

P19

**cDNA microarray and sequence analysis of wounding
and fungal elicitor-induced genes from wild rice
(*Oryza. grandiglumis*)**

Kyung-Mi Kim¹, Sang-Hyun Shin¹, Kyung-Ho Kang², Hae-Chune Choi²,
Jong-Chan Hong³, Sung Ki Cho⁴, Jeong-Sheop Shin⁴,
Won-Bok Chung¹ and Young-Soo Chung^{1*}

¹Dong-A University. Busan

²National Crop Experiment Station

³Kyung-Sang University

⁴Korea University

Oryza grandiglumis(CCDD, 2n=48), one of the wild rice species, has been known to possess fungal resistance against sheath blight, rice blast, bacterial leaf blight and insect resistance against brown plant hopper(*Nilaparvata lugens*).

To isolate differential genes expressed responding to fungal and insect attack, wounding and fungal elicitor(yeast extract) were applied to *Oryza grandiglumis* for 3, 6, 12, 24, 48, 72hrs, respectively.

Suppression subtractive hybridization(SSH) technique was used to normalize the both high and low abundance genes by incorporating a hybridization step, which can allow for the identification of differentially expressed low abundance mRNAs. The isolation of large amount of cDNA by SSH requires further confirmation of their differential expression. cDNA microarray was applied for a rapid and high-throughput screen of SSH cDNAs isolated. Three hundred and sixty eight clones out of 1,152 were identified as positive true by cDNA microarray analysis. 368 clones were sequenced and subjected to homology search to GeneBank sequence database. Northern blot further proved the differential expression of genes isolated and cloning procedure for whole gene is undergoing currently.