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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.

A total of 1,402 genome-specific primers have been designed and 814 loci containing SNPs have been discovered. SNPs were unexpectedly abundant in the A and B genomes, averaging 1 SNP/200 bp, but rare in the D genome. Most of the SNPs detected in the D genome were between *T. aestivum* and synthetic wheats. Some of the loci containing SNPs in wheat have been mapped using a highly polymorphic *Ae. tauschii* F₂ population. A public SNP database have been constructed. The data base shows among others sequences of the 23 wheat lines, indicates nucleotide showing a SNP in wheat, and the sequences of genome specific PCR primers for the amplification of target DNA from polyploid wheat.

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DNA marker를 이용한 벼멸구 저항성 선발

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본 연구에서는 자포니카형의 벼멸구 저항성 육종 효율을 향상시키기 위하여 벼멸구 저항성 유전자 *Bph 1*을 가진 '삼강벼'를 1회친으로 사용하고, 자포니카 감수성 품종인 '낙동벼'를 반복친으로 5회 여교잡한 집단(SNBIL; BC₅F₅)을 이용하여 벼멸구 저항성과 DNA marker간의 연관분석을 실시한 결과, RM28472, RM28479, RM28493 및 RM28504가 *Bph 1*과 완전연관되어 있었으며, 이 marker들은 12번 염색체의 물리지도 AP008218의 23.1 ~ 23.5 Mb사이에 위치하고 있었다. 완전연관된 marker들 가운데 agarose gel에서 다형성을 나타내는 RM28493을 벼멸구 저항성에 대한 marker assisted selection (MAS)용 DNA marker로 선발하였다. 여교잡집단에서 육성된 벼멸구 저항성 계통과 고품질인 '주남벼'를 교배하여 약배양 집단 38계통에 대해 RM28493의 MAS 활용성을 검토한 결과, 저항성 유전자형을 가진 계통은 20계통이었고 감수성 유전자형을 가진 계통은 18계통으로 나타났다. 이 결과는 생물검정 결과와 일치하여 RM28493이 MAS에 직접 사용될 수 있음을 입증할 수 있었다. 또한, 본 연구에서 개발된 벼멸구 저항성 연관 marker인 RM28493은 다양한 유전자원에서 저항성품종과 감수성품종을 뚜렷하게 구분하고 있어서 앞으로 DNA marker를 이용한 저항성 개체 선발에 광범위하게 활용될 수 있을 것으로 사료된다. 분자유종시스템에 적용하고자 RM28493을 이용하여 저항성 개체를 선발한 다음 2회 여교잡 하였으며, BC₂F₁세대에서 MAS를 실시하여 복교잡(A*3/C//B*3/C)을 실시하였다. 최종적으로 복교잡 F₁세대에서 MAS를 실시하여 Homozygous F₁ 식물체를 선발하였다.

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고추 탄저병 저항성 QTLs과 연관된 분자표지 개발

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