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Program & Abstracts

2016 Annual Autumn Conference of the Korean Society for Horticultural Science

주제 원예산업의 국제화 전략

일자 및 장소 2016. 10. 26(수)~29(토), 김대중컨벤션센터 중소회의실

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Program

- Title: 2016 Annual Autumn Conference of the Korean Society for Horticultural Science
- Theme: Global Strategy of the Horticultural Industry
- Date / Venue: October 26–29, 2016 / Conference Room, Kimdaejung Convention Center, Gwangju, Korea

October 26 (Wed)

16:00 - 21:00	**Executive Committee Meeting**

October 27 (Thu)

08:30 - 09:00	**Registration** (2F, Lobby) & **Poster Mounting (Odd Numbers)** (211~214)				
09:00 - 10:00	**Board Member Meeting** (206~207)				Exhibition
10:00 - 11:40	**Special Lectures** (301~306, Chairperson: Yong Pyo Lim) 1. Byeong Ryul Kim (Korea Rural Economic Institute) 2. Dream of Horticulture Industry, Pass The Great Wall of China (ChongSeo Park, Ministry of Agriculture, Food & Rural Affairs)				
11:40 - 12:00	**Awards** (301~306) - Scientific Achievement Award & Outstanding Industry Award - Society Achievement Award - Outstanding Poster & Oral Award				
12:00 - 13:00	**General Assembly Meeting** (301~306)				
13:00 - 14:00	**Lunch** (2F, LaBoum Wedding Hall)				
14:00 - 15:00	**Poster Presentation & Evaluation (Odd Numbers)** (211~214)			**Honorary Member Meeting** (206)	
15:00 - 17:00	**Oral Presentation 1**	**Vegetable Science** (301~306)	**Floriculture** (208~210)	**Pomology** (201~203)	
17:00 - 17:30	**Research Group Meeting**	**Vegetable Science** (301~306)	**Floriculture** (208~210)	**Pomology** (201~203)	
17:30 - 18:00		**Genetics and Breeding** (301~306)	**Protected Horticulture** (208~210)	**Postharvest Technology** (201~203)	

October 28 (Fri)

08:30 - 09:00	**Registration** (2F, Lobby) & **Poster Mounting (Even Numbers)** (211~214)				
09:00 - 10:00	**Editorial Board Meeting** (206~207)				Exhibition
10:00 - 12:00	**Oral Presentation 2**	**Vegetable Science** (301~306)	**Floriculture** (208~210)	**Pomology** (201~203)	
12:00 - 13:00	**Poster Presentation & Evaluation (Even Numbers)** (211~214)			**General Meeting & Workshop of Honam Branch** (208~210)	
13:00 - 14:00	**Lunch** (2F, LaBoum Wedding Hall)				
14:00 - 16:00	Symposia	**Joint Symposium by Genetics · Breeding of KSHS & Vegetable · Horticultural Seed Development of GSP** (301~306) 1. Byung Dong Kim (Seoul Natl. Univ.) 2. Jinman Lee (Bayer CropScience) 3. Byoung-Cheorl Kang (Seoul Natl. Univ.) 4. Seong Hwa Choi (Seoul Natl. Univ.) 5. Su Hyoung Park (Natl. Inst. of Hort. & Herbal Sci.) 6. Jinsu Go (G-Farm) 7. Chun-Hee Ahn (former Koregon Co., Ltd.) 8. Kang Jun Choi (Gangwondo Agr. Res. & Extension Services) 9. Kyeonggu Ahn (Joeun Seeds Co., Ltd.)	**Protected Horticulture** (208~210) 1. Dong-hang Shin (Whashin Agriconstruction Co., Ltd.) 2. Seungwan Lee (BK Greenhouses Ltd.) 3. Hye Min Park (Ministry of Agriculture, Food & Rural Affairs)	**Postharvest Technology** (201~203) 1. Yoon-Pyo Hong (Natl. Inst. of Hort. & Herbal Sci.) 2. Cheon-Soon Jeong (Kangwon Natl. Univ.) 3. JungMin Baek (Ecoplants Co., Ltd.)	
16:00 - 18:00		**Korean Society for Fruit Breeding and Varieties** (208~210)			

October 29 (Sat)

09:00 - 13:00	**Gwangju City Tour**

※ Each oral presentation including question-and-answer time will be limited to 15 minutes. All poster presenters must set up and tear down their posters during the designated times. The author must remain by his/her poster board for the duration of the one-hour poster session.

채소 – 조직배양/생물공학

182 P-1-④

Examining the Fuctions of the BrLKP2 Gene Family in the Circadian Clock in Brassica Rapa

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Light regulated protein turnover is a common feature among circadian clocks. In Arabidopsis, ZEITLUPE (ZTL) and its close relatives LOV KELCH PROTEIN2 (LKP2) and FLAVIN BINDING, KELCH REPEAT, F-BOX1 (FKF1) encode F-box proteins with an N-terminal LOV domain, and a series of Kelch repeats at the C terminus. ZTL is necessary for maintaining a normal circadian period whereas FKF1 and LKP2 play minor and primarily redundant roles in determining circadian period. In addition, FKF1 is a necessary component in the early steps of photoperiodic flowering. To define the extent to which the Arabidopsis model can be extrapolated to other species, including crops, we wished to examine the role of these F-box proteins in the agricultural crop, Brassica rapa, a close relative of Arabidopsis. Following divergence from Arabidopsis, B. rapa has undergone whole genome triplication and subsequent diploidization resulting in considerable gene loss. In B. rapa, ZTL and FKF1 have been lost, in sharp contrast to most other clock genes which have been preferentially retained in two or three copies. However, a single locus of LKP2 has been retained. Intriguingly, a tandem triplication event has resulted in three tightly linked copies of LKP2. This raises the question of whether these three copies of LKP2 in B. rapa have undergone functional specialization and now fulfill the functions of ZTL and FKF1. Accordingly, we transformed the B. rapa LKP2 genes into the Arabidopsis long period ztl mutant and the late flowering fkf1 mutant. Circadian period and flowering time analysis of these transgenic lines provides insight into the possible roles of these LKP2 genes in B. rapa.

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183 P-1-④

수박 유전자원의 원예적 형질 평가

Evaluation of Horticultural Characters for Watermelon Germplasm

정주형[1]*, 임정현[1], 김태복[1], 성문호[1], 전형권[1], 권성환[2]
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전라북도농업기술원 수박시험장에서는 2016년 국립유전자원센터 분양 자원 170계통 중 정상적으로 발아한 168계통의 종자를 증식하였다. 원예적 형질 평가는 양적형질 9종(과중, 과실길이, 과실너비, 과피두께, 당도, 종자길이, 종자너비, 종자의수, 잎몸 길이/너비의 비), 질적형질 9종(첫 번째 암꽃착생절위, 암꽃 개화기, 엽결각 깊이, 과실형태, 과실껍질의 바탕색, 과실 줄무늬색 강도, 과실 줄무늬, 과실 골, 과육의 주요색)에 대하여 실시하였고, 성분은 당류분석을 이미지 정보는 3종(수확기 잎, 수확 후 과일, 수확 후 종자)을 구축하였다. 이 유전자원들 중 적색과육 중과종 1계통, 고당도 1계통, 녹색과피 소과종 1계통, 녹색과피 중과종 1계통은 새로운 품종 개발 시 유용할 것으로 판단된다.

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184 P-1-④

오이모자이크 바이러스에 대한 새로운 고추 열성 저항성 유전자원 탐색

Identification of new Recessive Resistance Sources for *Cucumber mosaic virus* new Isolate-P1 (CMV-P1) in *Capsicum* spp.

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Cucumber mosaic virus is responsible for agronomic losses in many important crops worldwide. *Capsicum annuum* 'Bukang' Commercial F_1 hybrid shows resistance to CMV-P0 strains (CMV-Kor and CMV-Fny). And the single dominant resistance gene, *Cmr1*, is known to control CMV resistance in 'Bukang'. Recently, a new isolate, CMV-P1, breaking the *Cmr1*-mediated resistance, was identified in Korea. To find out the resistance sources, about two thousands of *Capsicum* germplasm collections comprising cultivated and wild species were screened for resistance to CMV-P1. For the selection of resistance sources, two criteria were established: 1) CMV-P1 inoculated plants were evaluated once a week for a month, compared with susceptible controls ('Jeju' and 'Bukang') and one resistant control *C. annuum* 'LAM'. Symptomless peppers were selected as potential resistance plants. 2) For these candidate plants, CMV accumulation levels were evaluated with a double antibody sandwich (DAS)-enzyme-linked immunosorbent assay (ELISA). Finally 'Kathmandu-1', 'Kathmandu-2a' and 'Kathmandu-2b' have been selected as resistant plants. Genetic analysis from all F_1 crossed with 'Jeju' showed that the new resistance sources were recessive gene. Further study with these newly identified CMV-P1 resistance sources can be used for CMV resistance pepper breeding.

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185 P-1-④

흰가루병 저항성 유전자, *PMR1*의 유전자 지도 작성

Molecular Mapping of a Novel Gene, *PMR1*, Conferring Resistance to Powdery Mildew in Pepper (*Capsicum annuum*)

CALS College of Agriculture and Life Sciences

Identification of new resistance sources for *Cucumber mosaic virus* new isolate-P1 (CMV-P1) in *Capsicum spp.*

Seula Choi[1], Myeong-Sook Han[1], Jin-Kwan Jo[1], Joung-Ho Lee[1], Eun-Ho Son[2], Byoung-Cheorl Kang[1]*

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ABSTRACT

Cucumber mosaic virus is responsible for agronomic losses in many important crops worldwide. *Capsicum annuum* 'Bukang' Commercial F_1 hybrid shows resistance to CMV-P0 strains (CMV-Kor and CMV-Fny). And the single dominant resistance gene, *Cmr1*, is known to control CMV resistance in 'Bukang'. Recently, a new isolate, CMV-P1, breaking the *Cmr1*-mediated resistance, was identified in Korea. To find out the resistance sources, about two thousands of *Capsicum* germplasm collections comprising cultivated and wild species were screened for resistance to CMV-P1. For the selection of resistance sources, two criteria were established: 1) CMV-P1 inoculated plants were evaluated once a week for a month, compared with susceptible controls ('Jeju' and 'Bukang') and one resistant control *C. annuum* 'LAM'. Symptomless peppers were selected as potential resistance plants. 2) For these candidate plants, CMV accumulation levels were evaluated with a double antibody sandwich (DAS)-enzyme-linked immunosorbent assay (ELISA). Finally 'Kathmandu-1', 'Kathmandu-2a' and 'Kathmandu-2b' have been selected as resistant plants. Genetic analysis from all F_1 hybrids, crossed with 'Jeju', showed that the new resistance sources were recessive gene. Moreover, the result of allelism test with all 'resistant lines x LAM F_1' showed, the genes of three resistant lines are alleles of *cmr2*.

INTRODUCTION

Cucumber Mosaic Virus (CMV), a member of the genus Cucumovirus in the family Bromoviriae, is one of the most destructive viruses worldwide, specially in temperate regions. It is responsible for important agronomic losses in many crops, infecting more than 1,200 plant species.

Capsicum annuum 'Bukang' commercial F_1 hybrid shows resistance to CMV-P0 strains (CMV-Kor and CMV-Fny) and the single dominant resistance gene, *Cmr1*, is known to control CMV resistance in 'Bukang'. However, a new isolate, CMV-P1, breaking the *Cmr1*-mediated resistance, has been identified in Korea (Kang et al., 2012). Recently, CMV-P1 resistance source, *C. annuum* 'LAM' was described as a resistance source to CMV-P1. The object of this study was to identify the additional CMV-P1 resistance sources against CMV-P1.

MATERIALS AND METHODS

Plant materials

Two thousands of *Capsicum* germplasm collections, provided by RDA-Genebank Information Center, were screened for resistance to CMV-P1. *Capsicum annuum* 'Jeju' and 'Bukang' were used as the susceptible controls. 'Bukang' is a commercial cultivar (Monsanto Korea Inc., Cheongwon-Gun, Korea) known to contain the CMV resistance gene, *Cmr1* (Kang et al., 2012). As a resistance control, *C. annuum* 'LAM' was used. 'LAM' is known to contain the CMV-P1 isolate resistance gene, *cmr2*.

For genetic traits study materials, resistance lines were crossed with 'Jeju' and 'LAM'.

Virus inoculation

The inoculum of CMV-P1 isolate was prepared from infected leaf material of *N. rustica* plants. Briefly, one gram of infected leaves were ground in 4 ml phosphate buffer. The seedlings were dusted with Carborundum #400 mesh (Hayashi Pure Chemical Ind., Japan) and inoculated by rubbing the virus onto the cotyledons. After 15-20 min, the inoculated plants were rinsed with tap water and then maintained in a growth chamber. The CMV-induced symptoms were recorded at 7, 14 and 21 day post inoculation (dpi) (Hoang et al., 2013).

Detection of CMV accumulation by ELISA

Twenty-one days of post inoculation, the coat protein (CP) of CMV was detected by an enzyme-linked immunosorbent assay (ELISA), performed according to the manufacturer's protocol (Agdia, Elkhart, IN, USA). Two leaf discs of CMV-infected plant were used for ELISA analysis. Each sample was measured at an absorbance value of 405 nm in an ELISA reader (Anthos, Eugendorf, Austria) (Kang et al., 2012).

ACKNOWLEDGEMENT

This research was supported by Golden Seed Project (213002-04-4-CG900), Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), Rural Development Administration (RDA) and Korea Forest Service (KFS), Republic of Korea.

RESULTS

Finding potential resistant plants

After inoculation, susceptible controls showed mosaic, leaf distortion and yellowing on their leaves at 21 dpi. Among the test plants, 16 potential resistant plants, 14 accessions of *C. annuum* and 2 accessions of *C. frutescens*, have been identified (Table 1). The potential resistance plants were tested by ELISA. only 3 out of 16 candidates had no accumulation of the virus CP. *C. frutescens* 'Kathmandu-1', *C. annuum* ' Kathmandu-2a' and *C. annuum* 'Kathmandu-2b' confirmed to have resistance to CMV-P1 (Fig.1).

Table 1. Summary of *Capsicum* germplasm screening against CMV-P1 isolate.

Capsicum species	Total number of accessions	Number of accessions	
		At 21 dpi	
		Susceptible	Resistant
C. annuum	1839	1826	14
C. baccatum	56	56	0
C. chinense	43	43	0
C. frutescens	60	58	2
C. pubescens	2	2	0
Total	2000	1985	16

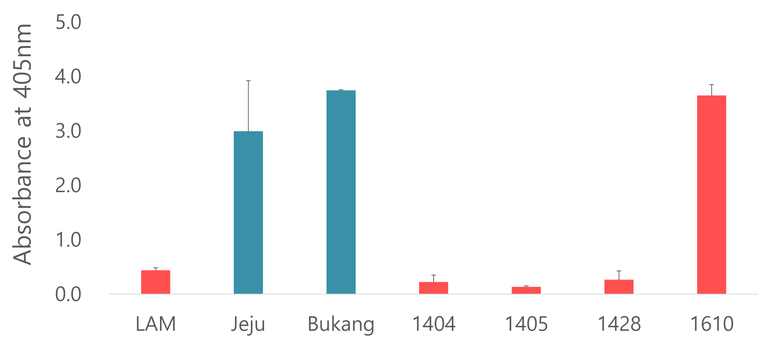

Figure.1. Detection of CMV accumulation by ELISA. ELISA result of resistance candidates. Only three lines were confirmed as resistance plants. (1404=Kathmandu-1, 1405=Kathmandu-2a and1428=Kathmandu-2b)

Genetic characteristics confirmation of resistance sources.

First, to test the genetic traits, 1404, 1405, and 1428 were crossed with 'Jeju'. Those F_1 hybrids were inoculated with CMV-P1. At 20 dpi, mosaic and yellowing were detected from the plants (Fig.2. (g),(h), and (i)). The new resistance sources were confirmed as recessive gene.

Second, for the allelism test, three lines were crossed with CMV-P1 resistance plant, 'LAM'. CMV-P1 virus inoculation test were performed with those F_1 hybrids. At 20 dpi, no symptom were detected from all the three resistance lines (Fig.2. (j), (k), and (l)). From the additional ELISA test, no CMV were detected (Fig.3). This result suggests CMV-P1 resistant genes of 1404, 1405, and 1428 are allele of same gene, *cmr2 of* LAM.

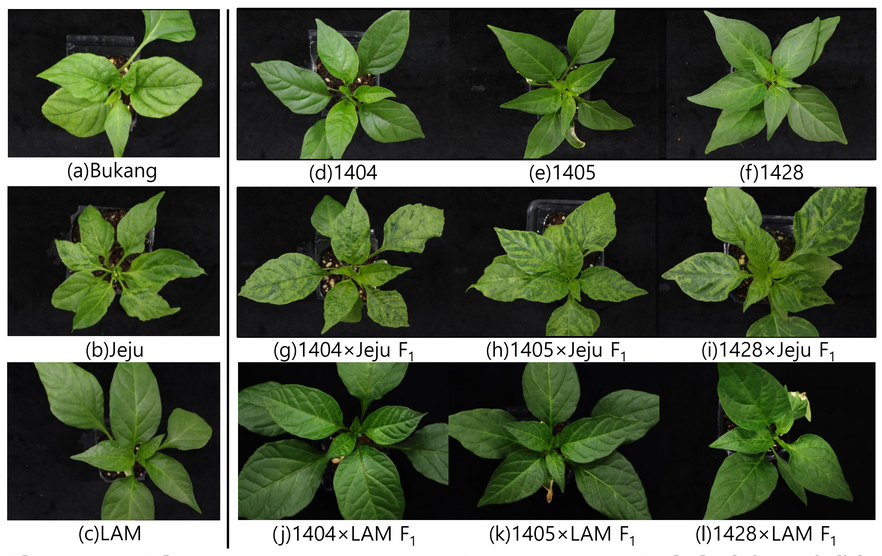

Figure.2. Disease responses to CMV-P1 at 20 dpi. (a) and (b) are susceptible control. (c) is resistance control. (d), (e), and (f) are identified resistance sources. (g),(h), and (i) are hybrid F_1 crossed with 'Jeju', showing CMV-P1 symptoms. (j), (k), and (l) are hybrid F_1 crossed with 'LAM', showing no CMV-P1 symptoms.

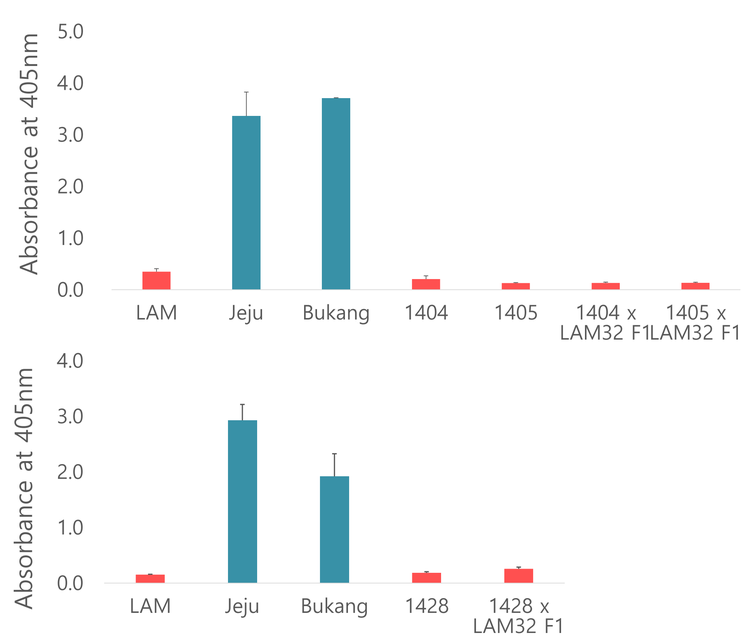

Figure.3. CMV detection for allelism test by ELISA. ELISA result of three resistance lines and F_1 hybrid crossed with 'LAM' for allelism test at 20 dpi.

DISCUSSION

With the new three resistance lines, we will find out the location of CMV-P1 resistance genes and develop close markers for breeding CMV-P1 cultivars. For further study, F_2 populations derived from *Capsicum annuum* 'Jeju' and *C. chinense* 'Habanero' are being cultivated in the Suwon farm. To identify more CMV-P1 resistance gene, additional *Capsicum* germplasm collections are being screened.

REFERENCES

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- Kang WH, Hoang NH, Yang HB, Kwon JK, Jo SH, Seo JK, Kim KH, Choi D, Kang BC (2010) Molecular mapping and characterization of a single dominant gene controlling CMV resistance in peppers (*Capsicum annuum L.*). *Theor Appl Genet* 120:1587-1596
- Kang WH, Seo JK, Chung BN, Kim KH, Kang BC (2012) Helicase domain encoded by *Cucumber mosaic virus* RNA1 determines systemic infection of *Cmr1* in pepper. *Plos One 7*

SUMMARY

- *Capsicum* germplasm collections were screened to identify CMV-P1 resistance sources.
- Three CMV-P1 recessive resistance sources were identified and those were appeared to be *cmr2* allele.
- Identification of additional CMV-P1 resistance sources would be useful for pepper breeding programs.