

## CALIFORNIA LEAFY GREENS RESEARCH PROGRAM

April 1, 2012 to March 31, 2013

### BREEDING CRISPHEAD AND LEAFY LETTUCE

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#### SUMMARY

The program continues to emphasize the identification and incorporation of genes for disease resistance, particularly to downy mildew, *Verticillium* and *Fusarium* wilts, corky root, lettuce mosaic virus, and anthracnose, into crisphead and four leaf horticultural types suitable for California. Resistance for downy mildew is being introduced from several new sources and combined with resistance to lettuce mosaic virus and corky root. We have continued to monitor variation in the ability of the downy mildew pathogen to overcome resistance genes. Of the known genes for resistance to downy mildew, only *Dm17* remains effective against all of the California isolates tested. Utilization of multiple new sources will minimize the chances that changes in the pathogen will render all cultivars susceptible simultaneously. Genetic studies are in progress to determine the genetic basis for the resistances and to identify molecular markers to increase the efficiency of generating resistant varieties.

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### OBJECTIVES:

- 1) To identify new genes for disease resistance in wild germplasm and incorporate multiple genes from diverse sources into advanced breeding lines to achieve durable resistance.
- 2) To monitor variation in pathogen populations, particularly downy mildew, to facilitate the deployment of effective resistance genes.
- 3) To determine the genetic basis of agriculturally important traits, particularly disease resistance.
- 4) To release advanced breeding lines which have resistance to multiple diseases, superior appearance and quality, high yielding ability, uniform maturity, and are slow bolting.

## PROCEDURES AND RESULTS:

### **Development of Disease Resistant Lines**

#### **Breeding Strategy**

The strategy used for the UC Crisphead and Leafy Lettuce Program is to initiate crosses and early generations at Davis; later generations are being trialed and selected at several different lettuce-growing areas in collaboration with USDA, Cooperative Extension in Salinas and California growers. Backcross or modified single-seed descent strategies are being employed for most of the early generations. We are selecting for type, color, slow bolting, and yield as well as disease resistance in the crisphead and the four leaf lettuce plant types. As far as possible we use different sources of resistance for each plant type. This will diversify the selection pressure on the pathogen. The use of multiple sources of resistance will tend to increase the longevity of each resistance gene and decrease the chances that a single change in the pathogen will render multiple lettuce types susceptible.

When resistant advanced lines of the desired plant type have been generated for individual resistances, they are intercrossed to create lines with multiple disease resistances for lettuce downy mildew (LDM), corky root (CR), anthracnose (ANT) and lettuce mosaic virus (LMV). Additionally we are screening germplasm to identify genetic resistances for *Verticillium* and *Fusarium* wilts, which are being incorporated into the breeding program.

Cultivars representing each type were selected to be the recurrent parents in backcross programs to introgress resistance genes based on their horticultural type and performance in California, their status in the public domain, and the presence of additional disease resistance genes. We are currently using Salinas, Green Towers, Tropicana, Red Fox, Red Tide, and Margarita for the crisphead, romaine, green leaf, red leaf, and butterhead programs, respectively (Tables 1 and 3). We welcome suggestions and further input on the field performance of these and other potential recurrent parents. The recurrent parents used in the final generations of backcrossing will be adjusted to reflect the industry standards as they change.

#### **Sources of Downy Mildew Resistance**

We are continuing to develop crisphead and leafy coastal lettuce lines with resistance genes from diverse sources to provide protection against downy mildew in California. Last year seventeen additional resistant accessions were identified in germplasm from Israel and Armenia. We are focused on generating advanced breeding lines with new resistance genes identified through germplasm screens in previous years (Tables 1 and 2). Mapping and characterization of the new sources are in progress to provide a pipeline of new sources of resistance. Two new resistance genes from *L. serriola* (R48, R49) were identified from germplasm provided by Ales Lebeda (Department of Botany, Faculty of Natural Sciences, Palacky University, Czech Republic). *L. saligna* acc. UC04US2509 from Davis (Yolo County, CA) was characterized genetically as containing a new resistance gene, *Dm45*. It was released with other four lines with resistances from earlier germplasm (Table 1). Backcrossing programs to introgress the next generation of genes for resistance to LDM into crisp and leafy types is in progress.

**Table 1:** Status of introgression of novel sources of LDM resistance into crisphead lettuce types.

Accession #	Source <sup>a</sup>	<i>Lactuca</i>	Type	Status		R gene
CGN9311	CGN	<i>saligna</i>	Crisphead	Release UC12100	Early Donor	?
CGN5318	CGN	<i>saligna</i>	Crisphead	Release UC12101	Early Donor	?
CGN5282	CGN	<i>saligna</i>	Crisphead	Release UC12102	Early Donor	?
CGN5147	CGN	<i>saligna</i>	Crisphead	Release UC12103	Early Donor	?
UC04US2509	UCD	<i>saligna</i>	Crisphead	Release UC12104	New Donor	45
UC04UK2507	UCD	<i>virosa</i>	Crisphead	BC6	New Donor	?
UC07CS100	LEB-CS	<i>serriola</i>	Crisphead	BC5	New Donor	48
UC07CS101	LEB-CS	<i>serriola</i>	Crisphead	BC5	New Donor	49
UC07CS102	LEB-CS	<i>serriola</i>	Crisphead	BC4	New Donor	?
UC07CS103	LEB-CS	<i>serriola</i>	Crisphead	BC4	New Donor	?
UC07CS104	LEB-CS	<i>serriola</i>	Crisphead	BC4	New Donor	?
UC07CS105	LEB-CS	<i>saligna</i>	Crisphead	BC3	New Donor	?
UC07CS106	LEB-CS	<i>saligna</i>	Crisphead	BC3	New Donor	?
UC07CS107	LEB-CS	<i>saligna</i>	Crisphead	BC3	New Donor	?
UC07CS108	LEB-CS	<i>saligna</i>	Crisphead	BC3	New Donor	?
UC07CS109	LEB-CS	<i>saligna</i>	Crisphead	BC3	New Donor	?
	Isr Col(8)	<i>saligna</i>	Crisphead	BC1	New Donor	?
	Isr Col(4)	<i>acuelata</i>	Crisphead	BC1	New Donor	?
	Arm Col(5)	<i>serriola</i>	Crisphead	BC1	New Donor	?

a: CGN: Centre for Genetic Resources, the Netherlands; UCD: University of California Davis;

LEB-CS: Ales Lebeda collection, Czech Republic; USDA: US Department of Agriculture

### Downy mildew virulence surveys

In order to ensure that we are breeding for resistance against virulence phenotypes of the pathogen currently present in California, we have continued to sample the downy mildew pathogen on an opportunistic basis with the collaboration of growers, the seed industry and extension personnel, particularly Steve Koike. Over the past year, 47 isolates of *B. lactucae* originating from several regions in California were characterized for virulence phenotype and a subset of them were characterized for fungicide sensitivity and mating type (Tables 3 & 4). This opportunistic sampling gives an indication of the diversity of *B. lactucae* isolates in the field but does not provide a comprehensive or quantitative measure of LDM variation.

**Table 2:** Status of introgression of novel sources of LDM resistance into leafy lettuce types.

	Type	Donor line	Donor species	Status
<b>Advanced breeding lines</b>	romaine	00G950	<i>L. saligna</i>	BC <sub>7</sub> S <sub>1</sub> to be released
	romaine	CGN5322	<i>L. saligna</i>	BC <sub>4</sub> S <sub>1</sub>
	red leaf	05G1411	<i>L. serriola</i>	BC <sub>6</sub>
	red leaf	PI509523	<i>L. saligna</i>	BC <sub>3</sub>
	green leaf	PI49100	<i>L. saligna</i>	BC <sub>7</sub> S <sub>1</sub> seed production
	butterhead	05G1421	<i>L. serriola</i>	BC <sub>3</sub>
	butterhead	CGN13330	<i>L. saligna</i>	BC <sub>2</sub>
<b>Early breeding lines</b>	romaine	09G1077	<i>L. saligna</i>	F <sub>2</sub> & BC <sub>2</sub>
	romaine	09G1080	<i>L. saligna</i>	BC <sub>3</sub>
	red leaf	09G1082	<i>L. saligna</i>	BC <sub>3</sub>
	green leaf	LB line	<i>L. saligna</i>	F <sub>2</sub>
<b>New donors</b>	Israel	5 lines	<i>L. saligna</i>	to be crossed
	Israel	5 lines	<i>L. aculeata</i>	to be crossed
	Armenia	5 lines	<i>L. serriola</i>	to be crossed

Thirty seven % of the isolates analyzed in 2012 were pathotype CAVIII; 33.3% were CAVII and 27% were had novel virulence phenotypes. Pathotype CAV was detected in one sample (2%). Pathotype VI isolates were not detected in 2012 (Figure 1). *Dm17* remains effective against most but not all isolates; it has not, however, been widely deployed and so has not been under extensive selection pressure. All isolates virulent on *Dm17* came from a single location as in 2011. *Avr36*, *Avr37* and *Avr38* were present in 29, 62 and 67 % of the isolates respectively. The frequency of *Avr18* was 0%; therefore *Dm18* is no longer effective against any of the isolates tested. *Avr4* was detected at a frequency less than 31%. Among the novel isolates, *Avr2*, *Avr3* and *Avr6* were all detected at frequencies of below 30 % (Fig. 2). This is interesting because until recently avirulence to *Dm2*, *Dm3* or *Dm6* was very rarely detected in California. The presence of *Avr2*, *Avr3* and *Avr6* may indicate that the recently identified novel isolates have originated from different source(s) than isolates characterized in previous years.

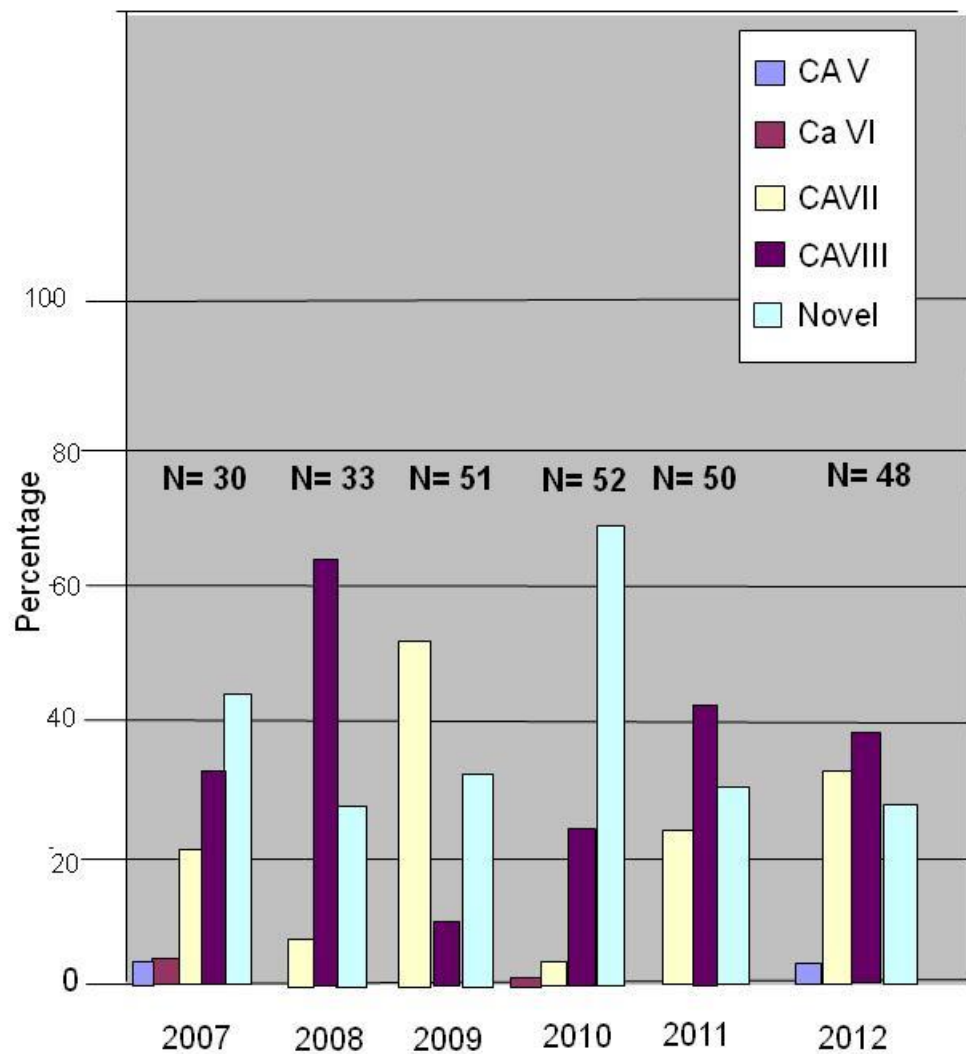
Of the 30 isolates tested for sensitivity to Ridomil in 2012, the majority, 27 isolates, were insensitive to Ridomil and three had an intermediate level of insensitivity. No fully sensitive isolates were detected. Therefore, insensitivity to Ridomil once again seems to be widespread and applications of Ridomil are likely to be ineffective.

One 2012 isolate was mating type B<sub>1</sub> and had a novel virulence phenotype. It was also insensitive to Ridomil indicating control of this isolate by this chemical is not possible. The continued detection of isolates of the B<sub>1</sub> mating type opens up the possibility of greater variation in LDM due to sexual reproduction as well as survival in the soil as oospores.

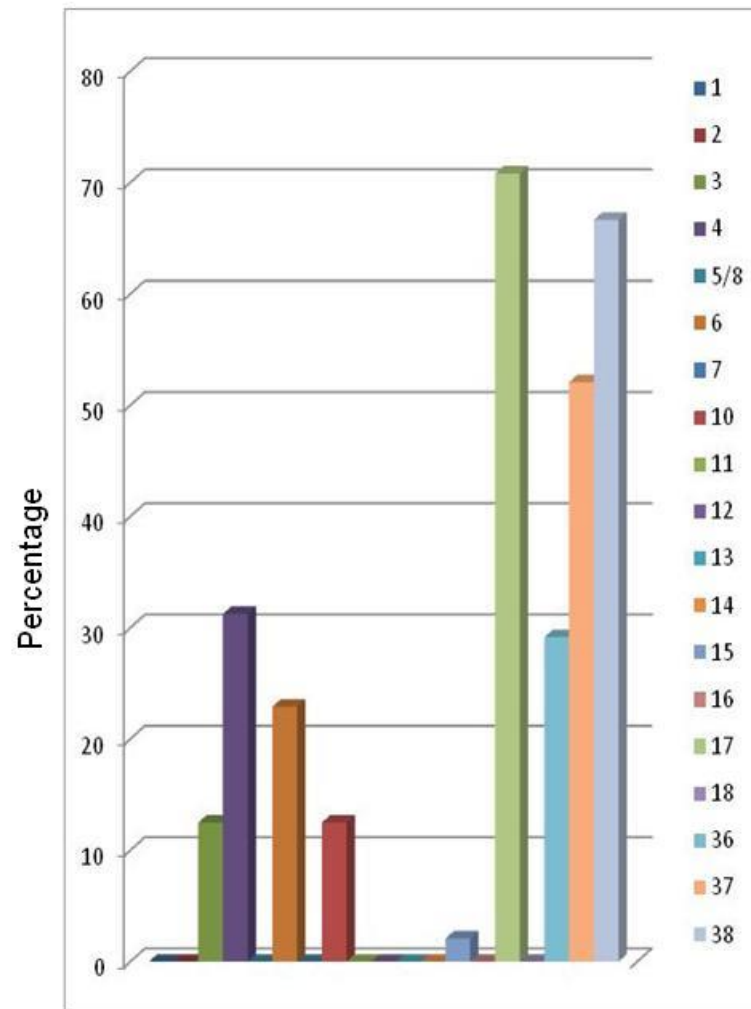
**Table 3.** Origin of *B. lactuca* isolates characterized in 2012.

Isolate ID	Collection	Location	Collector	On:
2012	Date			
A12O1359	3/23/12	Yuma AZ	Darryn Gibson, Progeny Adv genetics INC	Main Man
A12O1360	3/23/12	Yuma AZ	Darryn Gibson, Progeny Adv genetics INC	Main Man
A12O1361	3/23/12	Yuma AZ	Darryn Gibson, Progeny Adv genetics INC	Main Man
A12O1362	3/23/12	Yuma AZ	Darryn Gibson, Progeny Adv genetics INC	Speedway
A12O1363	3/23/12	Yuma AZ	Darryn Gibson, Progeny Adv genetics INC	Speedway
A12O1364	3/23/12	Yuma AZ	Darryn Gibson, Progeny Adv genetics INC	Speedway
C12O1365	4/19/12	?	Steven Koike/Joe Santiago	Fortress
C12O1368	6/5/12	Chualar	J. Heintzberger	Regency
C12O1369	6/5/12	Chualar	J. Heintzberger	"X", Iceberg
C12O1370	7/11/12	Salinas, Ca	J. Heintzberger	Regency
C12O1371	7/11/12	Salinas, Ca	J. Heintzberger	Regency
C12O1372	7/11/12	Salinas, Ca	J. Heintzberger	Black Belt
C12O1373	7/11/12	Salinas, Ca	J. Heintzberger	Black Belt
C12O1374	7/3/12	King City, Ca	Darryn Gibson, Progeny Adv genetics INC	Romaine
C12O1375	7/3/12	King City, Ca	Darryn Gibson, Progeny Adv genetics INC	Romaine
C12O1376	7/3/12	King City, Ca	Darryn Gibson, Progeny Adv genetics INC	Romaine
C12O1377	7/3/12	King City, Ca	Darryn Gibson, Progeny Adv genetics INC	Romaine
C12O1378	7/12/12	Salinas, Ca	Darryn Gibson, Progeny Adv genetics INC	Black Belt
C12O1379	7/12/12	Salinas, Ca	Darryn Gibson, Progeny Adv genetics INC	Black Belt
C12O1380	7/12/12	Salinas, Ca	Darryn Gibson, Progeny Adv genetics INC	Black Belt
C12O1381	7/12/12	Salinas, Ca	Darryn Gibson, Progeny Adv genetics INC	Black Belt
C12O1382	7/25/12	South County	Steven Koike/Shamrock	?
C12O1383	7/25/12	South County	Steven Koike/Shamrock	?
C12O1384	8/1/12	Spence, USDA, Salinas	Ivan Simko	s1118-2
C12O1385	8/1/12	Spence, USDA, Salinas	Ivan Simko	s1136-4
C12O1388	8/1/12	Spence, USDA, Salinas	Ivan Simko	line 1
C12O1393	8/1/12	Lucky Stricke Farms	J. Heintzberger	Regency
C12O1394	10/1/12	Spence, USDA, Salinas	Ivan Simko	Gran Rapids
C12O1395	10/1/12	Spence, USDA, Salinas	Ivan Simko	GR x ICE 1078
C12O1396	10/1/12	Spence, USDA, Salinas	Ivan Simko	LSE 57/15
C12O1397	10/1/12	Spence, USDA, Salinas	Ivan Simko	Balady Ash Green
C12O1398	10/1/12	Spence, USDA, Salinas	Ivan Simko	PI-536699
C12O1399	10/1/12	Spence, USDA, Salinas	Ivan Simko	GR X ICE 1053
C12A1400	10/1/12	Spence, USDA, Salinas	Ivan Simko	Balady Bauha
C12A1401	10/15/12	?	Steven Koike	Romaine Salvius
C12A1402	10/15/12	?	Steven Koike	Romaine Salvius
C12A1403	10/15/12	?	Steven Koike	Romaine Salvius
C12A1404	10/15/12	?	Steven Koike	Romaine Salvius
C12A1405	10/15/12	?	Steven Koike	Romaine Salvius
C12A1406	10/15/12	?	Steven Koike	Romaine Salvius

**Figure 1: Frequency of downy mildew pathotypes observed in California in 2007-2012.**



**Figure 2: Frequency (%) of avirulence genes detected in 2012.**



**Table 4.** Virulence phenotypes of isolates of *B. lactucae* characterized in 2012.

	Cobham Green	Lednický	UC DM2	Dandle	R4T57D	Valmaine	Sabine	LSE 57/15	UC DM10	Capitan	Hilde II	Pennlake	UC DM14	PIVT 1309	LSE /18	LS-102	Colorado	Ninja	Discovery	Argelés	Mariska	El Dorado	R32	Amplus	Sextetblok 1	Sextetblok 2	Sextetblok 3	Sextetblok 4							
	0	1	2	3	4	5/8	6	7	10	11	12	13	14	15	16	17	18	36	37	38	18m	18ed	18/32	40											
Isolate ID	1	2	4	8	16	32	1	2	4	8	16	32	1	2	4	8	16	32	1	2	4	8	16												Fung Test
2012	Fully avirulent																								Pathotype	Mating	Alliote	Ridomil							
A12O1359	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	-	+	+	+	+	63	63	11	0	17,36,37,38,	CAVIII	B2	NT	Ins			
A12O1360	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	-	+	+	+	+	63	63	11	0	17,36,37,38,	CAVIII	B2	NT	Ins		
A12O1361	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	-	+	-	-	-	+	-	-	-	31	63	11	0	6,17,36,37,38,18ed,18/32,	Novel	B2	NT	Ins		
A12O1362	+	+	+	-	+	+	-	+	+	+	+	+	+	+	+	-	+	-	-	-	+	+	+	-	27	63	11	0	3,6,17,36,37,38,	Novel	B2	NT	Ins		
A12O1363	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	-	+	+	+	+	63	63	59	0	17,38,	CAVIII	B2	NT	Ins		
A12O1364	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	-	+	+	+	+	63	63	11	0	17,36,37,38,	CAVIII	B2	NT	Ins		
C12O1365	+	+	+	-	+	+	-	+	+	+	+	+	+	+	+	-	+	-	-	-	+	+	+	+	27	63	11	0	3,6,17,36,37,38,	Novel	B1	NT	Ins		
C12O1368	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+	+	+	+	-	55	63	59	0	4,17,38,	CAVII	B2	NT	Ins		
C12O1369	+	+	+	-	+	+	-	+	+	+	+	+	+	+	+	-	+	-	-	+	+	+	+	27	63	11	1	3,6,17,36,37,	Novel	B2	NT	NT			
C12O1370	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	-	+	+	+	-	55	63	59	0	4,17,38,	CAVII	B2	NT	Ins		
C12O1371	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	-	+	+	+	-	55	63	59	0	4,17,38,	CAVII	B2	NT	Ins		
C12O1372	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	-	+	+	+	-	55	63	59	0	4,17,38,	CAVII	B2	NT	Ins		
C12O1373	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+	+	+	+	-	55	63	59	0	4,17,38,	CAVII	B2	NT	Interm		
C12O1374	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	-	+	+	+	+	63	63	27	0	17,37,38,	CAVIII	B2	NT	Ins		
C12O1375	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	-	+	+	+	+	63	63	27	0	17,37,38,	CAVIII	B2	NT	NT		
C12O1376	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	-	+	+	+	-	55	63	27	0	4,17,37,38,	CAVII	B2	NT	Ins		
C12O1377	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	-	+	+	+	+	55	63	27	0	4,17,37,38,	CAVII	B2	NT	Ins		
C12O1378	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+	+	+	+	-	55	63	59	0	4,17,38,	CAVII	B2	NT	Ins		
C12O1379	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+	+	+	+	-	55	63	59	0	4,17,38,	CAVII	B2	NT	Ins		
C12O1380	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	-	+	+	+	+	63	63	27	0	17,37,38,	CAVIII	B2	NT	Ins		
C12O1381	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	-	+	+	+	-	55	63	59	0	4,17,38,	CAVII	B2	NT	Ins		
C12O1382	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	-	+	+	+	+	63	63	11	0	17,36,37,38,	CAVIII	B2	NT	NT		
C12O1383	+	+	+	-	+	+	-	+	+	+	+	+	+	+	+	-	+	-	-	-	+	+	+	+	27	63	11	0	3,6,17,36,37,38,	Novel	B2	NT	NT		
C12O1384	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	+	+	+	+	+	63	63	11	1	17,36,37,	CAVIII	B2	NT	Ins		
C12O1385	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	-	-	-	-	+	59	63	10	0	3,15,17,36,37,38,18m,18ed,18/32	Novel	B2	NT	NT		
C12O1388	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	-	+	+	+	+	59	63	11	0	3,17,36,37,38,	Novel	B2	NT	NT		
C12O1393	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	-	+	-	-	-	-	-	-	+	55	63	11	0	4,17,36,37,38,18m,18ed,18/32,	CAV	B2	NT	Ins		
C12O1394	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+	+	+	+	+	63	63	59	0	17,38,	CAVIII	B2	NT	Ins		
C12O1395	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+	+	+	+	-	55	63	59	0	4,17,38,	CAVII	B2	NT	Interm		
C12O1396	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+	+	+	+	+	63	63	59	0	17,38,	CAVIII	B2	NT	Ins		
C12O1397	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+	+	+	+	-	55	63	59	0	4,17,38,	CAVII	B2	NT	Ins		
C12O1398	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+	+	+	+	+	63	63	59	0	17,38,	CAVIII	B2	NT	Interm		
C12O1399	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	-	+	+	+	-	55	63	11	0	4,17,36,37,38,	CAVII	B2	NT	Ins		
C12A1400	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+	+	+	+	-	55	63	59	0	4,17,38,	CAVII	B2	NT	Ins		
C12A1401	+	+	+	+	+	-	+	-	+	+	+	+	+	+	-/3+	+	+	-	+	+	+	+	+	+	31	61	27	1	6,10,37,	Novel	B2	NT	NT		
C12A1402	+	+	+	+	+	-	+	-	+	+	+	+	+	+	-/2+	+	+	-	+	+	+	+	+	+	31	61	27	1	6,10,37,	Novel	B2	NT	NT		
C12A1403	+	+	+	+	+	-	+	-	+	+	+	+	+	+	-/3+	+	+	-	+	+	+	+	+	+	31	61	27	1	6,10,37,	Novel	NT	NT	NT		
C12A1404	+	+	+	+	+	-	+	-	+	+	+	+	+	+	-/3+	+	+	-	+	+	+	+	+	+	31	61	27	1	6,10,37,	Novel	B2	NT	NT		
C12A1405	+	+	+	+	+	-	+	-	+	+	+	+	+	+	-/3+	+	+	-	+	+	+	+	+	+	31	61	27	1	6,10,37,	Novel	B2	NT	NT		
C12A1406	+	+	+	+	+	-	+	-	+	+	+	+	+	+	-/1+	+	+	-	+	+	+	+	+	+	31	61	27	1	6,10,37,	Novel	B2	NT	NT		



## Screening for resistance to *Verticillium* wilt

Resistance to *Verticillium* wilt is a top priority for our program. We previously developed an efficient, reliable, and contained method for screening for the reaction of lettuce to *Verticillium dahliae* in the greenhouse. We utilize microplots within the greenhouse with restricted access to minimize the opportunity for spread of the pathogen. We are screening for resistance to *V. dahliae* strain VdLs17 (race 2) provided by Dr. Krishna Subbarao. We include cv. Salinas as the susceptible control genotype with cv. La Brillante representing a genotype that has resistance to race 1 and that has shown less disease in the field.

We have continued to screen germplasm for resistance to race 2. In 2012, 47 new accessions received from Israel and Russia were increased prior to screening for resistance; these are currently being screened. The majority of accessions screened over the past five years have been highly susceptible, although differences in symptoms have been observed. A few accessions of *L. serriola* showed delayed development of symptoms or were asymptomatic. In particular, seven lines from Armenia showed no symptoms when initially screened against Vdl 17 (race2) and exhibited no seed transmission. These were inter-mated as well as crossed to *L. sativa* genotypes; 196 F<sub>2</sub> plants from a cross between *L. serriola* acc. Arm09-170-1-5 and a *L. sativa* breeding line were challenged with race 2. Disease severity and the frequency of seedborne *Verticillium* seemed to segregate and show transgressive segregation. Some lines showed no symptoms and had no seed transmission. However, QTL analysis failed to detect significant QTL. Moreover, progeny testing of F<sub>3</sub> families derived from asymptomatic plants showed some susceptibility. The same potentially resistant F<sub>3</sub> families were analyzed by USDA personnel at Salinas who also observed delayed symptoms but all lines showed some level of susceptibility. We re-genotyped this population and F<sub>3</sub> seed from 169 F<sub>2</sub> individuals were tested for resistance to *Verticillium*. Few inconsistencies with prior data were detected and QTL analyses were inconclusive. Using information from our ultra-dense lettuce map, we are identifying additional polymorphic markers to provide better genome coverage and populate regions with low marker density, including one in LG9 where the resistance for *V. dahliae* race 1 is located (CLGRP 2012-2013 Variation Report). QTL analysis will be performed again once we have a more complete map.

Evaluations of resistance to *Verticillium* are confounded by differences in plant development and maturity. Therefore, we crossed between *L. serriola* acc. Arm09-170-1-5 to *L. serriola* PI251246 and are generating RILs; the latter is highly susceptible to *Verticillium* race 2. These will be ready for screening for resistance later this year.

## Multiple Disease Resistances

Crosses between advanced breeding lines, field selections, and released lines have been made to generate lines with multiple disease resistances. Screening for multiple diseases, including lettuce downy mildew, corky root, anthracnose and lettuce mosaic virus, continues.

## Supply of Isolates

We have continued to supply California isolates of downy mildew and corky root to breeding companies and other research groups. We have trained personnel from the seed industry and others to handle lettuce downy mildew, corky root, anthracnose and other diseases.

## **(Re)Announcement of Releases of Advanced Breeding Lines of Crisphead Lettuce**

Advanced breeding lines of crisphead lettuce are available for use by plant scientists and breeders in public and private institutions. These lines were developed by Richard Michelmore and Oswaldo Ochoa at University of California, Davis. When this germplasm contributes to a new cultivar, appropriate recognition should be given as to its origin.

These lines have been developed to provide new sources of disease resistance to downy mildew in a Salinas horticultural type by backcrossing resistant genotypes with cv. Salinas as the recurrent parent.

UC12100 is a BC<sub>7</sub>S<sub>2</sub> line with resistance derived from *L. saligna* acc. CGN9311.

UC12101 is a BC<sub>7</sub>S<sub>2</sub> line with resistance derived from *L. saligna* acc. CGN5318.

UC12102 is a BC<sub>7</sub>S<sub>2</sub> line with resistance derived from *L. saligna* acc. CGN5282.

UC12103 is a BC<sub>7</sub>S<sub>2</sub> line with resistance derived from *L. saligna* acc. CGN5147.

Resistant individuals were selected in each generation. These lines are now homozygous for resistance to California pathotypes CAVI, CAVII and CAVIII and several novel California isolates. We have not observed susceptibility to any California isolate; however, given the variability of *Bremia lactucae*, this does not preclude the existence of virulent isolates currently or in the future. We would be interested in receiving isolates in any cases where one of these lines appears to be susceptible.

To the extent possible, the Salinas plant type was selected in each generation. Field evaluations of the final two selfed generations were made in Salinas, California. These lines are close to horticultural types used in the coastal production areas of California. However, residual variation remains in these lines and further selections may be required to fix plant type. Trials and selections should be made to determine specific areas and seasons to which these lines are best adapted.

Requests for seed should be made to Richard Michelmore at [rwmichelmore@ucdavis.edu](mailto:rwmichelmore@ucdavis.edu) with copies to Maria Truco at [mjtruco@ucdavis.edu](mailto:mjtruco@ucdavis.edu).