



Recurrent selection resulted in rapid genetic gain for upland rice in Brazil

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Populational recurrent selection (RS) has been used for rice breeding at the Brazilian Agricultural Research Corporation (Embrapa) since the early 1990s. One of the populations under RS is named CG3, developed in 1997 by intercrossing 59 selected families, representing Embrapa’s elite early-flowering upland rice germplasm. This note reports the results of the ongoing RS applied to the CG3 population.

The RS scheme is based on a 3-year, four-step cycle (Fig. 1)—year 1 selection of F₁ single plants; year 2 selection between F₂ progenies to advance to yield trials and selection of five plants within selected F₂ progenies, of which F₃ seeds are kept in storage; year 3, evaluation of 250–300 F_{1:3} families, in multiple-environment yield trials; and off-season recombination of approximately 50 selected F_{1:3} families, by manual crossing, using F_{2:3} seeds in storage. Single-plant selection was based on plant architecture, phytosanitary aspect, and grain type, whereas family-based selection depended on grain yield, lodging resistance, heading date, disease resistance, and grain quality.

The results reported here are based on data from field evaluation of F_{1:3} families in three RS cycles (trials in 2000, 2003, and 2006), conducted in four to five environments/year, in an augmented block design (Federer 1961), with four

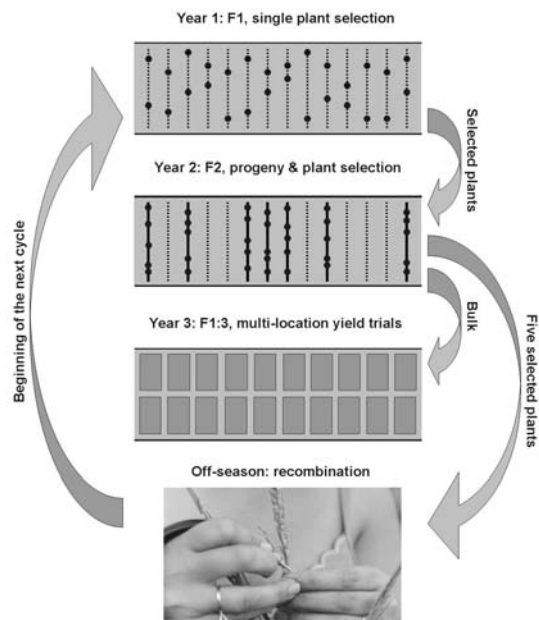


Fig. 1. Recurrent selection scheme used for upland rice improvement at Embrapa.

early-flowering rice cultivars used as checks, replicated in each block. Plots were dry-seeded in 4 rows × 5 m, spaced at 0.3 m, with 60 seeds m⁻¹. Data were analyzed in SAS/GLM, with the interactions family × cycle and family × environment within a cycle bulked into the experimental error. Genetic gain was estimated by comparing the adjusted means for each cycle (Bresseghele et al 1998, modified by Morais et al 2000).

RS resulted in rapid gain for grain yield (Table 1). In cycle 1, the mean yield of F_{1.3} families from the population was significantly lower than the mean of the checks. In cycle 2, there was no significant difference. In cycle 3, the population was more productive than the checks. The mean genetic gain for grain yield was 103.4 kg ha⁻¹ y⁻¹, corresponding to 3.6% of the initial population mean. This gain is three to four times as high as the genetic gain from other rice breeding programs in Brazil, using pedigree schemes (Bresseghele et al 1999). Some increase in days to flowering was observed, whereas plant height showed a small change. Lodging and blast disease severity decreased significantly in the population (data not shown).

Table 1. Adjusted means of groups of families from the population CG3, evaluated in three cycles of recurrent selection, compared with the mean of checks, for grain yield, flowering time, and plant height.

Group	Year	Number of materials	Grain yield		Flowering time		Plant height	
			(t ha ⁻¹)	(%)	(days)	(%)	(cm)	(%)
Checks	Average	4	3.18 b	100	76.9 a	100	104 b	100
Cycle 1 families	2000	131	2.87 c	90	71.3 d	93	105 ab	101
Cycle 2 families	2003	269	3.19 b	100	73.3 c	95	106 a	102
Cycle 3 families	2006	244	3.49 a	110	74.7 b	97	105 a	101
Gain per year			0.103	3.6	0.6	0.8	0.0	0.0

Means followed by the same letter do not differ by Tukey's test at $\alpha=0.05$.

Yield histograms of families from each cycle revealed an increasing mean and a somewhat decreasing variance in grain yield (Fig. 2). Maintenance of genetic variation is important in populational breeding. To evaluate the remaining variability in CG3, 96 F_{1.4} families were genotyped with three fluorescent-based multiplexes, comprising 15 SSR markers (Pessoa Filho et al 2007). Each family was represented by a bulk of six plants. The number of alleles was computed as total, common, and effective alleles. Results indicated an

intermediate to high remaining genetic diversity (Table 2), which should allow further gains through RS.

Two factors may have contributed to the rapid gains observed: (1) in the first two cycles of selection, low-yielding families were easily detected and eliminated, raising the population mean; (2) blast disease incidence in the checks increased through the cycles, and the consequent decay in the performance of the checks may have partially inflated the estimate of genetic gain. Nevertheless, the improvement in CG3 is corroborated by the fact that the best inbred lines from cycle 3 are proving to be competitive with elite lines from the pedigree program (evaluation in progress).

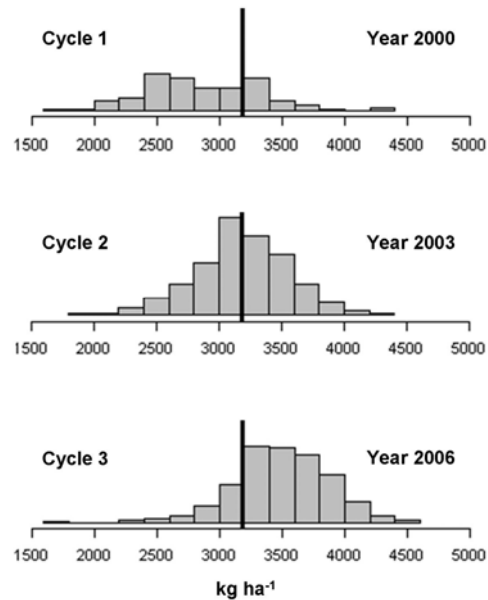


Fig. 2. Histograms of the distribution of grain yield of F1:3 families from upland rice population CG3 in three consecutive cycles of recurrent selection. Heavy lines indicate the adjusted mean of four checks across cycles.

Table 2. Number of total, common, and effective alleles detected in the populations of CG3 on 15 unlinked SSR loci.

Marker	Alleles (no.)		
	Total (all alleles)	Common ($p_i > 5\%$) ^a	Effective ($N_e = 1/\sum p_i^2$)
OG05	6	2	1.3
OG106	11	5	4.5
OG44	11	7	4.7
OG61	8	4	3.9
OG81	7	4	2.4
OS19	6	3	2.0
RM224	13	5	4.5
RM248	10	3	2.0
RM252	5	2	2.0
RM259	9	3	1.3
RM263	4	3	2.4
RM335	9	5	3.1
RM418	5	3	2.2
RM420	5	2	1.9
RM475	5	2	1.5
Av	7.6	3.5	2.64

^a p_i =frequency of the i^{th} allele.

Considering the progress achieved so far and the remaining genetic variability in the population, it is reasonable to expect that inbred lines from CG3 may soon take the yield of upland rice beyond current levels in Brazil.

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