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Genotypic analysis of receptor-like protein kinases with leucine-rich repeat motifs

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Receptor-like protein kinases (RLKs) are transmembrane proteins that transmit extracellular signals across a membrane with the use of an intracellular kinase domain. RLKs play important roles in plant growth and development, plant-microbe interactions, and defense responses. In *Arabidopsis thaliana*, a commonly used genetic model system for plants, 417 genes encode RLKs. Though plant RLKs have a monophyletic origin and belong to a clade that also contains the animal Pelle cytoplasmic kinases, they can be divided into distinct families based on their extracellular motifs. The most common extracellular motif in plant RLKs are the leucine-rich repeat that are thought to be involved in protein-protein interactions. Over half of RLKS found in *Arabidopsis thaliana* have leucine-rich repeat extracellular motifs. As a genetic model, the genome of *Arabidopsis* has been fully sequenced; however, the functions of many genes are still unknown. To uncover their function, experiments are being done using the principles of reverse genetics. By inserting T-DNA segments into the genome, the function of a gene can be disrupted. The T-DNA insertion into a gene would prevent a functional protein from being produced. Without the production of this protein, a specific mutant phenotype is likely to result. However, duplication of genes with similar sequences and therefore, possibly similar functions, may hinder the production of a mutant phenotype. As such, all the genes must also be rendered functionless. Our experiment consisted of creating functional knock-outs for genes found in families XIe, XIh, XIg, and XId. Single and double mutants were then genotyped to see if any heterozygous or homozygous progeny had been produced and had survived. Sequencing of the flanking regions of the t-DNA insert was also completed. Twelve of thirteen genes yielded single mutant homozygotes. Of the six double mutant crosses genotyped, all yielded heterozygotes. Crosses were then made between homozygotes of one line of a particular gene with those from another line of a different, but related gene. Results for function and phenotype are pending.