were screened in the field during the main season.

In F_1 progenies from all crosses, dominance of fertility over complete sterility was observed. F_2 populations from P1/P5 and P1/P6 showed segregation for fertility and complete sterility in a ratio of 15:1. This indicated that thermosensitive male sterility was controlled by two pairs of recessive genes with duplicate inheritance. The remaining three crosses displayed monogenic control of this trait. The test cross progenies from P1//P1/P5 showed 3:1 segregation (χ^2=0.0126). The results suggested two pairs of independent recessive genes controlling the TGMS trait in UPRI 95-140. Monogenic inheritance observed in the F_2 populations of crosses P1/P2, P1/P3, and P1/ P4 was due to the allelic nature of one of the two pairs of recessive genes present in both the parents involved.

Fertility transformation of TGMS plants in segregating populations of crosses depended on the genetic background of the male parents used. In the F_2 generation, average maximum fertility of TGMS plants during spring 1996 was 37.7, 45.3, 60.5, and 65.4% in crosses P1/P5, P1/P6, P1/P2, and P1/P4, respectively, as compared with 41.5% in UPRI 95-140, the female and TGMS donor parent. Differential behavior of TGMS plants in the F_2 for transformation from fertility to complete sterility was observed during the heading period: 25 Apr to 20 May for cross P1/P5, 1-10 May for P1/P6, 1-25 May for P1/P2, 1-10 May for P1/P4, and 1 May for the TGMS female parent. Eight lines identified with early transformation behavior were 97-7S from P1/P2; 34-2S and 69-2S from P1/P5; 206-8S, 206-9S, and 206-10S from P1/P4; and 79-2S and 79-4S from P1/P6. These lines are being further evaluated for their agronomic performance and for possible exploitation in hybrid breeding.■

Biochemical markers for characterizing rice genotypes

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Eight frequently used genotypes in the hybrid rice program were characterized on the basis of (1) phenol color reaction; (2) electrophoresis profiles of total soluble seed proteins, albumin, and globulin; and (3) polymorphism with respect to esterase (EST), malate dehydrogenase (MDH), peroxidase (POX), alcohol dehydrogenase (ADH) and glutamate dehydrogenase (GDH) isozymes. These genotypes were IR58025A, IR58025B, IR62829A, IRR62929B, IR54742-22-19-3R, IR40750-82-2-2-2-3R, IR10198-66-2R, and IR20933-68-21-1-1-2-1-R.

Seven genotypes were grouped into two classes on the basis of phenol color reaction; IR20933-68-21-1-1-2-1R was distinct from the others because it did not develop color. A comparison of sodium dodecyl sulfate polyacrylamide gel electrophoresis profiles of soluble proteins, albumin, and globulin revealed maximum polymorphism among the genotypes for the albumin fraction. All the genotypes were distinct from each other except for the A and B lines, in which only the presence of a weak band of approximately 14,000 kD molecular weight differentiated IR58025A from its maintainer line.

Maximum polymorphism was detected in the isozyme patterns of EST and POX, which differentiated all A and R lines. The greater intensity of a POX band having an Rm of 0.93 differentiated IR58025A from its B line. A faint MDH band having an Rm of 0.67 was detected in IR62829A, but was absent in its corresponding B line. Thus, a combination of the albumin profile with a POX, EST, or MDH isozyme pattern could identify all eight lines studied. The phenol color reaction was useful in verifying the identity of IR20933-685-21-1-1-2-1R. Such characterization is useful in establishing or verifying the identity of a genotype and in differentiating one genotype from another. The uniformity of these patterns within the population of a genotype needs to be tested. The possibility of using isozyme markers to test genetic purity, particularly of A lines, is now being investigated.■

Identifying molecular markers for the gene(s) governing thermosensitive genic male sterility in rice

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Thermosensitive genic male sterility (TGMS) in rice is advantageous in hybrid seed production compared with three-line breeding. Genetic studies revealed four putative genes imparting thermosensitive male sterility in rice. It was observed that the segregation pattern of this trait in the F_2, F_3, and backcrosses indicated that sterility caused by the TGMS trait was controlled by a single recessive gene. It was noted, however, that individual TGMS segregants drawn from the same F_2 population exhibited a differential pattern for fertility alteration, suggesting the influence of modifier genes. This makes the transfer of this character difficult to achieve, as selection has to be made for the appropriate fertility alteration level in addition to selection for the TGMS trait. Identifying a suitable molecular marker linked to genes of the TGMS trait may therefore aid in selection. The present study aimed at tagging genes pertaining to TGMS through a bulked