

## Deep Transcriptome Analysis of the Rice and Rice Genome Using LongSAGE and MPSS Technologies

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LongSAGE (LongSerial Analysis of Gene Expression) and MPSS (Massively Parallel Signature Sequencing) are two new 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 not available in the ETS and KOME full-length cDNA collections.

Recently, we started to make 65 MPSS rice libraries of different tissues and treatments to comprehensively characterize the transcriptome of the rice genome. So far, 22 libraries have sequenced and the sequence data are available for the public at <http://mpss.udel.edu/rice/>. In these libraries, a total of 24,495 genes were identified. The detailed results from the analysis of these libraries will be presented. The MPSS data provide experimental support for thousands of genes not previously identified by EST or full-length cDNA approaches."

### Reference:

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