

P004 Construction of T-DNA inserted rice populations for functional genomics

Guocheng Hu, Yaping Fu, Wenzhen Liu, Huamin Si, Dekai Wang, Zongxiu Sun

State Key Lab of Rice Biology, China National Rice Research Institute, Hangzhou 310006, P. R. China

As the rice genome sequence is completed, a large effort is in progress to elucidate the biological function of rice genes. Inserted mutagenesis is a powerful method for functional analysis of a large number of rice genes. A rapid and highly efficient *Agrobacterium tumefaciens*-mediated rice transformation protocol was developed by our laboratory to construct rice mutant pool. Up to now, approximately 45,000 independent T-DNA inserted lines were obtained using japonica varieties Nipponbare and Zhonghua 11, and the seeds of 30,000 lines were stored in the germplasm bank, CNRRI. Among them, approximately 60% of the lines had only one inserted locus. More than 1,500 mutants (variants) were isolated by its phenotype, and more than 500 flanking sequences were analyzed by Tail-PCR. Some interesting mutants (such as premature senescence, lesion mimic, low chlorophyll b, male sterility and leafy) have been studied by genetic and molecular analysis. Some mutants which induced by T-DNA insertion were also selected, and cloning the related genes is in process. To isolate more useful rice mutants, more available screen techniques are needed, scientists are welcome to use the collection for cooperation.