A Comprehensive Analysis of Agronomic and Disease Resistance Gene Mutations in Katy Rice Mutants through DNA Next-generation Sequencing

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Mutagenesis induces artificial genetic variation which allows breeders to discover the functions of genes previously unavailable. This project looked for yield and disease resistance-related traits in the next-generation DNA Illumina sequence (Novogene) of wild-type rice cultivar Katy versus two previously mutated strains, M2354 and LMM1. M2354 was mutated via fast neutrons (FN) and LMM1 was mutated via ethyl methanesulfonate (EMS). In M2354, 115 insertions and 55 deletions (Indels) and 257 single nucleotide polymorphisms (SNPs) were detected and 217 SNPs in LMM1 were detected compared to Katy. Rice blast inoculation was performed and it was found that M2354 was susceptible to both tested isolates while LMM1 and Katy were only susceptible to the fungi isolate not carrying the AVR-Pita gene. Contrary to previous work, large insertions were discovered in addition to previously reported deletions in M2354. The presence of the previously identified two base-pair deletion found in the Ptr region of M2354 that knocks out a broad-spectrum blast disease resistance gene was verified. There were no detected differences in the genes in the Pi-ta region, a region on chromosome 12 also associated with blast resistance. This suggests that Ptr is more responsible for broad-spectrum blast resistance than Pi-ta. Mutations within candidate genes for significant agronomic traits and disease resistance were discovered that may contribute to M2354's extreme susceptibility to rice blast disease. Work is currently underway to verify indels and SNPs using gel electrophoresis for further functional genomic analysis. Thus far, only three indels on M2354's chromosome 12 have been conclusively verified.

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Fourth Award of $500