W04

Genetic diversity and phenotype variation analysis among rice mutant lines (Oryza sativa L.)

Truong Thi Tu Anh, Do Tan Khang, Phung Thi Tuyen, Pham Thi Thu Ha, Tran Dang Xuan*

Graduate School for International Development and Cooperation, Hiroshima University 1-5-1 Kagamiyama, Higashi-Hiroshima city, Hiroshima 739-8529, Japan

Abstract

Genetic diversity is one of fundamental parameters for rice cultivar improvement. Rice mutants are also a new source for rice breeding innovation. In this study, ninety-three SSR markers were applied to evaluate the genetic variation among nineteen rice mutant lines. The results showed that a total of 169 alleles from 56 polymorphism markers was recorded with an average of 3.02 alleles per locus. The values of polymorphism information content (PIC) varied from 0.09 to 0.79. The maximum number of alleles was 7, whereas the minimum number of alleles was 2. The heterozygosity values ranged from 0.10 to 0.81. Four clusters were generated using the unweighted pair group method with arithmetic mean (UPGMA) clustering. Fourteen phenotype characteristics were also evaluated. The correlation coefficient values among these phenotye characteristics were obtained in this study. Genetic diversity information of rice mutant lines can support rice breeders in releasing new rice varieties with elite characteristics.

Keywords: genetic diversity, polymorphism information content, alleles, rice mutant lines, SSR markers

Corresponding author*
Tran Dang Xuan

Graduate School for International Development and Cooperation, Hiroshima University Address: 1-5-1 Kagamiyama, Higashi-Hiroshima city, Hiroshima 739-8529, Japan

Tel: +81-82-424-6927; Fax: +81-82-424-6927

E-mail: tdxuan@hiroshima-u.ac.jp