



**GENETIC VARIABILITY IN EARLY INBREEDING GENERATION OF
YELLOW POOL BASE POPULATION
A). BASE POPULATION, B). S₀ GENERATION IN MAIZE (ZEA MAYS L.)**

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Abstract

Study was conducted to assess the magnitude of heterosis and combining ability in the line × tester cross material involved 100 hybrids generated by crossing 25 lines with four testers and 3 commercial hybrid check (900 M, DMH-2 and Prabha) in maize during 2005-06 at Agricultural Research Station, Arabhavi. The analysis of variance indicated significant amount of variability among the genotypes for yield and yield contributing traits. Among the hybrids, ARYP-24 × CM-111 and ARYP-15 × CM-111 were found to be the best cross combinations for grain yield and its components.

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. 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).

Maize is physiologically more efficient crop with high grain yield and wide adaptation. It is grown from 58° N to 40° S, from below sea level to altitudes higher than 3000 m and in areas of lower rainfall (250 mm) to high rainfall (5000 mm) (Shaw, 1988 and Dowswell *et al.*, 1996). However, it is mainly grown in the warmer parts of temperate regions and in humid-subtropical climate. The highest production is in areas with the warmest month isotherms from 21° to 27°C and a frost-free season of 120 to 180 days duration. Today, maize has become an all season crop in India.

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.

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.

The efficiency and success of hybrid maize breeding depends on the contribution of heterotic effects from the superior inbred lines. The superior cross combination may be exploited as commercial single cross. Usually, the hybrid development programme in maize involves development of inbred lines, evaluation of inbred lines, crossing of selected inbreds and production of hybrids. In this context, a programme on development of inbred lines was initiated by using inbreeding system utilizing yellow pool as the base population. Yellow pool is a blend of 50 elite lines received from Directorate of Maize Research (DMR), New Delhi and inter mated for four cycles at Agricultural Research Station, Arabhavi. The S_2 lines derived from this population were evaluated by line \times tester analysis involving four diverse testers in *kharif* season (2005) to know their performance, combining ability and nature of inheritance of different quantitative traits. The line \times tester (L \times T) design is basically an extension of top cross analysis involving more than one tester (Kempthorne, 1957). Thus, keeping these views in background, the proposed work was undertaken to develop hybrids suitable for *kharif* season.

II. MATERIAL AND METHODS

Fifty elite breeding lines (Table 1) were received from Directorate of Maize Research (DMR), IARI, New Delhi for development of full season heterotic yellow pool. These lines were raised and allowed to open pollinate for four generations (intermating) without exercising any selection. In each generation, the plants were raised in half-sib family method and at the end of fourth generation, the seeds were collected and grown as base population at College of Agriculture, Dharwad in isolation and allowed to open pollinate. Sufficient care was taken to maintain more than 10 thousand plant population. Out of this population, 150 plants were tagged in each grid by dividing entire population into 10 grids of 150 sq. mt. at the time of tassel emergence, based on vigour, standing ability, silk and tassel traits and free from disease incidence, 800 cobs were selected based on grain yield (*per se*) performance and this material formed basis for further inbreeding and isolation of inbred lines. The experiments were laid out at Agricultural Research Station, After thorough land preparation, hand dibbling was done with two seeds per hill and thinned out to maintain single plant per hill during second week after sowing (10-15 days after sowing). The crop was applied with recommended dose of fertilizers. The crop was raised with the recommended package of practices as per schedule.

Observations on quantitative traits:-

In these investigations, data were collected in respect of quantitative traits. Observations on quantitatively inherited traits were recorded on five competitive randomly selected plants. The average was taken as the mean of the treatment. The way in which observations were recorded is described below.

Plant height at 30 days after sowing (cm), Plant girth / stem thickness at 30 days after sowing (cm), Leaf area at 30 days after sowing (cm²), Plant height at 60 days after sowing (cm), Ear height at 60 days after sowing (cm), Leaf area at 60 days after sowing (cm²), Ear weight (g), Ear length (cm), Ear circumference (cm), Number of kernel rows per cob, Number of kernels per row, Number of kernels per ear, Hundred grain weight (g), Shelling percentage, Pith / shank / heart weight (g), Kernel yield per plant (g), Kernel yield per plot (kg/plot), Kernel / grain yield per hectare (q/ha).

Observations on qualitative traits:-

The data were collected in respect of 12 qualitative characters and procedure of recording is described below. Seedling vigour, Seedling colour, Leaf shape, Tassel size, Tassel shape, Silk colour, Anther colour, Kernel type, Kernel / grain size, Kernel colour, Pith colour, Tip filling of cob,

Statistical analysis :-

Analysis of variance:-The data were subjected to statistical analysis for randomised block design (RBD) as described by Panse and Sukhatme (1962). The mean values of the entries in each replication were used for analysis of variance (ANOVA). The significant difference among genotypes was tested by

'F' test at one per cent and five per cent levels of probability. The significance was tested by referring to table given by Snedecor and Cochran (1967).

Estimation of variance:-Phenotypic and genotypic components of variance were computed according to the formula given by Lush (1940) and Choudhary and Prasad (1968).

Coefficient of variability:-Genotypic and phenotypic coefficients of variability were computed according to Burton and Devane (1953).

Estimation of Heritability:-Broad sense heritability was estimated as the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Hanson *et al.*, 1956).

Genetic advance (GA) :-Genetic advance (GA) was computed according to the formula given by Johnson *et al.* (1955a).

Genetic advance over mean (GAM) :-

Genetic advance over mean was computed by the formula:

$$GAM = \frac{GA}{\bar{x}} \times 100$$

Where \bar{x} = mean of the population

Combining ability analysis:-

Analysis of variance:-The mean of each character for each entry were subjected to line \times tester analysis and the variance of general combining ability of different cross combinations were estimated by the procedure developed by Kempthorne (1957).

Estimation of variance components:-From the mean squares, covariance of full sibs (FS) and covariance of half sibs (HS) were estimated as per Singh and Choudhary (1985).

Estimation of heterosis:-Heterosis expressed as per cent increase or decrease of F₁ hybrid over mid-parent (average or relative heterosis), better parent (heterobeltiosis) and commercial checks (standard heterosis) were computed for each character using the following formulae (Turner, 1953 and Hayes *et al.*, 1955).

III. RESULTS AND DISCUSSION

Performance of Yellow Pool Base Population:-

Mean and range values for ten quantitative traits among selected progenies in yellow pool base population:-

The yellow pool base population comprising of 10,000 plants was raised during *khariif* season. A total of 1500 plants were initially tagged based on plant morphological traits and finally 800 cobs were selected based on plant morphology and cob characters. The cobs harvested from such selected plants were assessed for following ten quantitative traits whose results are presented below.

Cob weight (g) :-

The cob weight among 800 progenies ranged from 91.90 to 375.00 g. and the mean cob weight was 160.35g (Table 5). However, the median value (155.31g) was comparatively lower than mean value, while the mode value (170.00g) was relatively higher than the mean cob weight. The skewness of the results indicated the negative distribution in the base population. The kurtosis (1.57) and skewness (0.89) values supported the deviation from normal distribution. The cob weight trait recorded higher coefficient of variance (23.49%) with coefficient range value of 0.61.

Cob length (cm) :-

The cob length ranged from 9.00 to 23.00 cm (Table 5).The median (15.00 cm) and mode (15.00cm) values were comparable with the mean value (15.08 cm). The mode value (15.00cm) was equal to the mean value indicating a positively skewed distribution in the base population and a marginal deviation from the normal distribution. The cob length recorded higher coefficient of variance (13.89%)

with a coefficient range of 0.44. As many as 312 progenies (39%) recorded cob length ranging from 15.08 to 17.17 cm (Table 6).

Cob girth (cm) :-

The cob girth in population ranged from 10.00 to 18.00 cm with a mean of 13.08cm (Table 5). The magnitude of median (13.00) and mode (13.00) were comparable with mean value. This indicated the positive skewness and narrow deviation from the normal distribution. The cob girth recorded relatively lower coefficient of variation (9.25) with a coefficient range of 0.29.

Number of kernel rows per cob:-

The number of kernel rows per cob ranged between 8.00 to 20.00 rows per cob (Table 5). The magnitude of median (14.00) and mode (14.00) were comparable with the mean number of kernel rows per cob (13.79). The magnitude of kurtosis indicated negative distribution (-0.19) while the skewness indicated positive distribution (+0.19). The data indicated negatively skewed distribution with narrow deviation from the normal distribution. The coefficient of variance with respect to number of kernel rows per cob was 14.69 with a coefficient range value of 0.43.

Number of kernels per row:-

The number of kernels per row ranged from 18.00 to 48.00 with a mean value of 30.90 (Table 5). The magnitude of median (31.00) was comparable with the mean value, while, the mode value (28.00) was relatively lower than mean value. The skewness recorded positive distribution (0.30), while the kurtosis (-0.40) recorded negative distribution indicating the deviation from normal distribution. The coefficient of variation was 18.38 per cent with a co-efficient range of 0.45.

Number of kernels per cob:-

The number of grains per cob ranged from 200.00 to 774.00 with a mean of 428.09 (Table 5). The magnitude of median (420.00) and mode (336.00) were relatively lower than mean value. This indicated negatively skewed distribution from the normal distribution. The kurtosis was negative (-0.02) while skewness (0.58) had positive. The number of grains per cob recorded higher coefficient of variation value (25.64%) with a coefficient of range of 0.60.

Hundred seed weight (g) :-

The range of 100-seed weight was between 16.53 to 46.53 g with a mean value of 29.55g (Table 5). The median value (29.21) and mode value (29.28) were relatively lower than the mean (29.55 g). This indicated negatively skewed distribution and deviation from the normal distribution in the base population. However, the kurtosis (0.42) and skewness (0.42) indicated relatively lesser deviation. The 100-seed weight recorded coefficient of variation of 16.88 per cent with a coefficient range of 0.48.

Shelling percentage (%):-

The shelling per cent in the base population ranged between 74.71 to 95.60 per cent (Table 5). The mean shelling percentage was 86.05. The magnitude of median (86.24) and mode (86.65) were comparable with the mean value (86.05) indicating negatively skewed distribution. The kurtosis value of 0.76 and skewness of -0.43 were recorded for the shelling percentage. The shelling percentage recorded minimum coefficient of variation (3.14) with a coefficient of range of 0.12.

Grain yield per plant (g) :-

The grain yield per plant ranged between 72.73 to 318.18g, with a mean value of 138.15 g (Table 5). The median (133.93) was lesser than the mean value (138.15), while the mode value (151.91) was relatively higher than mean value. This indicated both negative and positive skewed distribution in the base population. The kurtosis (1.45) and skewness (0.90) were appreciably deviated from the normal distribution. The grain yield per plant recorded coefficient of variation of 24.27 per cent with a coefficient of range of 0.63.

Frequency distribution of progenies for various quantitative traits in maize yellow pool base population:-

The frequency distribution of the progenies for different quantitative characters such as cob weight, cob length, cob girth, number of kernel rows per cob, number of kernels per row, pith weight, 100-seed weight, shelling percentage, number of kernels per cob and grain yield per plant are presented here under.

Cob weight (g) :-

Out of 800 progenies in the base population, the class, mean minus one standard deviation to mean ($M - SD$ to M) comprised of 277 progenies with a range of 122.70 to 160.35 g, while the class, mean to mean plus one standard deviation (M to $M + SD$) comprised of 176 progenies with a range of 160.35 to 198.01 (Table 6). As many as 96 progenies belonged to class mean plus one standard deviation to mean plus two standard deviation ($M + SD$ to $M + 2 SD$) with range between 198.01 to 235.67 and 31 progenies (3.88%) exhibited higher values belonging to class ($>M + 2 SD$) values greater than 235.67g. As many as 453 progenies recorded higher cob weight than the population mean (160.35 g) which accounted for 56.63 per cent of total progenies.

Cob length (cm) :-

Among the 800 progenies in the base population, five recorded cob length with class value of less than 10.80 cm that belonged to the class less than $M - 2 SD$ (Table 6). Equal number of progenies (312) belonged to the class $M - SD$ to M (12.99 to 15.08) and M to $M + SD$ (15.08 to 17.17). Large number of progenies (406) belonged to the higher class M to $M + SD$ to $>M + 2 SD$ (>19.26) accounting for 50.75 per cent of the 800 progenies.

Cob girth (cm) :-

The frequency distribution for cob girth based on the class values indicated that maximum number of progenies (259) belonging to $M - SD$ to M (11.87 to 13.08) followed by 258 lines to the class values of M to $M + SD$ (13.08 to 14.29) (Table 6). The minimum numbers of progenies (12) belonged to the class value of less than 10.66cm. The total number of progenies belonging to the higher class commencing from M to $M + SD$ to more than $M + 2 SD$ (363) accounted for 45.38 per cent of the total base population based on cob girth.

Number of kernel rows per cob:-

The frequency distribution recorded equal number of progenies (266) under both classes $M - SD$ to M (11.76 to 13.79) and M to $M + SD$ (13.79 to 15.82), followed by 167 progenies (20.88%) belonging to the class $M + SD$ to $M + 2 SD$ with a class value of 15.82 to 17.85 number of kernel rows per cob (Table 6). The progenies which belonged to higher class values were 477, accounting for 59.63 per cent of the base population.

Number of kernels per row:-

The frequency distribution for 800 progenies based on the class values revealed that 300 progenies belonged to the class values of $M - SD$ to M to M to $M + SD$ (25.22 to 30.90) to (30.90 to 36.58) (Table 6). As many as 145 progenies belonged to a class value of 36.58 to 42.26 ($M + SD$ to $M + 2 SD$). The total number of progenies in the favourable class values (461) accounted for 57.63 percentage of the base population.

Number of kernels per cob:-

Out of 800 base progenies frequency distribution revealed equal number lines (153) belonged to two classes *viz.*, 318.35 to 428.09 (M to $M + SD$) to 428.09 to 537.83 (M to $M + SD$) kernel number (Table 6). The maximum numbers of progenies (268) belong to the class value ranging from $M + SD$ to $M + 2 SD$ (88.75 to 91.45). The total number of progenies with desirable number of kernels per cob were 471, accounting for 58.88 per cent of the total progenies in the base population.

100 seed weight (g) :-

Out of 800 progenies, 282 belonged to the class M-SD to M followed by 281 belonging to the class M to M+SD (29.55 to 34.54) (Table 6). Minimum number of lines (8) was recorded in a class with value less than 19.57g of 100-seed weight. The total Number of progenies which belong to higher seed weight category (M to M+SD to > M+2 SD) (401) accounted for 50.13 per cent of the total progenies.

Shelling percentage (%):-

The frequency distribution of 800 progenies revealed equal number of progenies (393) belonging to the two classes viz., M-SD to M and M to M+SD (83.35 to 86.05 and 86.05 to 88.75) (Table 6). None of the lines belonged to the class value of more than 91.45 shelling per cent under the category >M+2 SD. The total number of progenies with better shelling values (402) accounted for the 50.25 per cent of the base population.

Grain yield per plant (g) :-

Out of 800 progenies, thirty five per cent (280) exhibited grain yield per plant between 104.62 to 138.15g (M-SD to M) per plant followed by 279 (34.88%) progenies, whose class values were between 138.15 to 171.68g (M to M+SD)per plant (Table 6). As many as 85 progenies belonged to the class of M + SD to M + 2 SD (171.68 to 205.21g), accounting nearly for 10.63 per cent of the total progenies. However, there were only 33 (4.13%) progenies which recorded grain yield per plant higher than 205.21g per plant.

Distribution of progenies for various qualitative traits in base population:-

The distribution for qualitative traits of the progenies in yellow pool base population were studied for grain colour, grain size, grain texture pith colour and tip filling and the same is presented here under.

Grain colour:-

Out of 800 progenies in the base population, 369 progenies were with yellow colour followed by 309 with orange yellow and 122 progenies had yellow orange grain colour (Table 7). The frequency of yellow population was relatively high (46.13%) followed by orange yellow (38.63%). The frequency of yellow orange progenies was minimum with per cent value of 15.25.

Grain size:-

Among the 800 progenies, 546 had medium grain size accounting for 68.25 per cent of the population followed by 219 progenies with bolder grain size (27.37%) (Table 7). Thirty four progenies recorded smaller grain size, while only one progeny recorded very bold grain size. Highest number of progenies (95.6%) recorded grain size which ranged between bold to medium grain size.

Grain texture:-

Out of the 800 progenies, 713 possessed flint grain texture accounting to 89.13 per cent of the population (Table 7). The other progenies exhibited grain texture such as dent (8 progenies), semident (26 progenies) and semi-flint (53 progenies) accounting to 10.87 per cent of the base population.

Tip filling:-

Moderate tip filling was recorded by 437 progenies accounting to 54.63 per cent, while 326 lines exhibited no tip filling accounting to 40.75 per cent of the base population (Table 7). Only 37 progenies recorded complete tip filling accounting for 4.63 per cent of the base population.

IV. DISCUSSIONS

Characterization Of Yellow Pool Base Population Based On Quantitative And Qualitative Traits:-

The proportion of superior inbred lines is determined by the proportion of the superior genotypes in the base population and the effectiveness of selection during the inbreeding. Hence, selection of proper germplasm source is an essential part of breeding programme. The breeding methods, efficiency of selection and final success are highly dependent on the base population chosen. Tannar and Smith (1987) studied various maize population derived from synthetics using two methods of recurrent

selection and population derived from open pollinated variety based on the changes in grain yield, grain moisture and lodging. The study indicated the importance of effective population size and selection during S_1 or S_2 was more effective in eliminating unfavourable allele in the population.

In an another attempt, made to establishing inbreeding tolerant base population, Choudhary and Choudhari (2001) using DH-8644 and Jogia local as a base population indicated the possibilities of establishing inbreeding tolerant base population by selecting crosses which showed non-significant inbreeding depression with better yield performance.

Out of ten quantitative characters recorded in 800 selected progenies on cob characters, the progenies exhibited very high coefficient of variation for cob weight, pith weight, number of kernels per cob and grain yield per plant coupled with relatively high estimates of coefficient of range values indicating the presence of high variability in the base population. Further the median and mode values indicated positive skewed distribution for pith weight with high mode value suggesting the greater scope for selection of progenies for lower pith weight there by shelling percentage can be improved. It is interesting to note that out of the traits which recorded high estimates of coefficient of variability, cob weight and the grain yield per plant revealed platykurtic distribution with a high mode value than their respective mean values indicating the presence of relatively high proportion of superior progenies with higher mean values for both the characters in base population. Carlone and Russell (1989) selected 247 progenies from BSSS population and advanced to S_2 generation. Similarly, Venkatesh *et al.* (2001) selected 500 progenies from CMIP2-7 population and selfed it for two generation to obtain S_2 generation. The results on the *per se* performance of line, crosses vis-à-vis revealed that high yielding sister line crosses (SLCs) recorded high values for various yield related traits.

Cob girth and shelling percentage exhibited lower coefficient of variability with a 0.29 and 0.12 coefficients of range values, respectively with a platykurtic distribution in both the cases. However, shelling percentage had the greater mode value than the mean indicating the presence of superior progenies with a high shelling percentage in the base population comparatively with cob girth. It is interesting to note that cob length, number of kernels per cob, number of kernels per row and 100-seed weight had more or less a similar coefficient of range value varying from 0.43 to 0.48 revealing the presence of moderate variability for these traits in the selected progenies in base population. Wide range of cluster mean, for various traits were observed by Saxena and Sandhu (1989) in a divergence study involving 140 genotypes belonging to diverse geographic region.

Selected 800 progenies were grouped into different classes based on their superiority over the mean (Table 4). When superior progenies were scored based on greater values than mean + two standard deviation ($>M + 2 SD$) for ten quantitative traits, two traits namely number of kernels per cob and number of kernel rows per cob had high frequency of progenies *i.e.*, 6.25 per cent for number of kernels per cob and 5.50 per cent for number of kernel rows per cob followed by 100-seed weight and grain yield per plot. However, there were no superior progenies for shelling percentage under this class. Similar results were quoted by earlier workers. Marker and Joshi (2005) reported genetic gain for two traits *vis-à-vis* 100-grain weight and ear diameter through full sib family selection.

In a similar frequency classification made considering the class value of $M + SD$ to $M + 2 SD$, high frequency of superior progenies were scored for number of kernels per cob (33.50%) and number of kernel rows per cob (20.88%). These two traits also had similar trend in the higher class value. However, as many as 49.00 per cent progenies had shelling percentage between M to $M + 2 SD$ followed by cob length with 39.00 per cent of the progenies. Out of ten traits under study, the base population had maximum number of superior progenies in higher class values for number of kernel rows per cob and number of kernels per cob which are important components of a grain yield, revealing the importance of the Yellow pool population for isolation of productive inbred lines at later generations.

These were also scored for grain colour, grain size, grain texture, pith colour and tip filling characters. As many as 713 (89%) progenies were flint type, 546 (68.25%) with medium grain size and

437 (54.60%) with a medium tip filling traits. However, there were only 37 (4.60%) plants with a complete tip filling and 122 progenies with a yellow orange grain colour. Majority of the progenies (87.40%) had the white pith colour.

The grouping made on the basis of qualitative cob character clearly revealed the presence of desirable alleles for grain texture, grain size and tip filling in the Yellow pool population.

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