

measured and the indices of tolerance to stress including Fischer and Fernandez were calculated within them. The results showed
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Identification of Broad Spectrum Resistance Locus Pi41(t) to Blast Magnaporthe Grisea in Korean Weed Rice

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Rice blast continues to be a potentially devastating disease of rice, affecting yield and decreasing its quality. It is necessary to look for novel resistance gene(s) for blast that can express a broad spectrum of resistance in diverse environmental conditions. In this study, we have made an attempt to search for the new gene/QTL from Korean weed rice germplasm, GL33. A major QTL qBL4 was mapped to a spanning 1.3cM region at RM5586-RM6679 on chromosome 4, and explaining 43.5-53.1% and 26.1-28.1% of total phenotypic variation for blast nursery test and isolate inoculation by the GL33 allele, respectively. This major QTL was designated as Pi41(t) gene. Two SSR markers RM5586 and RM6679 were landed at a BAC clone OSJNB0012E08, and RM5586 was specified to the locus Os04g32940 including the LRR family protein related to disease resistance gene through BLASTN analysis. We were developed a few candidate R gene markers based on the sequence downloaded from the RGP web site for fine-scale mapping the Pi41(t) locus. A few promising BC₂F₂ lines based on backcross method to develop Pi41(t)(QTL)-NIL were selected and would be evaluated for the resistance effect to diverse spectrum of blast in the field and by isolate inoculation.

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Identification of Maize Germplasm for Resistance to Maize Weevil (*Sitophilus Zeamais Motsch.*) in Thailand

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Maize weevil, *Sitophilus zeamais* Motsch. is the most serious stored product insect pest in Thailand. It caused grain losses up to 90% particularly where grain are stored without chemical protectants. The objective of this study was to evaluate the maize germplasm for maize weevil resistance. Fourteen inbreds and 50 hybrids from maize breeding project were evaluated separately in no-choice test in laboratory at Nakhon Sawan Field Crops Research Center, Thailand, 2006. Thirty grams grain samples of each inbred and hybrid were infested with 25 un-sexed and approximately 1-7 days old adults weevil in a glass bottle to allow oviposition to take place for 7 days and then removed parental adults. The samples were incubated for 90 days in the laboratory (27 °C and 75% RH) after which the percentages of grain damaged and grain weight losses were recorded. There were not statistically significant differences among inbreds and hybrids for the two parameters. However, in this study, the percentages of grain weight losses was used as the resistance parameter. The average of percentages of grain weight losses were 7.04 and 12.86 for inbreds and hybrids respectively. Fifteen hybrids and 11 inbreds were identified as resistant to maize weevil. Hybrids which have common parent: Nei 452008, were less percentages of grain weight losses than others. Therefore these superior maize genotypes will be considered to further use in maize breeding project for weevil resistance.

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Dissection of Factors Affecting Age-Related and Race-Specific Resistance Conferred by Xa21 and Xa26 in Rice

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XA21 and XA26 are two R proteins mediated resistance to rice bacterial blight caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo). Although they share a typical structure of leucine rich repeat (LRR) receptor kinase-like (RLK) proteins, the extracellular domain of LRR, the transmembrane region, and the cytoplasmic domain of protein kinase (PK) and 53% sequence similarity (E-

Value = e⁻¹³⁵), they had distinct resistance spectrum and different growth stage-related resistance. To examine how sequence diversity and genetic background influence the resistance specificity and developmental related resistance, four chimeric genes encoding different part of XA21 and XA26 were constructed by domain swapping and transformed to susceptible rice variety Mudanjiang 8. Two of the four chimeric genes mediated compromised resistance; the plants carrying the two chimeric proteins had a similar resistance spectrum as the plants carrying the protein which provided the LRR domain. Further more, this two chimeric genes and Xa21 conferred whole growth stage resistance to Xoo in Mudanjiang 8 background. These results suggest that sequence diversity of LRR determines the resistance specificity and genetic background is responsible for the development related resistance of XA26 and XA21.

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Induction of Systemic Resistance in Tomato Against Root-knot Nematode by *Pseudomonas Fluorescens*

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The biocontrol agent, *Pseudomonas fluorescens* CHA0, was evaluated for biological control of root-knot nematode, *Meloidogyne javanica*. The biocontrol effects of *P. fluorescens* CHA0 on *M. javanica* were evaluated under glasshouse. In glasshouse experiments *Pseudomonas fluorescens* CHA0 (1.8 x 10⁸ CFU/ml) used as bare shoot -spray treatment reduced the numbers of galls and egg mass caused by *M. javanica* in per plant but no effected on plant growth in to tomato under glasshouse was shown. The potential of the biocontrol agent *P. fluorescens* CHA0 to trigger plant defense responses was investigated by inoculating shoot of tomato seedlings. The results showed that peroxidase, polyphenoloxidase and catalase activities were increased after nematode inoculated within 24-96 h in roots of bacterized seedlings. These results provided evidences that *P. fluorescens* CHA0 may induce systemic resistance mechanisms in tomato plants against *M. javanica*

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Milyang237, A New Japonica Rice Variety with Xa5 Gene to Bacterial Blight

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Milyang237 is the first japonica resistant variety carrying xa5 gene, a broad spectrum gene for bacterial blight resistance, in korean japonica varieties. It was developed from the cross between Iksan469 and HR23966-22-1-2. The HR23966-22-1-2 has xa5 gene introgressed through backcrossing IRBB5 two times to the recurrent parent, Suwon345. This variety is 74cm tall, produces 12 tillers per plant and 127 spikelets per panicle, has 1,000-grain weight of 23.9g and matures in 145 days from seeding to harvest. It is resistant to races K1, K2, K3, K3a, K4 and K5 of bacterial blight, rice stripe virus, moderately resistant to blast and tolerant to lodging. This variety is translucent with non-glutinous endosperm, 19.8% amylose content, 5.9% protein content and has excellent palatability of cooked rice. The yield performance is about 5.97MT/ha, 9% higher than that of check variety, Nampyeongbyeol.

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Chemical Composition, Antibacterial and Antifungal Activities of the Essential Oil of *Hymenocrater Platystegius* Rech.f. from Iran

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The essential oil composition of the aerial parts of *Hymenocrater platystegius* Rech.f. (Labiatae), which is endemic to Iran, was studied by GC and GC/MS. The oil was obtained by hydrodistillation of air-dried samples. The yield of the oil was 0.1% (based on dry weight) and the oil was pale yellow in color. Forty-two compounds were identified representing about 99.8% of the total oil. Monoterpene hydrocarbons (45.3%) constituted the principal fraction of the oil, followed by oxygenated monoterpenes (26.7%). The main components were found to be α -pinene (20.6%), 1,8-cineole (18.6%), β -pinene (9.9%), δ -cadinene (4.2%), myrcene (3.5%) and linalool (3.3%). Evaluation of the in vitro antibacterial and antifungal activities of the essential oil against four fungi (*Rhizopus stolonifera*, *Aspergillus niger*, *Botrytis cinerea* and *Penicillium digitatum*) and bacteria (*Xanthomonas campestris*, *Pectobacterium carotovorum*, *Pseudomonas fluorescens* and *Bacillus subtilis*) is also reported.

Key words: *Hymenocrater platystegius*, Labiatae, essential oil, antibacterial activity, antifungal activity, α -pinene, 1,8-cineole

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Genetic and Transcriptome Analyses of Resistance to Rice Tungro Spherical Virus

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Rice tungro disease is caused by the interaction between rice tungro spherical virus (RTSV) and rice tungro bacilliform virus (RTBV), both of which are transmitted by green leafhoppers (GLH). Genetic analysis revealed that RTSV resistance is governed by a single recessive locus. Near-isogenic lines (NIL, BC¹) were produced from Utri Merah and RTSV-susceptible variety Taichung Native 1 (TN1). The association analysis between genotypes and phenotype in regard to RTSV infection showed that RTSV resistance locus is mapped between 22 to 23Mb of chromosome 7. Further analysis of RTSV resistance using a population derived from the cross between one of the RTSV-resistant NIL (TW16) and japonica variety Unkwang mapped RTSV resistance between 22.1 to 22.2Mb. Genome-wide gene expression analysis for RTSV-resistant TW16 and susceptible TN1 using *c*-oligonucleotide microarray showed that the expression levels of genes common and distinctive between the resistant and the susceptible plants were regulated in response to inoculation with RTSV. Collectively these results suggested that infection of RTSV in rice is suppressed due to the lack of or low expression of gene(s) required for the replication and/or the movement of RTSV.

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Cropview: Attracting Non-science Undergraduates to Crop Science

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Major USA Land-Grant Universities are experiencing difficulty attracting students to crop science undergraduate majors. These universities require undergraduates to complete a diverse group of "general education" courses that include biological science classes. Students may elect classes in Colleges of Agriculture to satisfy these requirements. We have developed an internet based learning system to complement our traditional crop science general education classes. The program known as CROPVIEW is composed of four learning modules followed by two game role play modules. The four learning modules are: 1. Introductory Module - overview of major groups of plants, plant nutrition, photosynthesis, and biome adaptation, 2. Nutrition Module - how plants provide energy and protein for human nutritional needs, 3. Biome Module - characteristics that delineate biomes and where they occur in the world, and 4. Seed Plant Module - descriptive information and interactive images of 20 of the world's most important crops. The Feast or Famine game is an interactive game that evaluates comprehension and retention of module

information in an entertaining way. The game consists of scenarios with increasing difficulty where people groups are faced with natural disasters leading to possible food deficits. The game player is presented the challenge of accepting the mission to identify plants that are adaptive to the disaster biome and that will satisfy human nutritional needs. The Crop Science Investigation (CSI) game is designed to help students learn about biological nitrogen fixation by investigating factors in a greenhouse environment that could have resulted in unhealthy plants.

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Resistant Soybean Varieties to Frogeye Leaf Spot Disease (*Cercospora Sojina*) in Korea

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Frogeye leaf spot (FLS) is an important disease in many soybean production areas of the world. Nowadays in Korea, FLS comes to be a new problem disease in the main soybean cultivated region. Therefore, this study was conducted to investigate the distribution of FLS races in Korea and to select the standard varieties based on the different responses to isolated 6 FLS races. The mobility rate of FLS in Korea were Gangwon-do(78%) > Gyeonggi-do(62%) > Chungcheongbuk-do(54%) > Gyeong sangbuk-do(43%) > Jeonlabuk-do(36%) > Chungcheongnam-do(33%), respectively. And six *C. sojina* races were isolated from the infected plant collected from 52 areas based on the morphological characteristics and pathogenicity. Responses of 63 soybean varieties to 6 races (*C. sojina*) were different respectively. Soybean cultivars, Bogwang and Geomjeong 4 showed resistant response to all FLS races. On the other hand, Taekwang was susceptible to all races. As a results of this test, ten soybean cultivars showed different responses against the six FLS races were selected. And these selected standard cultivars can be used as parents in breeding programs to develop the soybean varieties with resistance to FLS caused by *C. sojina*.

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Durable Blast Resistance in Rice Cultivars Developed Last Four Years in Korea

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Blast resistance of fifty-five rice cultivars which were developed from 2004 to 2007 was screened to identify durable blast resistance in blast nursery, fields and by sequential planting. Fourteen cultivars, early heading type showed under 2.9 of disease severity in blast nursery and twenty-one of medium heading type and twenty mid-late heading type were 4.4 and 4.9, respectively. Early heading type rice cultivars were compatible with 18.4% of representative isolates that are typical races collected in Korea and medium and mid-late heading type was 36.9% and 42.1%, respectively. In the field test, early heading type was resistant leaf blast while mid-late heading type was to panicle blast. In sequential planting test, forty-two rice cultivars, all of Tongil type and short term grown rice cultivars represented high durability to rice blast. 86.2% of cultivars having high eating quality, 60% of cultivars for direct seeding and 57.1% of special purpose cultivars were proved to have high durable blast resistance. However, seven cultivars having high eating quality such as Gounbyeol, Odae 1, Hwangkeumbora, Cheongdam, Cheonga, Hwasin 1, Juan 1 and six special purpose cultivars such as Keunnoon, Hongjinju, Goami 3, Heugseol, Sinnongheugchal, Sinmyeongheugchal was proved having low durability. These results indicated that some of rice cultivars developed for last four years don't have durable resistant to rice blast even though most of cultivars has high durability. Therefore, proper managements would be needed to prevent damage caused by rice blast when cultivating these susceptible cultivars.

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Durable Blast Resistance in Rice Cultivars Developed Last Four Years in Korea