Differentially expressed gene for allelopathic potential of "Sathi" rice in response against barnyardgrass

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Differentially expressed gene (DEG) was discovered in Sathi variety, an indica rice showed high allelopathic potential against barnyardgrass (Echinochloa crus-galli Beauv. var. frumentaceae). Rice plants were grown with and without barnyardgrass and total RNA was extracted from rice leaves at 45 days after seeding. DEG full-screening was done by GeneFishingTM method (Seegene, Korea) to discover cDNA sequences related with allelopathic potential. The differentially expressed bands were extracted from the gel and re-amplified, then sequenced with ABI PRISM and identified by BLAST searching. GeneFishing screening discovered 9 possibility genes associated with expression of allelopathic potential of Sathi rice. The gel electrophoresis showed 4 genes were more expressed when rice grew with barnyardgrass, and 2 genes were more expressed when rice grew without barnyardgrass. Whereas, DEG-6 was expressed only in rice without barnyardgrass and DEG-7 was expressed only in rice grown with barnyardgrass. The results of RT PCR confirmed the results of DEG from GeneFishing screening. BLAST searching resulted that 5 DEGs have no significant homology with rice genes reported. These mean the genes for allelopathic potential expression might be as novel genes. Whereas, DEG-1 shows homology with Oryza sativa mRNA for S-adenosylmethionine synthetase (SAMS gene), DEG-2 with Oryza sativa chloroplast gene for ribulose 1,5-bisphosphate carboxylase large subunit, and DEG-6 with identified Oryza sativa (japonica cultivar-group) m-RNA. From this result, we develop 7 primers as candidate marker of allelopathic expression gene in rice. Further works are in progress for clarifying the marker usefulness and identifying the gene function associated with the marker.

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SNP Discovery and Deployment in Polyploid Wheat

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Single nucleotide polymorphisms (SNPs) are exceptionally well suited for high-resolution gene mapping and high-throughput marker assisted selection schemes. The use of SNPs in wheat breeding and genetics is unfortunately complicated by polyploidy. We therefore developed a strategy for SNP discovery and deployment that is tailored to polyploid wheat but can be readily adapted to other polyploid plant species.