MONITORING A RICE RECURRENT SELECTION PROGRAM USING SSR AND RAPD MARKERS

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Recurrent selection (RS), based on the selection of superior individuals from a genetically variable group and their posterior recombination, is widely used for breeding allogamous species, and has been proposed as an alternative for autogamous species such as rice. The success of an RS program depends on the selection of the progenitors, based on their genetic variability. Rice male sterile lines are used in RS programs to facilitate recombination and seed production. Since the progenies of the superior plants are harvested from male sterile individuals after each cycle, three questions raised: (a) what is the genetic distance between the male sterile line and the other parental lines involved; (b) what is the effect of the male sterile line on the genotypic composition of the recombined progeny, and (c) what is the proper selection cycle to initiate the process of line recovery. An experiment was set up to answer these questions. A battery of 100 SSR (Simple Sequence Repeats) markers was recently developed from the genome of *O. glumaepatula*, a wild relative, native to Amazon Forest and Western Brazil. From these, fourty-eight SSR markers selected at random were used to genotype the 22 parental lines used to develop the RS superior population called CNA5. Fifteen of the most informative markers presented more than seven alleles usually observed as homozygotes in the parental lines. Only three of the tested marker loci were monomorphic for the parental sample genotyped. Allelic frequencies were estimated for each selected marker locus based on a sample of 104 rice varieties (reference collection) of *O. sativa* subspecies *indica* (irrigated rice) and *japonica* (upland rice). Genetic distances between each parental line and the rice varieties were estimated based on SSR- and RAPD-marker polymorphisms. The allelic contribution of parental lines to two selection cycles was estimated.

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