

Use of KitBase to Facilitate Forward and Reverse Genetics Research in Rice

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Project Goals: We are using whole-genome sequencing approach to establish a fully sequenced mutant collection in a model rice variety that is being used to identify genes involved in grass cell wall biosynthesis and modification.

To achieve cost efficient conversion of lignocellulosic biomass into biofuels, basic knowledge on the genes that control cell wall biosynthesis and modification is needed in grasses. To facilitate cell wall research, we have generated a mutant population using fast-neutron irradiation in the model rice cultivar Kitaake, a tractable model grass species. Kitaake is an early flowering, short-statured, short life cycle rice that is easy to transform, compared with other Japonica and Indica rice varieties. In collaboration with the Joint Genome Institute, we are sequencing 4,000 mutants. Genomic analysis of more than 1,000 mutants has been done, revealing that 13,469 genes are affected. Mutation types include single base substitutions, deletions, insertions, inversions, translocations, tandem duplications, and complex events. Single base substitutions predominate, but deletions affect the greatest number of genes, accounting for 57.2% of all affected genes. To make the genetic resource publicly available, we established KitBase, a comprehensive repository for rice mutant information. KitBase integrates JBrowse and BLAST to facilitate identification of mutations and searching of the database. KitBase includes genomic data, phenotypic data, and seed information for each of the mutant lines. Dozens of glycosyltransferase (GT) and glycohydrolase genes have been mutated in this mutant collection, and the function of multiple GTs in rice cell wall biosynthesis is being studied.

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