

Maythiya Changcharoen 2014: Assessment of Genetic Diversity of Water-Onion (*Crinum thaianum*) an Endangered Plant in Thailand Using Molecular Markers. Mater of Science (Genetics), Major Field: Genetics, Department of Genetics. Thesis Advisor: Assistant Professor Vipa Hongtrakul, Ph.D. 94 pages.

Microsatellite DNA markers were developed for classification and varietal specific identification of Thailand water-onion (*Crinum thaianum* J. Schulze) from the enrich library using biotin-oligonucleotide probes, B-(GA)₁₅, B-(CA)₁₅, B-(ACC)₁₀ and B-(CCT)₁₀. Twenty-six primer pairs were designed and were used to evaluate genetic relationship among 55 water-onion samples collected from natural water resources in Phang-nga and Ranong provinces, White Crane water plant export company and Chatuchak market. Cluster analysis using computer program NTSYSpc-2.20k was performed and could classify all 55 samples into 2 major groups and 7 sub-groups. AFLP markers were used to evaluate genetic diversity in seven populations. The result shows that, average percentage of polymorphic loci and expected heterozygosity were 31.45% and 0.129, respectively. The highest percentage of polymorphic loci (59.15%) and the highest expected heterozygosity (0.238) were found in water-onion from White Crane water plant export company. PCR-RFLP markers were developed specific to seven genes, *NADH dehydrogenase* subunit F (*ndhF*), *Acetyl-CoA carboxylase* beta subunit (*accD*), *NADH-plastiquinone oxidoreductase* subunit 7 (*ndhH*), *NADH-plastoquinone oxidoreductase* subunit 1 (*ndhA*), *Photosystem I P700 apoprotein A2* (*psaB*), 18srDNA and 26srDNA and used to evaluate genetic relationship among 77 water-onion samples and five other plants in family Amaryllidaceae, including *C. asiaticum* L., *Hymenocallis littoralis* Salish., *C. amabile* Don., *C. nathans* and *Hymenocallis* sp. All samples could be separated into two major groups and 4 subgroups. Group I consisted of two subgroups, one was all water-onion samples and the other was *C. asiaticum* and *C. amabile*. Group II also consisted of two subgroups, one was *Hymenocallis* sp. and the other was *H. littoralis* and *C. nathans*. Partial sequences of seven genes of water-onion were analyzed in order to confirm the gene specificity and for specific identification of Thailand water-onion. Five partial gene sequences (*accD*, *ndhH*, *ndhA*, *psaB*, 26srDNA) of water-onion were compared to other plant sequences available in database. The result indicated that water-onion was most closely related to *C. asiaticum*. The result indicated that water-onion in Thailand still maintain its genetic variation. This first report on genetic study of water-onion will be useful for the development of suitable DNA markers or genetic evaluation of water-onion and for conservation and sustainable use of Thailand water-onion in the future.

Student's signature

Thesis Advisor's signature