GENETIC PROGRESS OF THE CNA6 POPULACION AFTER FOUR CYCLES OF RECURRENT SELECTION

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Key words: *Oryza sativa* L., mixed model, population breeding

An important parameter to measure the success of breeding programs is the monitoring of their efficiency over time by estimating achieved genetic progress and identifying the factors that contributed to it. The objectives of this study were to estimate genetic progress in grain yield (GY) achieved in the CNA6 population of upland rice after four cycles of recurrent selection by the Brazilian Agricultural Research Corporation; and evaluate the genetic potential of this population to generate superior inbred lines after each cycle. This population was synthesized in the 1993/94 crop year by incorporating the alleles from 27 parents into the CNA-IRAT 5/2/1 population. The CNA-IRAT 5 population was a product of the partnership between Brazilian Agricultural Research Corporation (Embrapa) and the French Center for International Cooperation in Development-oriented Agricultural Research (CIRAD). This population was synthesized in 1984 by intercrossing 26 lines of the subspecies *japonica* and one line of *indica* originated from the mutation of IR6. This mutant possesses the recessive gene that affects genetic male sterility, which makes possible the recombination of progenies. The data set was unbalanced because in each cycle, the trials were composed of $S_{0:2}$ progenies from the respective cycle with at least three checks. As check cultivars (commercial) change over the time, some checks were substituted across the cycles; however, at least two common check cultivars were maintained between cycles. The Federer's augmented block design with one replication within the location was used. Plots consisted of four 5-m-long rows, spaced 0.30 m. The statistical analyses were performed using mixed model. The locations and cycles effects were treated as environments, because only two cycles with two locations were common to all periods; and there was no intention to analyze the effect of the interactions between genotype and environment partitioned into locations and cycles. Results revealed genetic progress for GY with total genetic gains of 375.87 kg ha^{-1} during the four cycles. The annual relative gain observed for GY was 1.54%. The genetic potential of the population was analysed by the expected proportion of superior inbred lines. The standard adopted as the limit for obtaining superior inbred lines was the average of checks. The genetic potential for GY increased during the study period, because the average of $S_{0:2}$ progenies increased and the genetic variance among $S_{0:2}$ progeny was maintained to allow the improvement by selection and recombination in subsequent cycles.

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