



**CALIFORNIA STATE SCIENCE FAIR  
2011 PROJECT SUMMARY**

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<b>Project Title</b> Phenotypic and Genotypic Analyses of Oryza sativa T-DNA Lines	
<p style="text-align: center;"><b>Abstract</b></p> <p><b>Objectives/Goals</b> Oryza sativa T-DNA lines were studied to better understand cell wall synthesis and function for the development of a new bioenergy crop. Mutant and wild-type rice plants were compared to determine whether they were significantly different in several phenotypic characteristics. T-DNA and gene-specific primers were then used to identify mutant plants and their genotypic status. If T-DNA is successfully inserted into the rice genome, then by analyzing and comparing the phenotypes and genotypes of mutant and wild-type rice lines, we can identify the functions of cell wall-related genes.</p> <p><b>Methods/Materials</b> Phenotypic analysis: Wild-type Dongjin (DW) rice seeds (the control) were first grown to study the developmental stages of the rice plant life cycle and to aid in the analysis of visible phenotypic differences in mutant plants. Qualitative and quantitative phenotypic traits were then observed. Genotypic analysis: Genomic DNA isolated from mutant lines were genotypically analyzed using PCR. Hygromycin phosphotransferase (hph) gene-specific primers were used to identify mutant plants. T-DNA border and gene-specific primers were used to confirm the location of T-DNA insertion and to identify the genotype of mutant plants.</p> <p><b>Results</b> Phenotypic analysis: Mutant and wild type plants were found to be significantly different for several phenotypic traits, including leaf color, leaf strength and flexibility, and number of tillers. Genotypic analysis: PCR results were used to categorize the plants as: wild type (T-DNA was not inserted into the rice genome), homozygous (T-DNA contained in both DNA copies), heterozygous (T-DNA contained in one DNA copy), and transgenic (for which zygosity cannot be determined due to insufficient information).</p> <p><b>Conclusions/Discussion</b> Our hypotheses are confirmed: rice mutant lines were found to have several significantly different phenotypic characteristics from wild-type plants, and mutants were confirmed for their transgenic and genotypic status using T-DNA and gene-specific primers. Homozygous plants of mutant lines with interesting phenotypes are chosen for and observed in future generations to correlate phenotype with genotype. Further phenotypic and genotypic analyses of plants will help elucidate gene functions, thereby increasing our understanding of cell wall-related genes to launch a future generation of bioenergy crops.</p>	
<b>Summary Statement</b> Oryza sativa transfer DNA (T-DNA) lines were phenotypically and genotypically analyzed to better understand cell wall synthesis and function for the development of a new bioenergy crop.	
<b>Help Received</b> Participant of UC Davis Young Scholars Program; Dr. Manoj Sharma, Dr. John C. Howe, and Dr. Charles Barker were mentors.	