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Deep Transcriptome Analysis of the Rice and Rice Blast Genomes Using LongSAGE and MPSS Technologies

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LongSAGE (Serial analysis of gene expression) and MPSS (Massively parallel signature sequencing) are two new powerful global expression analysis techniques for cataloguing known and novel genes experimentally. Millions of transcripts in certain tissues can be obtained from each LongSAGE or MPSS library. Except for transcriptome analysis, identified tags are useful for genome annotation. To identify novel transcripts involved in the rice and rice blast interaction, we generated five LongSAGE libraries from 3-week old plants of japonica rice cultivar Nipponbare infected with different rice blast isolates. From these libraries, over 1,000,000 LongSAGE tags have been identified with about 93,000 unique transcripts. Many of them are novel genes. To experimentally characterize the *Magnaporthe grisea* genome, the causal agent of the rice blast disease, one longSAGE and two MPSS libraries have been made. About 15,000 unique transcripts have been identified. Recently, we started to make 65 MPSS rice libraries of different tissues and treatments to comprehensively characterize the transcriptome of the rice genome. The detailed results from the analysis of these libraries will be presented.