INTRODUCTION

The genus Oryza consists of two cultivated rice species (O. sativa, and O. glaberrima) and about 20 related species (Vaughan et al., 2003), which represent a source of new alleles for improving the yield, quality and stress resistance of cultivated rice. Genome differentiation at the diploid and tetraploid levels has been considerable, which makes difficult the transfer of alleles of interest to cultivated rice by crossing. There are ten different genomes in Oryza genus, AA, BB, CC, EE, FF, GG, BBCC, CCDD, HHJJ and one unknown. Some interspecific crosses have been achieved, but mainly with diploids AA species due its close relation with O. sativa (Brar and Kush, 1997). Reports of diploid - tetraploid crosses did not use molecular markers to prove introgressions nor evaluated cytogenetics relationships (Mariam et al., 1996; Multani et al., 2003). In this work, we obtained diploid individuals from a cross between the cultivated rice O. sativa (AA genome) and the wild tetraploid O. latifolia (CCDD genome), evaluated cytogenetic process to recover fertility, and showed introgression from tetraploid to diploid rice by using SSRs markers.

MATERIALS AND METHODS

Figure 1 shows the crossing scheme used in this study. 80 SSRs markers out of 313 proved in O. latifolia were polymorphic and used to follow introgressions into O. sativa (figure 3). A total of 28 BC2 and BC3 individuals were obtained and evaluated using the polymorphic SSRs distributed throughout the whole genome. Molecular data were analyzed with the CSSL Finder software (Lorieux, 2006) to look for wild chromosomal segments introgressed into O. sativa.

RESULTS AND DISCUSSION

Triploid sterile F1 hybrids between an accession of allotetraploid species Oryza latifolia (2n=48) and the diploid O. sativa (2n=24) were obtained by embryo rescue. After three backcrosses towards O. sativa fertile progenies were obtained (figure 2). Cytogenetical evaluations in all generations showed some pairings between the O. latifolia and O. sativa chromosomes in F1, and a trend to complete diploidy in later generations. Additional chromosomes were observed in twenty-one BC2 and BC3 individuals (eleven individuals with one, and ten with 2), but seven of them had not additional chromosomes. SSRs showed clearly the additional chromosomes in some plants (figure 5).

CONCLUSIONS

• Use of wild allotetraploids of genus Oryza in cultivar rice improvement, by means of interspecific crosses is possible.
• Evaluation by SSRs demonstrated that pairing between homeologous chromosomes may produce recombination.
• Three backcrosses towards O. sativa were required to recover diploidy, and therefore, fertile individuals with wild introgressions.
• Additional work using other accessions and more markers would give more information about recombination capacity between these species and their evolutive relationships.

REFERENCES


