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Program & Abstracts

2016 Annual Spring Conference of the Korean Society for Horticultural Science

주제 스마트 원예(Smart Horticulture)의 현황과 발전방안

일자 및 장소 **2016. 5. 25**(수)~**28**(토), 창원컨벤션센터(CECO)

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Program

- Title: 2016 Annual Spring Conference of the Korean Society for Horticultural Science
- Theme: Smart Horticulture – Current State and Perspectives
- Date / Venue: May 25–28, 2016 / Changwon Exhibition Convention Center, Changwon, Gyeongnam, Korea

May 25 (Wed)

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

May 26 (Thu)

08:30 - 09:00	**Registration** (Conference Room 301 · 302, Lobby) & **Poster Mounting (Odd Numbers)** (Convention Hall, Lobby)				
09:00 - 10:00	**Board Member Meeting** (Conference Room 602)				Exhibition
10:00 - 11:40	**Special Lectures** (Convention Hall 3, Chairperson: Jung Eek Son) 1. Current status and Standardization Trends of IoT based Smart Horticulture (Hyun Yoe, Sunchon National University, Korea) 2. Strategy and Policy Direction of ICT convergency in Horticulture Industry (Hong Sang Kim, Korea Rural Economic Institute, Korea)				
11:40 - 12:00	**Awards** (Convention Hall 3) - Outstanding Paper Award - Best Associate Editor & Best Reviewer Award - Outstanding Poster & Oral Award				
12:00 - 13:00	**General Assembly Meeting** (Convention Hall 3)				
13:00 - 14:00	**Lunch** (Convention Hall 1)				
14:00 - 15:00	**Poster Presentation & Evaluation (Odd Numbers)** (Convention Hall, Lobby)		**Horticultural Industry Promotion** (Convention Hall 3)	**Honorary Member Meeting** (Conference Room 602)	
15:00 - 17:00	**Oral Presentation 1**	**Vegetable Science** (Convention Hall 3)	**Floriculture** (Convention Hall 2)	**Pomology** (Conference Room 301 · 302)	
17:00 - 17:30	**Research Group Meeting**	**Vegetable Science** (Convention Hall 3)	**Floriculture** (Convention Hall 2)	**Pomology** (Conference Room 301 · 302)	
17:30 - 18:00		**Genetics and Breeding** (Convention Hall 3)	**Protected Horticulture** (Convention Hall 2)	**Postharvest Technology** (Conference Room 301 · 302)	

May 27 (Fri)

08:30 - 09:00	**Registration** (Conference Room 301 · 302, Lobby) & **Poster Mounting (Even Numbers)** (Convention Hall, Lobby)				
09:00 - 10:00	**Editorial Board Meeting** (Conference Room 301 · 302)		**Outstanding Undergraduate Award** (Convention Hall 2)	**International Student & Scholar Gathering** (Conference Room 602)	
10:00 - 12:00	Symposia	**Vegetable Science** (Convention Hall 3, Chairperson: Il Seop Kim) 1. Jeong Wook Heo (Rural Development Administration) 2. Chongrae Roh (Inst. of Convergence Technol.) 3. Changhoo Chun (Seoul Natl. Univ.)	**Floriculture** (Convention Hall 2, Chairperson: Byoung Ryong Jeong) 1. Kwang Jin (Natl. Inst. of Hort. & Herbal Sci.) 2. Jongyun Kim (Korea Univ.) 3. Kyeong-Hwan Lee (Chonnam Natl. Univ.)	**Pomology** (Conference Room 301 · 302, Chairperson: Ki Woong Nam) 1. Hae Keun Yun (Yeungnam Univ.) 2. Byung Woo Moon (M · Hort. Technique Reserch Inst.) 3. Dong Hyuk Lee (Natl. Inst. of Hort. & Herbal Sci.)	Exhibition
12:00 - 13:00	**Poster Presentation & Evaluation (Even Numbers)** (Convention Hall, Lobby)				
13:00 - 14:00	**Lunch** (Convention Hall 1)				
14:00 - 16:00	**Oral Presentation 2**	**Vegetable Science** (Convention Hall 3)	**Floriculture** (Convention Hall 2)	**Pomology** (Conference Room 301 · 302)	

May 28 (Sat)

09:00 - 13:00	**Field Trip**

※ 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.

135 P-1-③ Quality Change of Baemoochae Plant (X*Brassicoraphanus*) during Postharvest Cold Storage
..... NaRae Han, Soo-Seong Lee, and Jongkee Kim

채소 – 유전육종

136 P-1-④ 팁번에 강하고 다수성 청치마 상추 '삼복하청' 육성
..... 장석우, 박수형, 채원병, 정승룡, 이종남, 서명훈, 이민정, 인민식, 김은지, 김희대, 고순보

137 P-1-④ QTL Mapping of CMV_{P1} Resistance in Pepper with a Genotyping-By-Sequencing Approach
..... Min Ho Eun, Jung-Heon Han, Jae Bok Yoon, Ye Rin Lee, Kyumi Jeong, Haein Kim, and Jundae Lee

138 P-1-④ 내염성 박 대목 우량 계통의 수박 접목 후 생육 비교 ..... 안세웅, 문지혜, 허윤찬, 박태성, 김수, 서태철, 전희, 김영철, 남춘우, 김선민

139 P-1-④ Fine Mapping of the Genic Male-Sterile Gene (*msk*) in Pepper (*Capsicum annuum* L.)
..... Kyumi Jeong, Ye Rin Lee, Haein Kim, and Jundae Lee

140 P-1-④ 딸기 품종의 역병(*Phytophthora cactorum*) 저항성 분석 ..... 이예린, 정규미, 김해인, 이준대

141 P-1-④ RAPD-SCAR Molecular Markers Related to Powdery Mildew Resistance in Squash .. Ha-Jin Jeon, Sang-Ki Seo, and Young-Doo Park

142 P-1-④ High-throughput SNP 분자표지 개발을 통한 배추 MAB 육종체계 구축 ..... 김진희, 안율균, 이은수, 박수형, 김정호

143 P-1-④ 수출용 사계성 딸기 '무하' 육성 ..... 이종남, 김혜진, 최미자, 김기덕, 남정환, 홍수영, 김수정, 손황배, 김율호, 서종택

144 P-1-④ 다공성 세라믹 큐브를 활용한 쉽고 빠른 토마토 DNA 추출 ..... 김태언, 성시영, 김현정

145 P-1-④ 덩굴쪼김병 저항성 수박 대목용 박 선발 ..... 문지혜, 김수, 박태성, 허윤찬, 조명철, 양은영, 채수영

146 P-1-④ 다양한 토마토 유전자원 수집, 평가 및 선발 결과 ..... 조명철, 양은영, 김수, 채수영, 김정호, 허온숙, 최학순

147 P-1-④ 위도와 지리적 위치에 따른 전 세계 무 재래종의 개화시기 변이 ..... 강은선, 장석우, 박수형, 하선미, 김혜림, 채원병

148 P-1-④ Molecular Mapping of the Root-Knot Nematode (*Meloidogyne incognita*) Resistance Gene *Me7* in Pepper and Histological Characterization of the Parental Lines
..... Amornrat Changkwian, Jin-Kyung Kwon, Ji-Woong Han, Joung-Ho Lee, Gyung-Ja Choi, Yong-Ho Kim, and Byoung-Cheorl Kang

149 P-1-④ 감자의 Genotype에 따른 효소적 갈변특성 ..... 임주성, 이슬기, 한다솜, 김미옥, 조지홍, 조광수, 장동칠, 유홍섭, 진용익, 김화영

150 P-1-④ A Study on the Characteristics of Various Morphology to Double Haploid Population of *Brassica rapa*
..... Mi-Suk Seo, Kyoung-Ah Lim, Mi-Sun Moon, Hye-Young Seo, Seung-Ah Choi, Ji-Yun Lee, and Jung Sun Kim

151 P-1-④ 파프리카 CMV, TSWV 저항성 계통 육성 ..... 박종숙, 장지혜, 이재택, 권성환, 송영주

152 P-1-④ 다수성 미니 파프리카 '미니팡' 육성 ..... 전수경, 이문중, 황지은, 장길수, 김찬용, 권오훈, 권오흔

153 P-1-④ 전국 재배용 다수성 6쪽 마늘 '홍산' ..... 곽정호, 안율균, 김철우, 권영석, 최근진, 윤무경

154 P-1-④ Inheritance Study of a CMV Resistance Gene in Cucumber (*Cucumis Sativus* L.) and Candidate Gene Analysis
..... Jelli Venkatesh, Joung-Ho Lee, Seula Choi, Byoung-Cheorl Kang, and Kihwan Song

155 P-1-④ 휴면기간이 짧은 칩가공용 감자 신품종 '남선'
..... 조지홍, 천충기, 이영규, 한선경, 이형운, 김성용, 김태균, 조광수, 임주성, 장동칠, 진용익, 유홍섭, 양석철, 박영은, 조현묵, 정진철, 조혜윤, 박미경

156 P-1-④ 파 F1 종자생산용 만추대성 웅성불임계통 '원예 27005' ..... 김철우, 최민선, 권영석, 곽정호

157 P-1-④ Carotenoids Profiling to Infer Genetic Determinants of Tomato Fruit Colors
..... Hee Ju Yoo, Gyu Myung Lee, Chang-Sik Oh, Inhwa Yeam, and Je Min Lee

158 P-1-④ 양파 F1종자생산용 중만생계 웅성불임계통 "원예 30011"육성 ..... 김철우, 권영석, 최민선, 황엄지, 최인후, 배상경, 장영석

159 P-1-④ Characterization of Ethylene Biosynthesis and Signaling Genes in Cucumber
..... Jeong Hwan Lee, Daeun Choi, Youjin Jung, Hye Jin Kwon, Ji Hoon Han, and Sanghyeob Lee

160 P-1-④ 수집지역별 한지형 마늘 유전자원의 알린 함량 비교 ..... 박영욱, 전종옥, 정재현, 권영희, 이상영

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최근 토마토는 국내·외적으로 기능성 건강식품에 대한 관심이 증가되면서 지속적으로 소비가 증가되고 있다. 이에 따라 국내에서도 토마토 재배면적과 생산량이 지속적으로 증가되고 있다. 아직까지 토마토 종자는 국내육성 품종보다는 외국에서 수입한 품종의 재배가 많이 이루어지고 있다. 일반 토마토의 경우 재배면적의 70% 이상이 일본, 네덜란드, 이스라엘 등에서 육성된 수입 품종들이 재배되고 있는 것으로 추정하고 있다. 반면에 방울토마토의 경우는 국내 육성 품종들이 보급되면서 최근 급속히 재배면적이 증가하여, 2015년 현재 국내 방울토마토 재배면적의 약 70% 이상을 점유하고 있는 것으로 추정된다. 본 논문에서는 국내·외에서 도입된 다양한 토마토 유전자원 123점을 대상으로 초형, 과중, 과장, 당도, 과형 등 주요 원예적 특성과 토마토 황화일말림바이러스(TVYLCV), 시들병 레이스 2(I2), 3(I3) 등 개발된 11개 분자마커를 이용하여 검정을 수행하였다. 농업유전자원센터에서 도입한 유전자원 79점, 시판 중인 F1 품종 20점 및 대만 AVRDC에서 도입한 유전자원 24점의 원예적 특성 조사 결과, 초형은 무한형이 108점(유전자원 77점, F1 품종 20점, AVRDC 11점), 준 유한형이 9점이었다. 그 밖에 평균과중은 9.5-447g, 과장은 14.0-78.3mm, 과경은 7.1-112.8mm, 당도는 2.8-10°Brix까지 유전자원 별로 다양하게 분포되었다. 성숙 시 과실의 색은 노란색, 오렌지색, 빨간색 및 검정색을 띤 빨간색 등이 분포되었다. 분자마커를 이용하여 내병성 검정을 실시한 결과 유전자형이 동형접합체 또는 이형접합체 상태가 1개에서부터 많게는 9개까지 존재하였다. 특히, 유전자원 중에서 분자마커 8개를 보유하고 있는 TG108(AVTO1422), 109(AVTO1424), 112(AVTO1458), 113(AVTO1219), 116(AVTO1315), 120(AVTO1174) 등 6 계통은 내병성 육종소재로 활용 가치가 높아서 선발하였다. 선발된 자원들은 유전자원으로 등록하여 토마토 병저항성 품종육성을 위한 재료로 활용할 수 있도록 할 예정이다.

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147 P-1-④

위도와 지리적 위치에 따른 전 세계 무 재래종의 개화시기 변이

Flowering Time Variation among Radish (*Raphanus sativus* L.) Accessions Depending on Latitudes and Geographic Regions

강은선*, 장석우, 박수형, 하선미, 김혜림, 채원병
국립원예특작과학원 채소과

Eun Seon Kang*, Suk Woo Jang, Su hyoung Park, Sun Mi Ha, Hye Lim Kim, and Won Byoung Chae
Vegetable Research Division, National Institute of Horticultural & Herbal Science, RDA, Wanju 55365, Korea

개화시기는 다양한 기후대 및 지역에서 작물의 적응 및 생존, 육종 방법에 영향을 미치는 중요한 요소이다. 본 연구는 전 세계에서 수집된 무의 개화시기를 조사하기 위하여 실시하였다. 농촌진흥청 농업유전자원정보센터의 데이터베이스를 검색하여 기후대 및 대륙별로 무 유전자원을 분류한 후 약 500여 점의 유전자원을 분양 받았고, 최종적으로 모든 기후대와 대륙에 골고루 분포하는 64점의 무 재래종 유전자원을 선발하였다. 선발한 유전자원 64점은 2013년과 2014년 봄 국립원예특작과학원(수원) 시험포장에 유전자원 1점당 18립씩 35cm × 25cm 간격으로 난괴법 3반복으로 파종하였으며 봄 재배 작형에 준하여 재배하였다. 무 유전자원을 수집한 지역별로 유라시아대륙 6개 지역으로 분류하여 파종 후 30일부터 70일까지 개화시기를 조사하였다. 동남아시아 원산지의 모든 개체는 35일 안에 꽃이 개화하였으며 동남아시아, 남아시아, 동아시아, 서아시아, 중앙아시아, 유럽 순으로 통계적으로 유의하게 개화시기가 늦어졌다. 동일한 유전자원을 위도에 따라 10°N에서 60°N까지 위도 10° 간격, 5단계로 나누어 개화시기를 조사한 결과, 적도 근처의 무 재래종은 개화시기가 가장 빨랐고, 위도가 증가할수록 통계적으로 유의하게 개화시기가 늦어지는 것으로 나타났다. 경도에 따른 개화시기에서는 60°E에서 150°E에서 수집한 재래종의 개화시기가 가장 빨랐으나 이 지역의 유전자원은 대부분 남아시아 및 동남아시아의 낮은 위도에서 수집된 것으로 나타났다. 따라서 무의 경우 저위도에서 고위도로 갈수록 개화시기가 늦어지고 이는 무의 전 세계 분포에 일정 부분 영향을 미친 것으로 판단된다.

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148 P-1-④

Molecular Mapping of the Root-Knot Nematode (*Meloidogyne incognita*) Resistance Gene *Me7* in Pepper and Histological Characterization of the Parental Lines

Amornrat Changkwian[1], Jin-Kyung Kwon[1], Ji-Woong Han[1], Joung-Ho Lee[1], Gyung-Ja Choi[2], Yong-Ho Kim[3], and Byoung-Cheorl Kang[1]*
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The famous pepper accession (*Capsicum annumm*) CM334 is known to be a resistant source against several pathogens including root-knot nematode (*Meloidogyne incognita*). This line carries the resistance gene *Me7* that triggers a hypersensitive response (HR) resulting in reduction or halt egg-mass production on root surface. This study was aimed to map the *Me7* gene using the F2 populations derived from a cross between ECW30R, a susceptible line and CM334. The previously developed molecular markers were analyzed to delimit the genomic region of *Me7*. A YAC clone corresponding to the genomic region was sequenced. To confirm the resistance phenotype, resistant and susceptible plants were compared after root inoculation with *M. incognita* race 4 at the second juveniles stage (J2). The test plants were inoculated with 1,000 J2 approximately, four weeks of post planting. Disease reaction on plants roots were observed at 5, 10 and 15 days of post inoculation. The roots of infected plants were characterized by examining histological variations, number of gall formation and comparing gall size on root surface. Further study will confirm and distinguish the resistance and susceptibility

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The famous pepper accession (*Capsicum annumm*) CM334 is known to be a resistant source against several pathogens including root-knot nematode (*Meloidogyne incognita*). This line carries the resistance gene *Me7* that triggers a hypersensitive response (HR) resulting in reduction or halt egg-mass production on root surface. This study was aimed to map the *Me7* gene using the F_2 populations derived from a cross between ECW30R, a susceptible line and CM334. The previously developed molecular markers were analyzed to delimit the genomic region of *Me7*. A YAC clone corresponding to the genomic region was sequenced. To confirm the resistance phenotype, resistant and susceptible plants were compared after root inoculation with *M. incognita* race 4 at the second juveniles stage (J_2). The test plants were inoculated with 1,000 J_2 approximately, four weeks of post planting. Disease reaction on plants roots were observed at 5, 10 and 15 days of post inoculation. The roots of infected plants were characterized by examining histological variations, number of gall formation and comparing gall size on root surface. Further study will confirm and distinguish the resistance and susceptibility mechanism at cellular level.

Introduction

Root-knot nematode (RKN) is a major pest of Solanaceae family. *M. incognita* is one of the most virulent species. A second stage juvenile (J_2) can penetrate to roots immediately after hatching. Then, successful nematode is able to induce giant cells close to vascular cylinder and this feeding site is essential for reproduction. The giant cell starts inhibiting transfer of water and nutrient, which causes low yield of crops. *M. incognita* usually completes life cycle in 45 days after penetration. Unsuccessful feeding site causes incomplete life cycle of the pest. The *Me* gene mediates hypersensitive reaction which causes cell necrosis and inhibits feeding site establishment in resistance pepper plants. This study aims at observation of the cellular level of parents line and for mapping of gene using a second filial generation (F_2) of pepper derived from the crossed between Early Calwonder 30R (ECW30R) and Criollo de Morelos 334 (CM334) which are susceptible and resistance lines, respectively.

Methodology

Plant Material and Inoculation

A total of 199 F2 plants derived from a cross between *C. annuum* 'Early Calwonder 30R (ECW30R)' and 'Criollo de Morelos 334 (CM334)' were used in phenotype screening and fine mapping analysis. *M. incognita* egg masses were extracted using 1% NaOCl solution, and J_2 nematode was collected by using Baerman funnel technique. The four week-old plants were inoculated with 1,000 J_2.

Histological Study

The inoculated plants were kept in the growth chamber at 24 °C. After 5, 10 and 15 days after inoculation (dai), plants were uprooted and fixed with modified Karnovsky's fixative and post fixation steps followed according to Moon, et al., (2010) procedure. The tissue sectioning was done using ultramicrotome and stain with 1% toluidine blue O in 1% tetraborate and observed under a light microscope.

Phenotype Screening

The gall formation screening was done after 60 dai. An uprooted plant was washed and monitored (**Figure 3**). Criteria of resistance was carried out using gall index system, which is categorized on percentages; equal or less than 10% was presented highly resistant, 11-25% was moderate resistant, and over 25% was scored as susceptible.

Genotype Screening

The genotype screening was done initially using SCAR and CAPS markers (Djian-Caporalino et al., 2007; Fazari et al., 2012). To develop closer map, we used BLAST with the pepper CM334 genome reference, Pepper.v.1.55 (http://peppergenome.snu.ac.kr/). Further development of SNP markers were based on PCR and high resolution melting (HRM) techniques.

Mapping Analysis

The *Me7* linked markers were analyzed by Carthagene ActiveTcl 8.4 and mapping distance was calculated by Kosambi's mapping functions, LOD threshold 3.0 and distance threshold 0.5. The genetic linkage chart was organized by MapChart 2.2 software.

Results and Discussion

Histological Study

External root characteristic study (**Figure 1**) of the parental lines ECW30R (A, C, E) and CM334 (B, D, F) were conducted at 5, 10, and 15 dai, respectively. At 5 dai, gall formation was hardly identified in both lines (A; ECW30R, B; CM334) due rather small. At 10 dai, the susceptible root (C) were clearly distinguished with more swollen than the resistant (D). At 15 dai, there were large well-developed gall in ECW30R (E), and small gall size in CM334 (F). These swollen roots were selected for further study at tissue level.

The tissue sectioning illustrated normal vascular cylinder in non-infected roots (**Figure 2**; A, D, H). At 5 dai, both parents (ECW30R; B, CM334; C) were detected with nematode but no sign of giant cell formation and cell necrosis. At 10 dai, giant cell development were showed in both parents. Nonetheless, only in ECW30R (E) the cells close to the feeding sites were observed to be narrow and dense compared with the CM334 (F). At 15 dai, the infected cells in ECW30R (H) grow much larger than CM334 (I) and causes compact cell layers in vascular tissue.

Figure 1. The physical appearance of ECW30R (A, C, E) and CM334 (B, D, F) roots and galls formation at 5, 10, and 15 dai. Arrow pointing the clear well-developed gall on the roots, Bar= 1 cm.

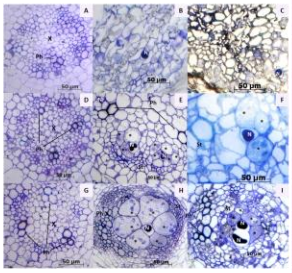

Figure 2. The cross sections of roots of a susceptible female parent ECW30R (B, E, H) and a resistant male parent CM334 (C, F, I) at 5, 10, and 15 dai; nematode (N), enlarged multinucleate giant cells (*), phloem (Ph) , xylem (X), stele (St).

Phenotype Observation

From total 199 F_2 population the phenotyping showed 163 resistant and 36 susceptible plants (X^2= 5.067 and $P > 0.01$). The 3:1 phenotypic ratio confirmed that resistance phenotype is controlled by a single dominant gene. The gall counts were categorized in to 3 groups, highly resistant, moderate resistant and susceptible (**Figure 3**). The resistant plant roots usually showed no or very small number of gall (CM334 (A), F_1 (D) and F_2 (E)). Plants with moderate resistance showed around 1-10 galls (G). The number of gall formed varied from over 10 to 180 in susceptible parent (B) and F_2 (F).

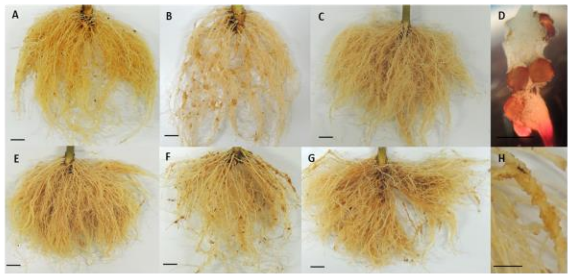

Figure 3. The parents and F_2 root characteristic at 60 dai; Resistant roots CM334 (A), F_1 hybrid (C), F_2 (E) have low reproduction and single small galls; susceptible roots ECW30R (B) and F_2 (F) have heavy galls; and the size of gall that was counted were medium (D) and large size (H); bar=1 cm

Genotype Screening and Map Analysis

The screening was performed using PCR based markers which included SCAR, CAPS, and HRM. All of the markers were co-dominant markers. The closest flanking markers, SCAR_PM6a (Fazari et al., 2012) and a newly developed HRM_SF551511 were 3.9 cM and 4.5 cM away from the *Me7*(**Figure 4**), respectively. In the previous research, a *Bs2* marker was mapped around 4.6 cM from the *Me7* gene in the population derived from CM334 (Fazari et al., 2012), and the *Bs2* gene was reported to located on a YAC clone (550 Kb), YCA22D8 (Tai, et al., 1999). Therefore, to know if this clone would provide the *Me7* gene sequence information, the YAC clone was sequenced. Assembled YAC contigs were used for marker development for fine mapping. The fine mapping showed that the molecular markers, CAPS_22D8, HRM_YAC35b, YAC58, and YAC135 were found to be located about 35 cM away from the *Me7* gene. Besides the YAC clone marker screening, NB-LRR candidate gene markers from the Renseq screening (HRM_NBLRR6b, NBLRR7b1 and NBLRR12) were also analyzed, nevertheless, none were found to be in the vicinity of the target gene. Further studies with more markers will be developed from the chr.09 scaffold A.

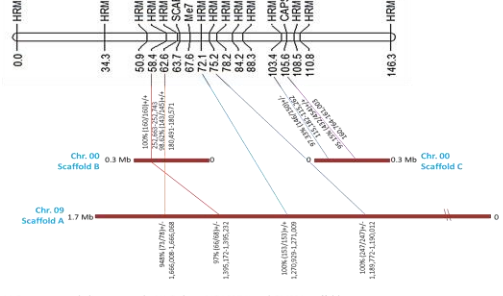

Figure 4. Position of the *Me7* gene mapped alignment to the YAC clone (YCA22D8) and CM334 scaffold sequences

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