

## ABSTRACT

*Oryza sativa* consists of two major subspecies: *indica* and *japonica*. There are four methods that have been used to classify between these two subspecies including phenol reaction (PHR) phenotype. In phenol solution, the *indica* and *japonica* subspecies show discoloration and non-discoloration on paddy rice, respectively. The PHR phenotype is controlled by *Phr1* gene which encodes a polyphenol oxidase. In this study, 53 upland rice varieties were used to classify subspecies using PHR phenotype (phenol solution assay and PPO activity) and molecular markers (pSTS18, pSTS29 and PPO-E3-29). The pSTS18 marker was used to identify varieties with deletion at 18 bp ( 18) in *Phr1* gene and pSTS29 and PPO-E3-29 markers for 29 bp ( 29) deletion. The results showed that forty three varieties carry 29 as well as non-discoloration and low PPO activity. Therefore, they were classified as putative *japonica* subspecies. On the other hand, ten varieties were classified as putative *indica* subspecies because of no-deletion at 29 bp, discoloration and high PPO activity. In addition, seed morphology of all varieties was studied for genetic diversity. The dendrogram showed 1) two main clusters corresponding to rice type (glutinous and non-glutinous rice), 2) three main clusters for brown rice shape, 3) two main clusters for hair of husked and 4) three main clusters for brown rice color. The obtained results from this study can be used to select the parental lines for rice breeding program.