

Performance of upland rice families selected from segregant populations

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ABSTRACT

The objective of this research was to analyze the agronomic performance of rice (*Oryza sativa* L.) families selected from divergent populations evaluated under different sowing times and locations in 1996/97. The source populations for the families were CNA x 5496, CNA x 6001, CNA x 6063 and CNA x 6102. A hundred families from each cross (population) were evaluated and submitted to five common treatments, which originated a three-replicate 20x20 lattice, grown at two locations, Lavras and Patos de Minas in 1997/98. In the next year (1998/99), the ten best and the ten worst-performing families from each population were again evaluated to confirm the superiority of families selected from the CNA x 5496 and CNA x 6001 populations. A 9x9 lattice with three replications experimental design was used. The two populations selected as the most promising in 1996/97 yielded the best families upon selection. Therefore, in a similar breeding program, it would be advantageous to carry out a high number of crosses, originating a great number of segregant populations, and to select the best ones, concentrating efforts on the evaluation of families extracted from superior populations. Such results confirm the efficiency of selection of source populations for family extraction.

KEY WORDS: *Oryza sativa*, breeding, yield.

INTRODUCTION

Rice, as the majority of other cultivated crops, carries in its germplasm bank, several thousands of accesses which permit an infinite number of two-by-two or multiple-parent breeding combination possibilities. However, this infinite number of possibilities makes the decision-making process of choosing parents to generate genetic variable populations very difficult for the plant breeder. In any breeding program, the number of families to be evaluated is limited by space and budget constraints. A question, which is frequently raised among researchers, is whether to evaluate a small number of families from the largest possible number of segregant populations or to work alternatively with a great quantity of families from a restricted number of source populations is the best option.

In order to answer this question, some simulation experiments were carried out to show the advantage of evaluating a smaller number of families out of the largest possible number of populations (Baker, 1984; Fouilloux and Bannerot, 1988). Such research however, assumed that h^2 estimates equal to 100%, which normally does not occur for the great majority of economically important characters. In this context, experiments with field beans (Ferreira, 1998) and

maize (Pinto, 1996) were conducted under field conditions, which revealed the need to evaluate a large number of families within each population, especially if character heritability is low.

All things considered, the breeder should try to obtain the greatest number of populations possible, evaluate them early in the F_2 , F_3 and F_4 generations, and concentrate efforts on evaluating a great number of families from the best populations. To make this procedure effective, it is important to establish criteria for choosing the best segregating populations. Some procedures for choosing superior populations have already been described by Jinks and Pooni (1976) and Abreu (1997). Performance evaluation of families extracted from such populations is an important stage in a breeding program. It is fundamental that families are tested in replicated experiments and in several environments so that possible effects of family by environment interactions, which may interfere in the process of family selection, can be evaluated.

The present research was designed with the purpose of evaluating the performance of families derived from populations with divergent agronomic performance, and to confirm the efficiency of early selection in such segregating populations.

MATERIAL AND METHODS

Families evaluated in this experiment were obtained from upland rice segregating populations selected during the 1996/97 growing season by Santos et al. (2001), who utilized the procedure proposed by Jinks and Pooni (1976). Out of a total of 23 populations, the two best-performing, CNAx 5496 (Caiapó/IAC 84-198//CNA 7680) and CNAx 6001 (CNAx 4442-6-1-B-1/4001.BC 92/93), and the two worst, CNAx 6102 (BSL/CNA 8217) and CNAx 6063 (CNAx 1722-9-1-1-1/L 141) were selected. The method utilized for the analysis of the populations was bulk inside family. Within each family a sample of 100 plants was randomly chosen, originating 400 families, which were grown at Formoso do Araguaia, State of Tocantins, Brazil, from May to September 1997, to increase the number of seeds for the 1997/98 study. Families from population CNAx 5496 were in the F₆ generation whereas families from the other three populations were in the F₄ generation.

In the 1997/98 growing season, the 400 families were evaluated in Lavras and Patos (both locations in the State of Minas Gerais, Brazil). Sowing was carried out on November 18, in Lavras, MG, and on November 25, in Patos de Minas, MG. A lattice 20x20 with three replicates was the experimental design used in this study. Five common treatments were added to the experiment: four populations, which originated the families and the cultivar Canastra. Plots were sown in 1.5m-long rows, 40 cm apart, with 90 seeds per meter at planting. Next, 400 kg/ha of the NPK: 4-30-16 + Zn fertilizer was used followed by a side-dressing application of 150 kg/ha of Ammonium Sulfate 45 days after planting. The experiments were sprinkle-irrigated whenever long periods of drought occurred. Standard practices for dryland rice plot cultivation were also used.

The following plant characters were evaluated: plant height (cm), flowering date (days to flower) and grain yield (kg/ha). Evaluation of these traits was based on EMBRAPA (1977).

In the following growing season (98/99), the ten best and the 10 worst families by grain yield from each population were evaluated. The total number of families went under 80 treatments, which were analyzed together with the check treatment "Canastra". A three-replicate 9x9 lattice experimental design was used and plots were sown in two 2m-long rows, 40 cm apart. Sowing was carried out on November 13th and 26th, respectively, in Lavras and Patos de Minas. Fertilization and irrigation were similar to those of the previous year and the traits

evaluated were the same.

Individual analysis of variance was performed for each trait under study in both years and locations. Treatment effects were considered random and the following statistical model was used for the lattice with common treatments:

$$y = m + t_i + r_j + b_{(j)k} + \bar{e}_{ijk}$$

where:

Y_{ijk} : is the observation of the *i*-th treatment in the *k*-th block of the *j*-th replication

m: the overall mean

t_i : effect of the *i*-th treatment (*i* = 1,2,...,v')

r_j : effect of the *j*-th replication (*j* = 1,2,...,j)

$b_{(j)k}$: effect of the *k*-th block within the *j*-th replication (*k* = 1,2,...,k)

\bar{e}_{ijk} : experimental error associated with observation Y_{ijk}

The t_i effect involves t_s (*s* = 1,2,...,v) and $t_{s'}$ (s' = 1,2,...,c), which are the effects of the regular and the common treatments respectively, and $v' = v + c$ ($v=400$ e $c=5$).

A joint analysis of variance over locations was performed later for each year, in which treatment effects were considered random and location effects fixed.

From the mathematical expectations of mean squares, variance components were estimated as well as phenotypic and genotypic parameters according to Vencovsky and Barriga (1992). For the heritability estimates of families evaluated in 1997/98, lower and higher confidence limits at the probability level of 1 - α = 0,95 (Knapp et al., 1985) were established.

In order to study the effect of location and year on families, a joint analysis of variance was carried out with the 80 treatments in common, namely the ten best and the ten worst in each population evaluated in both years and locations. In this case, the effects of years and locations were considered fixed and treatments random.

Since 80 families were evaluated (20 from each population) for two years, a study on the efficiency of selection was done by means of the following estimates:

a) realized heritability for families within each population, utilizing mean data from both generations, according to the procedure proposed by Fehr (1987)

and by Ramalho et al. (1993):

$$h_{ij}^2 = \frac{GS_j / m_j}{ds_i / m_i} \quad \text{where:}$$

GS_j : performance on generation j of the ten families selected in generation i, minus the overall mean of the 20 families of generation j;

ds_i : selection differential, i.e. the average of the ten selected families in generation i, minus the overall mean of the 20 families of this generation;

m_i and m_j : means of the 20 families in generations i and j, respectively.

i: generation in which selection of the ten best-yielding families and the ten poorest-yielding was made.

j: generation in which selected families in each population were evaluated.

b) Gain due to selection of best-yielding and poorest-yielding families in each population, utilizing the following expression:

$GS(\%) = [(Average\ of\ the\ ten\ best\ -yielding\ or\ poorest\ -yielding\ families,\ selected\ in\ generation\ i,\ evaluated\ in\ generation\ j - overall\ mean\ of\ the\ 80\ families\ evaluated\ in\ generation\ j) / (overall\ mean\ of\ the\ 80\ families\ of\ generation\ j) \times 100]$.

c) Correlation between the phenotypic performance of the families in generation i and the genotypic performance in generation j (r_{FiGj}), according to the expression presented by Bernardo (1991):

$$r_{FiGj} = r_{GiGj} \sqrt{h_i^2} \quad , \quad \text{where:}$$

r_{GiGj} : genetic correlation which is function only of the inbreeding coefficient (I) in the generations considered, i.e., $r_{GiGj} = \sqrt{\frac{(1+I_i)}{(1+I_j)}}$;

h_i^2 : heritability of the trait in generation i, in which selection is performed.

It is important to emphasize that the inbreeding coefficient (I) was different amongst families in each population. Thus, the following inbreeding coefficients were used:

1 - For families of population CNAx 5496:

$$I_6 = 15/16 \quad \text{and} \quad I_7 = 31/32$$

2 - For families of populations CNAx 6001, CNAx 6102 and CNAx 6063:

$$I_4 = 3/4 \quad \text{and} \quad I_5 = 7/8$$

RESULTS AND DISCUSSION

A summary of the joint analysis of variance for grain yield, plant height and flowering date, evaluated in Lavras and Patos de Minas in 1997/98, is presented in Table 1. The experimental precision, judged by the coefficient of variation estimated for grain yield ($CV_e = 28,1\%$), may be considered high when compared with other rice experiments (Santos, 1996; Rangel et al., 1998). This could be due to the size of the experiment, in which variations in soil fertility and lack of stand uniformity are common. Furthermore, practices such as irrigation, weed control and side-dressing fertilization in large areas are generally done with low precision, affecting treatments and increasing values of CV_e 's.

All sources of variation for the three characters were statistically significant, except "populations + check" for plant height. The presence of treatment x location interaction confirmed the need for family evaluation in more than one environment. σ_{TxL}^2 was around 11 % and as large as σ_G^2 for all characters. Family mean square for grain yield in population CNAx 6063 was quite different from those found in the other three populations; consequently, σ_G^2 for grain yield in those other families was large (Table 2). Such families, however, were extracted from a population that did not have high grain yield in the previous growing season and was selected based on its poor performance.

Estimates of genetic parameters (CV_g , b e h^2) displayed in Table 1 were considerable for the three traits, indicating great variability among materials, and the genetic gain upon selection can be large.

In selecting promising materials, plant breeders normally take into consideration estimates of heritability. An isolated estimate is not a good evidence of a breeding program success since it may be associated with lower mean yields, reinforcing the idea that the best population is that one associated with higher mean values and sufficient variability.

The σ_G^2 and h^2 mean values for grain yields of families within each population, together with the lower and upper limits of the latter estimates, are presented in Table 2. It is clear that families of the

Table 1. Joint analysis of variance for the characters grain yield (kg/ha), plant height (cm) and flowering (days), evaluated in Lavras-MG e Patos de Minas-MG in 1997/98.

Sources of variation	DF	Mean squares		
		Grain yield	Plant height	Flowering
Block/location	4	87268563.59**	12427.12**	175.42**
Location (L)	1	1408618993.00*	157957.70*	49042.07**
Treatment (T)	404	4229259.02**	406.42**	292.15**
CNAx 5496	99	1650358.70**	199.68**	113.75**
CNAx 6001	99	1849181.06**	330.72**	134.76**
CNAx 6102	99	1477361.83**	544.98**	145.70**
CNAx 6063	99	3959957.70**	404.94**	71.94**
Pop + check	4	3466392.26**	127.34 ^{ns}	330.22**
Between families	3	4234703.46**	410.19**	292.37**
P vs families	1	797301884.00**	15901.56**	69.682.27**
T x L	404	1024021.37**	139.72**	48.52**
Effective error	2072	616755.74	106.73	15.07
Mean		2793.71	95.53	88.61
σ^2_G		602083.88	49.95	46.18
σ^2_{TxL}		67877.60 (11%) ^{1/}	5.50 (11%) ^{1/}	5.58 (12%) ^{1/}
CV _e (%)		28.10	7.14	4.54
CV _g (%)		27.77	7.40	7.67
b (CV _g /CV _e)		0.99	1.04	1.69
h ² (%)		85.42	73.74	94.84

** , * significant at 0.01 and 0.05 level by F-test, respectively; ^{1/} percent of s^2_G .

two first populations have presented intermediate average h^2 ; such families were extracted from the populations with better performance in the 1996/97 growing season. The h^2 values are quite large for the trait in discussion and the range of variation between the lower and upper limits was quite low, indicating the good precision of the estimate. The h^2 estimates of the worse populations have also presented good precision (small variation between the lower and upper limits). Some discrepancies were present among the estimates, the greatest being found among the families within population CNAx 6063. Thus, it may be inferred that the variability generated through crossing was quite high despite the condition of the segregant populations (promising or not promising). This result is expected since the procedure utilized for the choice of populations (Jinks and Pooni's) takes into consideration only the probability of obtaining lines superior to a predetermined standard and not the genetic variability liberated by advanced generations. This is a restriction of the method, since it should consider also the potential variability of the

population (Abreu, 1997).

The performances of the populations evaluated in the first stage and their families were consistent, except in the case of CNAx 6063. Such result may be explained by the occurrence of interaction. In this context it is worth noting that the interaction populations x environments found by Santos et al. (2001) was quite large, reinforcing the idea that the population selection process must be based on experiments conducted in many different environments (years and locations).

The potential of the material evaluated can be confirmed by the percent of families with performance superior to that of the check treatment. In this study, 24% of the families have presented means higher than those of the check, which demonstrate the possibility of obtaining genetic gains upon selection (Table 3). The percent of families, in each population, with better performance than cultivar "Canastra" (check) was superior in the families selected out of the populations with high performance.

The percentages of the 40 highest-yielding and the

40 poorest-yielding families from each population are also displayed in Table 3. 70% of the best families came from the best populations and the other 30% originated from the worst population evaluated in 1996/97 (CNAx 6063). Despite having contributed with a significant number of superior families, population CNAx 6063 has also produced 20% of inferior families. On the other hand, population CNAx 6001 contributed with only 7,5% of inferior families, which indicates its superiority. This leads to the conclusion that there is no advantage in keeping population CNAx 6063 in the breeding program due to the great number of low-performing materials that must be submitted to evaluations with no possibility of genetic advances, therefore rising the costs of the program. As for the effect of years, it was not detectable since the populations submitted to selection were evaluated only during one growing season.

Tables 4 and 5 summarize the analysis of variance for each location. The highly significant differences among families for all traits under evaluation are noteworthy. Differently from the two previous growing seasons, the trial in Patos de Minas presented the best value for

CV_e 's in this particular growing season; however, the values found were within the limits established for the rice crop. The low mean grain yield presented by Patos de Minas has probably conditioned a high CV_e , since its error mean square was even lower than the one obtained for the Lavras trial.

The increments on the CV_g , b and h^2 estimates for the trait grain yield are also highly significant. All estimates are dependent on σ^2_G , which was quite large in both locations, specially in Lavras, contributing to the increase of estimates in the three parameters. In the summary of the joint analysis of variance (Table 6), family x location interaction is present, indicating the inconsistency of family performances over the two locations for grain yield and plant height. The contribution of σ^2_{FXL} to the genetic variance (σ^2_G) was around 11%, the same value found in the previous experiment, in which all 400 families were evaluated (Table 1).

Means for the grain yields obtained by the families and the averages for the 10 highest-yielding and the 10 poorest-yielding families for each population are

Table 2. Genetic variance (σ^2_g) and heritability (h^2) for grain yields (kg/ha) of families from upland rice segregant populations together with the lower and upper limits of the latter estimate. Lavras-MG and Patos de Minas-MG, 1997/98 ^{1/}.

Families	σ^2_g	$h^2(\%)$	LL	UL
CNAx 5496	172267.16	62.63	49.28	71.41
CNAx 6001	205404.22	66.65	54.74	74.48
CNAx 6102	143434.35	58.25	43.34	68.06
CNAx 6063	557200.33	84.42	78.86	88.08
Pop + check	474939.42	82.21	-46.97	93.63

^{1/} LL: lower limit and UL: upper limit.

Table 3. Means for the grain yields (kg/ha) of populations, of families and percent of superior families to cultivar Canastra (PSFC), percent of superior families to populations (PSFP) and percent of 40 highest-yielding families (PHYF) and 40 poorest-yielding families (PPYF). Lavras and Patos de Minas-MG, 1997/98.

Populations	Populations means	Families means	PSFC	PSFP	PHYF	PPYF
CNAx 5496	3656.58	3550.40	14	38	60	0
CNAx 6001	2990.61	2817.87	1	36	10	7.5
CNAx 6102	2065.62	1920.09	0	36	0	72.5
CNAx 6063	3228.11	2866.00	9	33	30	20
CANASTRA	4078.11					

presented in Table 7. The hypothesis confirms that the best families are obtained from the best populations. In this case, populations CNAx 5496 and CNAx 6001, which were the best in 96/97, yielded most productive families, with means of 5404 and 4613 kg/ha, respectively. CNAx 6102 and CNAx 6063, on the other hand, originated less productive families with averages of 2489 and 3913 kg/ha, respectively. The overall family mean also reinforces this result. Families from population CNAx 5496 distinguished from others as far as their average yields, since it overcame the check (Canastra) even when the best and worst yielding families were considered. These results demonstrate that this population is promising for breeding and that selection for the best populations will produce the best families and consequently the best lines.

To study the effects of year and location on the 80 families, a joint analysis of variance was performed with the common treatments (Table 8). The significant family x year and family x location interactions indicate the inconsistency of performance of the families studied over the two years and the two locations. Family x year interaction variance, which was much more pronounced than the family x location variance, represented 9% and 5%, respectively of the σ^2_G . This result is corroborated by Santos et al. (2001) in a study carried out in the 1997/98 growing season, when the families of population CNAx 6063 performed satisfactorily.

To support the previous observations, the families means for the two growing seasons are shown in Table 9. The most productive families from population CNAx 6063 performed well only in 97/98 without repeating the same performance in the following year. The performance of families from populations CNAx 5496 and CNAx 6001 were quite superior to the other families and their improvement was quite expressive from one year to the other.

Family selection efficiency could have been evaluated in the present research since families were tested during two growing seasons. The parameters used to attain the objectives are presented in Table 10. It is clear that the h_r estimates, which reflect the real gains breeders are supposed to obtain, are quite superior for the families from the best populations (CNAx 5496 and CNAx 6001). Such results were inferior to the ones found by Santos (1996) in segregant populations from flood-irrigated rice.

The estimates of the correlations between family phenotypes in generation i and genotypes in generation j are displayed in table 10. Values obtained were quite high which indicated the efficiency of the selection. For this research in special, this result means that the best and the worst families from a superior population were also the best and the worst, respectively, in the two growing seasons. The same can be said about families from inferior populations. The r_{FiGj} values obtained were higher than those for a

Table 4. Analysis of variance for the characters grain yield (kg/ha), plant height (cm) and flowering (days), evaluated in Lavras-MG, 1998/99.

Sources of variation	DF	Mean squares		
		Grain yield	Plant height	Flowering
Replication	2	343157.99	85.38	3.17
Block/replication	24	673222.49	94.82	9.44
Families	80	8343929.40**	223.14**	259.04**
Effective error	136	541996.67	61.50	4.70
Mean		4003.50	109.67	90.49
σ^2_G		2,600,644.25	74.38	86.35
CV _e (%)		18.39	7.15	2.40
CV _g (%)		40.28	6.69	10.18
b (CV _g /CV _e)		2.19	0.94	4.25
h ² (%)		93.50	72.44	98.18

** , * significant at 0.01 and 0.05 level by F-test, respectively.

Table 5. Analysis of variance for the characters grain yield (kg/ha) and plant height (cm), evaluated in Patos de Minas-MG, 1998/99.

Sources of variation	DF	Mean squares	
		Grain yield	Plant height
Replication	2	4543190.78	117.44
Block/replication	24	1098263.81	67.67
Families	80	52622229.05**	339.80**
Effective error	136	371828.21	51.48
Mean		2822.81	106.22
σ^2_G		1754076.35	96.10
CV _e (%)		21.60	6.75
CV _g (%)		45.23	9.23
b (CV _g /CV _e)		2.09	1.34
h ² (%)		92.93	84.85

** , * significant at 0.01 and 0.05 level by F-test, respectively.

Table 6. Joint analysis of variance for grain yield (kg/ha) and plant height (cm), evaluated in Lavras-MG and Patos de Minas-MG, 1998/99.

Sources of variation	DF	Mean squares	
		Grain yield	Plant height
Block/location	4	2,443,174.39**	101.41 ^{ns}
Location (L)	1	169,372,610.10**	1,440.88*
Families (F)	80	11,893,148.45**	470.03**
F x L	80	1,713,017.27**	92.93**
Effective error	272	456,912.44**	56.49
Média		3413.16	107.95
σ^2_G		1,906,039.34	68.92
$\sigma^2_{F \times L}$		209,350.81 (11%) ^{1/}	6.07 (9%) ^{1/}
CV _e (%)		19.80	6.96
CV _g (%)		40.45	7.69
b (CV _g /CV _e)		2.04	1.10
h ² (%)		96.16	87.98

** , * significant at 0.01 and 0.05 level by F-test, respectively; ^{1/}percent of s^2_G .

field bean crop found by Rosal (1999), demonstrating the efficiency of early-generation selection. Thus it can be assumed that both selections of the best and worst families were quite effective. Since selection was based on family means, the efficiency of this parameter for the purpose of selection was reinforced.

For the divergent families selection evaluation, the ten highest and the ten lowest productive families from each generation (i and j) were used. Results are presented in Table 10 and it shows the gains in both directions. Gains for increasing yields were higher than gains for reducing the expression of the character,

Table 7. Means for grain yield from the 10 highest-yielding families and from the 10 poorest-yielding families from populations evaluated in Patos de Minas-MG and Lavras-MG, and overall mean, 1998/99.

Population	Families	Lavras	Patos de Minas	Overall Mean
CNAx 5496	Highest	6367	4441	5404
	Poorest	5150	3207	4179
Mean				4791
CNAx 6001	Highest	5030	4196	4613
	Poorest	3341	2521	2931
Mean				3772
CNAx 6102	Highest	2814	2163	2489
	Poorest	1995	1055	1525
Mean				2007
CNAx 6063	Highest	4356	3470	3913
	Poorest	2847	1401	2124
Mean				3018
CANASTRA	Check	5278	4107	4692

especially for the best populations such as the CNAx 6001, which obtained gains of 63,7 and 4,0%, for the highest and lowest-producing , respectively. Gains for the inferior populations were relatively small regarding trait expression increase.

Such comparisons support the previous conclusions about the performance of families from inferior populations in the 1996/97 growing season. To keep these families in the program would not be justifiable since their gains were inexpressive. Breeding efforts should be concentrated on the evaluations of most promising families. For low-yielding families, gains were negative in populations with poor performance; there was no genetic advance for such materials, whereas families from populations CNAx 5496 and CNAx 6001 presented real genetic gains even in the less productive families.

Results have shown that early selection on segregant populations was effective and that the Jinks and Pooni method utilized by Santos et al.(2001) was efficient. The absence of dominance effects was assumed upon the application of this method. Such assumption has not brought major consequences to the estimates obtained by this study. In general the method was particularly efficient for both biparental and multiple crosses.

Some important published researches have concluded that, whenever a choice was given, it was preferable to take a small number of families from the highest possible number of populations (Baker, 1984; Fouilloux and Bannerot, 1988). This strategy has been utilized in some breeding programs involving autogamous plants (Cooper, 1988). However, if populations are to be advanced in bulk, and, in the

process of family evaluation, an experimental design is used, in some environments breeders could concentrate their efforts and resources on the most promising populations, thus evaluating a greater number of families. This strategy is recommended especially when selection is aimed at low heritable

Table 8. Joint analysis of variance for the characters grain yield (kg/ha) of common materials in Lavras and Patos de Minas, 1997/98 and 1998/99.

	FV	GL	QM
Block/year/location	8		44855868.99**
Year (Y)	1		77971972.80 ^{ns}
Location (L)	1		6942238.38 ^{ns}
YxL	1		442675641.90*
Families (F)	80		18961665.90**
F x Y	80		2266353.68**
F x L	80		1517920.64**
F x Y x L	80		1560154.41**
Effective error	544		598207.38
Mean			3129.93
σ^2_G			1530288.21
$\sigma^2_{F \times L}$			76642.77 (5%) ^{1/}
$\sigma^2_{F \times a}$			139012.19 (9%)
CV _e (%)			24.71
CV _g (%)			39.52
b (CV _g /CV _e)			1.60
h ² (%)			96.85

**, * significant at 0.01 and 0.05 level by F-test, respectively; ^{1/}percent of s^2_G .

Table 9. Means for grain yield from 10 highest-yielding families, 10 poorest-yielding families and general mean from families evaluated in Lavras-MG and Patos de Minas-MG, 1997/98 and 1998/99.

Populacion	Families	1997/98	1998/99	Mean Two years	General Mean of families
CNAx 5496	Highest	4577	5404	4990	4230
	Poorest	2760	4179	3469	
CNAx 6001	Highest	3815	4613	4214	3298
	Poorest	1833	2931	2382	
CNAx 6102	Highest	2817	2489	2653	1985
	Poorest	1110	1525	1317	
CNAx 6063	Highest	4263	3913	4088	2944
	Poorest	1475	2124	1800	
CANASTRA	Check	4078	4692	4385	

Table 10. Realized heritability (h_r^2), correlation between the phenotypic performance of generation i and the genotypic performance in generation j and gain due to selection of highest-yielding and poorest-yielding families. Lavras-MG and Patos de Minas-MG, 1997/98 and 1998/99.

Families	h_r^2 (%)	r_{FiGj} (%)	GS (%)	
			Highest	Poorest
CNAx 5496	19.40	79.0	52.2	17.7
CNAx 6001	20.60	81.0	63.7	4.0
CNAx 6102	15.60	76.0	29.6	-20.6
CNAx 6063	15.70	91.0	36.5	-25.9

traits (Ferreira, 1998). The results obtained in the present work emphasize the importance of carefully choosing the segregant populations to work with.

CONCLUSION

The best families originated from the best segregant populations, reinforcing the efficiency of Jinks and Pooni method in selecting early-generation of populations and in allowing the breeder to concentrate greater efforts on the evaluation of a greater number of families within those populations.

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RESUMO

Desempenho de famílias de arroz de terras altas selecionadas de populações segregantes

O objetivo do trabalho foi analisar o desempenho de famílias de arroz (*Oryza sativa* L.) derivadas de populações divergentes avaliadas em diferentes épocas de semeadura e locais em 1996/97. As famílias avaliadas foram extraídas das populações CNAx 5496, CNAx 6001, CNAx 6063 e CNAx 6102. Avaliaram-se 100 famílias de cada população, juntamente com cinco tratamentos comuns, originando um látice 20 x 20 com três repetições, analisado em Lavras e Patos de Minas, em 1997/98. No ano agrícola seguinte (98/99), foram avaliadas as dez melhores e as dez piores famílias de cada população, visando confirmar a superioridade das famílias das populações CNAx 5496 e CNAx 6001. O delineamento utilizado foi um látice 9x9 com três repetições. As duas populações selecionadas em 1996/97 como mais promissoras originaram as melhores famílias. Assim, em um programa de melhoramento, seria vantajoso realizar um maior número de cruzamentos, originando mais populações segregantes, selecionar as melhores e concentrar os esforços na avaliação das famílias dessas populações superiores. Esses resultaram também comprovam a eficiência da seleção das populações de onde as famílias foram extraídas.

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