

Genetic diversity analysis of traditional rice *Sudu Heenati* (*Oryza sativa* L.) based on seed morphology and Simple Sequence Repeat (SSR) markers

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Abstract

Knowledge and assessment of the genetic diversity of genetic resources are important foundations for germplasm management process and crop improvement. This study was conducted to assess the genetic diversity and to identify representative sample among 19 accessions of *Sudu Heenati*, which are conserved in the seed gene bank of the Plant Genetic Resource Centre (PGRC), Gannoruwa. Seed morphological characters were assessed in accordance with the standard PGRC descriptors for rice. Grain shape, grain width, grain length, sterile lemma colour, seed coat colour, pubescence of lemma, lemma and palea colour were used as morphological descriptors and 26 polymorphic SSR markers were used for molecular analysis. Data were scored manually and a statistical analysis was done for morphological and molecular data using MINITAB 16 and POWERMAKER 3.25 software, respectively. Results revealed that there is a considerable amount of genetic diversity among the tested accessions of *Sudu Heenati* both at morphological and molecular levels. According to the morphological analysis of *Sudu Heenati*, accessions were grouped into 8 clusters. Molecular analysis identified a total of 75 alleles across 19 populations ranging from 3 to 5 alleles per locus with the average of 3.12 alleles. The measure of genetic diversity varies from 0.29 to 0.7 and a higher level of genetic diversity was observed at the locus RM259 (0.70), low level of genetic diversity was observed at RM207. The average PIC value of *Sudu Heenati* was observed as 0.48. The highest PIC value was observed at the locus RM259 (0.64) while the lowest was observed at RM207 (0.31) with a mean of 0.4. Nei's genetic distance ranged from 0.01 to 0.83. Constructed phylogenetic tree using UPGMA algorithm grouped these accessions into eight main clusters. Based on the molecular analysis and morphological data, nine accessions; 011828, 012825, 002088, 006332, 003993, 004354, 005670, 003355 and 003874, were identified as representative set of *Sudu Heenati* for seed production.

Keywords: Genetic diversity, Germplasm, Seed morphological characters, Simple Sequence Repeat marker, *Sudu Heenati*

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