

Early Generation Selection for Amylose Content in Rice Grain: Heritability and Response to Selection

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ABSTRACT

Landraces of glutinous rice contain many desirable traits, but many consumers do not prefer its glutinous grain characteristic. Genetic variability in the glutinous grain type exists, suggesting that it should be feasible to select for non-glutinous grain type. The aim of the present study was to accelerate the selection of non-glutinous rice grain type by examining the amylose content of F₃ and F₄ lines.

The grain amylose content of two hybrids of rice combinations was investigated: Kao Dok Mali 105 (non-glutinous) x Kum Doi Saket (glutinous) and RD15 (non-glutinous) x Kum Doi Saket. The amount of amylose was measured as an extraction from the unmilled ground grains, using 2N NaOH in 95% ethyl alcohol. Fifty F₂ plants were selected randomly to build up the F₃ families and, after harvesting, seeds of the 50 F₃-derived lines were divided into two halves. One half was used for analyzing amylose while the remainder was used to produce 50 F₄ families. In the F₄ generation, 20 plants were sown from each family and the amylose means and variance values of the 50 F₄ families were calculated as a within family variance. Heritability was calculated based on the linear regression coefficient value (b), which was obtained from the regression of the within family mean of F₄ families on its relative derived F₃ mean ($h_{ns}^2 = b \times 4/7$). The response to selection (R) for amylose content was then estimated by using a mathematical model, $R = i\sigma h^2$, with 5% of selected proportion ($v = 5\%$).

Variation in rice grain amylose content was detected in F₃ and F₄-derived lines in both combinations of parents, with a population mean intermediate between the two parents' values but closest to the value of the higher parent. This indicated the occurrence of the partial dominant action of gene segregation. Therefore, a selection for the character could be achieved in the F₃ generation. In the F₄ generation, family variance of the derived lines varied little with standard deviation (σ) = 2.24 and 2.35 in the two combinations. Regression of these variance values on its family mean showed a considerable number of families that regressed closely to the parents, thereby, indicating the homozygosity of genotypes in some F₄-derived lines. There were 14 lines (28%) in Kao Dok Mali 105 x Kum Doi Saket combination and 2 lines (4%) in RD15 x Kum Doi Saket combination that showed homozygosity. A significant linear regression