

Genetic variability studies in banana hybrids

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Accepted : August, 2008

ABSTRACT

Genetic Variance, Heritability, genetic advance and correlation coefficient components were studied in 19 hybrids in order to identify desirable genotypes for crop improvement programme. On the basis of fruit quality characters along with more number of fruits/hand, bunch weight and early crop duration, the hybrids NPH-02-01 and h-03-19 were observed to be more potential. The estimates of GCV and PCV were high for bunch weight, moderate GCV and PCV for number of hands/bunch and pseudostem height indicated better scope of improvement through selection. The genetic advance as percentage of mean ranged from 35.86 to 96.88. High estimates of heritability values accompanied with high genetic gain were observed for bunch weight, number of fruits/hand, days taken from planting to shooting, number of leaves at shooting and crop duration. A very strong positive and significant correlation was recorded between bunch weight and number of fruits/hand (0.752) and number of hands/bunch (0.632) indicating that effective improvement through these characters could be achieved in banana.

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Key words : Genetic variability, Banana hybrids, Heritability, Genetic advance.

Banana is the important staple and commercial crop world wide, but its improvement through artificial selection has proven difficult due to a limited understanding of the genetic organization and meiotic behaviour of the species (Ortiz and Vuylsteke, 1996). Genetic improvement of musa has traditionally been carried out through interspecific and interdiploidy crosses, with the major objective of producing hybrids that are high-yielding per unit area and time (Buddenhagen, 1997). Hence, improved hybrids should be photosynthetically efficient, early to mature in the first production cycle, and display minimum delay between consecutive harvests (Eckstein *et al.*, 1995; Ortiz and Vuylsteke, 1994). The present investigation was taken up in TNAU, Coimbatore, India, to evolve banana hybrids resistance to nematodes involving the resistant male parents like Anaikomban and Pisang Lilin with the commercial cultivar Karpooravalli.

MATERIALS AND METHODS

The hybridization resulted in 19 hybrids with 15 tetraploids (AABB), 2 triploids (AAB) and 2 diploids (AB). These hybrids were evaluated in their phase I generation (seed to sucker- single plant segregant) by Damodaran, 2003 for agronomic traits as a single plant. These hybrids were taken for their phase II generation (sucker to sucker) and their performances were recorded. The experiment was laid out in Randomized Block Design with three replications and five plants per replication. The observations *viz.*, days taken from planting to shooting, height of pseudostem, height of the following sucker,

number of leaves at shooting, number of leaves at harvest, crop duration, girth of pseudostem, number of hands / bunch, number of fruits / hand and bunch weight. To characterize and categorize the hybrids, the fruit quality characters were also assessed but not included for the variability studies.

The replicated values were subjected to statistical analysis of variance as prescribed by Panse and Sukhatme (1984).

The phenotypic and genotypic variances were computed as per the methods suggested by Johnson *et al.* (1955).

$$\text{Phenotypic variance } (\sigma^2_p) = (\sigma^2_g) + (\sigma^2_e)$$

where,

$$(\sigma^2_e) = \text{error variance}$$

$$\text{Genotypic variance } (\sigma^2_g) = \frac{M_1 - M_2}{r}$$

where,

M_1 = Mean sum of squares for genotypes

M_2 = Mean sum of squares for error

r = Number of replications

$$\text{Environmental variance } (\sigma^2_e) = S(X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X})$$

where,

X_{ij} = Mean sum of treatments and replications

\bar{X}_i = Mean of treatments

Table 1: Details of the hybrids used in the study

Sr. No.	Hybrid	Genome	Planting to shooting (days)	Height of pseudo stem (cm)	Height of Following sucker (cm)	No. of leaves at shooting	No. of leaves at Harvest	Crop cycle Duration (days)	Girth of pseudo stem (cm)	Bunch wt (kg)	No. of hands/ bunch	No. of fingers/ bunch
1.	H-03-04	AABB	360.50	395.00	160.00	19.00	15.00	476.00	68.00	4.50	5.00	60.00
2.	H-03-05	AABB	295.60	402.80	87.60	18.00	11.00	400.50	83.50	6.00	11.00	138.00
3.	H-03-06	AB	265.00	248.60	109.30	12.80	9.50	356.60	61.50	10.00	7.40	105.00
4.	H-03-07	AABB	298.30	260.00	122.60	14.00	10.00	420.00	60.00	2.50	3.00	18.00
5.	H-03-08	AB	260.00	218.40	115.50	14.00	11.00	352.80	52.80	4.00	5.00	70.00
6.	H-03-09	AABB	296.50	420.00	120.00	17.50	15.50	418.20	102.60	8.50	12.00	186.00
7.	H-03-10	AABB	292.00	386.60	95.00	20.00	16.00	426.00	89.00	6.50	8.70	98.00
8.	H-03-11	AABB	306.00	435.70	128.30	18.00	14.50	420.00	92.20	9.50	15.00	230.00
9.	H-03-12	AABB	314.20	423.20	118.00	22.50	17.00	434.70	78.50	9.00	12.00	156.00
10.	H-03-13	AABB	334.50	482.00	102.50	21.00	16.00	446.20	98.40	12.00	14.50	198.00
11.	H-03-14	AABB	308.00	392.00	133.90	17.00	12.00	442.00	88.00	3.50	7.00	69.00
12.	H-03-15	AAB	316.20	388.10	85.50	16.50	13.00	448.20	90.60	8.00	14.00	125.00
13.	H-03-16	AABB	286.70	493.70	69.60	23.00	16.50	396.20	100.70	6.00	9.00	144.00
14.	H-03-17	AABB	326.00	458.00	100.80	19.60	12.00	431.10	112.00	10.50	9.00	120.00
15.	H-03-18	AABB	410.50	398.00	92.60	19.00	12.50	522.00	92.50	5.00	6.00	86.00
16.	H-03-19	AABB	312.00	470.20	70.80	19.00	14.30	437.50	96.00	14.00	12.60	206.00
17.	H-03-20	AABB	428.40	398.60	108.00	18.70	14.00	553.90	76.00	6.50	11.00	132.00
18.	H-03-21	AABB	300.50	349.50	90.50	17.00	11.00	418.60	74.50	10.00	11.20	128.00
19.	NPH-02-01	AAB	220.00	360.00	74.00	12.00	9.00	342.00	72.50	19.00	11.00	213.00

\bar{X}_j = Mean of replications

\bar{X} = Grand mean

Heritability and genetic advance as percentage of mean:

Heritability in the broad sense (h^2) was derived based on the formula proposed by Lush (1940) and expressed in percentage.

$$h^2 = \frac{(\sigma^2_g)}{(\sigma^2_p)} \times 100$$

where,

(σ^2_g) = Genotypic variance

(σ^2_p) = Phenotypic variance

Genetic advance was estimated by the following formulae as per the methods of Johnson *et al.* (1955).

$$\sqrt{\sigma^2_{pxh^2k}}$$

where,

σ^2_p = Phenotypic variance

h^2 = Heritability

k = Selection differential constant, 2.06 at 5% selection intensity (Falconer, 1967).

Classification of genetic parameters proposed by Philomina (2000) was followed

Genetic parameter	Low	Moderate	High
GCV and PCV	0 to 20 %	20 to 30 %	30% and above
Heritability	0 to 30 %	30 to 60%	60% and above
Genetic advance as per cent mean	0 to 10%	10 to 20 %	20% and above

Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV):

The phenotypic and genotypic coefficient of variation was worked out as per the methods suggested by Burton (1952).

$$\text{Genotypic coefficient of variation} = \frac{\sqrt{\frac{2g}{\text{Mean}}}}{\text{Mean}} \times 100$$

$$\text{Phenotypic coefficient of variation} = \frac{\sqrt{\frac{2g}{\text{Mean}}}}{\text{Mean}} \times 100$$

Correlation coefficients:

Phenotypic and Genotypic correlation coefficients were worked out using the following formula as outlined by Johnson *et al.* (1955).

Genotypic correlation coefficient:

$$r_{g.x.y} = \frac{\text{Genotypic covariance between x and y}}{(\text{Genotypic variance of x} \times \text{Genotypic variance of y})^{1/2}}$$

where,

r_g = Genotypic correlation coefficient
 x and y = Variables or characters under consideration

The significance of these correlation coefficients was tested by referring to the table given by Panse and Sukhatme (1984).

Path coefficient analysis:

The direct and indirect effect of component characters on number of flowers per candle was estimated through path analysis technique (Wright, 1954 and Dewey and Lu, 1959).

Lenka and Mishra (1973) suggested the following scales for the categorization of direct and indirect effects.

Scale	Category
0.00 to 0.09	Negligible
0.10 to 0.19	Low
0.20 to 0.29	Medium
0.30 to 0.99	High
≥ 1.00	Very High

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant genotypic difference for all the ten characters depicting greater diversity studies in the experimental material under study (Table 2).

Results on phenotypic co-efficient of variability (PCV), genotypic co-efficient of variability (GCV), heritability (h^2 per cent) and genetic advance as per cent

of mean (GA per cent) for ten characters are furnished in Table 2. High GCV of 47.57 and PCV of 48.11 were recorded for the characters bunch weight and for weight of fruits, high GCV of 44.88 and PCV of 45.63 were recorded. Similarly, for number of hands/bunch, a moderate GCV of 27.29 and PCV of 29.34 were recorded and for pseudostem height, a moderate GCV of 28.75 and PCV of 30.52 were recorded.

With the help of GCV alone, it is not possible to determine the amount of variation that is heritable. Heritable variation can be found out with greater degree of accuracy when heritability (h , broad sense) is taken into consideration along with genetic advance (GA). Hence, both heritability and genetic advance were determined to get a clear picture of the scope of improvement in various characters through selection.

All the ten characters showed high heritability. However, considerable variations were noted for genetic advance. High genetic advance was observed for bunch weight (96.88) and number of fruits/hand (90.95), while low amount of genetic advance was recorded by number of leaves at harvest (41.05) and crop duration (35.86). Rest of the traits exhibited moderate genetic advance of mean.

The genotypic correlation values for the ten characters revealed that all the characters except the height of the following sucker were positively associated with bunch weight. Except days taken from planting to shooting, numbers of leaves at shooting and harvest and crop duration, all the other characters are significantly associated with bunch weight. Among the traits, positive and significant correlation was found in number of leaves at harvest, crop duration and pseudostem girth with all the other traits.

The components, days taken from planting to shooting, pseudostem height, crop duration and number

Table 2: Variability, heritability and genetic advance as percentage of mean for phenotypic characters in banana hybrids

Sr. No.	Character	GCV	PCV	Heritability (%)	Genetic advance (%) of mean
1.	Days taken from planting to shooting	21.1996	21.6272	96.08	42.8078
2.	Height of pseudostem (cm)	28.7532	30.5278	88.71	55.7884
3.	Height of following sucker (cm)	24.4277	25.9424	88.66	47.3831
4.	Number of leaves at shooting	21.8748	22.3577	95.73	44.0889
5.	Number of leaves at harvest	22.2288	24.7945	80.37	41.0528
6.	Crop Duration (days)	17.9049	18.4133	94.55	35.8657
7.	Girth of pseudostem (cm)	27.2912	29.3472	86.48	52.2811
8.	Number of hands/bunch	39.1812	40.6343	92.98	77.8270
9.	Number of fruits/hand	44.8891	45.6375	96.75	90.9553
10.	Bunch weight (kg)	47.5700	48.1150	97.75	96.8841

of fruits/hands alone exerted positive and direct effects on bunch weight. However, their effects were significant only with pseudostem height, pseudostem girth, number of hands/bunch and number of fruits/hand. The pseudostem height had high and positive indirect effect on bunch weight via number of fruits/hand (0.5313), while high and negative indirect effect via number of leaves at shooting (-0.4196). The pseudostem girth had high and positive indirect effect on bunch weight via pseudostem height (0.4238) and number of fruits/hand (0.5055) and high and negative indirect effect via number of leaves at shooting (-0.3573).

Phenotypic variance was relatively higher than the genotypic variance for all the traits. However, the magnitude of difference for most of the traits indicates that there was lesser influence of environment on these characters. This reveals that selection based on any traits would definitely reflect on bunch weight in these hybrids. Azhakiamaavalan (1979), Nayar (1952), Rangasamy (1980) and Tenkouano (1998) earlier made similar observations.

High genotypic and phenotypic co-efficient of variation was recorded for bunch weight and weight of the fruits while moderate GCV and PCV was observed by number of hands/bunch and pseudostem height (Table 3). This was further supported by the higher magnitude of heritability coupled with higher magnitude of genetic advance registered for most morphological traits especially for bunch weight, number of fruits/hand, days to shooting, number of leaves at shooting, crop cycle duration and number of hands/bunch. Burton (1952) suggested that genetic co-efficient of variability estimate would furnish the most reliable information on the amount

of advance expected from the selection. Correlation studies also further emphasized the association of bunch weight with pseudostem height, girth, number of leaves, days to shooting, number of hands / bunch and number of fruits / bunch. Hence in any hybrid before selection apart from bunch, due weightage should be given for their morphological traits also. The high variability and heritability along with genetic advance as percentage of mean expressed by the above mentioned traits indicated that the potential hybrids could be tested in multi-local traits and selected as donors for these characters or used as parent in hybridization programme.

The complexity of yield makes the total correlations insufficient to explain the true association between the characters. In this situation, path analysis serves as a tool for separating the total correlations into direct and indirect effects of different characters influencing the yield (Table 4). In the present investigation, among the nine characters correlated with yield, direct significant positive effect was obtained only with pseudostem height, girth, number of hands/bunch and number of fruits/hand. For the rest of the characters, the magnitude of direct effects was negligible. This is because these characters exerted high and positive indirect effect on bunch weight via pseudostem height, number of fruits/hand and negative indirect effect via number of leaves at shooting. Studies indicating increase in girth increases bunch yield in banana was earlier reported by Mahalakshmi, 2000; Nalina, 2002 and Damodaran, 2003. The residual value ($r=0.34$) indicated that nearly 70 per cent of the yield influencing characters were covered in the study and hence selection criteria based on this study would be reliable.

Additive gene effects may be more important for

Table 3: Genotypic correlation co-efficient matrix for bunch weight

Sr. No.	1	2	3	4	5	6	7	8	9	10
1.	1.000	0.684**	0.541**	0.592**	0.594**	0.954**	0.596**	0.262	0.112	0.125
2.		1.000	0.420*	0.819**	0.746**	0.683**	0.929**	0.655**	0.622**	0.443*
3.			1.000	0.312	0.470**	0.502**	0.366*	0.117	-0.033	-0.042
4.				1.000	0.870**	0.569**	0.697**	0.443*	0.351	0.058
5.					1.000	0.554**	0.650**	0.530**	0.450*	0.137
6.						1.000	0.598**	0.286	0.123	0.148
7.							1.000	0.655**	0.591**	0.442*
8.								1.000	0.906**	0.632**
9.									1.000	0.752**
10.										1.000

r table values: p-0.05 : 0.463,

p-0.01 : 0.361

* and ** indicates significance of values at P=0.01 and P=0.05, respectively

List of characters

1. Days taken from planting to shooting, 2. Height of pseudostem (cm), 3. Height of following sucker (cm), 4. Number of leaves at shooting, 5. Number of leaves at harvest, 6. Crop Duration (days), 7. Girth of pseudostem (cm), 8. Number of hands/bunch, 9. Number of fruits/hand, 10. Bunch weight (kg)

Table 4: Direct and indirect effects of characters on bunch weight

Sr. No.	Correlation co-efficient	Effects of characters on bunch weight (via characters)								
		1	2	3	4	5	6	7	8	9
1.	0.131	0.0908	0.3120	-0.0328	-0.3034	-0.0605	0.0910	-0.0199	-0.0476	0.0957
2.	0.439*	0.0621	0.4563	-0.0255	-0.4196	-0.0760	0.0651	-0.0310	-0.1192	0.5313
3.	-0.030	0.0491	0.1916	-0.0607	-0.1601	-0.0478	0.0479	-0.0122	-0.0212	-0.0279
4.	0.064	0.0537	0.3736	-0.0189	-0.5125	-0.0886	0.0542	-0.0233	-0.0806	0.3004
5.	0.0139	0.0539	0.3404	-0.0285	-0.4457	-0.1019	0.0528	-0.0217	-0.0964	0.3845
6.	0.155	0.0866	0.3116	-0.0305	-0.2914	-0.0564	0.0954	-0.0200	-0.0520	0.1049
7.	0.436*	0.0541	0.4238	-0.0222	-0.3573	-0.0662	0.0570	-0.0334	-0.1193	0.5055
8.	0.627**	0.0237	0.2988	-0.0070	-0.2271	-0.0539	0.0272	-0.0219	-0.1820	0.7740
9.	0.753**	0.0101	0.2836	0.0019	-0.1801	-0.0458	0.0117	-0.0198	-0.1649	0.8547

* and ** indicate significance of values at P=0.01 and P=0.05, respectively

yield determination in secondary triploids than dominance interactions (Tenkouano *et al.*, 1998). Thus greater yield gains may be more predictable by alleles in a diploid male background through recurrent selection prior to cross-breeding with a tetraploid female. Moreover, genetic manipulations for traits with complex inheritance are easier to carry out in a diploid background than in higher ploidy states.

Conversely, non-additive genetic effects appeared to control the number of days to shooting and suckering behaviour. This was not surprising since a dominant gene controls the expression of apical dominance (Ortiz and Vuylsteke, 1994a) and a major dominant gene determines the response to black sigatoka (Ortiz and Vuylsteke, 1994b), which affects the number of standing leaves at shooting. This would suggest that selection for these traits could be carried out in the tetraploid progeny with desirable plant phenology and architecture. While suckering behaviour was shown to be controlled by a single major gene (Ortiz and Vuylsteke, 1994a). However, these traits are often used as morpho taxonomic descriptors (Swennen *et al.*, 1995), suggesting that they are controlled by a relatively small number of genes, which would minimize non-hereditary variation for these traits. Therefore, selection for these attributes in a tetraploid background should not be as difficult as would be expected for traits with complex inheritance. The proportion of phenotypic variance attributed to genetic effects was smallest for crop cycle duration (18.41) and days taken for shooting (21.62), reflecting low genetic variability for these traits in the population studied. This was expected since parents were selected for earliness (Vuylsteke *et al.*, 1997).

Considerable scope exists for improvement of yield, plant phenology and reproductive ontogeny through increased individual plant performance for these traits using recurrent selection. However, major gains in fruit quality would be achieved by restoration of the seedlessness character in the resulting 3x offspring.

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