Genetic progress of selections between and within caribbean cherry open pollination progenies

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ABSTRACT

The objective of this study was to estimate the genetic parameters of Caribbean cherry tree populations and select the most favorable individual plants by using the between-and-within a progeny selection method, as well as the index selection method which simultaneously takes into account the performance of each progeny for all the assessed traits. The experiment was carried out in April 1996 in a randomized complete block design with 62 treatments (open pollination progenies) and three replications at the Experimental Station at the Embrapa Tropical Agroindustry, in Pacajus, CE. Single row plots of four plants were used, and the spacing was 4 m between rows and 3 m between plants within rows. The progenies were assessed for fruit yield and physical-chemical traits of fruits according to vitamin C content, total soluble solids content (ºBrix) and mean fruit weight (PMF). The estimated monthly yield gains (in percentage) from selection between and within progenies varied from 3.68% to 44.98% respectively, in the June and May 1999 assessments. The variation for the other traits was from 28.3% to 327.2% respectively, for total titer acidity and pH. Plants in the next cycle population are expected to present a vitamin C content higher than 30% compared to those from the first selection cycle. The use of a selection index that simultaneously considered the classification of each progeny for the assessed traits screened progenies showed a coincidence of 84% progenies in relation to those selected using the between and within progeny selection method. This suggested that the index method was efficient compared to the traditional method.

KEY WORDS: *Malpighia emarginata*, caribbean cherry, variability and genetic parameters.

INTRODUCTION

There was great interest in the Caribbean cherry in the late 1980s with a rapid increase in commercial orchards. However, the lack of planning, the unavailability of good-quality genetic material, and the lack of a suitable infrastructure for processing and post-harvest fruit conservation caused frustration in many producers, and this eventually led to a change in their business activities.

The potential of the Caribbean cherry as a natural source of vitamin C in industrial juices, ice cream, preservatives, medicine and in mixtures with other juices to enrich the vitamin C content is undeniable. However, the production must be profitable and the fruit quality must be uniform; this is not easy to be done within the established orchards because the plants were obtained from seeds. It is well known that there is a great variation in fruit yield and quality (acidity, sugars and vitamin C content) in this type of

orchard, which makes standardization difficult (Paiva et al., 1999a).

In spite of the great expansion of the crop in Brazil, especially in the Northeast, only recently have selected cultivars (like the BRS Sertaneja released by Embrapa Semi Arid) become available for commercial planting (Acerola, 1999). Clones like Mineira, Barbados, Monami, CAMTA 40.2 and Okinawa are commercially planted in Tomé-Açu, PA, but were not released by a research institution.

In the state of Paraná, the Caribbean cherry breeding program at Londrina State University (UEL) began in 1992 with the establishment of a clone orchard from genotypes selected from orchards in the northern region of the state. The Dominga, Ligia and Natalia genotypes resulted from five assessment cycles for earliness, yield, fruit size, appearance and vitamin C content, as well as pest and disease tolerance (Pípolo et al., 1998).

Pests and diseases, especially fruit pests and root node nematodes, are limiting factors for cultivation in

Northeastern Brazil. Apparently, there is a biological balance related to the sexual reproduction of the species in the local commercial orchards. If this proves to be true, breeding research directed to clone development - that is, obtaining genetic uniformity in the orchards - must consider other ways of maintaining the existing genetic diversity in the orchards in order to ensure sustainability of the cultivation system.

In species that propagate by both sexual and asexual reproduction, genetic breeding can explore two paths: plant selection with progeny testing and plant selection with vegetative propagation. The advances obtained in population breeding can be used as predictors of the problems that may derive from future mass clone planting, since orchard uniformity may have disastrous consequences (Paiva et al., 1999b).

The objective of this study was to estimate the genetic parameters in Caribbean cherry tree populations and select the most favorable plants using between-and-within progeny selection and an index to simultaneously assess the performance of each progeny for the assessed traits.

MATERIAL AND METHODS

The experiment was carried out in April 1996 in the Pacajus Experimental Station at Embrapa Tropical Agroindustry Research Center, located in the city of Pacajus, CE at 4º10´S and 38º27´W and 60 m altitude. A randomized complete bock design with three replications and 62 treatments, and single row plots of four plants were used. Spacing was 4 m between rows and 3 m between plants within rows. The treatments consisted of open pollination progenies derived from plants selected in the FRUCESA – Frutas do Ceará, S/A - a commercial orchard located in Jaguaruana, CE.

Assessments involved the evaluation of progeny fruit yield (kg/plant) from July 1998 to June 1999, in weekly harvesting of individual plants, and the determination of the fruits physical-chemical properties, C vitamin (mg/100g) and total soluble solids (SST - ºBrix) content, and mean fruit weight (PMGF –in grams).

The transformation $(x + 0.5)^{1/2}$ was applied prior to the analysis of the fruit yield data. The analyses of variance of all traits were carried out at individual plant levels within plots using the GENE's program (Cruz, 1997). The following expressions were used to estimate the genetic parameters: $\sigma^2_{ge} = (QMp - QMe)$

$/ rn$; $\sigma^2_{gd} = (\theta_d / \theta_e). \sigma^2_g$; $\sigma^2_T = \sigma^2_d + \sigma^2_e + \sigma^2_g + \sigma^2_b$; $h^2_e = (\sigma^2_g) / (QMp / nr)$; $h^2_d = (\sigma^2_{gd}) / (\sigma^2_d)$; $h^2 = (\sigma^2_g + \sigma^2_{gd}) / (\sigma^2_d + \sigma^2_e + \sigma^2_g + \sigma^2_b)$; $CV_{ge}\% = [100 . (\sigma^2_g)^{1/2}] / m$; $CV_{gd}\% = [100 . (\sigma^2_{gd})^{1/2}] / m$; $CV\% = [100 . (\sigma^2_e)^{1/2}] / m$; $b_1 = CV_{ge} / CV$; $b_2 = CV_{gd} / CV$; $r_{F(x,y)} = [Cov_{F(x,y)}] / [\sigma^2_{F(x)}. \sigma^2_{F(y)}]$; $r_{G(x,y)} = [Cov_{G(x,y)}] / [\sigma^2_{G(x)} . \sigma^2_{G(y)}]$. Where σ^2_{ge} means the between progeny means genetic variance; σ^2_{gd} the within progeny genetic variance; σ^2_T the total phenotypic variance; h^2_e, the between progeny means heritability; h^2_d the within progeny heritability; h^2 the plant level heritability; CV_{ge} the between progeny coefficient of genetic variation; CV_{gd} the within progeny coefficient of genetic variance; CV the experimental coefficient of variation; b_1 the relationship between the CV_{ge} and the experimental CV; b_2 the relationship between the CV_{gd} and the experimental CV; QMp the between progenies mean square; QMe the between plot mean square; r_F the phenotypic correlation coefficient; and r_G the genotypic correlation coefficient.

Progenies were selected based on total fruit yield, vitamin C content, total soluble solid contents and mean fruit weight. Initially, 30% of the best progenies were selected for each individual trait. Next, the outstanding progenies for pairwise combined traits were ranked. The accumulated yield individual plant and the plant phenotypic performance were taken into account for the within progeny mass selection. The genetic gain for each individual trait was estimated according to Vencovsky (1978).

The index selection considered the sum of the performance points of each progeny for the assessed traits (Cruz and Regazzi, 1997); it was used to estimate the genetic progress based on the mean of the next generation parental plants.

RESULTS AND DISCUSSION

Table 1 shows the mean squares of the analysis of variance for all traits. Significant differences were detected between progenies at the 1% level of probability per yield in August and March, Vitamin C content, pH, total soluble solid content, total titer acidity (ATT) and mean fruit weight (PMF). The between progeny yield was significant at the 5% level of probability in September, October, November, December, January, February and April, while no significance was detected in June. These results show differences in the progeny performance for the assessed traits.

Table 1 also presents the mean, minimum and maximum values of all the traits assessed in the progeny and the experimental variation coefficient.

The greatest fruit yield progeny mean occurred in March and June 1999 and September 1998, as shown in the total monthly yield graph (Fig. 1). The variation of the progeny vitamin C content, which showed a maximum value of 2.7%, indicate a very favorable condition for selecting more nutritive plants. The coefficients of experimental variation per yield were high, ranging from 22.5% to 40.2%, while those for the qualitative variables were at acceptable levels for field experiments ranging from 2.6% to 15.7% respectively for pH and C vitamin content.

Table 2 shows the estimates of the components of variance for all traits. The genetic variances within progenies were higher than those estimated for between progenies for all traits. The genetic variance observed among progenies represented approximately only 33% of the variation contained within progenies. These values were in the intermediary range among those estimated by Vencovsky (1978) for the ratio of between and within progenies genetic variance in half and full sib families, which ranged from 14% to 60%.

The fruit yield heritability estimates suggest that between progenies selection will result in larger gains compared to within progenies plant selection. For the other assessed traits the largest portion of the genetic variability was detected within progenies. The comparison of the values of the genetic coefficients of variation within and between progenies also suggested that the larger portion of the genetic variability can be found within progenies. The b_1 and b_2 indexes, which respectively quantify the ratio of the genetic variation and the between and within progenies environmental variation, showed a more favorable condition for within progenies selection.

The estimation of genetic parameters provided information on the nature of the gene action controlling the trait inheritance, and also a base for drawing the breeding plans. It may also allow the development of new focuses for plant breeding (Robinson and Cockerham, 1965). The partitioning of the additive genetic variance from the total genetic variance, for example, allowed better designing of the selection scheme. The within progeny and plant level heritabilities for the pH, total soluble solid contents and mean fruit weight traits were higher than 1%. Estimates of heritability coefficients above 1% are common for other traits in progeny tests with native tree species and in experiments with forest species. Several hypotheses can be formulated to explain these results: a) the estimates of the associated errors are much greater than those of heritability; b) the traits may present a significant maternal effect; and. c) there are low estimates of the phenotypic variances as a consequence of the greater environmental uniformity (Matziris and Zobel, 1973). Paiva et al. (1999c) estimated these same genetic parameters for morphological traits of these progenies when they are one year old, and found a similar distribution of the genetic variability.

The between progeny selection based on the accumulated fruit yield, vitamin C content, ºBrix and the mean fruit weight - first individually and then pairwise combined - screened the progenies of number 8. 12. 20. 23. 26. 38. 47. 51. 54. 56. 63. 66. 68. 72. 75. 79. 87. 91 and 92 when a 30% selection pressure was applied. Individual yield and the phenotypic aspect of each plant were considered in the within progeny selection. Four plants per progeny were selected to obtain a selection intensity of 33.3%.

All not selected plants were eliminated and the 76

Table 1. Mean squares for the between progeny (QMp), between plot (QMe) and within plot (QMd) components, with their respective significances, and the mean coefficient of experimental variations (CV), and maximum and minimum values of the first selection cycle of open pollination Caribbean cherry progenies assessed for the following traits: monthly fruit yield (grams/plant) from July 1998 to June 1999, vitamin C content (Vit. C) in mg/100g pulp, pH, total soluble solid contents (SST) in ºBrix, total titter acidity (ATT) and mean fruit weight (PMF) in grams.

Parameters [1]	Monthly Fruit Yield [2]												Vit. C	pH	SST	ATT	PMF
	Jul	Ago	Set	Out	Nov	Dez	Jan	Fev	Mar	Abr	Mai	Jun					
QMp	395.31[ns]	487.15[4]	639.67[3]	390.99[3]	542.90[3]	658.25[3]	563.93[3]	609.02[3]	1604.0[4]	698.15[3]	1515.8[4]	1228.2[ns]	228707.9[4]	0.225[4]	20.084[4]	0.165[4]	7.092[4]
QMe	294.21	269.05	421.45	246.51	373.52	422.08	349.08	399.53	688.23	472.47	834.18	1141.2	87729.4	0.015	1.4451	0.058	2.116
QMd	149.37	200.58	301.54	230.62	283.29	204.11	213.63	251.76	556.16	309.01	541.53	558.31	70147.9	0.011	1.0930	0.054	1.946
Média	834.7	993.0	2423.4	698.5	1461.7	1685.6	1185.2	2288.8	3817.8	1137.8	1958.7	3027.9	1336.6	3.27	9.06	1.30	5.74
CV (%)	33.88	29.85	22.55	36.95	28.60	27.42	30.79	22.96	23.43	39.20	40.20	35.07	15.67	2.64	9.38	13.16	17.91
Minimum value	297	261	1111	142	573	704	204	663	693	102	199	1090	523.32	2.72	5.4	0.58	1.22
Maximum value	2357	2115	4230	1834	2567	4018	2097	3741	6155	2390	5481	5455	2718.33	3.83	15.7	2.26	13.3

[1] Degrees of Freedom: QMp = 61; QMe = 122; QMd = 558; [2] Data transformed to $(x + 0.5)^{1/2}$; [ns] not significant; [3] $p < 0.05$; [4] $p < 0.01$.

remaining Caribbean cherry trees of the isolated experimental area were submitted to natural and artificial genetic recombination. The resulting fruits were collected to form new progenies of a second selection cycle.

The expected genetic progress from between and within progeny selection for each trait is presented in Table 2. The estimated percentage gain for monthly yield ranged from 3.68% to 44.98%, respectively for June and May 1999, while for the other traits the variation was from 28.33% to 327.17% respectively for total titer acidity and pH. Based on these data, fruits from the next generation are expected to present a 30% greater vitamin C content if compared to the plants of the first selection cycle.

The Caribbean cherry genetic breeding program in development at Embrapa Tropical Agroindustry uses clone selection in addition to population breeding. The association of these methods has the advantage of producing clones in the short term to meet the immediate demands of the productive sector, and maintaining an alternative research line to obtain results in the medium and long terms at the same time.

Population breeding would be used to prevent problems that might occur in the future mass planting of few clones. The extensive use of a single clone or few clones leads to a greater genetic uniformity and progress, but uniformity can lead to failure. The population breeding strategy resulted in obtaining improved Caribbean cherry seeds for commercial sowing. There might be a reduction in fruit yield compared to clone planting, but a reduction of phytosanitary problems would be expected.

Table 3 shows the progeny classification for total accumulated yield, vitamin C content, total soluble solid contents and mean fruit weight. In this table the values obtained for each individually assessed trait were ranked in ascending order, depending on the position that each progeny obtained in the ranking (r). The classification was also done later for the sum of these values. Applying a selection pressure of 30% on the progenies based on their smallest "r" sum - where the best progeny performances for the four traits is simultaneously considered - resulted in the identification of 16 progenies which were also selected by the between and within progenies selection method. This suggests that the proposed method is efficient compared to the traditional between and within progenies selection method.

The expected genetic progress, considering the mean of the progenies from the new population and the mean of the original population, ranged from 1.75% to 17.65% for mean fruit weight and accumulated fruit yield respectively (Table 4). Although lower than tandem selection gains considering the same traits, they are probably closer to the real results.

The estimates of the phenotypic and genetic correlation coefficients among the trait combinations, vitamin C and pH, pH and total titer acidity were 0.10 and 0.12 (low positive and non significant) respectively. The correlation estimates between the C vitamin and total litter acidity were relatively high

Table 2. Components of variation of monthly fruit yield (grams/plant) from July 1998 to June 1999, vitamin C content (Vit. C) in mg/100g pulp, pH, total soluble solid contents (SST) in ºBrix, total titter acidity (ATT) and mean fruit weight (PMF) in grams in first selection cycle of open pollination Caribbean cherry progenies.

Components of variation [1/]	Monthly Fruit Yield												Vit. C	pH	SST	ATT	PMF
	Jul	Ago	Set	Out	Nov	Dez	Jan	Fev	Mar	Abr	Mai	Jun					
σ^2_{ge}	8.4259	18.175	18.185	12.040	14.115	19.681	17.904	17.458	76.317	18.807	56.798	7.2546	23496.4	0.0351	3.1065	0.0177	0.8293
σ^2_{gd}	25.278	54.524	54.553	36.121	42.346	59.043	53.712	52.374	228.95	56.420	170.40	21.764	70489	0.1052	9.3196	0.0532	2.4880
σ^2_{T}	195.16	241.20	355.39	248.94	322.07	287.02	265.91	439.09	696.14	371.78	669.61	711.46	102424	0.0017	4.3728	0.0737	2.8597
h^2_{e}	0.25	0.45	0.34	0.37	0.31	0.36	0.38	0.34	0.57	0.32	0.45	0.07	0.62	0.93	0.93	0.64	0.70
h^2_{d}	0.17	0.27	0.18	0.16	0.15	0.29	0.25	0.21	0.41	0.18	0.31	0.04	1.00	9.16	8.53	0.98	1.28
h^2	0.17	0.30	0.20	0.19	0.17	0.27	0.27	0.16	0.44	0.20	0.34	0.04	0.92	2.90	2.84	0.96	1.16
CV_{ge}	11.46	15.52	9.37	16.33	11.12	11.84	13.94	9.60	15.60	15.64	20.97	5.59	11.47	5.72	19.46	10.25	15.85
CV_{gd}	19.86	26.88	16.23	28.29	19.26	20.51	24.15	16.62	27.03	27.09	36.33	9.69	19.86	9.91	33.70	17.74	27.46
Gs	3.79	7.23	6.16	4.87	4.99	7.29	6.78	6.21	17.55	5.66	16.16	1.77	423.06	10.70	11.09	0.37	2.77
Gs(%)	14.95	26.33	13.54	22.93	14.79	19.48	22.33	14.26	31.35	20.42	44.98	3.68	31.65	327.17	122.38	28.33	48.62
b_1	0.48	1.03	0.78	1.74	0.79	0.60	0.73	0.69	1.52	0.68	0.88	0.22	1.63	4.49	4.20	2.84	3.12
b_2	0.83	1.78	1.35	3.01	1.37	1.04	1.26	1.19	2.63	1.17	1.53	0.39	2.83	7.76	7.27	4.92	5.41

[1/] σ^2_{ge}: between progenies genetic variance means; σ^2_{gd}: within progenies genetic variance means; σ^2_{T} : total phenotypic variance; h^2_{e}: between progenies mean heritability; h^2_{d}: within progenies heritability; h^2: heritability at plant level; CV_{ge}: between progenies coefficient of genetic variation; CV_{gd}: within progenies coefficient of genetic variation; CV: coefficient of experimental variation; b_1: relationship between the CV_{ge} and the experimental CV; b_2: relationship between the CV_{gd} and the experimental CV; Gs and Gs (%) expected value and percentage of genetic progress from selection between and within progenies, respectively.

Table 3. Rank (r) of 62 Caribbean cherry open pollination progenies according to the increasing performance for accumulated fruit yield (PROD), vitamin C content, total soluble solid contents (SST) and mean fruit weight (PMF).

Progenies	PROD (kg)	r	Vit. C (mg/100g)	r	SST (°Brix)	r	PMF (g)	r	r amount
51	443.7	1	1711.6	3	10.9	12	6.8	11	27
20	370.9	3	1505.6	14	11.1	9	6.3	19	45
75	300.7	11	1522.0	11	10.9	13	6.2	20	55
91	322.9	7	1853.3	1	10.0	21	5.2	42	71
26	253.6	34	1519.4	12	10.3	18	7.1	9	73
92	359.2	4	1291.1	35	10.1	20	6.4	16	75
56	315.5	8	1631.2	4	11.3	8	4.1	60	80
59	416.4	2	1424.0	20	9.6	27	5.8	32	81
87	257.6	30	1458.5	17	11.7	5	5.9	31	83
47	311.3	10	1406.6	23	7.9	44	7.2	7	84
70	274.0	21	1597.7	6	8.7	35	6.1	26	88
63	333.7	5	1367.0	27	11.5	6	4.5	53	91
8	281.4	16	1841.0	2	9.9	24	4.6	49	91
79	273.6	24	1434.2	18	11.9	3	4.6	50	95
66	331.4	6	1244.7	39	12.2	2	4.5	54	101
48	262.5	29	1376.8	26	8.0	43	7.6	4	102
68	281.6	15	1154.9	51	9.8	25	6.7	12	103
54	218.5	48	1603.6	5	13.2	1	4.6	51	105
12	314.0	9	1388.3	24	10.5	16	4.3	59	108
93	235.8	42	1407.7	22	7.3	49	8.0	1	114
72	277.4	18	1584.2	7	9.4	30	4.0	61	116
64	255.5	32	1505.7	13	9.6	26	4.9	45	116
23	236.8	41	1532.7	10	11.4	7	4.3	58	116
86	254.1	33	1274.6	36	9.3	31	6.4	17	117
40	180.2	56	1581.8	8	8.1	40	6.4	15	119
22	204.4	52	1551.3	9	9.0	34	6.0	28	123
14	276.5	19	1384.1	25	8.1	41	5.2	40	125
10	239.4	40	1487.4	16	11.0	10	3.4	62	128
71	200.3	53	1300.7	33	11.8	4	5.4	39	129
74	274.5	20	1134.9	53	10.9	11	4.8	48	132
30	273.9	23	1229.3	41	6.0	62	7.3	6	132
13	269.0	26	1332.2	31	10.1	19	4.4	56	132
38	279.1	17	1059.3	60	6.9	53	7.6	3	133
27	274.0	22	1069.7	59	8.7	36	6.4	18	135
6	190.0	55	1412.6	21	8.2	38	6.2	21	135
97	268.5	27	1342.0	30	9.9	23	4.4	57	137
3	205.4	51	1221.2	42	10.5	17	6.0	27	137
90	272.2	25	1204.0	44	7.5	48	6.2	23	140
82	263.0	28	1104.4	57	10.7	15	5.2	41	141
41	244.4	37	1151.1	52	7.5	47	7.6	5	141
4	257.5	31	1236.1	40	6.3	59	6.6	13	143
98	283.6	14	1263.6	37	6.6	55	5.4	38	144
2	253.5	35	1349.6	29	8.2	39	5.1	43	146
37	287.9	13	1204.1	43	6.6	56	5.5	37	149
17	169.3	61	1495.9	15	8.6	37	5.5	36	149
5	225.1	46	1360.9	28	7.1	52	6.2	24	150
21	172.2	59	1257.5	38	9.3	32	6.2	22	151
77	239.8	39	992.0	62	9.9	22	6.0	29	152
100	191.6	54	1294.7	34	9.5	28	5.0	44	160
85	169.0	62	1426.8	19	7.5	46	5.6	35	162
78	287.9	12	1188.6	47	6.3	58	4.9	46	163
81	230.4	44	1321.9	32	6.7	54	5.6	34	164
84	206.6	50	1105.6	56	6.4	57	7.9	2	165
1	170.1	60	1089.4	58	9.1	33	6.6	14	165
94	233.0	43	1113.9	54	10.8	14	4.5	55	166
57	248.0	36	1017.2	61	6.2	60	7.0	10	167
69	223.8	47	1200.2	45	9.5	29	4.8	47	168
52	217.9	49	1113.1	55	6.2	61	7.1	8	173
9	173.7	58	1197.2	46	7.6	45	6.1	25	174
58	225.3	45	1161.2	49	7.1	51	6.0	30	175
67	244.1	38	1180.8	48	8.0	42	4.6	52	180
80	174.9	57	1155.5	50	7.1	50	5.6	33	190

positive and significant at the 1% level of probability by the "t" test. Moura et al. (1997) analyzed fruits from 55 Caribbean cherry plants and also found a high and significant correlation of 0.732 between vitamin C and total acidity. On the other hand, these authors reported a totally different result for pH and total titter acidity, a negative and significant correlation value of -0.728.

Table 4. Means of original (X_o) and selected (X_s) progenies, heritabilities at plant level (h^2) and indirect gains (Gs) from selection based on the index obtained by the sum of the progeny "ranks" for the total fruit yield (PROD), vitamin C content, total soluble solid contents (SST) and mean fruit weight (PMF) traits assessed in first selection cycle of Caribbean cherry open pollination progenies.

Character	X_o	X_s	h^2	Gs	Gs(%)
PROD (kg)	257.8	303.3	0.30	45.5	17.65
Vit. C (mg/100g)	1336.6	1479.5	0.92	142.9	10.69
SST (^{o}Brix)	9.06	10.6	2.84	1.54	16.99
PMF (g)	5.7	5.8	1.16	0.1	1.75
TOTAL					47.08

Table 5. Phenotypic (above the diagonal) and genotypic (below the diagonal) correlation coefficients among pairs of fruit of vitamin C content, pH, total soluble solid contents (SST) and total titter acidity (ATT) traits assessed in first selection cycle open pollination Caribbean cherry progenies.

Character	Vit. C	PH	SST	ATT
Vit. C	-	0.10	0.40[1/]	0.74[1/]
pH	0.25	-	0.53[1/]	0.12
^{o}Brix	0.47[1/]	0.57[1/]	-	0.33
ATT	0.72[1/]	0.31	0.39	-

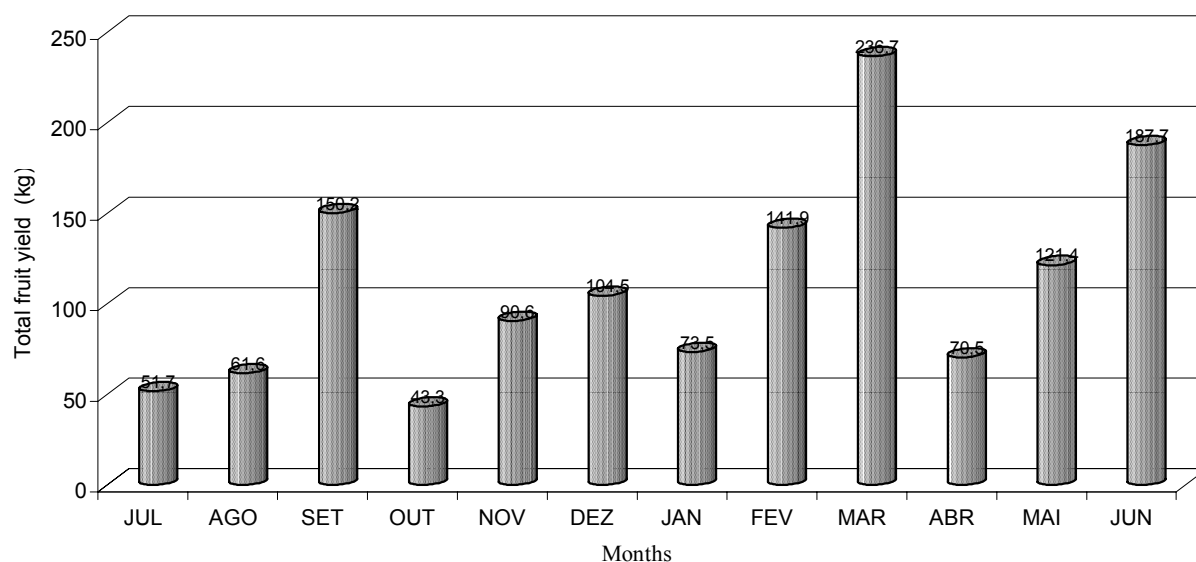[1/] significant at 1% probability by "t" test.

Figure 1. Total monthly fruit yield of 62 open pollination first selection cycle of Caribbean cherry progenies assessed in weekly harvests from July 1998 to June 1999.

CONCLUSION

The genetic variability parameters suggested that Caribbean cherry progeny selection is likely to be successful in the first cycle.

Progeny selection based on a proposed index showed a coincidence of 84% with the progenies select by the more traditional between and within progenies selection method, which indicates this method is relatively well efficient.

The genetic progress obtained from index selection is closer to the observed values.

RESUMO

Progresso genético com seleção entre e dentro de progênies de polinização aberta de acerola

O presente trabalho teve por objetivos estimar as magnitudes dos parâmetros genéticos populacionais de aceroleira e efetuar a seleção das plantas mais favoráveis utilizando os métodos de seleção entre e dentro de progênies e de um índice que considera simultaneamente o desempenho de cada progênie em relação aos caracteres avaliados. O experimento foi instalado no local definitivo em abril de 1996 na Estação Experimental da Embrapa Agroindústria Tropical, no município de Pacajus, CE, sob arranjo experimental de blocos casualizados com 62 tratamentos, 3 repetições e 4 plantas por parcelas, no espaçamento de 4 m entre linhas e 3 m entre plantas. Os tratamentos foram constituídos por progênies de polinização livre. A avaliação das progênies constou da medição da produção de frutos e avaliação físico-química dos frutos de cada progênie para determinação do conteúdo de vitamina C, teor de sólidos solúveis totais (ºBrix) e peso médio do fruto (PMF). O ganho percentual estimado para a produção mensal, com seleção entre e dentro de progênies, variou de 3,68% a 44,98%, respectivamente para os meses de junho e maio de 1999, enquanto que para os demais caracteres a variação foi de 28,3% a 327,2%. respectivamente para acidez total titulável e pH. É esperado que a próxima população apresente um conteúdo de vitamina C superior em mais de 30%, em relação as plantas do primeiro ciclo de seleção. A utilização de um índice que considera simultaneamente a classificação de cada progênie em relação as características avaliadas, mostrou uma coincidência de 84% de progênies entre aquelas selecionadas pelo método da seleção entre e dentro de progênies, indicando uma eficiência relativamente boa desse método em relação ao método tradicional.

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