (cm) :-

Plant height at 60 DAS among 350 S₂ progenies ranged from 120.00 to 205.50 cm with a mean value of 164.79 cm (Table 3 and 4). Genetic components of both PCV (11.05) and GCV (10.28) were moderate coupled with high heritability (93.02%). The GA (34.91) was high with GAM of 21.18 per cent.

Ear height at 60 DAS (cm) :-

The mean value of 350 S₂ progenies for ear height at 60 DAS was 75.44 cm which ranged from 45.30 to 115.50 cm (Table 3 and 4). The variability components of both PCV (15.49) and GCV (14.10) estimates had moderate value coupled with high heritability (90.99%). The genetic advance was 21.91 with GAM value of 29.04 per cent.

Leaf area at 60 DAS:-

The mean value of 350 S₂ progenies for leaf area at 60 DAS was 393.78 cm² and it varied from 163.40 to 600.10 cm² (Table 3). Higher PCV (21.85%) and moderate GCV (19.58%) and higher heritability (89.58%) values were observed. The GA (158.81) was high with GAM of 40.33 per cent for this trait.

Cob weight (g) :-

The character cob weight had a mean value of 144.13 g and it ranged from 56.55 to 276.90 g (Table 3 and 4). For variability parameters, progenies recorded higher value for both PCV (31.43) and GCV (29.63). The heritability estimate was 94.29 per cent and this trait also had higher GA (87.99%) coupled with GAM of 61.05 per cent.

Cob length (cm) :-

The mean value of 350 S₂ progenies for cob length was 15.83 cm and it ranged from 9.55 to 22.25 cm (Table 3 and 4). Critical observation of phenotypic and genotypic coefficient of variation revealed the moderate values of 14.99 and 14.04, respectively. The heritability recorded for this trait was higher (93.66%). The genetic advance estimate was low (4.58) with GAM of 28.53 per cent.

Cob girth (cm) :-

The mean value of 350 S₂ progenies for cob girth was 13.39cm with its values ranging from 10.15 to 17.30 cm (Table 3 and 4). The variability components, viz., PCV (9.54) and GCV (8.33) exhibited lower values coupled with higher heritability (87.30%). The genetic advance (2.30) was low coupled with GAM of 17.16 per cent.

Number of kernel rows per cob:-

The trait number of kernel rows per cob recorded mean of 14.40 which ranged from 10.60 to 19.20 (Table 3 and 4). The progenies recorded moderate PCV (10.88%) and low GCV (9.86%) values. The heritability was high (90.62%) and GA (2.93) was lower with GAM value of 20.31 per cent.

Number of kernels per row:-

The mean value of 350 S₂ progenies for number of kernels per row was 30.02 with wider range from 18.55 to 46.00 (Table 3 and 4). The variability parameters like PCV (16.30) and GCV (14.11) exhibited moderate values coupled with higher heritability (86.56%). The genetic advance (8.73) showed lower value coupled with GAM of 29.06 per cent.

Pith weight (g) :-

The character pith weight had population mean value of 25.01 g and values ranged from 10.84 to 47.19 g (Table 3 and 4). The progenies recorded higher value of both PCV (29.34) and GCV (27.86). High heritability (94.93%) were recorded for this trait. Genetic advance estimate was moderate (14.35) coupled with GAM of 57.38 per cent.

Hundred seed weight (g) :-

The 350 S₂ progenies recorded overall mean of 27.05 g and it ranged from 16.92 to 42.43 g (Table 3 and 4). Genetic variability parameters like PCV (16.52) and GCV (14.58) values were

moderate for this trait. However, higher heritability (88.23%) was recorded for this trait. The genetic advance (8.12) showed lower value coupled GAM of 30.03 per cent.

Shelling percentage (%):-

The mean value of 350 S₂ progenies for shelling percentage was 82.09 which ranged from 65.31 to 90.67 (Table 3 and 4). When the progenies were compared on the basis of variability parameters, the progenies exhibited lower PCV (5.17) and GCV (4.42) coupled with higher heritability value (85.46%). The genetic parameters like GA also exhibited lower value (7.47) coupled with GAM of 9.10 per cent.

Number of kernels per cob:-

The mean of number of kernels per cob of 350 S₂ progenies was 433.92. The range for this trait varied from 235.65 to 733.60 (Table 3 and 4). When the progenies were compared on the basis of variability parameters. The progenies recorded higher values for PCV (21.26) and moderate values for GCV (18.72) coupled with higher heritability (80.08%). Other parameters like GA was high (167.30) with GAM of 38.57 per cent for this trait.

Grain yield per plant (g) :-

Grain yield per plant is one of the important characters in selection of inbred lines. This trait is highly depending on many quantitative characters, namely cob weight, cob length, cob girth, number of kernel rows per cob, number of kernels per row, tip filling and 100-seed weight.

The mean of 350 S₂ progenies was 118.79 g per plant and it ranged from 44.65 to 232.86 g (Table 3 and 4). The variability components like, PCV (34.09) and GCV (31.79) exhibited higher values coupled with high heritability (93.26%). The genetic advance (77.80) estimate was high coupled with high GAM of 65.49 per cent.

Association studies:-

The results obtained in the present investigation on the basis of association of individual characters with grain yield in S₂ progenies is presented in Table 5 and 6.

Plant height at 30 DAS (cm) :-

A highly significant positive association was recorded at both genotypic and phenotypic levels for all the traits study, except for number of kernel rows per cob (0.112) at phenotypic level (Table 5 and 6).

Plant girth at 30 DAS (cm) :-

A highly significant positive genotypic association was recorded for all the traits, except number of kernel rows per cob which recorded non-significant association (0.008) and shelling percentage which exhibited significance only at five per cent level of probability (0.107) (Table 5). Similarly at phenotypic level, a highly significant positive association was recorded for all the characters, except for number of kernel rows per cob (0.018) and shelling percentage (0.091) (Table 6).

Leaf area at 30 DAS (cm²) :-

The leaf area at 30 DAS recorded a highly significant positive association for all the characters at genotypic level, except for number of kernels per cob (0.096) which recorded non-significant association (Table 5). Similarly, all the characters recorded highly significant positive phenotypic association with this trait except leaf area at 60 DAS which was significant only at five per cent of level of probability (0.132) whereas other characters namely number of kernel rows per cob (0.094), number of kernels per row (0.310) and pith weight (0.196) exhibited non-significant association (Table 6).

Plant height at 60 DAS (cm) :-

A highly significant positive genotypic association was recorded for all the traits, except for shelling percentage (0.107) which exhibited only significant positive genotypic association at five per cent level of probability (Table 5). Similar results were also observed at phenotypic level for all characters except for 100-seed weight (0.237) and shelling percentage (0.074) which had non-significant association (Table 6).

Ear height at 60 DAS (cm) :-

A highly significant positive association was recorded for ear height with all characters for both at genotypic and phenotypic levels (Table 5 and 6).

Leaf area at 60 DAS (cm²) :-

The leaf area at 60 DAS exhibited highly significant association both at one per cent and five per cent in positive direction for all the traits, except for shelling percentage (0.081, 0.057), which showed significance only at five per cent level of probability at both genotypic and phenotypic level (Table 5 and 6).

Cob weight (cm) :-

A highly significant positive association of cob weight with all the traits was recorded at both genotypic and phenotypic levels (Table 5 and 6).

Cob length (cm) :-

The character cob length showed highly significant positive association with all the traits, except for number of kernel rows per cob (0.071, 0.080) which recorded non significant association at both genotypic and phenotypic levels (Table 5 and 6).

Cob girth (cm) :-

Cob girth exhibited highly significant positive association with all the characters both at genotypic and phenotypic levels (Table 5 and 6).

Number of kernel rows per cob :-

For this character, highly significant positive genotypic and phenotypic association was recorded with all the traits, except for plant girth at 30 DAS (0.008, 0.018), leaf area at 30 DAS (0.096, 0.094), cob length (0.071, 0.080), and shelling percentage (0.064, 0.076), which exhibited non-significant association at both genotypic and phenotypic levels (Table 5 and 6). However, the character 100-seed weight exhibited significant correlation in negative direction at (-0.130) genotypic level and non significant association at phenotypic level.

Number of kernels per row:-

The correlation coefficient across traits revealed that a highly significant positive association of this trait with all the other traits was observed at both genotypic and phenotypic levels, except for leaf area at 30 DAS (0.310) which exhibited significance only at genotypic level (Table 5 and 6).

Pith weight (g) :-

The trait pith weight recorded highly significant positive association with all the characters except shelling percentage which recorded highly significant negative association both at genotypic (-0.239) and phenotypic (-0.241) levels and leaf area at 30 DAS (0.196) which recorded significant association at genotypic level (Table 5 and 6).

Hundred Seed weight (g) :-

Majority of the traits exhibited highly significant genotypic positive association with 100-seed weight except number of kernel rows per cob (-0.130) which recorded significant negative association (Table 5). Similarly, a highly significant positive phenotypic association was recorded with all the traits, except for plant height at 60 DAS (0.237) and number of kernel rows per cob (-0.103) (Table 6).

Shelling percentage (%):-

The character shelling percentage exhibited a lot of variation in association with different characters under study. A highly significant genotypic association was recorded for all the characters except for plant girth at 30 DAS (0.107) and plant height at 60 DAS (0.107) which recorded significant positive association at 5% level of probability and the other characters like leaf area at 60 DAS (0.081) and number of kernel rows per cob (0.064), which exhibited non-significant association (Table 5). Shelling percentage exhibited highly significant positive phenotypic association with majority of the traits, except for plant girth at 30 DAS (0.091), plant height at 60 DAS (0.074), leaf area at 60 DAS (0.057) and number of kernel rows per cob (0.076) traits (Table 6).

Number of kernels per cob:-

The character number of kernels per cob exhibited highly significant positive genotypic and phenotypic association with all the characters under this investigation (Table 5 and 6).

Grain yield per plant (g) :-

Study of nature of association in 350 S₂ progenies based on grain yield per plant is another important aspect which helps for selection of lines in early generation based on other traits. Hence, it is necessary to understand the nature of association existing among the different traits with grain yield per plant. The trait grain yield per plant exhibited highly significant association in positive direction with all the traits under study at both genotypic and phenotypic levels (Table 5 and 6).

EVALUATION OF S₂ GENERATION BY TOP CROSS TEST:-

The use of top cross test provides an efficient method for preliminary evaluation of inbred lines. The use of top cross evaluation is one of the methods for early testing of inbred lines. Top cross test is especially useful for determining general combining ability of a large number of inbred lines. The top cross test with a heterogeneous tester gives valuable information for characters which are not complex in inheritance.

Top cross testing of S₂ progenies with standard open pollinated line CM-501 was done for the early testing for general combining ability. ANOVA indicated the presence of highly significant differences among top crosses for all the 13 characters studied.

Wide range of performance for different growth and yield parameters was observed among 350 top crosses with CM-501. The overall mean grain yield per plot of top cross hybrids was 1.25 kg with a range from 0.74 to 1.77 kg per plot. Twenty four top cross hybrids were superior by exhibiting more than five per cent superiority for grain yield per plot over best check Cargil 900-M (1.42 kg/plot).

Among superior twenty five top crosses whose lines were further utilized for line × tester analysis were critically evaluated for their per se performance and growth parameters. It is found that 13 top cross hybrids 231 × CM-501, 249 × CM-504, 246 × CM-501, 269 × CM-501, 278 × CM-501, 236 × CM-501, 283 × CM-501, 315 × CM-501, 264 × CM-501, 398 × CM-501, 176 × CM-501, 365 × CM-501 and 185 × CM-505 recorded more than ten per cent superiority with respect to grain yield compare to best check Cargil 900-M (1.42 kg/plot). In general most of these hybrids had higher grain number per plant and lower pith weight compared to remaining identified hybrids. Davis (1927) evaluated the S₂ lines for combining ability by top cross test. The studies of Jenkins (1935), Lonquist (1950) and Wellhansen (1952) have clearly indicated the early detection of lines having high combining ability by early testing.

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