
OD-04

Comparative analysis of tea shrub(*Camelia sinensis*) using morphological character and RAPD markers in Kyungnam province

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RAPD and morphological traits of leaf blade were compared in terms of their information using genetic relationship analysis among 26 tea shrub samples of Kyungnam province. The 26 tea shrub samples were analyzed with 10 morphological traits of leaf blade. The genetic distance ranged from 0.59 to 1.00, thus reflecting phenotypic variation. The average of RAPD similarity coefficient among the samples was 0.66, it was very similar to the value obtained with morphological traits. The clustering based on RAPD was distinguished for four groups that were similar to the classification using morphological traits. In order to combine all the information that relates the samples, a new dendrogram was estimated by joining information for different genetic marker systems such as morphological traits and RAPD markers. The total of RAPD and phenotypic data of leaf blade were used to calculate genetic distance coefficients for cluster analysis using UPGMA. The dendrogram topology showed a similar degree of clustering of 26 samples in different marker systems, although there were differences in the positioning of some samples at the main group. No significance correlation was found between DNA markers and morphological data of leaf blade. Nevertheless, the combination of RAPD and morphological trait-based clustering was clearly differentiated for all the samples and indicates the genetic relationship of 24 tea shrub samples.

OD-05

The identification of candidate rice genes that confer resistance to the brown planthopper (*Nilaparvata lugens*) through representational difference analysis

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The development of rice cultivars (*Oryza sativa* L.) that are resistant to the brown planthopper (BPH; *Nilaparvata lugens* Stål) is an important objective in current breeding programs. In this study, we generated 132 BC5F5 near-isogenic rice lines (NILs) by five backcrosses of Samgangbyeo, a BPH resistant indica variety carrying the Bph1 locus, with Nagdongbyeo, a BPH susceptible japonica variety. To then identify genes that confer BPH resistance, we employed representational difference analysis (RDA) to detect transcripts that were exclusively expressed in one of our BPH resistant NIL clones, SNBC61, during insect feeding. Most of the RDA clones that we subsequently isolated were found to be exclusively expressed in SNBC61 and could be assigned to functional groups involved in plant defense. The chromosomal mapping of these RDA clones further revealed that they are located in close proximity to known either quantitative trait loci (QTLs) or to an introgressed SSR marker from the BPH resistant donor parent Samgangbyeo. These RDA clones therefore serve as candidate defense genes that confer BPH resistance. <Acknowledgements : This work was supported, in part, by a grant from the Crop Functional Genomic Center (CG1422, CG1510), as part of the 21 Century Frontier Program, the Biogreen 21 Program, Rural Development Administration, and from an SRC from the Plant Metabolism Research Center (PMRC), Korea Science and Engineering Foundation (KOSEF) Program.>