

1-07. cDNA Microarray Analysis of *Phytophthora* Resistance Related Genes Isolated from Pepper

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Phytophthora blight is a devastating disease of pepper and occurs almost anywhere peppers are grown. *Phytophthora blight* is caused by *Phytophthora capsici* and this pathogen can infect every part of the plant by moving inoculum in the soil, by infecting water on surface, by aerial dispersal to sporulating lesions. Management of *phytophthora blight* currently relies on cultural practices, crop rotation, and use of selective fungicides. Since these treatments are a short-term management, a classical breeding for development of resistant pepper against the *phytophthora* is an alternative. So far some of the resistant cultivars have been on the market, but those are limited regionally and commercially. Therefore, ultimately an elite line resistant against this disease should be developed, if possible, by biotechnology. We have set out a series of work recently in order to develop *Phytophthora* resistant pepper cultivar. For the first time, the cDNA microarray analysis was performed using an EST chip that holds around 5000 pepper EST clones to identify genes responsive to *Phytophthora* infection. Total RNA samples were obtained from *Capsicum annuum* PI201234 after inoculating *P. capsici* to roots and soil and exposed to the chip. Around 900 EST clones were up-regulated and down-regulated depending on the two RNA sample tissues, leaf and root. From those, we have found 55 transcription factors that may be involved in gene regulation of the disease defense mechanism. Further and in detail information will be provided in the poster.

1-08. Rice blast susceptible mutants of Taebaegbyeon and genes differentially expressed in the wild type rice.

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A rice cultivar, Taebaegbyeon, is highly resistant to rice blast and moderately resistant to bacterial leaf blight (BLB) caused by *Magnaporthe grisea* and *Xanthomonas oryzae* pv. *oryzae*, respectively. To study the rice disease resistance mechanism, we generated rice deletion M3 mutants by gamma-ray irradiation. Blast and BLB responses of 16,000 M3 mutants were screened by inoculating mixtures of 4 races (KJ-201, KI-1113a, KI-313, KI-409) of *M. grisea* and 3 Korean races of *X. oryzae* pv. *oryzae*. We selected so far 21 M3 mutants of Taebaegbyeon showing high susceptibility to the diseases. One of the mutants, KCT-6417, was susceptible to KI-1113a race of *M. grisea*, suggesting the deletion of a race-specific blast resistance gene in the mutant. To isolate rice genes involved in blast

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 Taebaegbyeon.

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 μ g/ml of hygromycin B but not 128 μ g 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 μ g/ml of hygromycin B. Fifty seven and 4 of hygromycin resistant isolates from strain R-34 and MUD, respectively, did not produce necrotic