October 2016 제34권 별호 II

광주관광컨벤션뷰로 Gwangju CVB

원예과학기술지

KOREAN JOURNAL OF HORTICULTURAL SCIENCE & TECHNOLOGY

2016 한국원예학회 임시총회 및 제105차 추계학술발표회 자료집

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

(사)한국원예학회 Vol.34 Supplement II (October 2016)

ISSN 1226-8763

주최 (사)한국원예학회 · GSP채소종자사업단 · GSP원예종자사업단

후원 광주관광컨벤션뷰로 · 몬산토코리아 · 코레곤종묘 · 아시아종묘 · 원예산업신문 · 일신화학공업 · 경농 · 그린씨에스 · 농우바이오 · 동일시마즈 · 비앤피인터내셔널 · 신젠타코리아 · 쏠단 · 씨앤와이 · 아름

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.

질의 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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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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Seul-A Choi[1], Myeong-Sook Han[1], Jin-Kwan Jo[1], Joung-Ho Lee[1], Eun-Ho Son[2], and Byoung-Cheorl Kang[1]*
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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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흰가루병 저항성 유전자, *PMR1*의 유전자 지도 작성

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

조진관, Jelli Venkatesh, 한고은, 이종호, 하예성, 정아영, 이혜영, 강병철*
식물생산과학부, 식물유전육종연구소, 채소육종연구센터, 농업생명과학대학, 서울대학교

Jinkwan Jo, Jelli Venkatesh, Koeun Han, Jon-ho Lee, Yeaseong Ha, Ayoung Jung, Hea-yong Lee, and Byoung-Cheorl Kang*
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Powdery mildew (*Capsicum annuum*) is a major fungal disease caused by *Leveillula taurica* in greenhouse. Although powdery mildew resistance has a complex mode of inheritance, resistant cultivars have been steadily developed. Therefore, our objective was to map the resistance gene to powdery mildew resistance in a breeding line, C. annuum 'VK515 R'. Based genetic analysis of an $F_{2:3}$ families derived from a cross between resistant parent 'VK515 R' and the susceptible parent 'VK515 S' we showed that powdery mildew resistant is controlled by a major gene, *PMR1*. Molecular mapping revealed that the *PMR1* locus is located at 1 cM genetic interval between CZ2_11628, and HRM4.1.6 markers on pepper chromosome 4. These results provide a solid foundation for map-based cloning of the PMR gene and helpful for development of marker-assisted selection in pepper breeding. This is the first report showing the localization of resistance genes against powdery mildew in pepper and the results offer the opportunity to increase the efficiency of breeding programs by means of marker-assisted selection.

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Candidate Gene Analysis of Carotenoids Synthesis in Pepper

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Carotenoids are vital pigments responsible for yellow, orange and red color in plants. In pepper, capsanthin-capsorubin synthase (*CCS*), phytoene synthase (*PSY*), β-Carotene hydroxylase (*CRTZ-2*) and lycopene β -cyclase (*LCYB*) were identified to be involved in the carotenoids synthesis pathway. Previously molecular markers based on the *CCS* and *PSY* genes have been developed to distinguish fruit colors in pepper. However, these markers can distinguish fruit colors of limited pepper genotypes. Therefore, there is need of developing additional markers for accurate prediction of fruit colors using molecular markers. In this study *CCS*, *PSY*, *CRTZ-2*, and *LCYB* genes of 134 pepper accessions were sequenced to identify the genes affecting the fruit color. Sequencing was performed using single molecule real time (SMRT) sequencing technology. We performed two step PCR experiment to reduce sequencing cost. With barcode sequence of primers in the second PCR, we were able to sequence all the samples at one time and detected sequence of each samples. We will develop markers using sequences of in *CCS*, *PSY*, *CRTZ-2*, and *LCYB* genes and these markers will be used for detecting the fruit colors of pepper.

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Molecular mapping of a novel gene, *PMR1*, conferring resistance to powdery mildew in pepper (*Capsicum annuum*)

Jinkwan Jo[1], Jelli Venkatesh[1], Koeun Han[1], Yeaseong Ha[1], Ayoung Jung[1], Hea-yong Lee[1] and Byoung-Cheorl Kang[1]*

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Abstract

Pepper powdery mildew caused by *Leveillula taurica* is considered to be the major fungal disease of peppers (*Capsicum annuum*) grown in greenhouse. Previous studies have demonstrated that powdery mildew resistance has a complex mode of inheritance. In the present study, a novel powdery mildew resistant gene, *PMR1* introgressed in a resistant breeding line, 'VK515 R' was investigated using the $F_{2:3}$ families derived from a cross between the resistant parent 'VK515 R' and the susceptible parent 'VK515 S'. Genetic analysis of the 'VK515' $F_{2:3}$ families showed a single dominant inheritance of the resistance. Genetic mapping showed that the *PMR1* locus is located on pepper chromosome 0 in a 4 Mb-region between CZ2_11628 and HRM4.1.6 markers. No recombinants were observed in 4 Mb-region, one SCAR marker and five SNP markers were found to be 0 cM apart from the *PMR1* locus, which could be due to the suppressed recombination, as revealed by the GBS analysis. In addition, comparison of species-specific InDel markers as well as GBS derived SNP markers indicated that *C. baccatum* as a possible source of alien introgression of powdery mildew resistance in 'VK515 R'. The molecular markers developed herein especially helpful in marker-assisted selection in pepper breeding programs against powdery mildew resistance.

Objectives

- To develop molecular markers linked to *PMR1* in *Capsicum*
- To conduct fine mapping of the *PMR1* gene
- To investigate the origin of the *PMR1* gene

Materials and Methods

Plant materials

- Resistant parent *C. annuum* 'VK-515 R' (Samsung Seeds Co., Ltd., Korea)
- Susceptible patent *C. annuum* 'VK-515 S' (Samsung Seeds Co., Ltd.)
- Resistant control is the commercial cultivar *C. annuum* 'PM Singang' (Nongwoo Bio Co., Ltd.)
- Susceptible control is the commercial cultivar *C. annuum* 'Bukang' (Hungnong Seed Co.)
- 'VK515' 102 $F_{2:3}$ families were derived from a 'VK515 R' X 'VK515 S' cross

Inoculum preparation and disease infection

- Infected 'Bukang' and 'VK515 S' plants were kept around $F_{2:3}$ plants grown in plastic trays (50 cell trays) at one-tray intervals.
- Presence or absence of white fungal hyphae observed on infected leaves 60 days after sowing was used as a measure of disease infection.

Chromosomal localization

- Genotyping was performed with the Fluidigm® EP1™ system (Fluidigm, USA), (Kang et al, 2014)

Genotyping-by-sequencing (GBS)

- Disestion: *Pst*I and *Mse*I
- Sequencing: Illumina Hiseq 2000
- CLC genomics workbench

Genetic mapping of *PMR1* locus

- CarthaGene Software and MapChart 2.3 software

Comparative map analysis of the *PMR1* locus using GBS derived SNP markers

- Genome: *C. annuum* L_Zunla-1, *C. chinense* v.1.2, C. *baccatum* v.1.2 (Prof. Choi of SNU)

Phygenetic analysis

- DARwin 6.0.9

Results and Discussion

Inheritance analysis of the *PMR1* gene

Among 102 'VK515' $F_{2:3}$ families, 24 families (a total of 451 plants) were resistant homozygous, 48 families (a total of 898 plants) were segregating, and 30 families (a total of 582 plants) were susceptible homozygous, which showed a good fit to 1:2:1 ratio (χ^2 = 1.06; P = 0.59), suggesting that resistant to powdery mildew is controlled by a single dominant gene, *PMR*1 in 'VK515 R' (Table 1).

Fig. 1 Phenotype analysis of powdery mildew resistance in pepper lines. Comparison of phenotypes of resistant, susceptible parental lines, and commercial pepper cultivar infected with *L. taurica*.

Table 1. Segregation analysis of powdery mildew resistance in VK515 families

Population	Number of plants/families	Phenotype			Expected ratio	χ^2	P-value
		R	H	S			
'VK515 R'	20	20					
'VK515 S'	20			20			
'VK515' F_1	20	20					
'VK515' $F_{2:3}$ families	102 (1931)	24 (451)	48 (898)	30 (582)	1 : 2 : 1	1.06	0.59

R, resistant; H, heterozygous; S, susceptible; Number of $F_{2:3}$ 'VK515' plants used were indicated in parenthesis.

Marker development and genetic mapping of the *PMR1* locus

Genotyping was performed with the Fluidigm® EP1™ system and *PMR1* locus were localized on chromosome 0. Therefore, more markers were tried to be added around the *PMR1* locus using genomic information of *Capsicum*.

A total of six polymorphic markers (ZL1_10691, CZ2_11628, ZL1_1826, KS16052G01, HRM2_A4, and HRM4.1.6) were developed and mapped in 102 'VK515' $F_{2:3}$ families (Fig. 2). Based on genetic analysis, the *PMR1* locus was delimited to a 1 cM-region between CZ2_11628 and HRM4.1.6 markers on chromosome 0 (Fig. 2). Among the six markers used, three markers, ZL1_1826, KS16052G01, and HRM2_A4, were co-segregated with powdery mildew resistant phenotype and found to be at a genetic distance of 0 cM from the *PMR1* locus (Fig. 2).

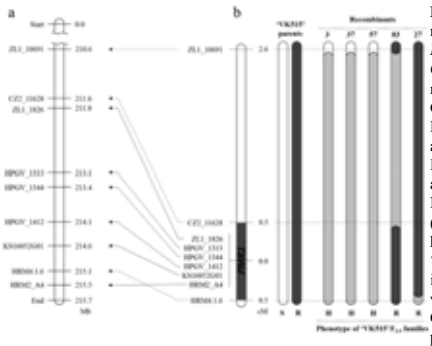

Fig. 2 Comparative genetic linkage and physical maps of the powdery mildew resistance gene *PMR1*. **a** Physical location of linked scaffolds in *C. chinense* v.1.2. **b** Physical location of linked markers in Zunla-1 genome chromosome 0 .**c** Genetic map of 'VK515' $F_{2:3}$ families. Recombinant heterozygous resistant plants 3, 37, and 57; homozygous resistant plants 27 and 83. Eight SNP markers linked to the *PMR1* locus are indicated next to pepper chromosome 0. Numbers on the right indicate genetic distances (cM). Black and white rectangles indicate the homozygous intervals of 'VK515 R' and 'VK515 S' chromosome 0, and gray rectangles indicate heterozygous intervals. The *PMR1* gene was delimited to a 4 Mb-region between the CZ2_11628 and HRM4.1.6 markers on the pepper 'L_Zunla-1' chromosome 0

Investigation origin of the *PMR1*

To know the origin of the *PMR1* gene, flanking markers (ZL1_1826 and HRM4.1.6) sequence were compared among *Capsicum* species. ZL1_1826 and Chr4.1.6 (HRM4.1.6) marker sequences with species-specific InDels indicated that the *PMR1* locus from 'VK515 R' are closely related to both *C. baccatum* and *C. chinense* than 'VK515 S' or *C. annuum* (Fig. 3a). And the GBS data were aligned with *C. annuum* 'L_Zunla-1', *C. chinense*, and *C. baccatum* genomic sequences. Based on GBS data 22 SNPs (Table 2) were detected in the *PMR1* locus. Phylogenetic analysis of the GBS data (Fig. 3b) from the *PMR1* locus revealed clustering of 'VK515 S', *C. annuum*, and *C. chinense*, whereas 'VK515 R' and *C. baccatum* shares a common node suggesting that the *PMR1* locus in the 'VK515 R' is closely related to *C. baccatum*. These results indicate that the *PMR1* locus might be introgressed from the *C. baccatum*.

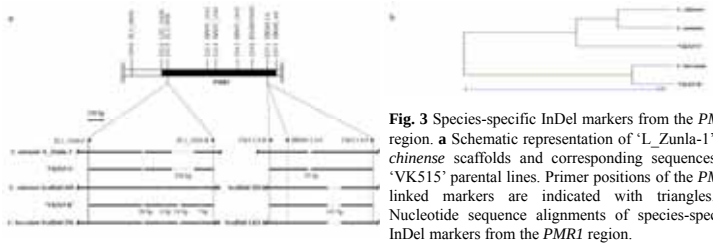

Fig. 3 Species-specific InDel markers from the *PMR1* region. **a** Schematic representation of 'L_Zunla-1', *C. chinense* scaffolds and corresponding sequences of 'VK515' parental lines. Primer positions of the *PMR1* linked markers are indicated with triangles. **b** Nucleotide sequence alignments of species-specific InDel markers from the *PMR1* region.

Table 2. Genotyping-by-sequencing of the *PMR1* locus

SNP marker	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6	SNP7	SNP8	SNP9	SNP10	SNP11	SNP12	SNP13	SNP14	SNP15	SNP16	SNP17	SNP18	SNP19	SNP20	SNP21	SNP22
C. chinense	G	G	G	A	G	C	G	C	G	G	G	C	T	T	C	A	A	T	T	G	G	G
C. annuum	A	G	G	A	G	C	T	C	G	G	G	C	T	T	C	A	A	T	T	G	G	G
'VK515 S'	A	G	G	A	G	C	G	C	G	G	G	C	T	C	C	A	A	T	T	G	C	A
C. baccatum	G	G	A	G	A	T	T	T	A	A	T	A	A	T	T	G	G	C	C	A	G	G
'VK515 R'	G	A	A	G	A	T	T	T	A	A	T	A	A	T	T	G	G	C	C	A	G	G

Conclusions

Phenotype and genetic analysis of powdery mildew resistance in pepper cv. 'VK15 R' identified a single dominant gene for powdery mildew resistance. We have mapped the *PMR1* locus to a 0 cM genetic interval on chromosome 0, co-segregating with six molecular markers. The molecular markers that we developed herein will be especially useful in MAS and pyramiding of powdery mildew resistance genes into an elite cultivar as they are tightly linked to the *PMR1* locus and the availability of efficient SNP marker detection platforms. Further fine mapping and candidate gene analyses are needed to reveal the relationship between the predicted receptor kinase/NBS-LRR genes and the *PMR1* gene.

References

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- Kim DH, Park JH, Lee JS, Han KS, Han YK, Hwang JH (2009) Effect of temperature, relative humidity on germination and development of powdery mildew (*Leveillula taurica*) on pepper and its inoculation method. *Res Plant Dis* 15:187-192.

Acknowledgement

- This research was supported by the 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.