California
CELERY RESEARCH
ADVISORY BOARD

2021-22 Annual Report

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The program was established in October 1976 under provisions of the California Marketing Act, following written assent of a majority of the industry's producers. The program is administered by the Celery Advisory Board, which is nominated at district meetings every three years by the industry and appointed by the Secretary of Food and Agriculture.

The function of the Board is to ascertain research needs that will benefit the widest spectrum of the industry in all producing districts, to establish priority of need, enter into agreements with approved agencies to initiate or continue such research, develop a budget for funding, give impetus, direction and evaluation to the conduct of the work, and report results to the industry periodically.

The Board represents the entire industry and all its actions and recommendations are subject to the approval of the California Secretary of Food and Agriculture. Board members serve without compensation. Funds budgeted by the Board for research projects amount to about one-fourth the total cost of the projects, with the University of California supplying the remaining three-fourths in supervisory research personnel, plant facilities and major equipment. Research initiated by the Board would not be conducted without the industry's contribution --- through equitable assessment --- for certain special equipment, supplies, staff research assistants, expenses, travel, etc., since neither funds nor nonpartisan direction are available from other sources.

RESEARCH PRIORITIES

Production

- ✓ Evaluate insect management tools, alternatives to organophosphates and carbamates (especially products which are subject to restriction or loss due to FQPA and other regulations - e.g., acephate, diazinon, carbamates)
- ✓ Study the biology and management of soil pests
- ✓ Study management of Sclerotinia (airborne and soil borne)
- ✓ Evaluate new celery varieties for resistance to insects and diseases
- ✓ Evaluate biofumigants as tools for pest control in celery
- ✓ Develop resistance management strategies for all pest categories
- ✓ Continue weed control research to find complimentary or replacement products for Lorox/linuron Caparol/prometry and Caparol/Prometryn
- ✓ Evaluate the secondary effect of loss of methyl bromide as a tool used in rotational crops on celery production areas

Regulatory

- ✓ Registrants should insure that air and chemigation labels are a part of all new product registrations
- ✓ Address REI issues/concerns for products used in late season (e.g. aphicides)
- ✓ Multiple products should be allowed under 24(c) and Section 18's for resistance management
- ✓ Expedite registration of Dual Magnum/S-metolachlor for nutsedge control

Educational

- ✓ Educate regulators, legislators, and policy makers on need for more than one product for a particular pest for effective resistance management
- ✓ Educate regulators on what a suitable replacement product is and what constitutes commercially acceptable levels of control
- ✓ Educate growers, PCAs, agencies and the urban community on the relationship of waterway management to weed and insect pests
- ✓ Educate the urban population about agricultural practices necessary for celery production
- ✓ Educate the public on the nutritional values of California grown celery and the high level of food quality standards established for this commodity

CALIFORNIA CELERY RESEARCH BOARD

September 1, 2021 through August 31, 2023

DIST	MEMBER	ALTERNATE
2	**Adrian Zendejas** Desert Mist Farms	**Jeff Percy** Desert Mist Farms
DIST	**MEMBER**	**ALTERNATE**
3	**Hank Laubacher Jr** Laubacher Farms	**Erik Heacox** Tanimura & Antle
3	**Geremy Olsen** Deardorff Family Farms	**Greg Lewis - RES COMM** Duda Farm Fresh
3	**Danny Pereira – Chairman** Rio Farms - **RES COMM**	**Bryson Daniel** Boskovich Farms
3	**Steve Adams – Res/Vice Chair** Boskovich Farms - **RES COMM**	**Mike Naumann - RES COMM** Naumann Farms
3	**Ryan Coultas** Coultas Vegetable	**Will Terry** Terry Farms
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4	**Phillip Adam** Innovative Produce	**David Ayala** Betteravia Farms
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DIST	**MEMBER**	**ALTERNATE**
5	**Alejandro Palma** Dole Fresh Vegetable	**Larry Knerr** Duda Farm Fresh
5	**Dean Diefenthaler** Duda Farm Fresh	**Julia Harshman - RES COMM** Duda Farm Fresh
5	**Kevin Brink - RES COMM** Ocean Mist Farms	**Paul Sheid** Ocean Mist Farms
PUBLIC MEMBER		
	Steve Donovan - RES COMM	

STAFF		
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CALIFORNIA CELERY RESEARCH ADVISORY BOARD
BUDGETARY COMPARISON SCHEDULE
YEAR ENDED SEPTEMBER 30, 2022

	Budget	Actual	Variance
Without Donor Restrictions			
REVENUE			
Assessments	$ 305,000	$ 294,304	$ (10,696)
Interest	4,000	3,073	(927)
Total Revenues Without Donor Restrictions	309,000	297,377	(11,623)
EXPENDITURES			
Administrative:			
Audit	4,450	4,450	-
Annual Report	50	-	50
Insurance	750	844	(94)
Management Services	55,440	55,440	-
Meetings	500	920	(420)
Office Supplies	600	666	(66)
Postage	600	-	600
Telephone	600	657	(57)
Travel and Mileage	1,200	1,136	64
Website	680	262	418
Miscellaneous	100	-	100
	64,970	64,375	595
Research:			
Production Research (1)	219,197	126,023	93,174
Departmental:			
Marketing Branch	16,500	18,136	(1,636)
Marketing Enforcement Branch	2,500	-	2,500
	19,000	18,136	864
Total Expenditures	303,167	208,534	94,633
INCREASE (DECREASE) IN NET ASSETS WITHOUT DONOR RESTRICTIONS	5,833	88,843	83,010
NET ASSETS, AT BEGINNING OF YEAR WITHOUT DONOR RESTRICTIONS	294,682	294,682	-
NET ASSETS, AT END OF YEAR WITHOUT DONOR RESTRICTIONS	$ 300,515	$ 383,525	$ 83,010

(1) For financial statement purposes the research activity was recorded during the period in which it was incurred, not based on the contracted budget. Therefore, with the audit adjustments, there are timing differences between the budget amounts and actual amounts.

See auditor's report and notes to financial statements.

Research Projects

2021-22

RESEARCHER	PROJECT TITLE		2021-22 FUNDED Annual Mtg	Inter-Term
Lynn Epstein *UC Davis*	**Next Step for Genomic Tools for Breeding for Resistance in Celery to F. oxysporum f. sp. apii Race 4 (*Foa Race 4*)**			**13,700**
Lynn Epstein *UC Davis*	**Completion of Challenger Genome Sequencing and Annotation *(Fusarium Yellows in Celery...)***		**20,029**	
Renee Eriksen *USDA - Salinas*	**Celery Breeding for Resistance to Fusarium Oxysporum f. sp. Apii Race 4**		**114,968**	
	Eriksen - USDA	*83,680.00*	*83,680*	
	Daugovish - UCCE ANR Ventura	*9,373.00*	*9,373*	
	Greer - UCCE ANR San Luis Obispo	*9,093.00*	*9,093*	
	Putman - UC Riverside	*12,822.00*	*12,822*	
Tom Perring/Greg Kund *UC Riverside*	**Integrated Pest Management on Celery**		**55,500**	
Perring/Chow-Yang Lee *UC Riverside*	**Insecticide Resistance of Celery Pests Focusing on the Lygus Bug, Lygus Hesperus**			**15,000**
TOTAL REQUEST			**190,497**	**28,700**
		Total 2021-22		**219,197**

Layperson's summary

CALIFORNIA CELERY RESEARCH ADVISORY BOARD
RESEARCH PROJECT REPORT
for the period of:
October 1, 2021 - September 30, 2022

PROJECT TITLE: Completion of Challenger genome sequencing and annotation

PROJECT LEADER: Lynn Epstein, Department of Plant Pathology, University of California, Davis, California 95616

COOPERATING PERSONNEL: Chaehee Lee, Armando Garcia-Llanos, Sukhwinder Kaur, Grey Monroe, Allen Van Deynze, Renee Eriksen, and Peter Henry

Before this grant, the only well-assembled genome of celery that was publicly available was for cv. Ventura (Song et al. 2021); but very few of the Ventura "gene models" have been publicly annotated, and this limits the utility of this genome. Also, Ventura is completely susceptible to *Fusarium oxysporum f. sp. apii (Foa)* race 4, and while Ventura is more resistant than Tall Utah types to *Foa* race 2, Ventura is what is now considered to be susceptible to *Foa* race 2 (Kaur and Epstein, unpublished)..

The Eriksen breeding program plans to continue using Challenger both as an open pollinated, celery-type parent in the public domain and for its resistance to *Foa* race 2. In addition, we have used Challenger as the celery parent for the cross with A0134 (USDA PI 181714) for race 4 resistance. Therefore, the complete, annotated genome of the Challenger parent will be extremely useful both to determine the gene(s) for resistance to *Foa* race 2 and as a susceptible reference compared to the F1S3 76-8-36-124 for resistance to *Foa* race 4.

Previously, two seed companies gave a grant during 2018-2020 to UC Davis (Van Deynze lab with cooperation from the Epstein lab) for the sequencing and assembly of the celery Challenger. That grant generated some high-quality data, with the then current latest technologies, but the complexity of the genome repeats made it difficult to assemble well. Here, the CCRAB gave us a grant to produce a longer-read library for PacBio HiFi sequencing. This PacBio HiFi long reads were assembled into highly contiguous contigs and the assembly is now being annotated with full-length IsoSeq transcriptome (from RNA), which were previously obtained from 15 different tissues/conditions including resistance to *Foa* race 2. Currently, we are anchoring the assembly to a "genetic map" for *Apium graveolens* with 1,725 "bins" in 11 linkage groups that was provided by one of the original sponsors. Primarily using some of the funds from our 2022-2023 CCRAB genomics grant, we are currently preparing to conduct analyses of three datasets that should provide us with candidates for the gene(s) in Challenger that confer resistance to *Fo*a race 2: 1) a comparison of the Ventura (*Foa* race 2-susceptible) vs. Challenger genomes; 2) a comparison from mapping "genome by sequencing" (GBS) Illumina (short read) sequences of restriction-enzyme digested, simplified genomes of 12 celery and celeriac accessions with documented *Foa* race 2 resistance or susceptibility; and 3) a quantitative comparison of the expression of genes using TagSeq (RNA) in crowns of Challenger that was grown in the greenhouse that was either uninfested, or infested with either *Foa* races 2 or 4.

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OBJECTIVES**:**

1. To complete the sequencing and assembly of the previously celery industry-sponsored UC Davis cv. Challenger Genome Project
2. To annotate the genes in the Challenger genome

RESULTS:

In 2018, the Van Deynze laboratory started a UCD Challenger celery genome project in collaboration with the Epstein lab; the project was sponsored by two vegetable seed companies and used two technologies for full genome assembly: "3rd generation" 10X Genomics Chromium Genome "linked read" and long read Nanopore PromethION genomic sequences. Although we made substantial progress, the complexity of the celery genome prevented an assembly. Ultimately, the 2018-2020 funds were insufficient to complete the assembly, and then to do the critical gene annotation. Nonetheless, the parts of the Challenger genome project that were finished also included the acquisition of several high-quality datasets: IsoSeq (full length) transcriptome sequencing (from RNA) from 15 different tissues/conditions including resistance to *Foa race 2*; and genome by sequencing data (GBS) from 12 lines that represent a variety of disease resistance in celery and celeriac, including the *Foa* race 4-resistant (and race 2-resistant) accession A0134 (synonym USDA PI 181714) (Epstein and Kaur, 2023).

For this grant, nuclear DNA was isolated and purified from two-week old, axenic Challenger seedlings in the Van Deynze lab, and made into a (long-read) PacBio HiFi library. The library was sequenced in four SMRT cells at the UC Davis Genome Center; we obtained 123.8 gigabasepairs (Gbp) in 9.2 million reads. The genome was assembled by Dr. Chaehee Lee in collaboration with the Monroe and Van Deynze labs. Our Challenger PacBio HiFi assembly has 36X coverage, an estimated haploid length of 3.3 Gbp, and a heterozygosity of 0.26%. Originally, the assembly was in 2,668 contigs (=segments), but some of these were low copy number repeats of relatively short length; after examination, some of them were eliminated as assembly artifacts based on coverage of PacBio HiFi read mapping, i.e., the number of contigs was reduced to 2,253. Celery has 11 chromosomes (Murata & Orton, 1984, Iovene et al. 2008), and based on the cv. Ventura assembly of the 11 chromosomes and their Hi-C data (Song et al. 2021), 96.6% of the 2,253 contigs

can be anchored to the 11 *Apium graveolens* chromosomes (Table 1). Finally, the 11 pseudochromosomes were improved based on multiple lines of evidence from genetic mapping, read mapping coverage, and location of telomeric repeats. Lengths of the scaffolds for each of the Challenger chromosomes is shown in Table 2; "scaffolds" are a stage of genome assembly in which multiple contigs are assembled into scaffolds.

Table 1. Statistics on the PacBio HiFi assembly of celery (*Apium graveolens* var. dulce) cv. Challenger

	Contigs	**Chromosomes**
# of sequences	2,253	11
Size (Gb)	3,428,536,321	3,267,747,404
Maximum	303,905,413	349,664,189
N50	162,067,254	320,415,245
N90	18,309,707	227,556,300
L50	8	5
L90	32	10
% of assembly	-	95.31
N's per 100 kbp		0.16

Table 2. Lengths of DNA sequence in each of celery cv. Challenger 11 chromosomes.

Chr ID	**# of contigs**	**Size (bp)**	**Telomeric repeats[a]**
Ap1	5	221,556,578	T2T
Ap2	4	340,104,542	T2T
Ap3	7	320,415,245	2T
Ap4	11	349,664,189	
Ap5	3	339,245,533	T2T
Ap6	5	339,388,289	T2T
Ap7	12	271,315,010	2T
Ap8	6	289,571,098	T2T
Ap9	2	313,448,105	T2T
Ap10	4	255,482,515	T2
Ap11	4	227,556,300	T2T
Total	63	3,267,747,404	

[a]T2T, telomeres at both ends of the chromosome; T2, a telomere only at the 0 bp end; 2T, a telomere only at the non-0 bp end.

All of the standard indicators of assembly quality indicate that our assembly has substantially better quality than the one for either celery cv. Ventura (Song et al. 2021), and particularly better than a genome for cv. Jinnan Shiqinm (Li et al. 2020), which is a Chinese local celery type, which is presumably in *A. graveolens* var. *secalinum*; celery is *A. graveolens* var. *dulce*. Based on the distribution of telomeric repeats at the ends of the chromosomes, 7 of the 11 chromosomes are assembled end-to-end, 4 are fully assembled on one end of the chromosome but not on the other, and only one chromosome is missing telomeres on both ends. The PacBio HiFi sequence is of extremely high quality, and our longer contigs are extremely long; ½ the length of entire genome is in 8 contigs, and 90% of the length of the entire genome is in 32 contigs (Table 1).

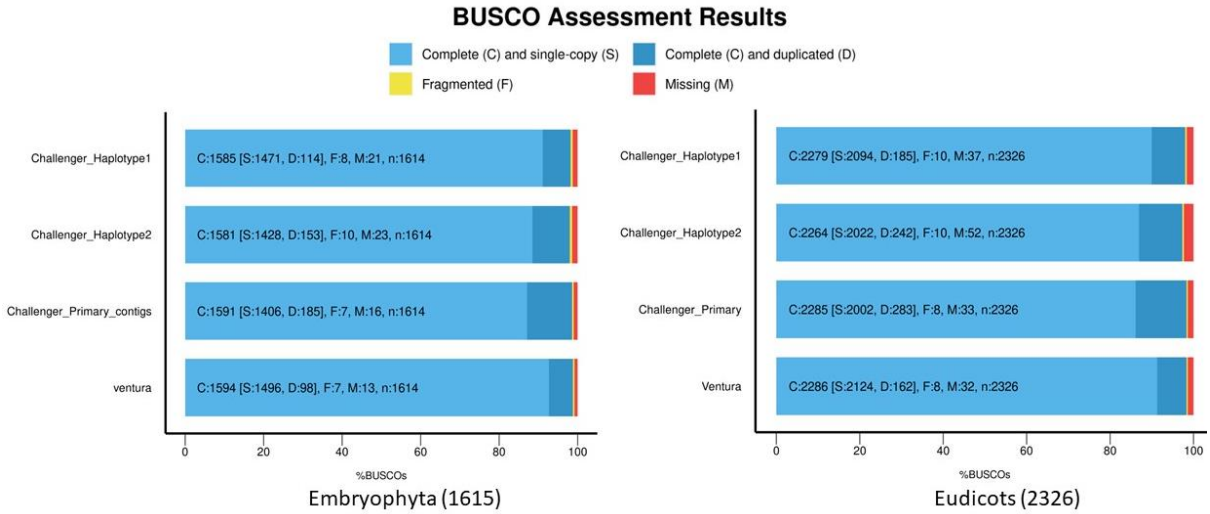

Fig. 1. A standard "BUSCO" assessment of the quality of three Challenger assemblies and the cv. Ventura assembly (bottom bars). Based on 1,615 highly conserved, typically single copy genes that are present in all land plants (left) or 2,326 highly conserved, typically single copy genes that are present in all dicots (right), the assessment indicates that the quality is very high.

Benchmarking Universal Single-Copy Orthologs ("BUSCO") is a standard method to assess genome quality by determining if our Challenger genome has complete copies of sets of the highly conserved, universal single copy genes (Manni et al. 2021a and 2021b). The best estimate so far in celery is that it probably has 31,000 genes (Song et al. 2021). The BUSCO project has selected 1,615 that are expected to be present in all Embryophyta (land plants) and 2,326 that are expected to be in all Eudicots (broad-leaved, flowering plants) (Fig. 1). Partly because the diploid Challenger genome is not completely homozygous (with an estimated heterozygosity of 0.26%), we can consider there to be two haplotype assemblies and a consensus assembly. Regardless, as shown in Fig. 1, our Challenger genome assemblies have approximately 98% of the expected genes in a complete form, 0.5% fragmented and only 1.5% genes not represented.

One of the great challenges of genome assembly is making sure that the DNA segments (contigs and scaffolds) are in the correct order and orientation. As mentioned above, we obtained an

Apium graveolens "genetic map" from an original sponsoring company; this map was obtained by evaluating progeny of two crosses: an *A. graveolens* var. *secalinum* x celery (*A. graveolens* var. *dulce*); and a *A. graveolens* var. *secalinum* x celeriac (*A. graveolens* var. *rapaceum).* Because high quality genetic maps can show the correct order of "markers" (or bins) along an entire chromosome, genetic markers are extremely useful in "anchoring" the DNA sequence. That is, we can be highly confident that our DNA sequence (physical map) has been ordered correctly. The data from a total of 1,725 bins with a minimum of 136 and a maximum of 191 bins/chromosome clearly show that recombination occurs far more frequently towards the ends of the chromosomes and far less often near the presumed centromeres, as is well-known. This is important in breeding because, for example, the ease of introgressing the resistance genes into celery cultivars and of replacing the non-celery genes depends upon where the genes are located within their chromosomes. In celery, the majority of the centromeres are located far closer to one end of the chromosome (Murata and Orton, 1984, Iovene et al. 2008), and we thought that this might affect the recombination rate. However, only on chromosome 10 is there very little recombination on the end of the chromosome that is presumably close to the centromere; there is a typical and high recombination rate on the other terminus of the chromosome that is relatively far from the centromere. Surprisingly, the high recombination rates in celery chromosomes are limited to a comparatively small portion of the length of the chromosomes (ca. 20%); we believe that this is less than what has been reported previously (Brazier & Glémin, 2022). That is, what has been historically interpreted as a suppression of recombination around the centromere extends further along the chromosomes in celery than what occurs in other species. Once we finish the Challenger annotation and know where the genes versus the repeat elements occur, we should be able to better interpret this finding and its potential relevance for breeding.

Fig. 2 shows an alignment of our Challenger chromosomes with those done for Ventura. If their DNA sequences were identical, there would be a single diagonal line. As would be expected, the two genomes are highly similar but not identical.

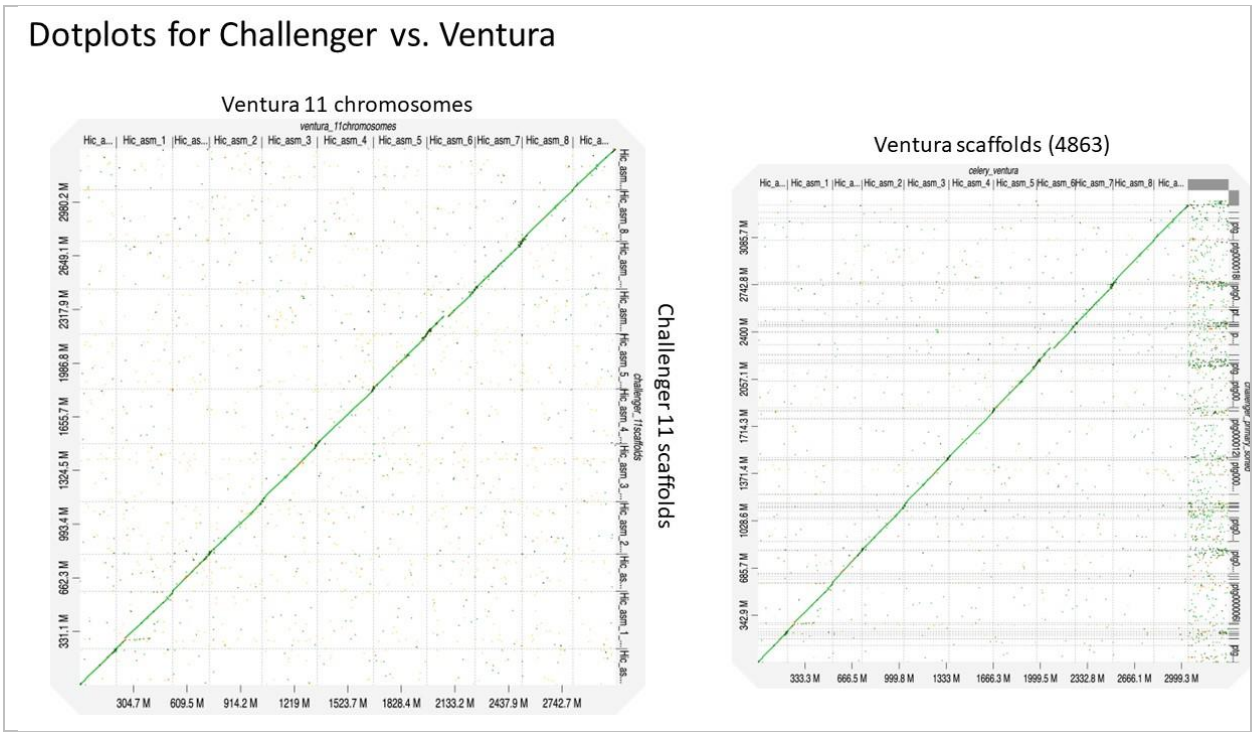

Fig. 2. A dot plot showing that the overall similarity of Challenger and Ventura genomic sequences. The chromosomes and scaffolds are compared on the left and right figures, respectively.

We are currently "annotating" the Challenger genome, a process of identifying the genes in the genome, using a combination of our IsoSeq sequences and on-line computer resources. Eighty five percent of the Challenger genome are repeat sequences (Table 3), or what used to be called "junk DNA." "Masking" this repeat DNA is an important step in the annotation process.

Table 3. “Repeat elements” in celery cv. Challenger.

Repeat Classes

Total Sequences: 3173

Total Length: 3403330603 bp

Class	Count	bpMasked	%masked
LTR	--	--	--
Copia	869390	1165228200	34.24%
Gypsy	456316	749466437	22.02%
unknown	633754	656241033	19.28%
TIR	--	--	--
CACTA	105637	67189353	1.97%
Mutator	240600	63209366	1.86%
PIF_Harbinger	19576	6240335	0.18%
Tc1_Mariner	43857	13556169	0.40%
hAT	48477	17633855	0.52%
nonLTR	--	--	--
LINE_element	1653	936099	0.03%
nonTIR	--	--	--
helitron	288739	94097493	2.76%
repeat_region	292132	69490028	2.04%
total interspersed	3000131	2903288368	85.31%
Total	3000131	2903288368	85.31%

Literature cited

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Iovene M, Grzebelus E, Carputo D, Jiang J, Simon PW. 2008. Major cytogenetic landmarks and karyotype analysis in *Daucus carota* and other Apiaceae. American Journal of Botany 95:793-804.

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Layperson's summary

CALIFORNIA CELERY RESEARCH ADVISORY BOARD
RESEARCH PROJECT REPORT
for the period of:
July 1, 2021 - September 30, 2022

PROJECT TITLE: Genomic tools for breeding for resistance in celery to *F. oxysporum* f. sp. *apii* race 4 (*Foa* race 4)

PROJECT LEADER: Lynn Epstein, Department of Plant Pathology, University of California, Davis, California 95616

COOPERATING PERSONNEL: Sukhwinder Kaur, Armando Garcia-Llanos, Allen van Deynze, Renee Eriksen, Peter Henry, Chaehee Lee and Grey Monroe

The new and highly aggressive *Fusarium oxysporum* f. sp. *apii (Foa)* race 4 first appeared in Camarillo, CA around 2013 (Epstein et al. 2017 and 2022, Henry et al. 2020, Kaur et al. 2022); at that time no commercial cultivars and no UC Davis germplasm had resistance to *Foa* race 4. Currently, the hybrid stalk cv. Earthrace has some resistance to *Foa* race 4, but overall, there is little or no resistance in the commercial marketplace. Because resistance is the best strategy for controlling crop diseases caused by *F. oxysporum*, Kaur and Epstein screened germplasm for resistance, and selected a celeriac/smallage accession (A0134, synonym USDA PI 181714) that is resistant to *Foa* races 4 and 2 and crossed it with race 2-resistant (but race 4-susceptible) celery cv. Challenger (Epstein and Kaur 2023). They then selected for race 4-resistance in lines with celery-type in now three subsequent selfed-generations, the F1S1, F1S2, and F1S3 generations. The F1S3, and if breeders want them the F1S2, will be useful germplasm for introduction of race 4 and race 2 resistance into their own lines. However, commercial breeding can be labor-intensive and take a long time period. In an effort to expedite both the CCRAB and commercial breeding programs, we are currently trying to identify the gene(s) that confer resistance, so that "marker-assisted" selection can be used to identify seedlings that have the desired genes for race 4 resistance. In this grant, we prepared materials for "bulk segregant analysis" of four populations that will assist in the identification of the resistance gene(s) to *Foa* race 4 that were introgressed from A0134 into the F1S3. A0134 and Challenger differ in at least one critical gene(s) for race 4 resistance. The bulk segregant analysis technique is very powerful because it lets us deduce which of the approximately 32,000 gene(s) are candidates specifically for disease resistance.

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PROJECT LEADER: Lynn Epstein, Department of Plant Pathology, University of California, Davis, California 95616, 530-754-7916, lepstein@ucdavis.edu

COOPERATING PERSONNEL: Sukhwinder Kaur, Armando Garcia-Llanos, Allen van Deynze, Renee Eriksen, Peter Henry, Chaehee Lee, Grey Monroe

OBJECTIVES**.** The overall objective was to acquire the DNA data that will at least start the process of the identification of markers and the genes in the celeriac/smallage A0134 that confer resistance to *Foa* race 4 when introgressed into celery. The specific objectives indicated in the proposal were:

1. To acquire short-read genomic (DNA) sequence of the race 4-resistant A0134, and for comparison, the race 4 susceptible parent Challenger;
2. To obtain DNA datasets from bulked segregant samples of two selected segregating populations of F1S2 individuals for resistance and susceptibility to *Foa* race 4 that will assist in the identification of markers and candidate genes for resistance to *Foa* race 4.

RESULTS. The tables and the figure only show data that were produced after our last report was submitted on Feb. 5, 2022. In our last year's report, we showed results from two field trials in infested soil that were harvested during the fall of 2022: from race 4-infested soil in Camarillo and from race 2-infested soil in Santa Maria. The field trials compared generations of one previously selected cross of Challenger (celery type, but susceptible to *Foa* race 4) X *Apium graveolens* A0134 (resistant to *Foa* race 4 but non-celery type). The trials either demonstrated or confirmed several hypotheses: 1) Based on a mini-trial of 5 F1S1 families, the F1S1 family 76-8 was a good selection for subsequent breeding lines. 2) Multiple F1S2 had acceptable resistance to *Foa* race 4 and race 2 in the field. 3) The F1S2 76-8-36 appeared to be closest to fixed (=homozygous) for resistance to *Foa* race 4. And 4) although the F1S2 families 76-8-4 and 76-8-27 were not as far along towards fixation for resistance to *r*ace 4 [i.e., some plants are heterozygous in the gene(s) for race 4 resistance], they carried race 4 resistance and had better celery-type. Here, we show the results of two subsequent greenhouse trials, which were used to identify suitable DNA for the current objectives.

Table 1 shows the results of a greenhouse assay in race 4-infested soil of the two parents (Challenger and A0134), the F1S2 76-8-36, and F1S3 families from nine selfed 76-8-36. We selected F1S3 76-8-36-124 as a genotype with fixed resistance for this project, partly because there were sufficient seeds (data not shown), the gene(s) for resistance were as fixed as in the resistant parent, and the line had reasonably good celery-type.

Table 1. The parents, F1S2 76-8-36 and F1S3 from nine selfed 76-8-36: vascular discoloration-based symptoms, and celery vs. celeriac type in *Foa* race 4-infested soil in the greenhouse[a]

		Plants in each category, %									
		Vascular discoloration (vd)-based score from 0 (asymptomatic) to 5 (dead)[b]									
Generation	Plant ID	0	1	2	3	4	5	Celery type[c]	Celeriac type[c]	Resistant, % (vd score ≤ 2)[d]	n
Parent of F1	A0134	95	0	2	2	0	0	0	100	98	44
F1S2	76-8-36	89	0	2	9	0	0	71	0	91	45
F1S3	76-8-36-124	96	0	2	2	0	0	82	0	98	45
F1S3	76-8-36-133	96	0	0	4	0	0	73	0	96	45
F1S3	76-8-36-151	84	0	2	14	0	0	93	0	86	44
F1S3	76-8-36-103	30	55	5	10	0	0	100	0	90	20
F1S3	76-8-36-127	91	0	0	9	0	0	54	0	91	35
F1S3	76-8-36-139	89	9	0	2	0	0	42	0	98	45
F1S3	76-8-36-146	95	5	0	0	0	0	35	0	100	20
F1S3	76-8-36-105	83	10	0	8	0	0	25	0	93	40
F1S3	76-8-36-148	93	0	2	4	0	0	98	0	98	44
Parent of F1	cv. Challenger	0	0	0	2	18	80	100	0	0	45

[a]Each trial also had 5 uninfested plants/family; all of the uninfested plants had a vd rating of 0 (data not shown). All plants in both the uninfested and infested treatments had solid petioles, expcept for all the plants in the *A. graveolens* A0134 parent, which had non-solid petioles.

[b]Disease scores are as follows: 0, asymptomatic; 1, some discoloration characteristic of *Foa* in the fine roots, but none elsewhere; 2, some characteristic discoloration in the main roots but none in the crown; 3, characteristic discoloration in the crown vasculature but on < 1/4 of the vascular ring; 4, characteristic discoloration in the crown vasculature on > 1/4 of the vascular ring; and 5, plant dead.

[c]Except for the dead plants (vd=5) in the cv. Challenger treatment, all plants were scored as either celery-type, celeriac-type, or an intermediate type. Celery petioles are wider and fewer than celeriac petioles, which are more numerous and less wide. The number of plants in the intermediate type can be calculated.

In a second greenhouse trial, we then tested a selected set of genotypes for *Foa* race 4 and race 2 resistance (Tables 2 and 3). Because F1S3 76-9-36-124 was fixed for resistance to race 4, i.e., all individuals in the population should be homozygous for the resistance gene(s), we modified Objective 2 in the current grant. For the current grant, just before we transplanted the seedlings into infested soil, we took the fourth leaf from genotypes of interest and stored them in the -80 C freezer for later selection and then DNA extraction, purification and library preparation by the van Deynze lab. (Because the grant didn't fit into the normal yearly grant cycle, we have a no-cost extension for another year to complete the isolation and purification of the DNA, and then the sequencing of the four populations by the UCD Genome Center). We now have 15 individuals from each of four populations: 1) (race 4-susceptible) Challenger with a disease rating of "5"; 2) (race 4-resistant) A0134 with disease rating of "0"; 3) segregating race 4-susceptible F1S2 76-8-27 with a disease rating of "4"; and 4) (race 4-resistant) F1S3 76-8-36-124 with the best celery type and a disease rating of "0".

As part of this year's companion grant on completion of the Challenger genome, we now have a well-assembled Challenger parent from PacBio HiFi long-reads. We will soon use our full length (IsoSeq) RNA transcripts to annotate the genome. As part of next year's genome grant, the van Deynze lab is working on preparing a high-quality library of long read DNA of F1S3 76-8-36-124 for PacBio HiFi sequencing by the UCD Genome Center; this DNA was prepared from hundreds of F1S3 76-8-36-124 seedlings. After we obtain the Illumina short read sequence from the four populations, the sequences will be "mapped" onto both (Challenger and F1S3) reference genomes. The data will show that both the F1S2 76-8-27 susceptibles and the F1S3 reference are heterozygous for a number of celery-type genes. However, the resistance gene(s) to *Foa* race 4 should be homozygous and the same in A0134 and the F1S3, and different from the homozygous but susceptible gene(s) in Challenger and the selected F1S2 76-8-27 individuals (Table 4).

In Tables 2 and 3, we show that the F1S3 76-8-36-124 were asymptomatic for race 4 and race 2 under very high disease pressure. In Fig. 1, we show that the F1S3 and the parent A0134 are resistant/immune to *Foa* race 4, rather than tolerant; in tolerance, the host is at least relatively asymptomatic, but the pathogen can still grow.

Table 2. The parents, F1S1 76-8, three F1S2, and F1S3 76-8-36-124: the percentage with symptoms of Fusarium wilt in *Foa* race 4-infested soil, and celery vs. celeriac type in a greenhouse trial†.

		Symptoms of Fusarium wilt from *Foa* race 4							Plant architecture§				
		Vascular discoloration-based score from 0 (asymptomatic) to 5 (dead)‡						Asymp-tomatic above-ground	All solid petioles	Growth habit			
		0	1	2	3	4	5			Celery	Mix of celery & celeriac	Celeriac	
Generation	Plant ID	Plants, %											n¶
F1 parent	A0134	**94**	0	0	4	2	0	**100**	0	0	0	100	47
F1 parent	cv. Challenger	0	0	0	0	38	63	0	**100**	**100**	0	0	48
F1S1	76-8	54	3	1	15	21	6	64	19	53	44	3	80
F1S2	76-8-4	49	11	0	11	16	11	73	100+	91	9	0	79
F1S2	76-8-27	68	0	2	12	18	0	82	100+	84	16	0	125
F1S2	76-8-36	84	13	4	0	0	0	100+	100+	63	37	0	80
F1S3	76-8-36-124	95+	0	0	5	0	0	99+	100+	85	15	0	80

†Two-month-old plugs were transplanted into a completely randomized design. There were three pathogen treatments: *Foa* race 4-infested soil (n shown in last column); *Foa* race 2-infested soil (n=20), with symptomatic scores shown in Supplemental Table 4; and uninfested soil (n=10), which were all asymptomatic. Values of parental phenotypes that are desired in the progeny are bolded.

‡0, asymptomatic; 1, characteristic discoloration in the fine roots, but none elsewhere; 2, characteristic discoloration in the main root but none in the crown; 3, discoloration in the crown but on < 1/4 of the vasculature; 4, discoloration in the crown on > 1/4 of the vascular ring; and 5, plant dead.

§ Data on plant architecture were based on the survivors from the *Foa*-race 4 treatment (because dead plants cannot be scored for these phenotypes) and the additional 30 plants. Celery has fewer and wider petioles than celeriac.

Table 3. The parents, F1S1 76-8, three F1S2, and F1S3 76-8-36-124: vascular discoloration-based symptoms **in *Foa* race 2-infested soil** in a greenhouse trial[a]

		Vascular discoloration (vd)-based score from 0 (asymptomatic) to 5 (dead)[b]						Asymptomatic above-ground	Resistant, (vd score ≤ 2)
		0	1	2	3	4	5		
Generation		Plants in each category, %							
Parent of F1	A0134	100	0	0	0	0	0	100	100
Parent of F1	cv. Challenger	95	0	0	5	0	0	100	95
F1S3	76-8-36-124	100	0	0	0	0	0	100	100
F1S2	76-8-36	95	0	0	5	0	0	100	95
F1S2	76-8-4	90	10	0	0	0	0	100	100
F1S2	76-8-27	100	0	0	0	0	0	100	100
F1S1	76-8	95	0	0	5	0	0	100	95

[a]The trial had three soil-infestation treatments; results from the *Foa* race 4-infestation are shown in Table 1. For each genotype, there were 10 and 20 plants/genotype in uninfested and *Foa*-race 2-infested soil, respectively. Pots were arranged in a completely randomized design. After 35 days post-transplantation, plants were evaluated. All of the uninfested plants had a vd rating of 0 (data not shown).

[b]Disease scores are as follows: 0, asymptomatic; 1, characteristic discoloration in the fine roots, but none elsewhere; 2, characteristic discoloration in the main root but none in the crown; 3, discoloration in the crown but on < 1/4 of the vascular ring; 4, discoloration in the crown on > 1/4 of the vascular ring; and 5, plant dead.

Table 4. Key characteristics of the pool populations for bulk segregant analysis.

Pool of 15 individuals	Trait fixed for *Foa* race 4?	Fixed for celery traits?	Criteria for candidates for DNA associated with *Foa* race 4 resistance
Challenger (parent)	Yes, susceptibility	Fixed, celery	100% Absent
A0134 (parent)	Yes, resistance	Fixed, Non-celery	100% Present
(Segregating) F1S2 76-8-27	Yes, susceptibility	Not-fixed	100% Absent
F1S3 76-8-36-124	Yes, resistance	Not fixed, but selected for best celery-type	100% Present

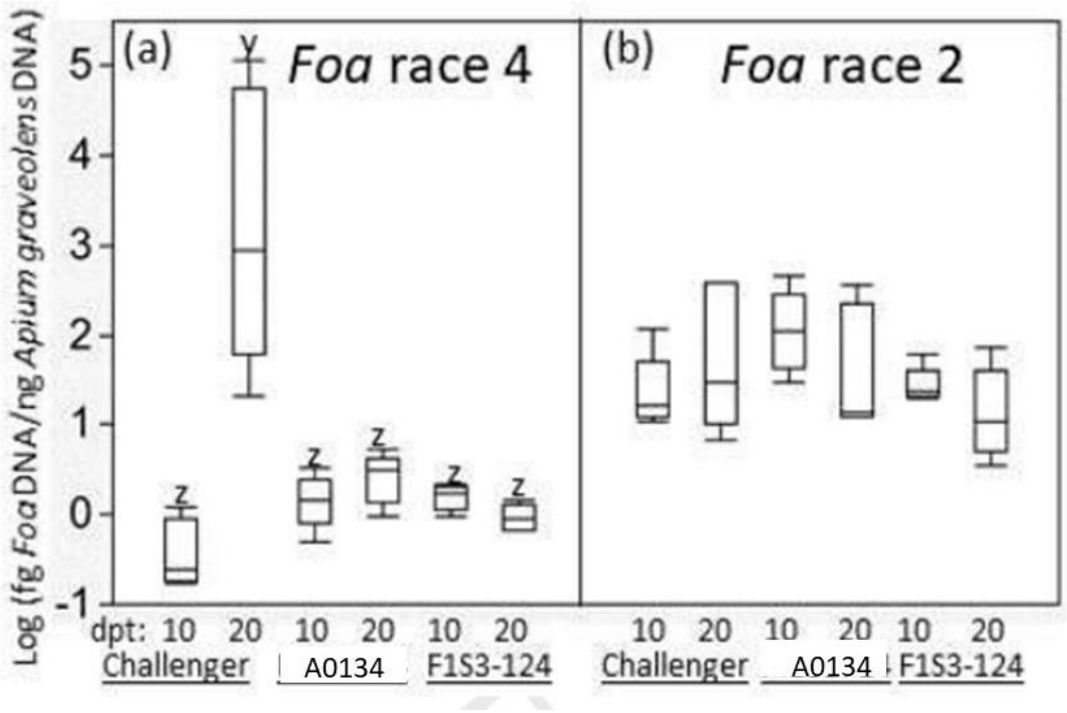

Fig 1. Box plots of the log concentration of *F. oxysporum* f. sp. *apii* (a) race 4 (*Foa*R4) and (b) race 2 (*Foa*R2) in *Apium graveolens* crowns 10- and 20- days post-transplantation (dpt) into either uninfested soil (data not shown), or soil that was infested with either *Foa*R4 or *Foa*R2 (n=5). Plants were either the parentals cv. Challenger and *A. graveolens* A0134 or their F1S3 76-8-36-124 (F1S3-124). No *Foa*R4 or *Foa*R2 DNA was detected in any of the crowns of plants in uninfested treatments (data not shown). For Figure 1a, means followed by the same letter were not significantly different by Tukey's HSD at α=0.05. The 10 and 20 dpt time points were pre-selected to represent pre-symptomatic and early-symptomatic times, respectively, for susceptible genotypes. Phenotypes of plants in a concurrent greenhouse trial 35 dpt are shown in Table 2 for *Foa*R4-infested soil and in Table 3 for *Foa*R2-infested soil.

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ERI-22

California Celery Research Advisory Board Report

Project title: Year 1: Celery breeding for resistance to *Fusarium oxysporum* f. sp. *apii* race 2 and race 4

Period of Funding: January 1, 2022 to September 30, 2022

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For questions or concerns, please contact Renee Eriksen at renee.eriksen@usda.gov

Objective 1 Activities:

1. Replication of UCD Foa race 4 greenhouse assays at the USDA in Salinas.
   The assay optimization is ongoing. We tested inoculation assays using race 4 isolates in growth chambers and two separate greenhouses under published temperature conditions, and while root discoloration symptoms were often apparent, we were not able to consistently induce disease or death of susceptible cultivars. We developed a new race 4 isolate from material collected from the Beardsley Road field, and with this new race 4 isolate we have been able to consistently induce disease and death of susceptible cultivars. In side-by-side trials with new and old isolates, we established that the old race 4 isolate has lost its pathogenicity. We are currently in the process of developing a new protocol for inoculation assays using the new race 4 isolates. Because of this delay, we were not able to meet this objective in 2022, however we are moving forward in developing a new assay.

2. Selections from the 2021 Foa race 4 field, vernalization, and selfing.
   Selected plants from the 2021 race 4 trial in Camarillo were returned to Salinas, and vernalized to induce bolting and flowering. Most plants were placed in a cold room with LED lighting, however some plants were permitted to be kept outside in compliance with a Monterey County Ag Commissioner's permit. 100% of plants flowered, and there was no difference in bolting among plants kept outside or in the cold room. All plants were placed in isolators for selfing, however all seed that was acquired was highly contaminated with white mold. A stringent fungicide application schedule was developed in consultation with Duda Farms, however not in time to save the seed from 2022. In future years, the fungicide application schedule will be initiated early in the season. We are moving forward in the process to hire a temporary technician to assist the breeding program with a regular fungicide application schedule.
3. Production of $F_{1.5}$s (new notation: F_1S_3).
   This activity was accomplished by Dr. Epstein and this line is available as "F_1S_3" via MTA (Material Transfer Agreement) with UC Davis. Dr Epstein published this work in the journal Plant Breeding, and interested individuals should contact Dr. Epstein or myself (renee.eriksen@usda.gov) to inquire about the MTA process to acquire 25 seeds of F_1S_3 or 50 seeds of the parental generation.

Objective 2 Activities:

1. *Fusarium oxysporum* f. sp. *apii* race 2 trial in Santa Maria
2. *Fusarium oxysporum* f. sp. *apii* race 4 trial in Camarillo

The trials were conducted during the following dates:

TRIAL	TRANSPLANT DATE	HARVEST DATE
SANTA MARIA	July 7, 2022	October 13-14, 2022
CAMARILLO	August 16, 2022	November 21 -22, 2022

Disease evaluation ratings were as follows:

SCORE	CRITERIA
0	No browning
1	Browning visible, particularly in feeder roots
2	Browning visible, particularly in primary roots
3	Browning visible, particularly around the crown
4	Browning in and/or around the crown
5	Extensive browning in crown, decay in crown tissue

Agronomic traits measured included:

TRAIT	UNITS	METHOD
PETIOLE LENGTH	inches	Petioles were cut at approximately 1-2 inches above the average petiole node and measured. This trait describes stunting due to disease as well as general agronomic characteristics, and was one of two quantitative measurements.
STALK WEIGHT	lbs	Ten trimmed plants were weighed to the nearest kg and an average stalk weight was calculated. Units were converted to pounds (lbs) for this report. As with petiole length, this trait captured stunting due to disease as well as general agronomic characteristics and was one of two quantitative measurements.
GREENNESS	Score 1-3	This trait describes the color of the stalk. A score of 1 was particularly light or yellow, and a score of 3 was particularly dark; red stalks were scored as a 3. Most plants received a 2. This trait was highly dependent on the individual conducting the scoring and on the light during which the evaluation was made. It could also be highly dependent on nitrogen fertilization, though we assume fertility was consistent among blocks.
CRACKING	Score 1-3	This describes cracking at the base of the stalk. We observed relatively little cracking. 1 = no cracking.
BOLTING	Score 1-5	This describes production of the flowering stalk. We observed no bolting in these trials. 1 = no bolting.
PITHINESS	Score 1-5	This trait describes hollow, pithy stems which are common in wild celery or lovage, but a defect in stalk celery. A score of 1 was no observed pithiness at any cut. A score of 2 was a small amount of pithiness in less than half of the stalks. A score of 3 was a small amount of pithiness in half of stalks. A score of 4 was pithiness in more than half of stalks. A score of 5 was pithiness or hollow stems in all stalks. This scale is still being developed, and may not have been consistently applied in 2022. Questions about this scoring system should be addressed to the researchers.
RIBBINESS	Score 1-3	A score of 1 was particularly smooth, and a score of 3 was particularly ribby or rough. Ribbiness appears to increase under disease pressure.
SUCKERING	Score 1-3	A score of 1 had no suckering, 2 had some suckering, and 3 had consistent suckers, similar to wild celery. Suckering seemed to increase with race 4 pressure in some cultivars.

Santa Maria race 2 trial

Methods: A total of 39 entries were received for the race 2 trial. Seeds were submitted by Bejo Seeds, Rijk Zwaan, Syngenta, and Tozer Seeds. Dr Epstein said she tested the majority of the USDA germplasm collection for race 2 and race 4 resistance, so additional, untested germplasm was requested from an open-pollinated germplasm bank in Iowa (Seed Savers Exchange, Ltd.) to test potential parental lines for breeding purposes. The Santa Maria trial was planted slightly later than historical plantings, resulting in a later harvest. There were 12 beds, with two beds filled with a border row of a field variety on either side. Beds were organized into four replicate blocks. Within each block, there were eight beds divided into five 20-foot plots. Germplasm entries were randomized within each block independently (see map in section Supplemental Materials). The susceptible control was cv. Tall Utah 52-70, acquired from Ferry Morse Seed Company. The resistant control was cv. Challenger derived from the UC Davis breeding program (Orton et al. 1984) by Pybus Seeds. Harvest and disease evaluation occurred on October 13-14, 2022. Twenty plants were removed from the center of each plot; ten were evaluated for root and crown discoloration indicative of disease, the other ten were evaluated for agronomic traits. Disease evaluations were conducted by one person per block to confine the assessors' scoring approaches to respective blocks.

Results: Disease Scores ranged from 0-5. The germplasm entries with the lowest average disease score (low disease score = healthy plant) were RZ2005, followed by TZ4, Merengo, Fandango, and RZ2008. The germplasm entries with the highest disease scores were Ventura, RZ2004, Tall Utah (susceptible control), Conquistador, and RZ2003. The resistant control cv. Challenger derived from UC1 germplasm had an average score of 1.9, which is a higher average disease score than 21 of the 39 germplasm entries. We observed stunting in susceptible Ventura and Tall Utah, but also in Sonora, Conquistador, and Mission. We also observed low average plant weight in Ventura, Sonora, Conquistador, Tall Utah, and RZ2002.

Conclusions: Germplasm entries such as RZ2005, TZ4, and RZ2008 as well as cultivars Merengo and Fandango had good field resistance to race 2 in this trial. Open-pollinated cultivars such as Wild Irish, Celeri a Couper, Zwolsche Krul, and Pink had lower disease scores than the resistant control Challenger derived from UC1, suggesting these lines may be good alternative sources of disease resistance to race 2, however they had very high suckering and pithiness, indicating association with wild or lovage celery.

Table 1: Cultivar entries in the **Santa Maria race 2 trial 2022**. Cultivars are arranged alphabetically by breeding company or contributor

Cultivar Entry	Contributor	
Merengo	Bejo Seeds	
Waltz	Bejo Seeds	
Fandango	Bejo Seeds	
Bolero	Bejo Seeds	
BJF5	Bejo Seeds	
BJF6	Bejo Seeds	
BJF7	Bejo Seeds	
Tall Utah 52-70	Ferry Morse	Susceptible control
Ventura	Ferry Morse	
CG390	Pybus	
RZ2001 Earthrace	Rijk Zwaan	
RZ2002	Rijk Zwaan	
RZ2003	Rijk Zwaan	
RZ2004	Rijk Zwaan	
RZ2005	Rijk Zwaan	
RZ2006	Rijk Zwaan	
RZ2007	Rijk Zwaan	
RZ2008	Rijk Zwaan	
RZ2009	Rijk Zwaan	
RZ2010	Rijk Zwaan	
Calmario	Seed Savers Exchange	
Celeri a Couper	Seed Savers Exchange	
Pink	Seed Savers Exchange	
Wild Irish	Seed Savers Exchange	
Zwolsche Krul	Seed Savers Exchange	
Celx147	Syngenta	
Celx767	Syngenta	
Challenger	Syngenta	Resistant Control
Command	Syngenta	
Conquistador	Syngenta	
Mission	Syngenta	
Sonora	Syngenta	
Stix	Syngenta	
TZ1	Tozer Seeds	
TZ2	Tozer Seeds	
TZ3	Tozer Seeds	
TZ4	Tozer Seeds	
TZ5	Tozer Seeds	
TZ6	Tozer Seeds	

Table 2: Average disease rating of cultivar entries in the **Santa Maria race 2 trial 2022**. Arranged from low to high rating. Low ratings indicate low disease and a healthy plant, and high ratings indicate more disease.

Cultivar	Average Disease Rating (0-5)
RZ2005	0.1
TZ4	0.1
Merengo	0.3
Fandango	0.4
RZ2008	0.5
TZ5	0.5
Celeri a Couper	0.6
Wild Irish	0.6
RZ2001	0.7
Stix	0.7
TZ2	0.9
Celx767	1
TZ3	1.2
TZ6	1.2
Bolero	1.3
Zwolsche Krul	1.3
Pink	1.4
Waltz	1.5
Celx147	1.6
TZ1	1.6
CG390	1.7
BJF5	1.9
Challenger	1.9

Cultivar	Average Disease Rating (0-5)
RZ2006	2
RZ2009	2.1
BJF6	2.2
RZ2010	2.3
RZ2007	2.4
Calmario	2.4
Command	2.4
Sonora	2.4
Mission	2.5
RZ2002	2.6
BJF7	2.7
RZ2003	2.7
Conquistador	2.8
Tall Utah 52-70	2.9
RZ2004	3.3
Ventura	3.6

Table 3: Average agronomic scores of cultivar entries in the **Santa Maria race 2 trial 2022**. Table is sorted alphabetically by cultivar name or germplasm code.

Cultivar	Petiole Length (in)	Weight (lbs)	Ribbiness (0-3)	Pithiness (1-5)	Bolting (1-5)	Greenness (1-3)	Suckers (1-3)	Cracks (1-3)
BJF5	9.5	0.7	2.5	0.5	0	2.5	0.3	0
BJF6	10.8	0.8	1.9	0.9	0	2.2	0.3	0
BJF7	6.4	0.2	2.1	0	0	2.4	2.6	0
Bolero	9.5	0.9	0.7	0.3	0	1.8	0	0.3
Calmario	6.9	0.5	2.5	0.3	0	2.5	1.3	0
Celeri a Couper	13.4	0.9	2.8	4.5	0	2.5	3	1.3
Celx147	8.7	0.7	1.5	0.1	0	2.2	0.6	0.3
Celx767	10.6	1.2	1.4	0.6	0	2	0	0
CG390	9.4	1	1.8	1	0	2.5	1	0
Challenger	9.8	0.9	1.3	0.6	0	2.3	0.3	0
Command	6.4	0.3	2.1	0	0	2.8	2	0
Conquistador	5.2	0.1	1.3	0	0	3	2.8	0
Fandango	10.4	1.3	1.4	0	0	2	0.3	0
Merengo	10.9	1.4	0.5	0.7	0	1.8	0.4	0
Mission	5.6	0.3	2	0	0	2.5	1.9	0
Pink	8.4	0.5	3	3.4	0	2.8	2.3	0
RZ2001 Earthrace	13.2	1.5	2.1	1.7	0	2.3	0.7	0
RZ2002	6.2	0.2	2.6	0.3	0	3	1	0
RZ2003	8.2	0.4	2.7	0.2	0	2.8	0.6	0
RZ2004	6.4	0.2	2.3	0.1	0	3	2.4	0
RZ2005	14.2	1.1	2.4	1.2	0	2.8	0.1	0
RZ2006	8.8	0.7	1.6	0.8	0	2.8	0.8	0
RZ2007	8.6	0.5	2.5	0	0	3	0.9	0.3
RZ2008	12.3	1	2	0.2	0.3	1.7	0.5	0
RZ2009	10.5	0.7	3	0.1	0	2.8	1.2	0
RZ2010	9.7	0.4	2.8	0	0	3	0.8	0
Sonora	4.8	0.1	1.5	0	0	3	2.2	0
Stix	13	1.4	2.4	0.8	0	2.5	0.7	0.3
Tall Utah 52-70	5.6	0.1	2.8	0	0	3	2.4	0
TZ1	9.1	0.7	2	0.4	0	2.4	0.9	0
TZ2	11.8	1.3	0.9	1.8	0	2	0.4	0.3
TZ3	10.3	1.1	1.6	0.5	0	2.6	0.1	0.3
TZ4	11.5	1.2	1.7	0.4	0	2.3	0.8	0
TZ5	11.2	1.1	1.9	1	0	2.1	0.8	0
TZ6	11.3	1.4	0.7	0.2	0	2.1	0.9	0
Ventura	4.8	0.1	2.4	0	0	2.5	1.7	0
Waltz	9.1	0.8	0.8	0.5	0	2.3	0.6	0
Wild Irish	14.2	1.1	2.8	4	0	2.5	3	1.3
Zwolsche Krul	14.1	0.9	3	3.5	0	2.5	3	1.3

Table 4: Ranking of germplasm and cultivar entries in the **Santa Maria race 2 trial 2022** for low disease ratings (under 2), lowest stunting or highest average trimmed plant weight (1 lbs and above), average petiole lengths greater than 10 inches, and average petiole length between 7-10 inches. Average agronomic scores of cultivar.

Lowest Disease Rating	Highest Average Trimmed Plant Weight	Average Petiole Length Greater than 10 inches	Average Petiole Length Between 7-10 inches
RZ2005	RZ2001 Earthrace	RZ2005	Merengo
TZ4	Merengo	Wild Irish*	BJF6
Merengo	Stix	Zwolsche Krul*	Celx767
Fandango	TZ6	Celeri a Couper*	RZ2009
RZ2008	Fandango	RZ2001 Earthrace	Fandango
TZ5	TZ2	Stix	TZ3
Celeri a Couper*	Celx767	RZ2008	Challenger
Wild Irish*	TZ4	TZ2	RZ2010
RZ2001	RZ2005	TZ4	Bolero
Stix	TZ3	TZ6	BJF5
TZ2	TZ5	TZ5	CG390
Celx767	Wild Irish*		Waltz
TZ3	CG390		TZ1
TZ6	RZ2008		RZ2006
Bolero			Celx147
Zwolsche Krul*			RZ2007
Pink*			Pink
Waltz			RZ2003
Celx147			
TZ1			
CG390			
BJF5			
Challenger			

*Indicates varieties with wild celery or lovage characteristics that were included to evaluate their genetic disease resistance rather than their agronomic traits under disease pressure.

Camarillo race 4 trial 2022

Methods: There were 41 germplasm and cultivar entries in the race 4 trial from the same seed companies that contributed to the Santa Maria trial. We planted four replicated blocks. Each block consisted of the four center beds, with unplanted border rows. Blocks consisted of four beds, each divided into ten 15-foot plots. Germplasm entries were randomized within each block independently (see map in section Supplemental Materials). The susceptible control was cv. Challenger, and no resistant control was planted. Soil temperatures were recorded at 6 and 12 inches throughout the growing season. Mortality rates were counted on September 14 (week 4), on September 26 (week 5), and at harvest. Harvest and disease evaluation took place on November 21-22, 2022 (about 14 weeks after transplant). Pathogen-caused mortality was sufficiently high in most plots that only ten plants were removed from the center of the plot; five were evaluated for root and crown discoloration indicative of disease, the other five were evaluated for agronomic traits. Disease evaluations were conducted by one person per block.

Results: Soil day-night average temperatures were measured at close to 80 degrees F at the start of recording, and remained above 70 degrees until October 23. Mortality at the first rating ranged between 2-69% of all plants. F11 and F10 from Bejo seeds as well as TZ5 and TZ3 from Tozer Seeds and 4005 from Rijk Zwaan had very low mortality rates during the first evaluation. The OP accession French Dinant also had very low mortality. Mortality increased at the second evaluation on September 26, and some cultivars such as Bachata, Conquistador, Command, Celx146, and Mission had over 90% mortality within 5 weeks after transplanting.

By 14 weeks after transplant, the lowest mortality was found in TZ5, RZ4005, and French Dinant. Mortality was less than 10% for cultivar entries such as TZ5 and French Dinant. Mortality was between 90-100% in cultivars such as Command, Conquistador, Bachata, Sonora, Celx147, Mission, Yellow-Stalked Verga d'Oro, Waltz, Stix, and RZ4003.

Disease pressure was not consistent among blocks or replicates. Mortality and Fusarium ratings were highest in block 1 and 2, and lowest in block 3.

Of the plants that survived until harvest, disease scores ranged between 0-5. Among all blocks, the accessions RZ4007 and RZ4001 Earthrace, RZ4009, TZ4, RZ2006 had the lowest Fusarium ratings (though mortality for these accessions was 43%, 31%, 21%, 31%, 31% respectively). TZ2, Qin, Conquistador, Sonora, and RZ4003 had the highest Fusarium ratings.

We observed stunted plants in most accessions. Without a nearby no-disease control, it was difficult to generalize from these data, however cultivars such as Yellow-stalked Verga d'Oro, Celx147, RZ4003, Mission, and TZ3 had average stalk lengths less than 7 inches indicating stunting. Cultivars such as Frevo, Fandango, Balada, Pink Plume, Qin, Waltz, Merengo, Stix, BJF8, Challenger, and TZ2 had average stalk lengths less than 10 inches, which also likely indicates stunting.

Conclusions: High temperatures after planting led to significant disease severity and mortality. Cultivars entries such as TZ5 had very low mortality, and cultivars such as RZ4007, RZ4009, RZ4006, RZ4001 Earthrace, RZ4005, TZ4, and BJF12 had low disease scores. The open-

pollinated cultivar French Dinant had very low mortality and relatively low average disease scores, but it had red stalks and high suckering, making it a poor cultivar for commercial traits, however it may be useful as a parental line for breeding.

Table 5: Cultivar entries in **Camarillo race 4 trial 2022.** Cultivars are arranged alphabetically by breeding company or contributor

Cultivar Entry	Contributor	
BJF8	Bejo Seeds	
BJF9	Bejo Seeds	
BJF10	Bejo Seeds	
BJF11	Bejo Seeds	
BJF12	Bejo Seeds	
BJF13	Bejo Seeds	
Merengo F1	Bejo Seeds	
Waltz F1	Bejo Seeds	
Bachata F1	Bejo Seeds	
Balada F1	Bejo Seeds	
Frevo F1	Bejo Seeds	
Fandango F1	Bejo Seeds	
RZ4001 Earthrace	Rijk Zwaan	
RZ4002	Rijk Zwaan	
RZ4003	Rijk Zwaan	
RZ4004	Rijk Zwaan	
RZ4005	Rijk Zwaan	
RZ4006	Rijk Zwaan	
RZ4007	Rijk Zwaan	
RZ4008	Rijk Zwaan	
RZ4009	Rijk Zwaan	
RZ4010	Rijk Zwaan	
French Dinant	SSE	
Boli Cui Qin Tsai	SSE	
Giant Pink	SSE	
Qin	SSE	
Yellow Stalked Verga d'Oro	SSE	
Pink Plume	SSE	
Challenger	Syngenta	Susceptible control
Command	Syngenta	
Conquistador	Syngenta	
Mission	Syngenta	
Sonora	Syngenta	
Stix	Syngenta	
CELx147	Syngenta	
CELx767	Syngenta	
Tozer1	Tozer Seeds	
Tozer2	Tozer Seeds	
Tozer3	Tozer Seeds	
Tozer4	Tozer Seeds	
Tozer5	Tozer Seeds	

Figure 1: Graph of soil temperatures at 6 inches (blue line) and 12 inches (orange line) across time. A mean percent mortality at September 11, 2022, and September 25, 2022 is also shown. Red bars represent mortality rates of the 10 cultivars with the lowest mortality. Yellow bars represent the mortality rates of the remaining cultivars with the highest mortality.

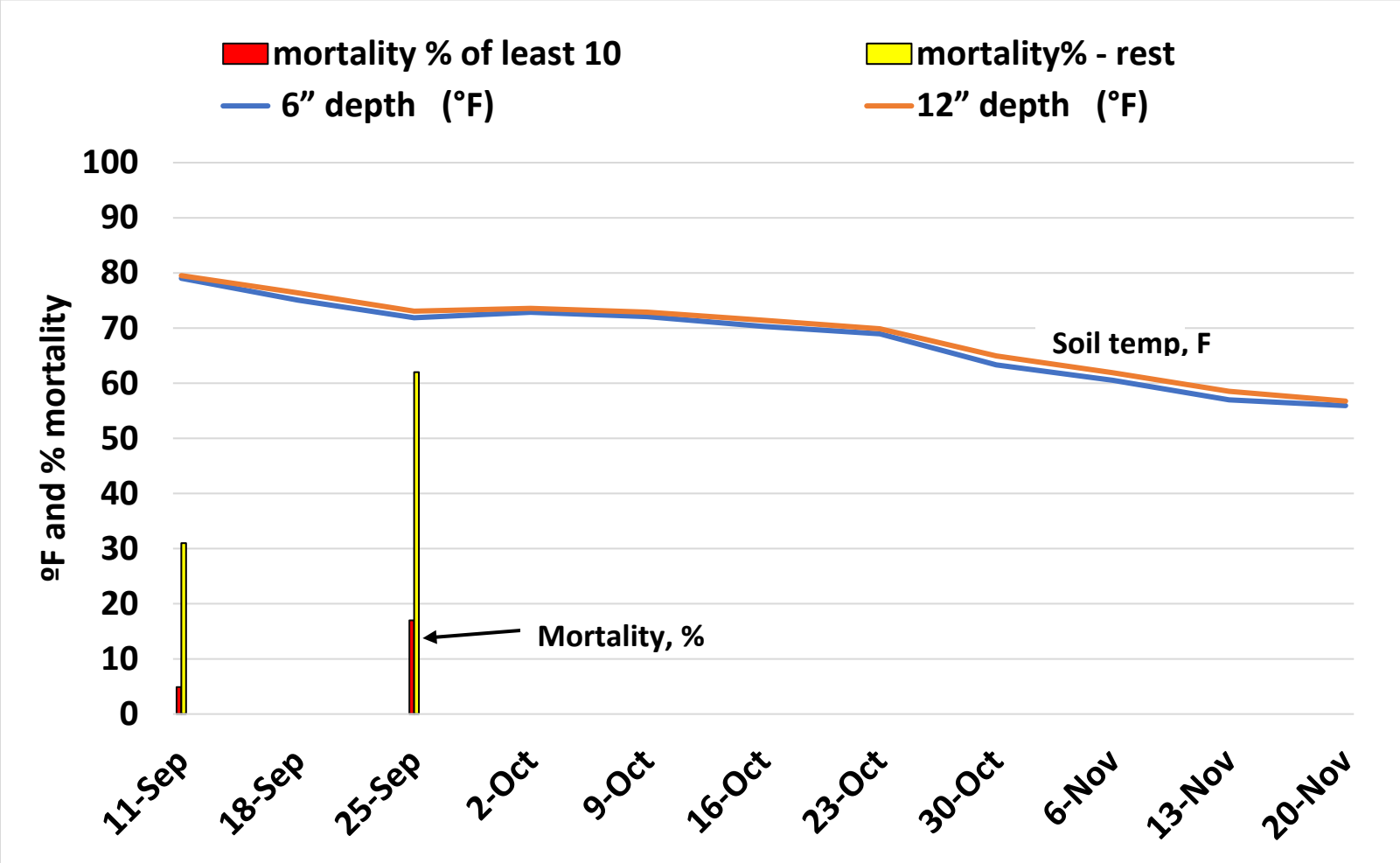


Table 6: Disease rating scores and mortality of cultivar entries in **Camarillo race 4 trial 2022.** Cultivars are arranged from low to high disease rating scores

Cultivar	Average Disease Rating (0-5)	Mortality Week4 (%)	Mortality Week5 (%)	Mortality Week14 (%)
RZ4007	1.0	8.5	23.0	43.0
RZ4001 Earthrace	1.5	13.0	30.5	30.5
RZ4009	1.5	7.3	21.3	21.3
TZ4	1.5	20.0	26.5	31.0
RZ4006	1.5	12.0	30.0	30.5
RZ4005	1.7	5.5	13.0	13.0
BJF12	1.8	6.5	29.0	29.0
French Dinant	2.0	4.0	8.0	8.0
BJF13	2.3	23.0	46.5	46.5
Fandango	2.3	26.5	76.0	89.0
TZ5	2.3	2.0	5.5	5.5
RZ4002	2.3	20.0	45.0	46.5
BJF8	2.5	27.5	50.5	50.5
Bachata	2.6	77.0	97.5	97.5
Yellow Stalked	2.6	73.0	89.0	91.0
Frevo	2.6	29.5	70.5	70.5
BJF11	2.7	1.5	16.5	16.5
RZ4010	2.7	27.5	51.5	51.5
BJF9	2.8	34.5	49.5	49.5
Waltz	2.8	33.5	87.0	90.5
Boli Cui	2.8	40.5	63.0	63.0
Pink Plume	2.9	50.0	83.5	84.5
BJF10	2.9	2.0	16.0	16.0
Merengo	3.0	23.5	77.5	77.5
Stix	3.1	42.5	86.0	90.0
RZ4008	3.1	22.5	54.5	54.5
Giant Pink	3.1	35.5	55.5	55.5
RZ4004	3.1	16.5	43.5	46.5
Challenger	3.1	43.5	79.5	81.5
TZ1	3.1	33.5	57.0	60.5
Celx767	3.2	20.0	60.5	60.5
TZ3	3.3	5.0	34.5	34.5
Balada	3.3	26.0	79.0	83.0
RZ4003	3.4	46.7	90.0	90.0
Mission	3.6	30.0	93.3	93.3
Conquistador	3.6	60.0	98.5	98.5
Qin	3.7	28.5	71.8	74.8
Sonora	3.7	46.0	93.0	96.5
Command	3.9	64.0	95.5	99.0
TZ2	4.0	16.7	34.0	34.0
Celx147	4.1	63.0	95.5	96.5

Table 7: Average agronomic scores of cultivar entries in the **Camarillo race 4 trial 2022**. Table is sorted alphabetically by cultivar name or code. NA indicates that too many of the plants were dead to rate.

Cultivar	Petiole Length (in)	Weight (lbs)	Ribbiness (1-3)	Pithiness (1-5)	Bolting (1-5)	Greenness (1-3)	Suckers (1-3)	Cracks (1-3)
Bachata	NA	NA	NA	NA	NA	NA	NA	NA
Balada	8.1	0.4	2	1	1	3	3	1
BJF10	11.9	0.6	2.5	1.3	1	2.5	3	1
BJF11	10.4	0.7	2.5	1	1	2.8	2.8	1
BJF12	11.9	1	2.3	1.8	1	2.8	1.8	1
BJF13	10.3	0.9	2	1	1	2.5	1.3	1
BJF8	9.7	1.2	1.7	1	1	2.7	1	1
BJF9	10.4	1	2.7	1.3	1	3	2.3	1
Boli Cui	10.7	0.6	3	2.5	1	3	3	1
Celx147	3.8	0.1	3	1	1	3	1	1
Celx767	10.7	0.7	2.3	1	1	2.5	2.5	1
Challenger	9.7	0.6	2.5	1	1	2	2.5	1
Command	NA	NA	NA	NA	NA	NA	NA	NA
Conquistador	NA	NA	NA	NA	NA	NA	NA	NA
Fandango	7.9	0.6	2.5	1	1	3	2	1
French Dinant	12.5	0.5	3	4.3	1	3	3	1
Frevo	7.4	0.4	2.3	1	1	2.7	2	1
Giant Pink	10.1	0.4	3	4.7	1	2.7	2.7	1
Merengo	9.5	0.8	1.3	1	1	2.3	2.3	1
Mission	6.1	0.2	3	1	1	3	2	1
Pink Plume	8.4	0.4	3	1	1	3	2.5	1
Qin	8.7	0.6	3	1	1	2.5	3	1
RZ4001 Earthrace	13.6	1	2	2	1	2.7	2	1.3
RZ4002	12.2	1.2	2	1	1	2.5	1	1
RZ4003	5.8	0.1	3	1	1	2	2	1
RZ4004	11.8	0.9	1.5	1	1	2.5	2.5	1
RZ4005	14.3	1	2.8	6.3	1	2.8	1	1.3
RZ4006	11.4	1	2.3	1.3	1	2.7	1.7	1.3
RZ4007	12.1	0.9	2	1	1	3	1.7	1
RZ4008	11.2	1	3	1	1	2.5	1.5	1
RZ4009	11.4	0.8	2.7	1.3	1	3	1.7	2
RZ4010	12.9	0.9	2.5	1	1	3	1.5	1
Sonora	NA	NA	NA	NA	NA	NA	NA	NA
Stix	9.6	0.6	3	1	1	2	1	1
TZ1	11.4	1	2	1	1	2.7	2.3	1.7
TZ2	9.9	0.5	3	1	1	2.5	1	1
TZ3	6.3	0.3	2.5	1	1	2.5	1.8	1
TZ4	11.9	1	2.3	1	1	2.3	1.7	1
Waltz	8.8	0.7	1.5	1	1	3	3	1
Yellow Stalked	2	0.1	3	1	1	3	3	1

Table 8: Ranking of entries in the **Camarillo race 4 trial 2022** for low mortality (under 10%), low disease ratings (under 2), lowest stunting or highest average trimmed plant weight (1 lbs and above), average petiole lengths greater than 10 inches, and average petiole length between 7-10 inches. Average agronomic scores of cultivar.

Lowest Mortality	Lowest Disease Rating	Highest Average Trimmed Plant Weight	Average Petiole Length Greater than 10 inches	Average Petiole Length Between 7-10 inches
TZ5	RZ4007	BJF8	RZ4005	Celx767
French Dinant*	TZ4	RZ4002	RZ4001 Earthrace	Boli Cui
RZ4005	RZ4001 Earthrace	BJF9	RZ4010	BJF9
	RZ4006	RZ4008	French Dinant*	BJF11
	RZ4009	RZ4006	RZ4002	BJF13
	RZ4005	TZ1	RZ4007	Giant Pink*
	BJF12	BJF12	BJF12	TZ2
	French Dinant*	TZ4	TZ4	BJF8
		RZ4001 Earthrace	BJF10	Challenger
		RZ4005	RZ4004	Stix
			RZ4006	Merengo
			TZ1	Waltz
			RZ4009	Qin
			RZ4008	Pink Plume*
				Balada
				Fandango
				Frevo

*Indicates varieties with wild celery or lovage characteristics that were included to evaluate their genetic disease resistance rather than their agronomic traits under disease pressure.

Photos from **Santa Maria race 2 trial 2022**


Command


RZ2004


RZ2008


Sonora


Celeri a
Couper


Tozer4

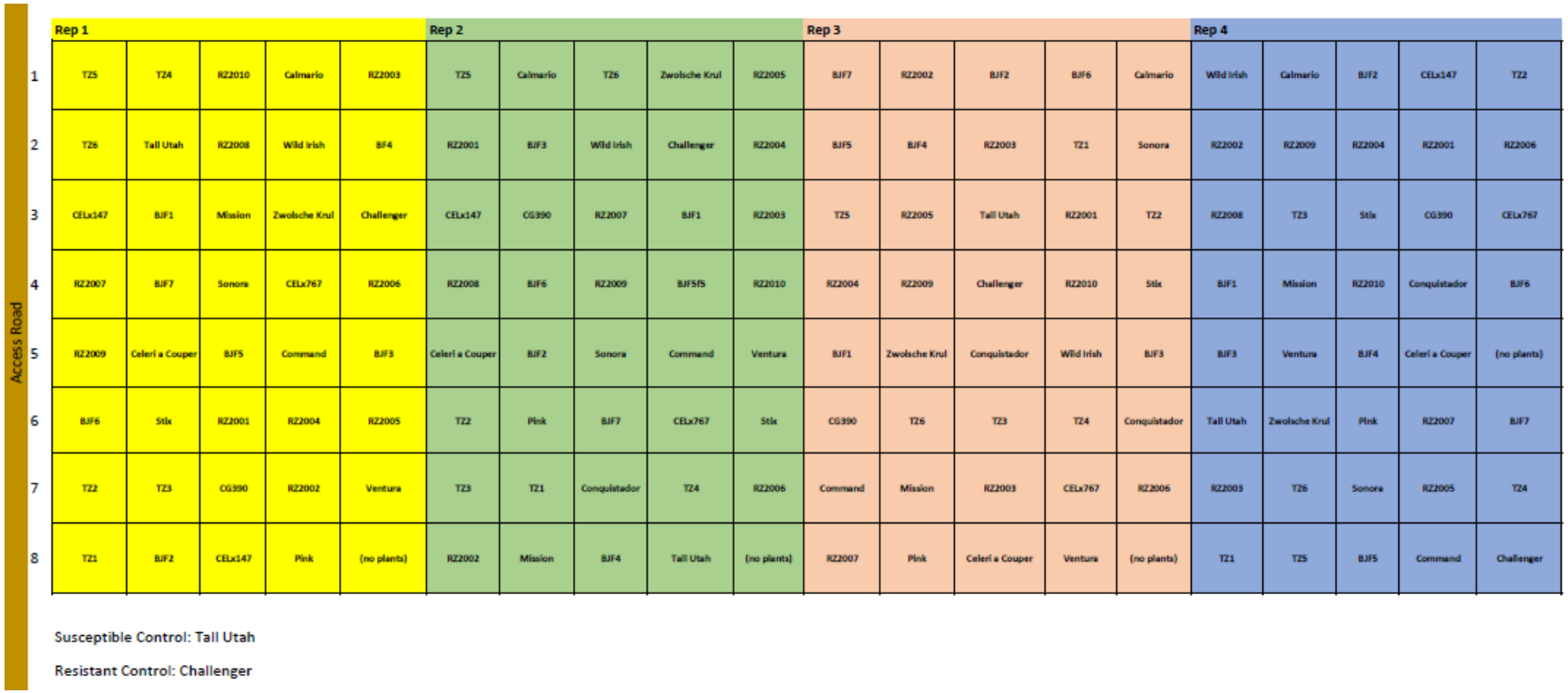
Photos from **Camarillo race 4 trial 2022**

RZ4006 on September 13, 2022

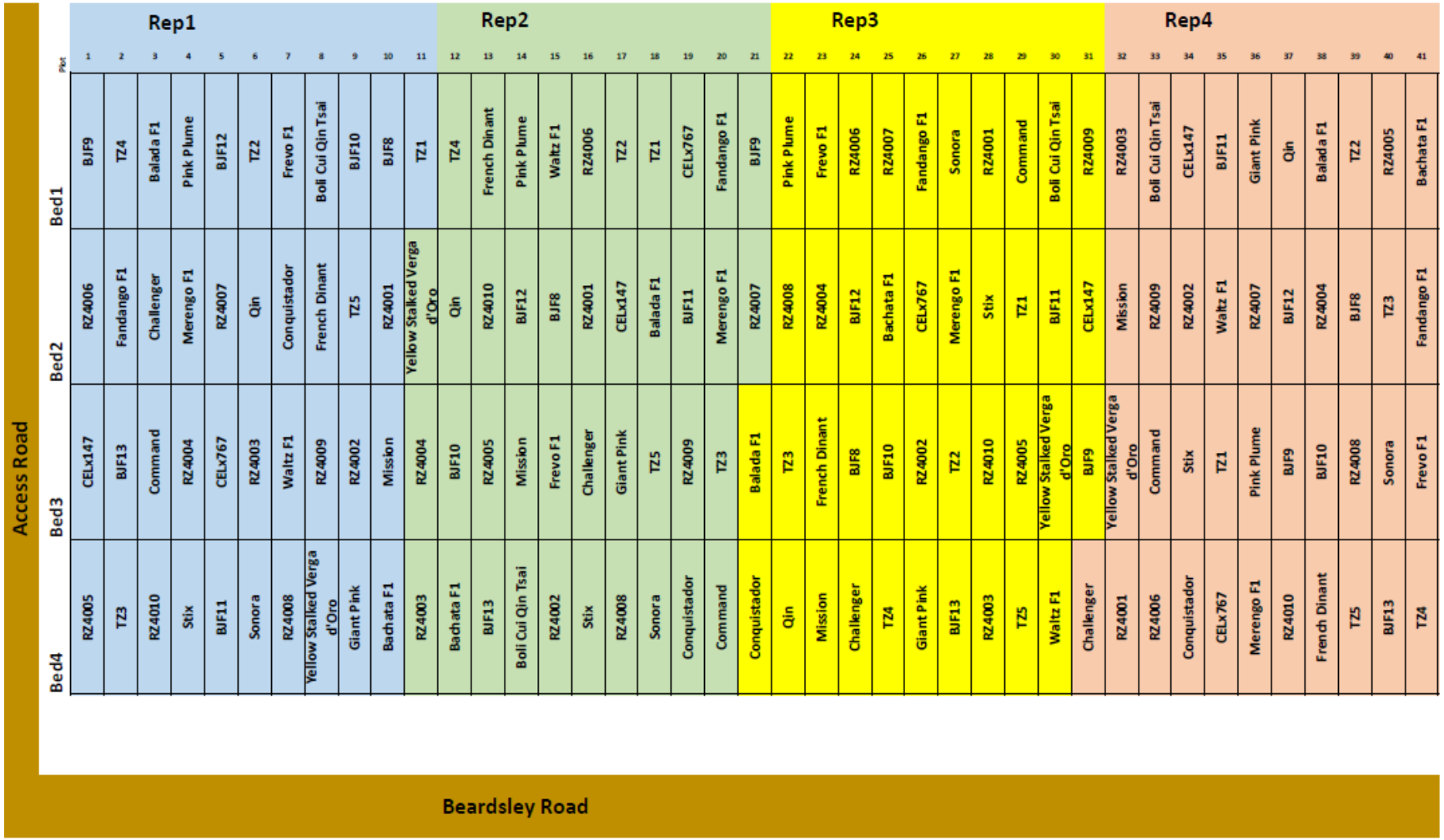
Challenger on September 13 2022

Supplemental Materials

Map Santa Maria race 2 trial 2022



Map Camarillo race 4 trial 2022



California Celery Research Advisory Board
Annual Report for 2021-2022
Management and Economics of Insect Pests on Celery

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Immediate Objectives:

I. Studies to minimize the negative effects of FQPA: Identifying control 'gaps' and finding solutions. Immediate goals are to screen new insecticides for insect control and resistance management programs on celery.

II. Continue economic analyses of IPM approaches developed through the support of the CCRAB using new insecticide chemistries. A comparison between the IPM and a "standardized" chemical approach has been evaluated.

Objective I. Screen new insecticides for insect control

Celery, variety "Command" celery was transplanted on 2 Nov 2021 at Agricultural Operations, University of California, Riverside, California (Figure 1A). The plots were three beds wide (two rows per bed on 60" centers) by 40 feet and were drip irrigated. Four replicates of each treatment were organized in a randomized complete block design. In addition to a non-treated control, a low input treatment had four applications using Exirel 100SE, Beleaf 50 SG, Radiant 1.0 SC, and Dipel DF (Table 1). The next treatment was a rate of Spear-Lep™ plus Leprotec DF, applied four times as a foliar spray with Vader used as a surfactant. Next was a rotation of Spear-Lep™ plus Leprotec DF, Radiant 1.0 SC, Beleaf 50 SG, and Dipel DF using Vader as a surfactant. The 5th treatment was Exirel 100SE plus Beleaf 50 SG, Spear-Lep™ plus Leprotec DF and Beleaf 50 SG, Exirel 100SE, and Spear-Lep™ plus Leprotec DF. The 6th treatment was Minecto Pro applied three times as an individual treatment. The 7th treatment was an organic rotation of Aza-direct EC, Dipel DF, Pyganic 1.4 EC plus Trilogy EC, Venerate XC, Grandevo WDG, and Entrust SC. The final treatment was the chemical standard of Asana XL, which was applied six times as a foliar spray. Treatments and spray dates are listed in Table 1.

In our studies, all chemicals were applied by tractor using a tractor-mounted boom sprayer operated at 100 PSI and 100 gal/Ac except the Spear-Lep and Leprotec treatments, which were applied at 50 gal/Ac (Figure 1B). Four, disc-type cone nozzles per bed incorporated D3 orifice disks, #25 cores, and 50 mesh screens.

Table 1. IPM Materials Evaluated:

Compound [b]	Formulation	Rate/Ac	MoA [a]	Supplier
1- Control-Non-treated	--	--	--	--
2- Low Input				
a-Exirel	100 SE	13.5 oz	28	Dupont
+ Beleaf	50 SG	2.8 oz	9C	FMC
b-Radiant	1.0 SC	8.0 oz	5	Corteva
+ Beleaf	50 SG	2.8 oz	9C	FMC
c-Exirel	100 SE	13.5 oz	28	Dupont
d-Dipel	DF	1 lb	11	Valent
Vader		0.125%		Loveland
(a=1/13,b=1/27, c=2/11, d=3/3)				
3- Spear-Lep +	--	32 fl oz	32	Vestaron
Leprotec	Btk	16 fl oz	11	AEF Global
Vader		0.125%		Loveland
(1/13,1/27,2/11,3/3)				
4- a-Spear-Lep +	--	32 oz	32	Vestaron
Leprotec	Btk	16 oz	11	AEF Global
b-Radiant 1.0 SC	--	8.0 oz	5	Corteva
+ Beleaf	50 SG	2.8 oz	9C	FMC
c- Spear-Lep +	--	32 oz	32	Vestaron
Leprotec	Btk	16 oz	11	AEF Global
d-Dipel	DF	1 lb	11	Valent
Vader		0.125%		Loveland
(a=1/13, b=1/27, c=2/11, d=3/3)				
5- a-Exirel	100 SE	13.5 oz	28	Dupont
+ Beleaf	50 SG	2.8 oz	9C	FMC
b- Spear-Lep +	--	32 oz	32	Vestaron
Leprotec+	Btk	16 oz	11	AEF Global
Beleaf	50 SG	2.8 oz	9C	FMC
c-Exirel	100SE	13.5 oz	28	Dupont
d- Spear-Lep +	--	32 oz	32	Vestaron
Leprotec	Btk	16 oz	11	AEF Global
Vader		0.125%		Loveland
(a=1/13, b=1/27, c=2/11, d=3/3)				
6- Minecto Pro	SC	10.0 oz	28,6	Syngenta
Dyne-amic		0.25%		Loveland
(1/13, 2/11, 3/3)				
7- Organic IPM				
a-Aza-direct		32 oz	UN	Gowan
b-Dipel	DF	1 lb	11	Valent
c-Pyganic +	5.0 EC	17.0 oz	3A	MGK

Trilogy	EC	128.0 oz	UN	Certis
d-Venerate	XC	128.0 oz	UNB	Marrone Bio
e-Grandevo + Oroboost	WDG	3 lb 0.25%	UNB	Marrone Bio Oro-Agri
f-Entrust (a=1/13, b=1/27, c=2/3, d=2/11, e=2/24, f=3/3)	SC	8.0 oz	5	Corteva
8- Asana (1/13,1/27,2/3,2/11, 2/24,3/3)	XL	9.0 oz	1	Dupont

[a] MoA – Mode of Action for insecticide resistance management
[b] Spray dates are included.

Figure 1. A is celery field plot at UCR Agricultural Operations in 2021-2022. B is the tractor setup for commercial scale application.

IRAC

Using the guidelines established by the Insecticide Resistance Action Committee (IRAC) we are classifying the compounds used in the field trial based on their mode of action (MoA) (see Table 1). The purpose is to assist growers in the development of insecticide resistance management (IRM) strategies. These strategies will improve the effectiveness of IPM programs, slow resistance development, and extend the life of the pesticides. The following language is from the IRAC; additional information and MoA classifications can be found in the IRAC handout or online at www.irac-online.org.

> "Resistance to insecticides may be defined as '*a heritable change in the sensitivity of a pest population that is reflected in the repeated failure of a product to achieve the expected level of control when used according to the label recommendation for that pest species*' (IRAC). This definition differs slightly from others in the literature, but IRAC believes it represents the most accurate, practical definition of relevance to farmers and growers. Resistance arises through the over-use or mis-use of an insecticide or acaricide against a pest species and results in the selection of resistant forms of the pest and the consequent evolution of populations that are resistant to that insecticide or acaricide.
>
> In the majority of cases, not only does resistance render the selecting compound ineffective but it often also confers cross-resistance to other chemically related compounds. This is because compounds within a specific chemical group usually share a common target site within the pest, and thus share a common mode of action (MoA). It is common for resistance to develop that is based on a genetic modification of this target site. When this happens, the interaction of the selecting compound with its target site is impaired and the compound loses its pesticidal efficacy. Because all compounds within the chemical sub-group share a common MoA, there is a high risk that the resistance that has developed will automatically confer cross-resistance to all the compounds in the same sub-group. It is this concept of cross-resistance within chemically related insecticides or acaricides that is the basis of the IRAC mode of action classification".

Field Counts:

The field was surveyed on 10 February and 11 March for Lepidopteran pests (primarily beet armyworm, (*Spodoptera exigua* (Hübner)) and cabbage looper (*Trichoplusia ni* (Hübner)), leafminer (*Liromyza trifolii*) (Burgess), cabbage aphid (*Brevicoryne brassicae*)(Linnaeus), lygus bug (*Lygus hesperus*)(Knight), greenhouse whitefly (*Trialeurodes vaporariorum*)(Westwood), and earwigs (*Forficula auricularia*) (De Geer) (Figure 2). Five plants from each plot were counted for a total of twenty plants per treatment. In addition to insect presence, insect damage was also assessed.

Of the insects listed we found aphids, Lygus bug, and beet armyworm, in numbers sufficient to analyze. Statistical differences between treatments were seen for Lygus on 10 February (Figure 3). Field assessments on 11 March showed statistical differences for aphids only (Figure 4).

Figure 2. Insects and damage seen in the Celery IPM Trials at the UCR Agricultural Operations research study. A. Aphids; B. Lygus bug damage; C. Beet armyworm damage; D. Earwig damage.

Figure 3. Field counts level of infestation on 10 February (insects plus damage)

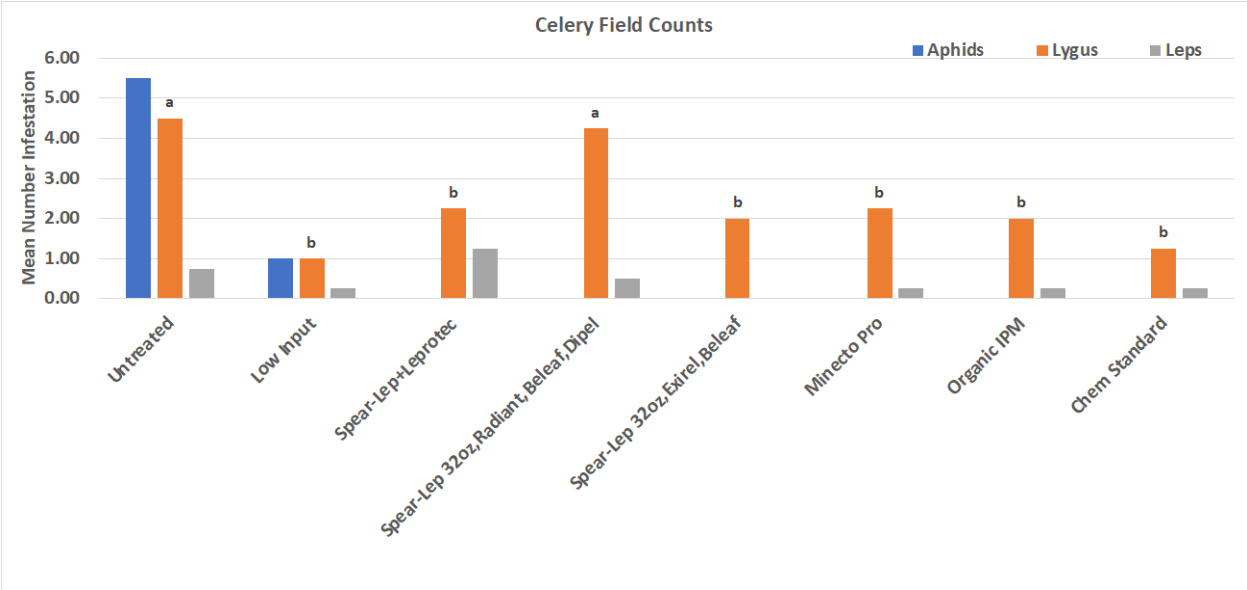
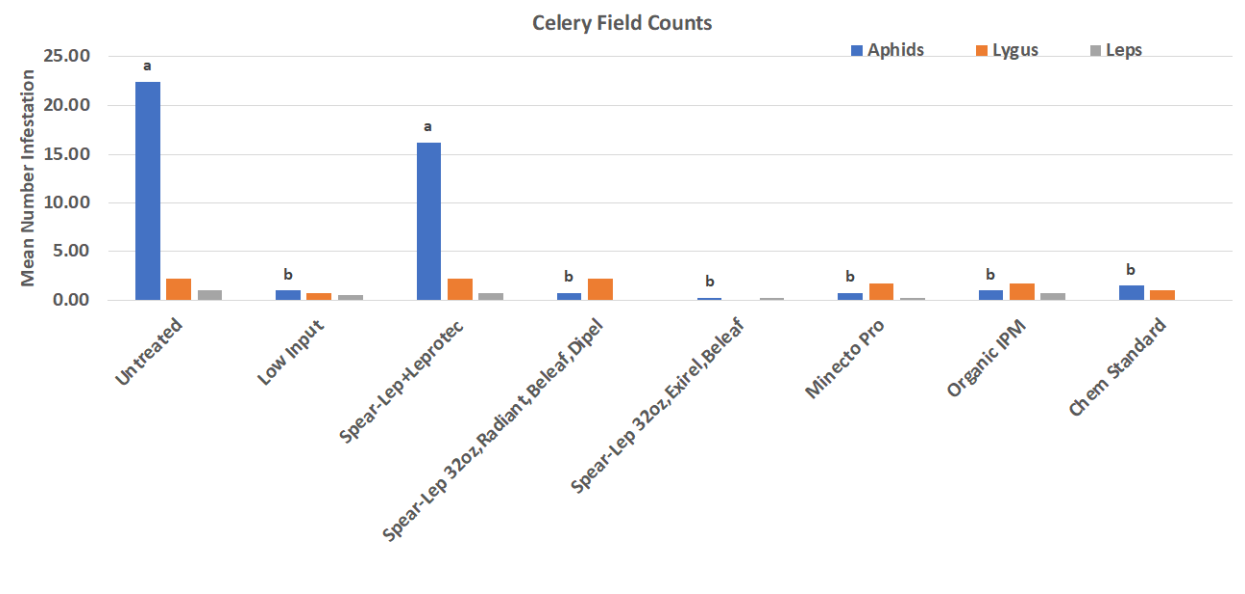


Figure 4. Field counts level of infestation on 11 March (insects plus damage)



Harvest Evaluations:

The field was evaluated at harvest on 24 March. The number of damaged plants found in 25 plants per replicate (4 replicates/treatment) from the center rows of each replicate were counted and recorded. Beet armyworm densities were high in the study; the control suffered 17% (4.25/25 plants) damage (Table 2). However due to variability there was no statistical separation of beet armyworm between the treatments. The field trials had high levels of pressure for Lygus bugs and aphids, and the harvest assessment results provided statistical separation between the treatments for Lygus damage. Spear®-Lep has been tested in our chemical trials for several years and is a biological product that was tested in IPM rotations as a substitute for Radiant® or Exirel®. Spear®-Lep performed well within the two IPM rotations, which may provide another product to use in rotations to reduce potential pesticide resistance of industry standard products. We also evaluated Minecto® Pro as a stand-alone product to see how it would perform against celery insect pests. Minecto® Pro is a broad-spectrum combination product composed of cyantraniliprole and abamectin. Results showed good efficacy against lepidopterans and lygus pests, but it did not perform as well on aphids. Beleaf® was used within rotations to target sucking insects such as aphids and Lygus bugs. Beleaf® performed well within the respective IPM rotations against lygus, but it did not provide significant control against aphids. The organic IPM rotation performed better than the chemical standard for lepidopteran control, had the highest number of aphid damage 58% (14.5/25), and was not significantly better than the untreated control for lygus damage. The Asana treated celery had the least damage from lygus pests. Asana is a pyrethroid product that should be used sparingly within IPM rotations to avoid increasing pest populations such as leafminers and aphids. Leafminers have not been included because of low pest pressure. Whitefly pressure also was very low. Adults were seen in the field, but nymphal densities were very low. No phytotoxicity was observed in any of the treatments.

TABLE 2. HARVEST MEAN NUMBER OF PLANTS DAMAGED

		Mean No. Plants Infested or Damaged by [a]		
Treatment	**Rate**	**Aphids**	**Beet Armyworm**	**Lygus Bug**
1- Control-Non-treated	--	12.75	4.25	9.25 a
2- Low Input		8.75	0.25	4.50 bc
a-Exirel	13.5 oz			
+ Beleaf	2.8 oz			
b-Radiant	8.0 oz			
+ Beleaf	2.8 oz			
c-Exirel	13.5 oz			
d-Dipel	1 lb			
Vader	0.125%			
(a=1/13,b=1/27, c=2/11,d=3/3)				
3- Spear-Lep +	32 fl oz	13.25	2.75	6.75 ab
Leprotec	16 fl oz			
Vader	0.125%			
(1/13,1/27,2/11,3/3)				
4- a-Spear-Lep +	32 oz	7.25	1.50	5.50 bc
Leprotec	16 oz			
b-Radiant 1.0 SC	8.0 oz			
+ Beleaf	2.8 oz			
c- Spear-Lep +	32 oz			
Leprotec	16 oz			
d-Dipel	1 lb			
Vader	0.125%			
(a=1/13,b=1/27, c=2/11,d=3/3)				
5- a-Exirel	13.5 oz	9.25	0.00	5.00 bc
+ Beleaf	2.8 oz			
b- Spear-Lep +	32 oz			
Leprotec+	16 oz			
Beleaf	2.8 oz			
c-Exirel	13.5 oz			
d- Spear-Lep +	32 oz			
Leprotec	16 oz			
Vader	0.125%			
(a=1/13,b=1/27, c=2/11,d=3/3)				
6- Minecto Pro	10.0 oz	11.75	0.50	5.25 bc
Dyne-amic	0.25%			
(1/13, 2/11, 3/3)				
7- Organic IPM		14.50	1.50	5.75 abc
a-Aza-direct	32 oz			
b-Dipel	1 lb			
c-Pyganic +	17.0 oz			
Trilogy	128.0 oz			
d-Venerate	128.0 oz			
e-Grandevo +	3 lb			

f-Entrust Oroboost (a=1/13, b=1/27,c=2/3, d=2/11, e=2/24, f=3/3)	8.0 oz 0.25%			
8- Asana (1/13,1/27,2/3,2/11, 2/24,3/3)	9.0 oz	9.75	1.75	2.50 c
ANOVA F_{value}		0.816	2.177	2.343
ANOVA P value		0.584	0.074	0.056

[a] Means in columns followed by the same letter are not significantly different ($P < 0.05$, Fisher's Protected LSD).

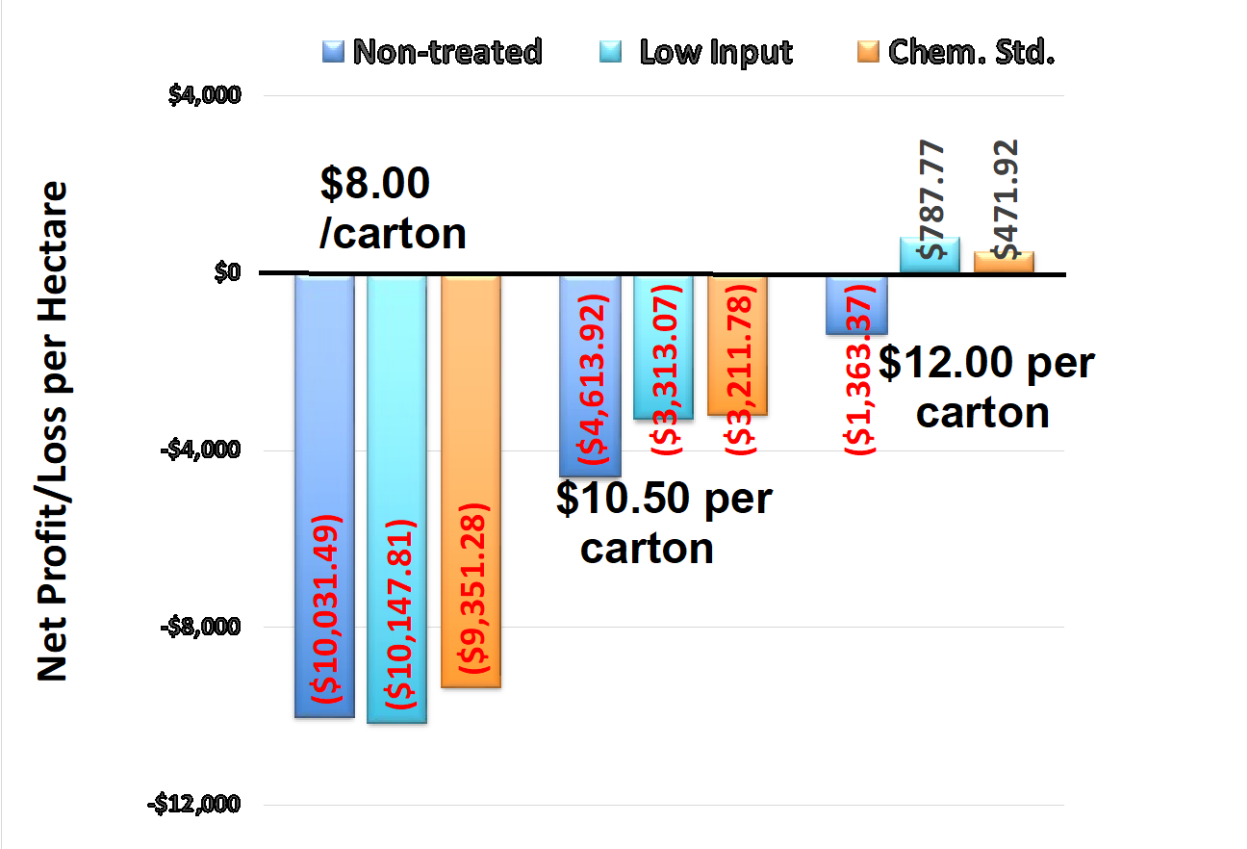
Objective II. Economic Analyses of an IPM and Chemical Standard Trial.

An economic analysis was prepared to compare harvest yields between treatments. Damage to the celery, costs of applications, and material costs were factored into the calculations. Figure 5 shows that the "Low Input" treatment performed the best at $12.00 per carton. The breakeven point for most growers is $10.50 per carton. An adjustment to the economic analysis was done to account for the high level of aphid damage that would have impacted the quality of the celery produced.

For this study, we tested new combinations of products designed to 1) reduce costs, 2) manage insecticide resistance, 3) increase harvest/yield, and 4) provide critical information to regulatory agencies on how products fit within an IPM program. The program consisted of a low input rotation of 1) Exirel®, Beleaf®, Radiant®, and Dipel® versus 2) Asana®. In the IPM plots chemicals were applied 4 times over the course of an 18 week season. In the 'chemical standard' treatment the materials were applied 6 times.

We used very progressive chemical treatments with fewer applications for the low input program. In spite of using chemicals that target specific insects, which in most cases have higher costs per application, we were able to increase net profits for the Low Input IPM program. Other benefits such as environmental effects and worker health and safety aspects are improved in the IPM programs and are necessary to conform with the FQPA. As reported to the Cal EPA, without some pesticidal control, celery damage by insects will be extensive, and losses would not allow a reasonable profit to be made. Thus, some pesticides must continue to be registered for celery for the crop to remain viable in California.

Figure 5. Net profit or loss in IPM, chemical standard, and control treatments in 2021. Numbers associated with each bar are net profits (if numbers are red and in parentheses, they represent net losses).



Celery Residue Concerns

We continued to address the concerns of celery being classified in a consumer advocates publication as part of the dirty dozen regarding pesticide residues. The amount of pesticides used in crop protection in California declined from 1997-2009. Examination of the "Pesticide Use Report" (PUR) from 2018 (web: https://www.cdpr.ca.gov/) shows a trend for the use of more biopesticides, which are generally safer for the environment, workers, and consumers. The goal of current pest management programs is to reduce the amount of pesticide applied, which minimizes environmental, occupational, and consumer exposures.

Future Research

In our 2022 celery field trials we will be utilizing promising compounds that may be included in an IPM program. We will be testing IPM programs against a chemical standard program to continue to identify the most effective and economical pest control strategies. Some new insecticide materials are being developed in the industry and some are being tested in laboratory and IR-4 trials. As these products prove to be effective, we will continue to support the registration of these new products for celery use, which will continue to support the goals of the FQPA. We will test Minecto® Pro to determine how it will fit into an IPM program after it showed promising results for the past two seasons. Additionally, we will continue to pursue organic treatments that could

fit into an IPM program for organic growers. We would like to test Grandevo® and Venerate® for a second season in our organic IPM treatment rotation to determine if these products are viable options.