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MASS PEDIGREE SELECTION IN ARECANUT (*ARECA CATECHU* L) - A CASE HISTORY ON THE APPLICATION OF THE METHOD IN A PERENNIAL TREE CROP[†]

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ABSTRACT

This paper deals with the results of a mass pedigree selection experiment carried out in the 'South Kanara' cultivar of arecanut. The data collected from the experiment has been utilised for various genetical studies, such as correlated responses, genotypic and phenotypic correlations, path coefficient analysis, heritability, and genetic gain achieved through selection. The results of these analysis are presented and discussed.

INTRODUCTION

Arecanut (*Areca catechu* L.) being a perennial naturally cross-pollinated and exclusively seed propagated tree crop application of well known breeding methods such as recurrent selection, reciprocal recurrent selection etc. have limitations. Because of the low heritability for yield, improvement in yield cannot be achieved by straight selection from high yielding mother palms (Bavappa and Ramachander, 1967a). Acute shortage of arecanut felt in internal market (during the early sixties), made it important to initiate a rapid yield improvement programme. When the available methods were examined, it was felt that the mass pedigree system enumerated by Harland (1949a, b) for the improvement of Peruvian Tangius Cotton would suit this crop (Bavappa and Ramachander, 1967b). This review presents of a mass pedigree selection experiment in the local arecanut cultivar 'South Kanara',

MATERIALS AND METHODS

The method adopted by Harland was modified by Bavappa and Ramachander to suit arecanut and is elaborated below (Bavappa and Ramachander, 1967a, b).

1. Fortyone mother palms having more than 60% yield over garden mean were selected from four gardens

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and from them about 3000 open pollinated progenies were raised under uniform conditions.

2. A norm of 30% above the mean yield of progeny garden mean was fixed and families screened (bulk norm test). Three families out of the 41 which satisfied the above norms were selected.

3. The palms of the selected three families were screened for yield using a norm of 30% above the respective family mean (single norm test). They were also screened for their age at first bearing (5 yrs after transplanting), number of leaves (having 5 or more leaves) at the time of transplanting, girth at collar (having more than 20 cm girth) after one year's growth in the main field, and number of nodes (more than 4 nodes) two years after transplanting. Sixteen palms that passed the screening were selected.

4. The progenies from these 16 palms were planted along with two controls (one progeny from phenotypically high yielding palms from farmers' garden, and the second progeny from phenotypically high yielding palms from the progeny garden of selected mother palms, selected based on 20% above garden mean). A randomized block design with three replications was used for the progeny testing. Each plot consisted of nine trees.

5. All the progenies from the 16 mother palms were screened for girth at collar (after one year) and number of nodes (after two years) and bulk norm test (30% above garden mean) was applied to eliminate undesirable lines; and single norm test (30% above family mean) to eliminate undesirable palms.

6. Collection of nuts from the selected palms, bulking and then distribution to farmers. Simultaneously emasculation of undesirable palms in order to avoid genetic deterioration.

This scheme differed from that of Harland mainly because of the introduction of screening palms based on characters of high heritability. In order to increase the selection efficiency, seedling characters having high correlations with yield were included. Number of leaves at the time of planting and number of nodes two years after planting have positive phenotypic and genotypic correlations with yield and these characters have high heritability (Bavappa and Ramachander, 1967a, b). These three characters were hence incorporated into the mass pedigree system, and it was thought that this sort of a modification will ensure efficient selection and better progeny performance.

The data from the experiment were analysed using the techniques given by Lerner (1958), Kempthorne (1957), Falconer (1960), Becker (1967) and Steel and Torrie (1960).

RESULTS

Table I gives results of the analysis of morphological data, collected in the 5th year after planting of the experiment, on the progenies of the 16 selected palms and two controls. Out of the

Table I. *Mean values for morphological characters and yield of selected areca palms (Quinquennial observations)*

Plant No.	1	2	3	4	5	6	7	8	9	10	11	12
SDK 15 (806)	4.08	39.06	29.86	11.10	6.16	47.53	83.13	35.83	8.73	1.82	46.94	1.51
,, (731)	5.65	43.20	34.20	14.70	9.10	46.16	85.96	38.93	9.46	1.84	30.19	1.15
,, (771)	5.00	45.30	34.60	13.70	6.83	48.53	87.26	39.13	8.90	1.89	70.70	2.42
,, (717)	5.16	46.16	34.23	13.13	5.90	50.66	88.33	35.63	9.40	1.80	233.12	6.95*
,, (774)	5.92	47.56	34.66	16.33	7.13	53.13	83.76	36.63	9.36	1.82	179.02	5.20*
,, (815)	6.65	47.80	36.13	16.30	7.80	57.93	93.46	38.33	9.90	1.90	144.26	5.71*
,, (690)	5.63	45.13	34.93	13.33	7.00	52.26	89.30	43.76	9.90	1.78	131.25	4.36*
,, (768)	4.88	44.00	32.73	12.70	8.53	43.80	85.53	33.90	9.20	1.83	70.79	2.22
,, (715)	4.97	40.90	33.06	13.30	6.40	49.56	86.70	35.73	9.10	1.57	81.85	2.64
KMJ 8 (35)	5.14	45.06	36.53	13.76	8.53	55.00	94.43	43.56	9.66	1.82	122.15	4.24*
,, (36)	4.40	50.93	31.06	14.06	5.33	52.80	87.96	38.16	9.16	1.75	78.63	2.27
,, (86)	5.15	46.06	33.63	13.13	7.56	50.73	95.73	36.43	9.76	1.68	66.24	2.31
,, (101)	6.30	45.36	37.56	14.56	5.50	59.83	96.43	40.56	9.80	1.81	90.44	2.87
,, (43)	4.24	42.93	30.90	14.00	5.83	47.23	92.90	34.03	8.43	1.79	160.18	5.44*
,, (45)	6.67	51.60	32.50	16.80	6.93	53.03	93.83	40.70	9.30	1.97	35.93	1·07
KMJ 3 (312)	5.50	47.13	36.50	13.16	7.96	50.06	86.36	39.66	10.10	1.72	88.94	2.75
Control 1	5.36	47.53	35.16	14.03	6.06	50.34	91.90	42.73	9.50	1.79	91.81	2.72
Control 2	5.37	47.20	34.16	14.40	7.46	51.36	90.86	33.16	9.23	1.79	78.27	2.52
CD (P=0.05)	1.30	5.17	4.13	N.S.	1.80	6.68	7.07	N.S.	N.S.	N.S.	82.61	2.18

* Families selected based on the bulk norm test

Explanation :

1. Height. 2. Girth at permanent mark. 3. Girth at last exposed node. 4. Internodal distance. 5. Internodal distance below the crown 6. Number of nodes 7. Leaf sheath maximum length 8. Leaf sheath maximum breadth 9. Number of leaves 10. Length of oldest leaf

11. Number of nuts } Mean of four years
12. Weight of nuts }

12 characters analysed, eight were significantly above the control in the selected palms. These characters were height, girth at permanent mark, girth at last exposed node, internodal distance below crown, number of nodes, leaf sheath maximum length, number of nuts and weight of nuts. In the case of height, KMJ 8(45),* SDK 15(815) and KMJ 8(101) gave the highest values. For girth at permanent mark, KMJ 8(43)* and KMJ 8(36) gave the highest values. In the case of girth at last exposed node, SDK 15(815),* KMJ 8(35),* KMJ (101), KMJ 3(312) and control 1 gave higher values than others. For number of nodes, SDK 15(774),* SDK 15(815),* SDD 15(717),* SDK 15(690),* KMJ 8(35),* KMJ 8(36), KMJ 8(86), KMJ 8(101), KMJ 8(45),* and controls 1 & 2 were on par among themselves and were above the rest. For number of leaves no significant differences were observed among the selected palms.

When yield was considered, SDK 15(717) significantly out-yielded all other families, excepting SDK 15(774) and KMJ 8(43). For weight of nuts also, SDK 15(717) was superior, but did not differ significantly from SDK 15(774), SDK 15(815), SDK 15(690) and KMJ 8(43).

All the above five characters showed significant correlation with yield and number of leaves had significant genotypic correlation, though between families there were no significant differences.

Table II gives the yields of mother palms and their progenies (5 years' average at comparable age). The data revealed a considerable reduction (over 70%) in yield of the progenies. This was rather unexpected. The yield reduction that has occurred over a single generation could be due to (i) the inbreeding depression resulting from limited population size and narrow genetic base of the population and (ii) environmental variation. These aspects are elaborated later.

Table II. *Yield data of mother palms and progenies*

Family & palm No.	Number of nuts per palm	Weight of nuts per palm
SDK 15 (806)	384.50 (47.0)	18.30 (1.5)
,, (731)	246.75 (30.2)	10.93 (1.2)
,, (771)	485.00 (70.7)	21.08 (2.4)
,, (717)*	528.75 (233)	19.48 (6 9)
,, (774)*	360.75 (179)	12.82 (5.2)
,, (815)*	388.25 (144.3)	20.53 (5.7)
,, (690)*	421.00 (131.25)	14.48 (4.4)
,, (768)	474.25 (70.8)	16.66 (2.2)
,, (715)	347.00 (81.8)	16.29 (2.6)
KMJ 8 (35)*	377.25 (122.2)	15.73 (4.2)
,, (36)	455.00 (78.6)	18.56 (2.3)
,, (101)	470.25 (90.4)	18.79 (2.9)
KJ 3 (312)	329.00 (89.0)	14.75 (2.75)
KMJ 8 (43)*	312.00 (160.2)	13.51 (5.44)
KMJ 8 (45)	182.47 (35.9)	12.74 (1.07)
MEAN:	395.55 (101.9)	16.33 (3.32)

Variances	Number of nuts	Weight of nuts
σ^2 g	2987.65	3.58
σ^2 e	16319.16	21.36
σ^2 p	19306.81	24.94
h^2	0.155	0.143

The values in parentheses are the mean yields of the progeny (at comparable age).

* Selected families in the progenies

The progenies marked with asterisks (Table II) are the selected palms, based on the selection norms (bulk and single norm tests). Even in the selected palms the yield-both number and weight of

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* Selected families

nuts were considerably lower than the parental means. The best progeny (SDK 15 717), gave only 233 nuts (7.0 kg) while its parental yield was 529 (19.5 kg) nuts and the parental population mean itself was 396 nuts (16.3 kg).

Table II also gives phenotypic and genotypic variances and heritability for the parent palms. The portion of genetic variance out of the total phenotypic variance was found to be rather low, and hence the heritability estimates calculated were also much low, only 0.15 and 0.14 for number and weight of nuts respectively.

Table III gives the parent–offspring correlation for the two yield parameters–number and weight of nuts. The data showed that for these characters, the correlation between parents and offsprings was very low.

The additive variance, regression coefficients (b) and heritability (h^2) are also given in Table III. The h^2 was calculated by parent–progeny regression. It may be noted that h^2 showed higher values for both number and weight of nuts (0.304 and 0.227 respectively) than those calculated using half-sib analysis (0.16 and 0.14 for number and weight of nuts respectively). This of course is understandable, because the regression method of heritability determination is known to be less accurate in the case of tree crops (Morgenstern, 1975).

Correlated responses

Correlated responses were also analysed using the data from the present experiment. Eight characters were used for this, namely, height of the palm, girth at permanent mark, girth at last exposed node, internodal distance, number of nodes, leaf sheath (maximum length), number of leaves and length of oldest leaf.

The yield characters considered were number and weight of nuts. The phenotypic correlations for these characters are given in Table IV. Height showed significant correlation with girth at permanent mark, girth at last exposed node, number of nodes, number of

Table III. *Correlation and regression coefficients of parents and progeny (one parent and one offspring)*

	No. of nuts (P)	Wt. of nuts (P)	No. of nuts (O)	Wt. of nuts (O)
No. of nuts (p)	1.000	0.7017*	0.2764	0.2555
Wt. of nuts (P)	—	1.000	0.1510	0.1910
No. of nuts (O)	—	—	1.000	0.9801**
Wt. of nuts (O)	—	—	—	1.000
Regression coefficient (b)	0.1521	0.1133		
h^2	0.3042	0.2266		
Additive variance (VA)	2927.69	0.18944		
Covariance (Cov)	1463.8457			

* P=0.05 ** P=0.01

Table IV. *Phenotypic (above diagonal) and genotypic (below diagonal) correlations of morphological characters with yield*

	1***	2	3	4	5	6	7	8	9	10
1		0.46*	0.78**	0.19	0.62**	0.38	0.67**	0.26	0.49*	0.58**
2	0.43		0.36	0.12	0.36	0.33	0.45	0.28	0.47*	0.47*
3	0.93**	0.33		0.18	0.58*	0.52*	0.61**	0.14	0.39	0.45
4	0.01	0.25	0.04		-0.34	-0.05	0.27	0.17	-0.19	-0.09
5	0.70**	0.47*	0.75**	-0.40		0.55*	0.53*	-0.08	0.47*	0.54*
6	0.55*	0.46*	0.92**	0.05	0.73**		0.50*	0.11	0.05	0.12
7	—	0.80**	0.62**	0.30	—	—		-0.10	0.30	0.36
8	—	0.01	0.02	0.02	-0.02	0.004	-0.02		0.10	0.16
9	0.50	0.68**	0.54*	0.45*	0.60**	-0.10	0.61**	0.23		
10	0.63**	0.69**	0.64**	0.26	0.67**	-0.01	0.62**	0.62		

* Significant at P=0.05 ** Significant at P=0.01 *** Designations as in Table I

leaves and yield characters. Girth at permanent mark was correlated with yield. Number of nodes had significant correlation with number of leaves and yield characters.

The genotypic correlations of these characters are given in Table IV. Here also, height was found to be significantly correlated with girth at last exposed node, number of nodes, leaf sheath (maximum length) and two yield characters. Girth at permanent mark is significantly correlated with the number of nodes, number of leaves, leaf sheath (maximum length) and yield. Girth at last exposed node showed significant correlation with number of nodes, leaf sheath (maximum length) and to the two yield characters. Number of nodes is significantly correlated with leaf sheath (maximum length) and yield characters. Number of leaves had significant correlation only with number and weight of nuts. Girth at last exposed node and number of leaves, though had no significant phenotypic correlation with yield, had been found to have significant genotypic correlation.

Heritability

Heritability for yield correlated morphological characters were computed using parent progeny regressions as well as by half-sib analysis. For the two economically useful characters–number and weight of nuts, the h^2 were 0.155 and 0.143 respectively in the case of parents. The h^2 worked out for the same characters for progeny were 0.334 and 0.227 for number and weight of nuts respectively. Half-sib analysis of the same data for yield gave the values $h^2 = 0.24$ and 0.27 for number and weight of nuts. Using a different population, Bavappa and Ramachander (1967) got $h^2 = 0.07$ for mean weight of nuts and $h^2 = 0.03$ for nut set.

A partitioning of the total variance into genotypic and phenotypic along with heritability were carried out for various characters (Tables V, VI). These computations were made only in the case of selected families, SDK-15 and KMJ-8. These two families differed in their heritability, and h^2 for KMJ-8 was more than that in SDK-15, for height, girth at permanent mark, girth at last exposed node, number of nodes, and number of leaves. For the yield characters, h^2 was more in SDK-15 (0.595 and 0.558 for number and weight of nuts, compared to 0.30 and 0.10 in KMJ-8).

Table V. *Components of variance for the significant characters*

	4	5	7	8	10
σ^2g	0.923	0.833	11.137	2.547	-0.0006
σ^2p	3.953	2.003	29.003	22.367	0.0233
h^2	0.233	0.416	0.379	0.112	—

4. Internodal distance 5. Internodal distance below the crown 7. Leaf sheath maximum length 8. i. s. m. breadth 10. Length of oldest leaf

SDK-15 and KMJ-8, when considered as a single unit (Table VII) did not exhibit any significant difference over control and population means, though SDK-15 was found to be slightly better.

Direct and indirect effect of yield components on yield

Table VIII presents the results of a path coefficient analysis to show the direct and indirect effects of yield components on yield.

Height of the palm showed high direct effect on both number and weight of nuts. It has indirect effect also on yield through girth at last exposed nodes, but it had negative effect indicating that taller palms with less girth at last exposed node contributed to high yield.

Table VI. *Characters with significant genotypic correlation with yield*

Characters	Family	σ^2g	σ^2p	h^2
1. Height	SDK 15	0.333	0.951	0.350
	KMJ 8	0.765	1.383	0.553
	Pooled	0.334	0.952	0.351
2. Girth (p. m.)	SDK 15	5.293	15.033	0.352
	KMJ 8	8.853	18.593	0.480
	Pooled	6.337	16.078	0.394
3. Girth (l.e.n.)	SDK 15	1.130	1.735	0.154
	KMJ 8	5.670	1.980	0.481
	Pooled	2.420	8.640	0.280
4. No. of nodes	SDK 15	12.050	28.330	0.425
	KMJ 8	12.390	28.670	0.432
	Pooled	10.243	26.523	0.386
5. No. of leaves	SDK 15	0.022	0.362	0.610
	KMJ 8	0.157	0.497	0.316
	Pooled	0.073	0.413	0.177
6. No. of nuts	SDK 15	3643.050	6126.810	0.595
	KMJ 8	1081.230	3564.990	0.303
	Pooled	1948.410	4432.170	0.439
7. Weight of nuts	SDK 15	3.301	5.917	0.558
	KMJ 8	0.185	2.801	0.066
	Pooled	1.948	4.564	0.427

Table VII. *Table of family means of morphological characters and yield*

Family	(1)	(2)	(3)	(4)	(5)	(6)	(7)
SDK 15	5.33	44.35	33.82	49.95	9.33	109.79	3.57
KMJ 8	5.32	46.26	33.70	53.10	9.35	92.76	3.03
Control	5.37	47.36	35.16	50.90	9.37	85.04	2.62
Pooled	5.38	45.47	34.10	51.12	9.38	100.04	3 24

1. Height 2. Girth at p. m. 3. Girth at l. e. n. 4. No. of nodes 5. No. of leaves 6. No. of nuts 7. Weight of nuts

Table VIII. *Direct and indirect effects of yield components on yield*

1.	3.55	0.24	-3.46	0.01	0.58	0.70	-0.09	-0.04	- (a)
	(3.27)	(0.16)	(-3.13)	(0.01)	(0.85)	(0.52)	(-1.02)	(-0.04)	- (b)
2.	1.53	0.55	-1.23	0.19	0.39	0.60	-1.30	-0.04	- (a)
	(1.41)	(0.39)	(1.12)	(0.26)	(0.57)	(0.45)	(-1.22)	(-0.04)	- (b)
3.	3.32	0.18	-3.71	0.03	0.62	1.18	-1.02	-0.07	- (a)
	(3.05)	(0.13)	(-3.36)	(0.04)	(0.91)	(0.88)	(-0.95)	(-0.07)	- (b)
4.	0.04	0.14	-0.16	0.74	0.33	-0.05	-0.82	-0.07	- (a)
	(0.04)	(0.10)	(-0.15)	(1.04)	(-0.49)	(0.04)	(-0.76)	(-0.08)	- (b)
5.	2.49	0.26	-2.78	-0.30	0.83	0.94	-0.86	0.03	- (a)
	(2.29)	(0.18)	(-2.52)	(-0.42)	(1.21)	(0.70)	(-0.81)	(0.03)	- (b)
6.	1.94	0.25	-3.41	0.04	0.60	1.29	-0.82	0.01	- (a)
	(1.78)	(0.18)	(-3.09)	(0.05)	(0.88)	(0.96)	(-0.77)	(0.02)	- (b)
7.	2.38	0.49	-2.31	0.37	0.44	0.65	-1.63	0.09	- (a)
	(2.19)	(0.31)	(-2.09)	(0.52)	(0.64)	(0.49)	(-1.53)	(0.10)	- (b)
8.	0.91	0.16	-1.86	0.39	-0.17	-0.14	1.09	-0.14	- (a)
	(0.84)	(0.11)	(-1.69)	(0.54)	(2.25)	(-0.11)	(1.02)	(-0.15)	- (b)

(a) No. of nuts (b) Weight of nuts

1. Height 2. Girth at permanent mark 3. Girth at last exposed node 4. Internodal distance 5. No. of nodes 6. Leaf sheath maximum length 7. No. of leaves 8. Length of oldest leaf

The girth at last exposed node (LEN), as stated above, shows a negative direct effect indicating lesser girth at LEN contributes towards higher yield. It has indirect effect through height, once again confirming the influence of girth at LEN and height on yield. Number of leaves had good indirect effect through height and girth at LEN. Number of nodes also did show good indirect effect on yield through height and girth at LEN. However, its indirect effect on yield was not conspicuous.

Observed and expected genetic gains through selection

The genetic gain achieved through selection has been worked out using the relationship $G = i\sigma ph^2$, where 'i' is the selection differential $\left(\frac{S}{\sigma P}\right)$, P standard deviation of the population, and h^2 the heritability (Becker, 1967 Table IX).

Out of the six selected families, only one, SDK 15(717), showed a genetic gain of 32% over garden mean for both number and weight of nuts. All the other families had genetic gains less than 20% over garden mean. Even in the case of SDK 15(717), the observed genetic gain was far below the parental mean yield (Table IX).

The expected genetic gain for the next generation was calculated based on the relationship, $g = i \sigma ph^2$, where 'i' is the selection intensity, 'σ p' the phenotypic S. D. and h^2 the heritability for the character under consideration. In the expected genetic gain, the selected families did not show practically any difference, thereby indicating that selection has been effective almost uniformly for all the families (Tables X, XI).

Table X. *Expected genetic gain for the next generation*

Palm No.	Genetic gain	
	No. of nuts	Wt. of nuts
SDK 15 (717)	9.10	1.93
SDK 15 (774)	11.00	2.34
SDK 15 (815)	10.20	2.17
KMJ 8 (43)	9.10	1.93
SDK 15 (690)	13.30	2.84
KMJ 8 (35)	12.50	2.66

Table XI. *Individual palms selected in each family and their yields*

Family No.	No. of nuts	Weight (kg)
SDK 15 (717)	351	10.850
SDK 15 (774)	350	10.600
SDK 15 (815)	222	8.300
SDK 15 (690)	277	8.800
KMJ 8 (35)	257	8.650
KMJ 8 (43)	244	8.400

DISCUSSION

The mass pedigree system of selection as outlined here has got much similarity with the 'plus tree selection', a breeding methodology developed by forest tree breeders in the 1950's and 60's (Morgenstern et al, 1975). In short, the plus tree selection as practiced by forest tree breeders consists of selecting superior (plus) trees in natural stands from varying ecological and geographic areas, collecting clones or seeds and raising a clonal/seedling orchard, where the progenies are subjected to progeny testing and selection. The selected lines then go to the seed production orchards. Special selection procedures

Table IX. *Genetic gain achieved through selection*

Family & Palm No.	No. of nuts	Wt. of nuts	Genetic gain		% gain over popl. mean	
			No.	Wt	No.	Wt.
SDK 15 (717)	233	7.0	31.8	32	32	32
SDK 15 (774)	179	5.2	18.9	16.9	19	17
SDK 15 (815)	144	5.7	10.5	21.1	11	21
SDK 15 (690)	131	4.4	7.3	10.1	7	10
KMJ 8 (43)	160	5.4	4.9	8.4	5	8
Control 1	92	2.7	..	..	..	..
Control 2	78	2.5	..	..	..	..
Popl. mean	100	3.2	..	..	..	..

have also been developed by forest tree breeders for selection of mother trees in the natural stands.

An important point to be considered in the plus tree selection, or for that matter any such mother plant selection programme, is the population structure itself. Arecanut is a tall palm, naturally cross-pollinated and the pollinating agent is wind. In this regard it is very similar to many conifers. In such a population, one naturally expects wide variability and high heterozygosity. In a natural stand this would be the rule. But in the case of arecanut the picture is different. Arecanut is exclusively cultivated, and no natural stands exist in India. Each traditionally areca growing tract has its own adapted cultivar where it was under cultivation perhaps from time immemorial. The continuous existence of a particular cultivar in a tract, combined with the conscious or unconscious selection practised by the farmers might have led to considerable homogeniety and stability in the local areca populations. The *South Kanara* (local) areca cultivar, represents such a climax population. The first cycle of selection from four farmers' gardens around the Research Institute (Vittal) was a very restricted selection, having an extremely narrow genetic base. The population thus selected was then subjected to further selection.

In the present selection programme, two types of selection pressures were imposed, namely, family selection (bulknorm test) and within family selections (single norm test). According to Falconer (1960), family selection is applicable in cases where the selected characters have a low heritability. The efficiency of this selection rests on the fact that environmental deviations of the individuals tend to cancel each other out in the mean value of the family so that the phenotypic mean of the family comes close to being a measure of its genotypic mean. The advantage gained through this selection is greater when environmental deviations constitute a large part of the phenotypic variance, or when the heritability is low. The individual palm selection (within the family selection), on the other hand, is useful where population size is small and the heritability of the characters selected are high. The combination of the two selection procedures imposed a tremendous selection pressure on the population which, in fact, as seen from the population performance, turned out to be disadvantageous, probably due to the small population size of selected palms-41 mother palms-and the consequent close breeding.

A study of Tables I and II will reveal the deleterious effect of close selection in a naturally outcrossed species. The 3000 progenies from the 41 mother palms from four gardens might have been quite uniform, forming a fragment of a 'climax population', as mentioned earlier. The sixteen selected palms gave a mean yield of 400 nuts (16.3 kg) while in the next generation, the mean yield (at comparable age) came down to 102 nuts (3.3 kg). This drastic reduction in yield that occurred in one generation could be due to close breeding resulting from a narrow selection base and small population size, as both parents and their progenies were grown under identical management conditions.

The analysis of correlated responses revealed that girth, number of nodes, and height were highly correlated with yield. In an earlier study, Bavappa and Ramachander (1967 a) found that number of leaves at the time of planting, and girth at collar after two years' growth had significant correlation with age at first bearing, which in turn was highly correlated with number of nuts. They also found that yield attributes such as number of bunches produced, number of female flowers, nut set and number of nuts per bunch were also highly correlated with yield. The morphological characters studied here also showed some difference in their genotypic and phenotypic correlations. Significant phenotypic correlations were observed in the case of height, girth at permanent mark and number of nodes. In addition to these three, girth at last exposed node and number of leaves also showed significant genotypic correlations. Internodal distance was found to have significant genotypic correlation with number of nuts only. The genotypic correlations worked out here are especially important because they result from pleiotropy and they can greatly influence the selection process (Becker, 1967). The poor parent–progeny correlation for the yield characters and their low heritability indicated that selection for these characters will be ineffective and cannot give any improvement in yield.

A partitioning of the total variance into genotypic, phenotypic and environmental were carried out in the case of the two selected families SDK–15 and KMJ–8. They were found to differ in their heritabilities; in KMJ 8, h^2 were more for morphological characters, while for yield components (number and weight of nuts) the h^2 were more in SDK–15. This suggests that the two families were in the past subjected to different degrees of selection pressures. This type of differential advance in heritability in the different cultivars is common in many crop plants (Lerner, 1958).

The data from this was also used for a path coefficient analysis, whose results indicate that height of palms influenced yield directly, as well as indirectly through girth at LEN (negative effect), thereby showing that taller palms with less girth at LEN are better yielding. Girth at LEN is thus having a direct negative effect on yield. Similarly, leaf number and node number were found to have good indirect effect on yield.

A final picture on the effectiveness of selection is available from the genetic gains due to selection. Only one family out of six selected, gave a genetic gain of over 32% and in the others the gains were below 20%. The expected genetic gain for the next generation did not reveal any significant differences among the selected families. Thus, selection has been effective in bringing in uniformity among the population. But with regard to the aim, selection itself was ineffective, as even the best family, SDK–15 (717), having a genetic gain of over 32%, came far below the parental mean yield. As mentioned earlier, this may be the result of close breeding with consequent inbreeding depression.

The present study points to the fact that though the mass pedigree selection is an effective method of improvement, selection in a population having little variation and a narrow genetic base may not be desirable or effective. Sampling from large and widely separated areas and from different ecological conditions become imperative for such a selection programme to be effective.

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