

# THE USE OF SIMPLE SEQUENCE REPEATS FOR DETECTING GENETIC DIVERSITY AND DIFFERENTIATION IN EGYPTIAN AND EXOTIC RICE (*Oryza sativa* L.) SUBSPECIES

By

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## ABSTRACT

A set of 16 rice simple sequence repeats (SSRs) markers was used for the assessment of genetic diversity in 21 Egyptian and exotic rice genotypes. A total of 66 alleles were detected at 16 loci using the above SSR markers pairs, the number of alleles per locus ranged from two for RM 161 and RM 162 to six for RM 22, RM 55, RM 413 and RM 271 with an average 4.125 per locus. The value of polymorphic information content (PIC) for the 16 microsatellite loci varied from 0.439 for RM 6 to 0.996 for RM 413 with an average of 0.705. The average of PIC for *O. sativa* and the two subspecies *indica* and *japonica* was 0.689, 0.619 and 0.501, respectively. Compared to *japonica* genotypes, the *indica* group showed significantly higher genetic diversity on chromosomes 2, 3, 4, 5, 6, 7, 11 and 12 and considerably lower diversity on chromosome 1, 9 and 10. Cluster analysis based on pair-wise comparison of genotype genetic similarities data resolved the *O. sativa* into two groups. Group I corresponds to the classical *japonica* subspecies, whereas group II belonged to the *indica* subspecies. The results demonstrated the utility of microsatellite markers for detecting polymorphism leading to genotype identification and for estimating genetic diversity to be used in rice breeding programs.

**Key Words:** Simple Sequence Repeats, Genetic Diversity, Egyptian And Exotic Rice