

## THESIS

**Do duc Tuyen.** 2007. Yield trait analysis of rice (*Oryza sativa* L.) using candidate gene approach. MS Thesis on Plant Biotechnology. Department of Biotechnology, University of Agricultural Sciences, Bangalore, India. 85 p.

### ABSTRACT

Eighty five diverse rice genotypes used in the present study, were obtained from IRRI, Philippines and evaluated the yield parameters under low moisture conditions. The results revealed that CV (coefficient of variation) among the genotypes varied from 4.5% (plant height) to 13.32% (number of panicles). The difference between genotypes with all traits was insignificant at 5%. Clustering genotypes was carried out using DIST coefficient and correlation coefficient for all traits. The differences among genotypes were evaluated with DIST coefficient varied from 2.89 to 62.36 and correlation coefficient from 95% to 99.98%. The rice genotypes were also used for candidate gene analysis to identify correlation with traits and evaluated diversity of the genotypes. Good bands were obtained from the 10 primer pairs and varied in size between 200 bp and 1700 bp. Polymorphism between genotypes was found with 9 primer pairs (ACCsyn, Chitinase, Chitinase basic, Gluc, LFY, Hsb, MBRL, PR10 and UBQ5). The correlation of morphological characters with candidate gene markers was evaluated by SMA and SMRA. Seven of ten primers (ACCsyn, Chitinase, Chitinase basic, Gluc, LFY, MBRL, PR10 and UBQ5) used in study show significant correlation with morphological traits. Clustering genotypes was also carried out using Dice coefficient for all candidate gene markers. The clustering was started at the Dice similar coefficient of 64% for WAB638-1 genotype which differed with other genotypes. The diverse genotypes were divided into many subgroups with increasing of the Dice similar coefficient. The diversity of eighty five diverse rice genotypes obtained from molecular marker analysis was higher than the one obtained from morphological marker analysis. Correlation between the clustering using morphological data and the clustering using marker data was significant at 1% probability level.