

Maytinee Kladmook 2009: Classification of Rice Germplasms Using DNA Markers for Hybrid Rice Production. Master of Science (Genetics), Major Field: Genetics, Department of Genetics. Thesis Advisor: Assistant Professor Vipa Hongtrakul, Ph.D. 102 pages.

Genetic diversity among 415 rice cultivars collected from Thailand and foreign countries was determined using 4 marker systems, Insertion/Deletion (InDel), Inter-Simple Sequence Repeat (ISSR), microsatellite and gene specific marker. A total of 34 alleles from InDel marker were generated with an average of 2.83 alleles per locus. Polymorphic Information Contents (PICs) or Expected heterozygosity (H_e) ranged from 0.2110-0.5563 with an average score of 0.3707. Phylogenetic tree was performed using NTSYS-pc version 2.20k program which could clearly identify rice samples into 2 groups, *indica* and *japonica*. Genetic similarity between two groups was 0.28. Principal Component Analysis (PCA) was also performed and the result was consistent with phylogenetic tree. Genetic diversity of rice germplasms was assessed by 4 ISSR primers and a total of 34 DNA bands were generated with an average of 8.5 bands per locus. Twenty seven out of 34 DNA bands were found to be polymorphic. PICs ranged from 0.0000-0.4998 with an average score of 0.1953. Eight microsatellite markers were also performed and 55 alleles were produced with an average of 6.88 alleles per locus. PICs ranged from 0.3821-0.7972 with an average score of 0.6219. Phylogenetic tree resulted from combining InDel, ISSR and microsatellite data could classify rice samples into 14 groups at genetic similarity of about 0.76. Tropical *japonica* samples were in group 12 and 13 while *japonica* samples were in group 13. Thai landraces were scattered in group 1, 2, 7 and 12. The TGMS lines (10 samples) were dispersed in group 2, 5 and 6. The TGMS line (1 sample) in group 2 has shown to carry high genetic distance as compare to the tropical *japonica* and *japonica* rice. This TGMS line in group 2 might be used as female parent in order to produce intersubspecific hybrid; whereas the TGMS lines in group 5 and 6, carried more genetic similarity to tropical *japonica* and *japonica*, could be used to produce *indica* intrasubspecific hybrid. Consideration of genetic distance and data from 4 functional markers, which specific to *Pi-ta* and *Pi-2t* gene conferring resistance to rice blast disease, *fragrance* gene (*fgr*), and *S-5* locus controlling spikelet fertility in hybrids between *indica* and *japonica*, will be very useful for selection of parental lines in hybrid rice breeding program.

Student's signature

Thesis Advisor's signature