resistance and defense response, we take a PCR-based suppression subtractive hybridization approach using cDNAs of blast-inoculated wild type and the KCT-6417 as a tester and a driver, respectively. Genes specifically expressed in the wild type will be presented. The selected genes would give us a clue to understand mechanism for the race specific resistance and defense responses against *M. grisea* KI-1113a in Taebaegbyeo.

1-09. Characterizing of Rice Blast Lesion Mimic

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When plants are infected by plant pathogens, typical disease symptom termed lesion, appears in compatible interaction. Whereas, in incompatible interactions, only small speck of lesions are visible on the leaf surfaces. Hypersensitive response (HR) of plant which is the result of infection by incompatible pathogens, is a well known defense response inducing rapid cell death resulting in complete resistance. However, some rice mutants show spontaneous disease symptoms during the growth stages without interaction with pathogens. We investigated the spontaneous cell death mutant called Blast Lesion Mimic(BLM) generated by EMS mutation, on the relationship with the hypersensitive response as well as resistant characteristics. Accumulation of phenolic compounds were detected around the lesions as lesions develop on leaf surface. Activation of PR gene was detected before the lesion appeared, and that result indicates the defense-related response are started earlier than lesion formation. The BLM mutant showed resistant response to inoculation of *Magnaporthe grisea* KJ201 with which the wild type Hwacheong is totally susceptible. Informations on the formation of spontaneous lesions and detail analysis of lesion mimic mutants and related genes are very limited to date. It is really important to understand the phenomenon of the defense-related lesion formation for developing resistant cultivar for rice blast pathogens.

1-10. Induction of pathogenicity mutants from *Elsinoe fawcettii*, the causal fungus of citrus scab by genetic transformation

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Genetic transformation carried out to induce the pathogenicity mutants from the two isolates, *Elsinoe fawcettii* R-34 and MUD of citrus scab fungus to hygromycin resistant by transferring plasmides (pUCATPH) that contain *hygB* gene. We produced protoplast for transformation by using of combinations of available enzymes including β-D-glucanase, β-glucuronidase, lyticase and driselase. The protoplasts regenerated at 64 μg/ml of hygromycin B but not 128 μg in sensitivity test to identify the concentration of useful marker for the selection of transformants. Approximately 1200 and 67 hygromycin resistant isolates from strain R-34 and strain MUD, respectively, were isolated on PDA added with 200 μg /ml of hygromycun B. Fifty seven and 4 of hygromycin resistant isolates from strain R-34 and MUD, respectively, did not produce necrotic

lesions on the leaf in detached-leaf assay. Finally, 9 isolates were isolated from strain R-34, and these isolates produced non or very few symptoms on seedlings of citrus in greenhouse pathogenicity test. And it's very interesting that some isolates produced melanose-like symptom on very young leaves which it was not typical symptom and somtimes produced on only expanded leaf.

1-11. Functional Analysis of PepRSH (Pepper *relA/spoT* homolog) cloned from *Capsicum annuum* showing Systemic Acquired Resistance against *Phytophthora capsici*

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RSH (relA/spoT homolog) has been known to determine the level of guanosine tetraphosphate (ppGpp) and guanosine pentaphosphate (pppGpp), which are the effector nucleotide of the prokaryotic stringent response and also play a role in antibiotic production and differentiation in *Streptomyces* species but not a little in eukaryotic organism, especially in plant. Salicylic acid (SA), a critical signal molecule of establishing systemic acquired resistance (SAR), could induce SAR in Pepper (*Capcicum annuum*) against *Phytophthora capsici*. And the extent of SAR induction was in proportion to the dosage of SA (or BTH). Suppression subtractive hybridization (SSH), a PCR-based method for cDNA subtraction, was carried out between SA-treated and non-SA-treated pepper leaves to isolate genes which may be responsible for defense signaling against pathogens. Early upregulated gene was selected from reverse northern and kinetics of SSH-genes transcripts in SA-treated pepper leaves upon SA treatment. Full-length cDNA of the gene (PepRSH ; Pepper *RelA* / *SpoT* homolog) had an open reading frame (ORF) of 2166 bp encoding a protein of 722 amino acids and a significant homology with (p)ppGpp phosphohydrolase or synthetase. Genomic DNA gel blot analysis showed that pepper genome has at least single copy of PepRSH. PepRSH transcripts was very low in untreated pepper leaves but strongly induced by SA and methyljasmonic acid (MeJA), indicating that PepRSH may share common SA and MeJA-mediated signal transduction pathway. Functional analysis in *E. coli* showed PepRSH confers phenotypes associated with (p)ppGpp synthesis through a complementation using active site mutagenesis.

1-12. EVALUATION OF DISEASE RESISTANCE AND SUSCEPTIBILITY TO CHESTNUT BLIGHT FUNGUS, CRYPHONECTRIA PARASITICA, OF CHESTNUT VARIETIES IN KOREA

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For the selection and breeding of chestnut varieties resistant to the chestnut blight fungus Cryphonectria parasitica, disease resistance and susceptibility of 28 varieties widely planted and growing in Korea were evaluated by artificial inoculation of a pathogenic fungus. For this