2022-23 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 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

Terms Ending August 31, 2023

DIST	MEMBER	ALTERNATE
2	**Adrian Zendejas** Desert Mist Farms	**VACANT**

DIST	MEMBER	ALTERNATE
3	**Hank Laubacher Jr** Laubacher Farms	**Erik Heacox** Tanimura & Antle
3	**Geremy Olsen** Deardorff Family Farms	**Jackson Duda** 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

DIST	MEMBER	ALTERNATE
4	**Phillip Adam** Innovative Produce	**David Ayala** Betteravia Farms
4	**VACANT**	**Tyler Grosini** Campbell Ranches

DIST	MEMBER	ALTERNATE
5	**Alejandro Palma** Dole Fresh Vegetable	**Larry Knerr** Duda Farm Fresh
5	**Greg Lewis - RES COMM** Duda Farm Fresh	**Julia Harshman - RES COMM** Duda Farm Fresh
5	**Kevin Brink - RES COMM** Ocean Mist Farms	**VACANT**

PUBLIC MEMBER	NON-BOARD/RES COMMITTEE MEMBER
Steve Donovan - RES COMM	**Meadow Englund,** Ocean Mist - **RES COMM**

STAFF	**Oleg Daugovish** UC Liaison UCCE – Ventura County 805-645-1454 odaugovish@ucanr.edu	**Ben Kardokus** CDFA 560 J St, Ste 170-A, Sacramento 95814 916-900-5018 ben.kardokus@cdfa.ca.gov
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CELERY RESEARCH ADVISORY BOARD

FISCAL YEAR ENDING 9/30/23

April 30, 2024

INCOME		**CARRYOVER**	**312,270**	
		BUDGET	**YTD**	**BALANCE**
30-110	Current	280,000	280,671	(671)
30-111	Prior	-	-	-
30-120	Interest Income	4,150	9,377	(5,227)
30-140	Other Income	-		-
TOTAL INCOME		**284,150**	**290,048**	**(5,898)**

EXPENSES				
30-305	Management Services	55,440	55,440	-
30-315	Audits	4,450	4,750	(300)
30-320	Office Supplies	600	988	(388)
30-330	Telephone	640	937	(297)
30-335	Postage	400	350	50
30-355	Travel & Mileage	1,200	1,719	(519)
30-360	Meetings	2,000	1,907	93
30-365	Annual Report	50	-	50
30-370	Insurance	1,000	938	62
30-390	Miscellaneous	100	-	100
30-392	Website	500	274	226
30-530	No Cost Extension	-	26,043	(26,043)
30-551	Production Research - UC Davis	74,722	41,571	33,151
30-552	Production Research - UC Riverside	83,322	53,858	29,464
30-554	Production Research - UCCE	18,466	18,466	-
30-556	Production Research - Outside	4,077	4,077	-
30-710	Marketing Branch	18,500	14,689	3,811
30-711	Market Enforcement Branch	2,500	-	2,500
TOTAL EXPENSES		**267,967**	**226,009**	**41,958**

NET INCOME	**$ 64,039**
CASH BALANCE	**$ 376,309**

Research Projects

2022-23

RESEARCHER	PROJECT TITLE	2022-23 Funded
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*)**	**74,722**
Renee Eriksen *USDA - Salinas*	**Celery Breeding for Resistance to Fusarium Oxysporum f. sp. Apii Race 4** *Eriksen - USDA* *4,077* *Daugovish - UCCE ANR Ventura* *9,373* *Greer - UCCE ANR San Luis Obispo* *9,093* *Putman - UC Riverside* *12,822*	**35,365**
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 2022-23 FUNDED	**$180,587**

Layperson's summary

CALIFORNIA CELERY RESEARCH ADVISORY BOARD
RESEARCH PROJECT REPORT

for the period of:
October 1, 2022 - September 30, 2023

PROJECT TITLE: Next Step for Genomic Tools for Breeding for Resistance in Celery to *F. oxysporum* f. sp. *apii*

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

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

Genetic resistance is the best method for control of pathogens in the *Fusarium oxysporum* species complex. The *F. oxysporum* strain that causes disease on celery is called *F. oxysporum* f. sp. *apii* (*Foa*). Celery grown in infested areas in California can succumb to two different, and distantly related *Foa*: *Foa* race 2, which was first reported in 1976 (Hart and Endo, 1976), and *Foa* race 4, which was first detected in Camarillo in Ventura County in 2013 (Epstein et al. 2017). Before our recent research program, the only assembled genome of celery that was publicly available was 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 *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).

In the 1980's, UC Davis (UCD) researchers identified *A. graveolens* accessions that were resistant to *Foa* race 2; after initial breeding at UCD (Orton et al. 1984), the celery cultivar Challenger was developed in the private sector by Rob Pybus. More recently, we used Challenger as the celery parent for the cross with USDA PI 181714 for race 4 resistance (Epstein and Kaur, 2023). We then selfed the F1 three consecutive times with selection for both resistance and celery-type; resistance to both *Foa* race 4 and race 2 appear to be fixed in the line that we used here (F1S3 76-8-36-124), which we simply call the "F1S3" in this report.

In last year's report, we reported the completion of the chromosomal level DNA sequence of Challenger. This complete, and well-annotated genome of the Challenger parent will be extremely useful both to help determine the gene(s) for resistance to *Foa* race 2 and as a race 4-susceptible reference for comparison to the F1S3. Here, we report a high-quality, chromosomal-level DNA sequence of F1S3 and show regions of dissimilarity between the F1S3 and Challenger. A bulk segregant analysis that will facilitate identification of markers and/or genes for *Foa* race 4 resistance is in progress. We are continuing our analysis for genes for race 2 resistance in Challenger. Finally, we report that we have developed a Genotyping-by-Sequencing (GBS) protocol for celery and its potential breeding partners in *Apium graveolens*; GBS is a low cost and data-rich method that is ideal for assistance in molecular screening of germplasm of interest.

CALIFORNIA CELERY RESEARCH ADVISORY BOARD
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OBJECTIVES**:**
The overall objective is to acquire the DNA and RNA data that will allow the identification of markers and genes that confer resistance to *Foa* race 4 in celery. The specific objectives are:

1. To acquire the long-read genomic (DNA) sequence of the race 4-resistant celery breeding line (F1S3 76-8-36-124), which is fixed for race 4 resistance;
2. To acquire full-length gene transcripts (IsoSeq of RNA) of the genes in F1S3 76-8-36-124 under race 4 disease pressure;
3. To acquire a TagSeq (RNA) dataset of genes expressed in race 4-resistant vs. susceptible celery;
4. To use the data to identify candidate resistance genes for race 4 resistance;
5. To use previously-obtained datasets (the Challenger genome assembly, a genome by sequence dataset, and TagSeq data particularly of Challenger-*Foa* race 2 interactions) to identify markers and genes that confer resistance to *Foa* race 2 in celery.

RESULTS: The Tables and Figures below show new data for this report, except in some cases where we compare the F1S3 genome to those that we previously showed for the Challenger genome. (Challenger is resistant to *Foa* race 2 but susceptible to *Foa* race 4.) To introgress resistance to *Foa* race 4 into celery germplasm, Challenger was crossed with *Apium graveolens* PI 181714, which is probably in var. *secalinum* (Epstein et al. 2023) and then selfed the F1 three times; PI 181714 is resistant to both *Foa* races 2 and 4. One selection from the breeding is called F1S3 76-8-36-124, which we abbreviate as F1S3 here; resistance to both races appears to be fixed in this line. Results are shown by Objective.

Objective 1. Acquisition (and assembly) of the F1S3 genome. For this grant, DNA was isolated and purified from a population of two-week old, axenic F1S3 76-8-36-124 seedlings in the Van Deynze lab, and made into a (long-read) PacBio HiFi library. The library was sequenced in one SMRT cell on a Revio system at the UC Davis Genome Center; we obtained 85.5 gigabasepairs (Gbp) in 7.1 million reads; average read length was 12,060 bp. The sequence is good quality with a Q30 score of 92.8 % and a Q20 score of 97%. The genome was assembled by Dr. Chaehee Lee in collaboration with the Monroe and Van Deynze labs. Our F1S3 PacBio HiFi assembly has a 26.7X coverage, an estimated haploid length of 3.27 Gbp, and a heterozygosity of 0.23%. Originally, the assembly was in 368 contigs (=segments), but some of these appeared to originate from organelle genomes, either chloroplasts or mitochondria; after examination, 44 contigs were excluded from our assembly resulting in 324 contigs from the nuclear genome. Table 1 has additional details on the assembly.

Celery has 11 chromosomes (Murata & Orton, 1984, Iovene et al. 2008), and based on the cv. Ventura assembly of the 11 chromosomes and Song et al. (2021) Hi-C data, we previously anchored 95.3% of the Challenger contigs to the 11 *Apium graveolens* chromosomes. We improved the 11 Challenger "pseudochromosomes" based on multiple lines of evidence from genetic mapping, read mapping coverage, and location of telomeric repeats. The Challenger genome was then used to anchor the F1S3 genome. Lengths of the segments for each of the F1S3 chromosomes are shown in Table 2; "scaffolds" are a stage of genome assembly in which multiple adjacent contigs are connected into longer sequences.

Table 1. Statistics of the PacBio HiFi assembly of the *Apium graveolens* F1S3 76-8-36-124 germplasm, which is fixed for resistance to *Foa* races 4 and 2.

Assembly	Sequences, #	Total length (Gb)	Length of longest sequence, (Mb)	N50[a] (Mb)
Hap1	757	2.99	148.7	43.1
Hap2	689	3.05	91.8	13.5
Primary	368	3.34	182.2	74.2
Primary-nu	**324**	**3.33**	**182.2**	**74.2**

[a]N50 is a common statistic. To explain the N50, we use the data for the "Primary-nu" assembly, which is our final assembly. Here, the F1S3 genome is in 324 segments. (Ideally, there would be only 11 with each entire chromosome in a single segment.) If we were to sort the 324 segments by length, the longest is 182.2 Mb, and the 74.2-long segment separates the rest of the segments into two parts, each of which contain ½ of the entire genome.

The PacBio HiFi assembly of F1S3 is high quality, and our longer contigs are extremely long; ½ the length of the entire genome is in 14 contigs, and 90% of the length of the entire genome is in 52 contigs (Table 1). All of the standard indicators of assembly quality indicate that our F1S3 assembly has higher 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, six of the 11 chromosomes are assembled end-to-end and 5 are fully assembled on one end of the chromosome but not on the other (Table 3).

Table 2. A comparison of the quality of the genome assemblies of the F1S3 and its celery parent Challenger

Statistic	Genome	
	F1S3	Challenger
No. of chromosomes	11	11
(Haploid) size (Gb)	3.27	3.29
Largest chromosome size, Mb	350.55	349.66
N50, Mb	319.5	330.4
N90, Mb	225.04	227.56
L50	5	5
L90	10	10
% of assembly in the 11 chromosomes	98.62	95.31
No. of anchored contigs in the 11 chromosomes	138	63
N’s per 100 kbp	0.39	0.16

Table 3. Statistics on the assembly of the F1S3: the number of contigs/segments in each of the 11 chromosomes, their length, and whether there are telomeres at each end of the chromosome (T2T), or a telomere at only one end (designated as either T2 or 2T)

Chr	# of contigs	Size (Mb)	Telomeric repeats
Ap01	7	222.02	T2
Ap02	12	339.85	**T2T**
Ap03	8	319.46	**T2T**
Ap04	8	350.55	2T
Ap05	17	336.55	**T2T**
Ap06	21	332.94	**T2T**
Ap07	11	293.41	2T
Ap08	12	292.25	**T2T**
Ap09	7	316.86	**T2T**
Ap10	20	258.98	2T
Ap11	15	225.04	T2
Total	138	3.29 Gb	17

Benchmarking Universal Single-Copy Orthologs (BUSCO) is a standard method to assess genome quality by determining if our F1S3 genome has complete copies of sets of highly conserved, universal single copy genes (Manni et al. 2021a and 2021b). The BUSCO project has selected 1,614 genes that are expected to be present in all Embryophyta (land plants) (Table 4). As shown in Table 4, our F1S3 genome assembly has 99.2% of the expected genes in a complete form, with only 0.4% fragmented and 0.4% missing.

Table 4. A standard "BUSCO" assessment of the quality of the F1S3 and the Challenger assemblies. Based on 1,614 highly conserved, typically single copy genes that are present in all land plants.

BUSCOs	**F1S3**		**Challenger**	
	%	n	%	n
Complete BUSCOs, total	**99.2**	1601	98.6	1591
Complete BUSCOs with a single-copy	**93.4**	1508	87.1	1406
Complete BUSCOs, with a duplicated copy	5.8	93	11.5	185
Fragmented BUSCOs	**0.4**	6	0.4	7
Missing BUSCOs	**0.4**	7	1.0	16
Total BUSCO genes analyzed	-	1614	-	1614

Fig. 1 shows an alignment of our F1S3 chromosomes (or technically pseudo-chromosomes) with those done for Challenger. If their DNA sequences were identical, there would be a single diagonal line. As expected, the two genomes are highly similar but not identical. Because "structural rearrangements" might conceivably be involved in *Foa* race 4 resistance, we performed a structural analysis of differences between the F1S3 and Challenger (data not shown but include a few inversions, duplications and translocations). We'll wait to include the structural analysis in next year's report in case it's important for our identification of resistance gene candidates.

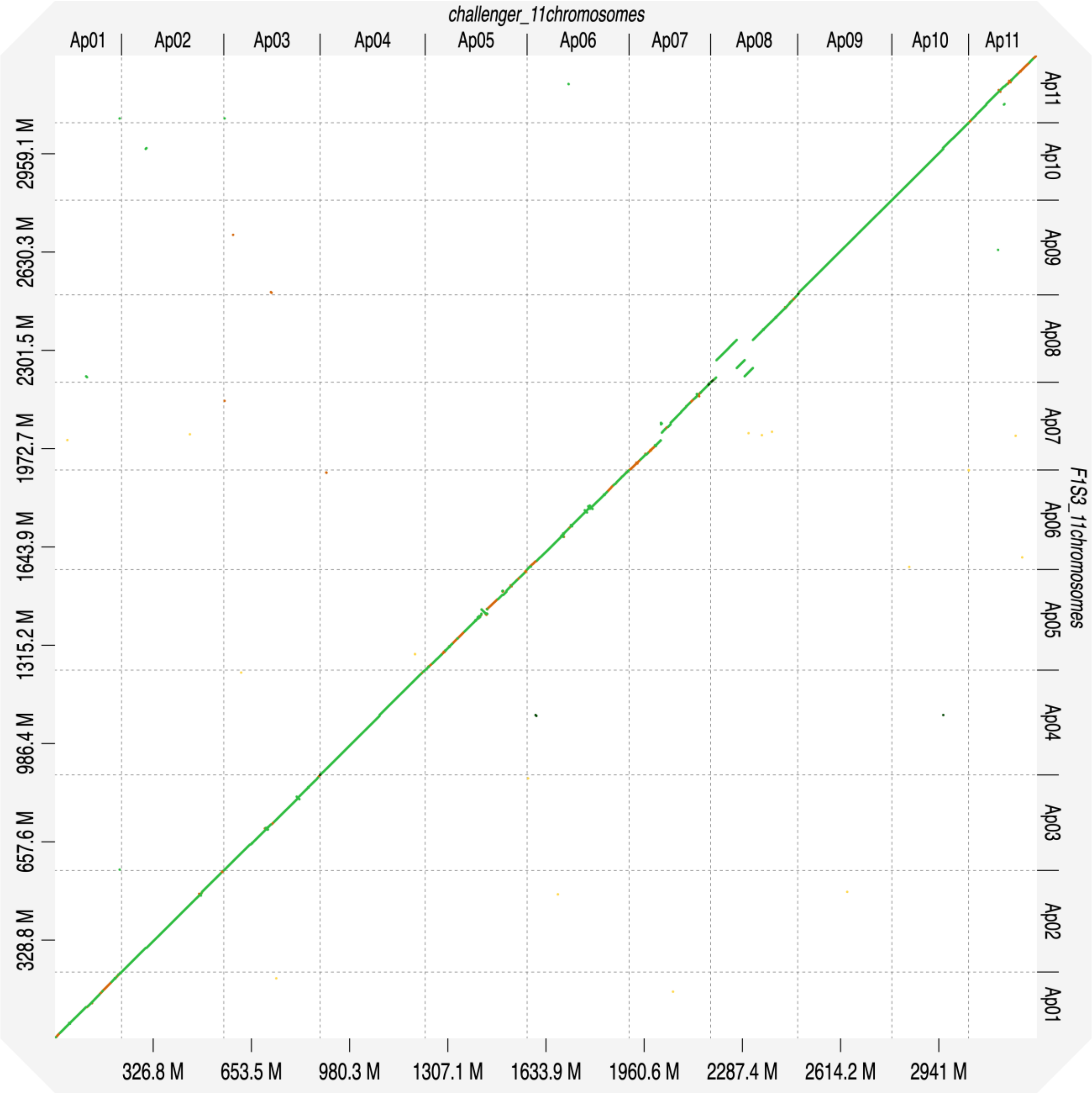


Fig. 1. A dot plot showing that the overall similarity of the F1S3 genomic DNA sequence in 11 scaffolds on the y axis with the Challenger genome by chromosome number on the upper x axis. Information on the assembly of the Challenger genome was shown in last year's report. We improved the F1S3 genome assembly by careful examination and manual correction of some of the regions with mis-assemblies.

An initial part of the process of "annotating" the F1S3 genome requires "masking" the repeat regions of what used to be called "junk DNA.". The *A. graveolens* genomes are large; 86.3%

of the F1S3 genome is comprised of what used to be called “junk DNA” (Fig. 2). More than ¾ (78.6%) of the F1S3 genome is comprised of retroviral elements.

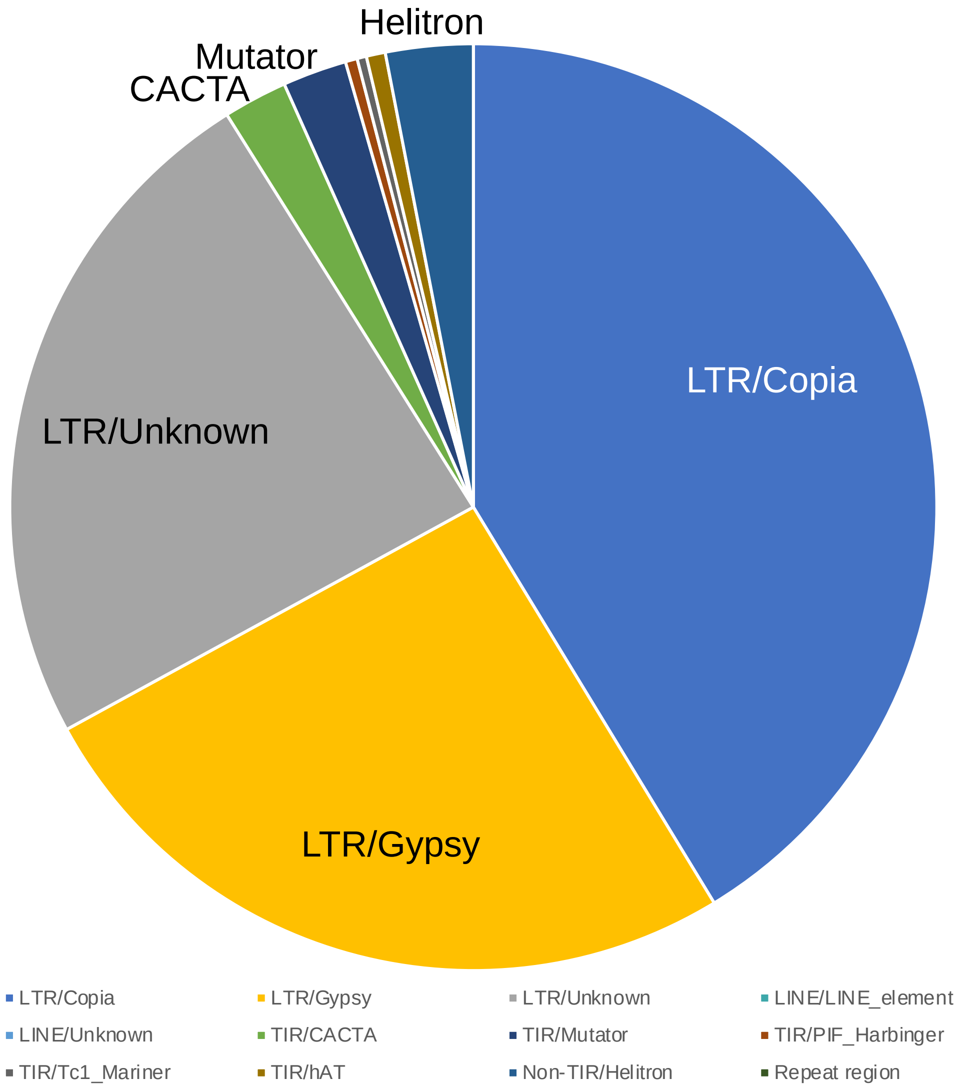


Fig. 2. The types of transposable elements in the F1S3 genome**.** The F1S3 genome is 86.3% transposable elements, which are primarily retroviral elements with long terminal repeats (LTR). Approximately 2/3 of the transposable elements are in either retrotransposon Copia or Gypsy types.

Objectives 2 and 3. Acquisition of IsoSeq and TagSeq datasets. Eriksen and Soule at USDA Salinas produced seedlings for one experiment that was performed at a UC Davis greenhouse in Dec. 2023 through Jan. 2024. The total RNA was extracted from the collected samples for Iso-Seq and are currently being sequenced at the UC Davis Genome Center. For the requisite TagSeq trial (and a more comprehensive IsoSeq backup), we are prepared to conduct a replicated trial at the UC Davis greenhouse starting in mid-April 2024.

Objective 4. Towards identification of markers and genes for resistance to *Foa* race 4 in celery. Analysis of two datasets are in progress: (Bulk segregant analysis, or BSA), which is described below and will be particularly useful for identifying candidate genes for resistance to *Foa* race 4 in the F1S3; and Genotyping-by-Sequencing (GBS). Genotyping-by-sequencing is a low-cost method of identifying differences in celery accessions; we believe that this is the first use of GBS in *Apium graveolens*. We remind the reader that previous evidence indicates that the race 4-resistance gene(s) in this F1S3 is fixed, i.e., is homozygous or invariant, and was inherited from the resistant parent. In contrast, there are many nucleotides (or genes) in the F1S3 that are a mix of those from both parents; portions of the genome that are heterozygous, or variable, do not contain the resistance gene(s) of interest. Fig. 3 shows, for each chromosome, the number of positions ("loci") along the chromosome within each consecutive "window" of 1 million nucleotides (1 Mb) long where the F1S3 population is either a mixture or heterozygous. For example, chromosome 3 is a mix of the two parents along the length of the chromosome, chromosome 6 is a mix of the two parents on one side of the chromosome and chromosome 10 has a mixture of heritage mostly in the middle region of the chromosome; these highly mixed or heterozygous regions inthe chromosomes are unlikely to contain the resistance gene. In Fig. 4, we used the GBS sequences from the susceptible mother and the resistant father, and selected for those SNPs that were homozygous/invariant within three accessions, i.e., in each the F1S3, the susceptible (S) parent , and and the resistant (R) parent, but that differed between S and R parents. Since the resistance gene(s) was inherited solely from the R parent, we can exclude the portions of the genome that have a large number of SNPS/high inheritance from the S parent, shown in orange, and close to 0 inheritance from the R parent, shown in black. We know from Fig. 3 that chromosome 4, for example, is homozygous except in the region of one narrow peak. Fig. 4 indicates that chromosome 4 was inherited mostly fromthe S parent, and only in the region on the very right side from the R parent.

For the Bulk Segregant Analysis (BSA), we first selected the two parents of the F1S3: the susceptible Challenger and the resistant PI 181714. We next selected two populations derived from the F1: 1) the resistant F1S3, in which resistance is fixed, and, 2) a F1S2 line that was segregating for resistance and susceptibility. We next stored a leaf from each individual that was going to be bioassayed for *Foa* race 4-resistance. Then we performed a bioassay for *Foa* race 4 resistance or susceptibility. Because, as expected, the parent, PI181714, and the F1S3 were all resistant, and Challengers were all susceptible, we simply selected a pre-stored leaf from 16 individuals in those populations. Of the 125 F1S2 76-8-27 that we assayed, the progeny were segregating approximately 3 resistant:1 susceptible. As with most plant-pathogen interactions, susceptibility is a recessive trait, i.e., susceptible individuals (in both the susceptible F1S2 and in Challenger) have an "allele" for the resistance gene that is homozygous (the two copies of the resistance gene are the same) and different from the allele in the two resistant lines. Importantly, because the two resistant lines appear to be fixed for resistance, their resistance alleles are also homozygous. Both the F1S3 and the F1S2 have a presumably large number of celery and smallage associated alleles, but with 16 individuals in each population, the F1S3 population and susceptible F1S2 populations will tend to be heterozygous in non-resistance genes that differ between the two parents. Consequently, after "mapping" the DNA sequences onto the F1S3 genome, we can look for differences where the loci (single nucleotide polymorphisms or indels) are homozygous (i.e., different in the resistant vs. the susceptible populations, and the same/homozygous in all the resistant, and the same/homozygous in all the susceptible. Current graphics indicate that the data will be very useful, but are not sufficiently refined to show in our report yet.

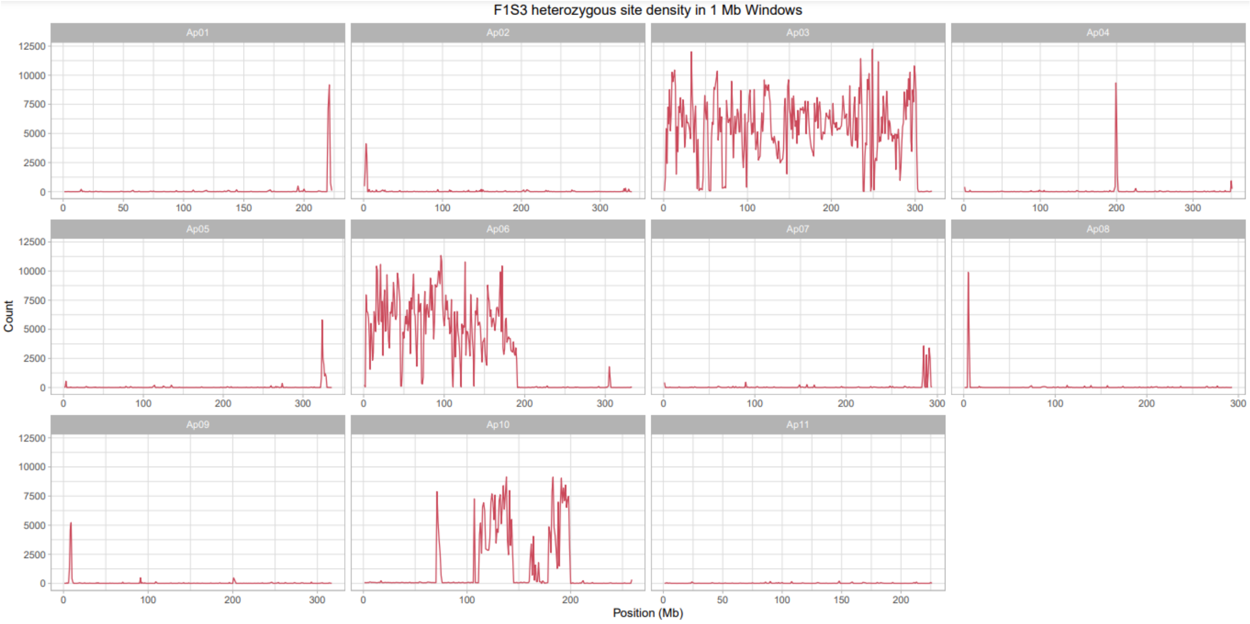


Fig. 3. The F1S3 PacBio (long read) full genome sequence was constructed from the DNA of hundreds of seedlings, i.e., from a mixed population. Each nucleotide in the genome sequence was scored as either variable/heterozygous or homozygous within the F1S3 population. The y axis shows the number of variable nucleotides in a 1 Mb window across the chromosomes. Because resistance is fixed in the F1S3, we can assume that the resistance gene(s) are in a region of very low variability (near 0), and that the resistance gene(s) is very unlikely to be located on, for example, Chromosome 3 (Ap03), which, at least on a population level, contains a mixture of DNA from both parents.

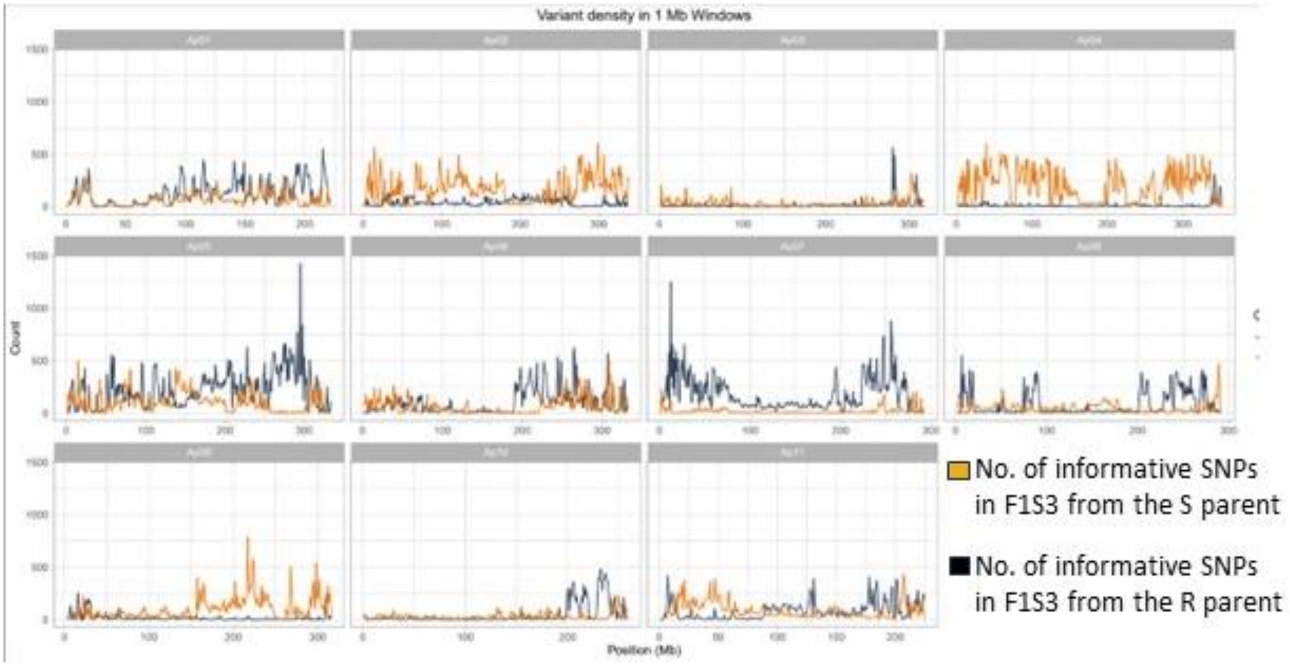


Fig. 4. An analysis of inheritance in the F1S3 population from each of the two parents: the celery Challenger in orange (the "S parent") and the resistant PI 181714 in black (the "R parent"). GBS data of 572,799 differential SNPs were "mapped" onto the F1S3 full genome sequence. The y axis shows the number of SNPs from each parent in each 1 Mb window. We can assume that the resistance genes (or alleles) are 1) fixed, i.e., homozygous, 2) resistant gene SNP(s) are the same in the F1S3 and PI 181714 and differ from the one in Challenger, and 3) expected inheritance within a chromosome in the F1S3 tends to be in "blocks," except where heterozygosity is maintained (which we are included in Fig. 3). As an example, Ap07 (=Chromosome 7), except for a relatively short region on the right, is largely inherited from the race 4-resistant parent and chromosome 4 is largely inherited from Challenger, the susceptible parent, except for a relatively short region on the right.

<u>Objective 5.</u> Towards identification of markers and genes that confer resistance to *Foa* race 2 in Challenger celery.

The Challenger genome is comprised of 3.3 billion nucleotides. Our IsoSeq and TagSeq data indicate that Challenger celery **expresses** 40,464 genes. From IsoSeq, we can publish full-length annotation of 24,064 gene models, and from TagSeq, we have support for expression of an additional 16,400 genes.

The genes in celery are highly concentrated near the ends of the chromomes (Figs. 5A and in Fig. 6, as shown with the red coloring inside the chromosomes. The comparatively long regions across the center of the chromosomes have a high density of retroviral elements, i.e., Copia, Gypsy, and an uncharacterized element with long terminal repeats (LTR), and a comparatively low density of genes. The gene-rich regions towards the ends of chromosomes are associated with a lower density of uncharacterized LTR (Fig 5C).

We can think of disease resistance as involving an initial celery surveillance gene(s), called an R gene, that activates many other "downstream" genes that successfully do the activities required for resistance. As background for readers, resistance to *F. oxysporum* pathosystems in which the resistance (R) genes have been molecularly identified indicate that R genes are generally in either of two groups that are involved in pathogen surveillance: 1) intracellular nucleotide-binding and leucine-rich repeat (**NLR**) groups of proteins with either Toll/Interleukin-1 receptor (TIR)- nucleotide binding (NB) -leucine rich repeat (LRR) or coiled coil (CC)- NB-LRR; or 2) transmembrane or extracellular pattern recognition receptors (PRR). In melon, the gene *Fom-1* encodes a TIR-NB-LRR protein (Brotman et al., 2013). The cabbage gene *FOC1* apparently encodes for a TIR-NB-LRR NLR, and presumably confers resistance to *F. oxysporum* f. sp. *conglutinans* race 1 (Lv et al., 2014). Also in melon, the R gene *Fom-2* encodes for a CC-NB-LRR and confers race-specific resistance (Joobeur, King, Nolin, Thomas, & Dean, 2004). In tomato, the R gene *I-2* encodes for a NLR with a CC-NB-LRR-receptor-like protein (RLP) (Simons et al., 1998) The banana gene RGA2, which is a CC-NB-LRR, may be an important gene for resistance to *F. oxysporum* f. sp. *cubense* race 1 (Dale et al., 2017). PRRs have also been identified as R genes; two *I* genes that were introgressed from *Solanum pennelii* can induce resistance in tomato depending on the pathogen race: the *I-3* gene encodes for a transmembrane protein with an extracellular S-receptor domain and an intracellular serine/threonine kinase domain (SRLK) (A. M. Catanzariti, Lim, & Jones, 2015) and the *I-7* gene encodes for a transmembrane receptor protein with extracellular leucine-rich repeats and short cytoplasmic receptor-like domains (LRR-RLP) (Gonzalez-Cendales, Catanzariti, Baker, McGrath, & Jones, 2016). Two other *I* genes were introgressed from *S. pimpinellifolium; I,* which is also called *I-1*, also encodes for a LRR-RLP (A. Catanzariti et al., 2017). In Arabidopsis, the **r**esistance to ***F. o****xysporum* f. sp. *matthioli RFO3* encodes for a β-lectin receptor-like kinase (Cole & Diener, 2013). A LRR-receptor like kinase *RLK7* and a receptor kinase *MIK2* confers resistance to *F. oxysporum* and other pathogens (Hou et al., 2021; Hou, Shen, & Shao, 2019). The Arabidopsis gene *WAKL22*, which encodes for a protein with a wall-associated receptor-like kinase domain and a second kinase domain also confers resistance to multiple *F. oxysporum f. spp.* that infect Arabidopsis (Diener & Ausubel, 2005).

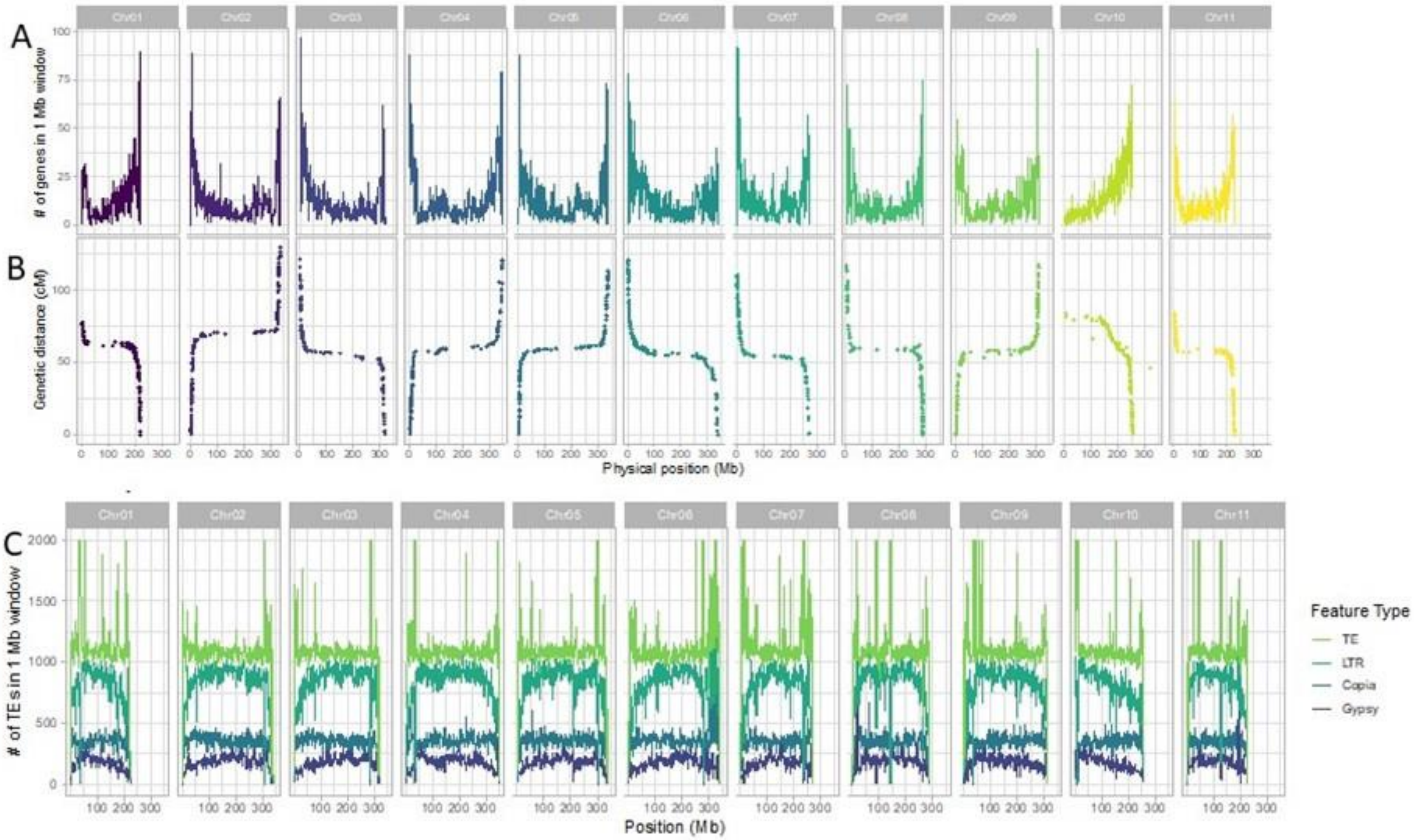
Because of the importance of NLRs in both other *F. oxysporum* and other pathogen pathosystems in plants, we have investigated whether NLRs are candidates for the resistance gene in the Challenger-*Foa* race 2 interaction. We first examined the NLRs in Challenger, shown outside the chromosome diagrams (Fig. 6). These 477 are predicted by DNA sequence, and may or may not be expressed in the plant; any NLRs that are functional in resistance to *Foa* race 2, must be expressed in the roots and crown. We have two types of datasets that show gene **expression**, i.e., the production of an RNA template that actually encodes for the protein: TagSeq and IsoSeq. TagSeq generates a quantitative dataset that estimates how many copies of the template RNA, i.e., how much "gene activity" there was of each of the genes in the genome.

IsoSeq generates a qualitative dataset that indicates the amino acid sequence of the entire protein that the gene encodes for. Based on just the IsoSeq dataset of Challenger tissue that was infested with *Foa* race 2, remarkably, we detected 231 NLRs from the crowns at day 7, 271 NLRs at day 14 and 267 NLRs at day 21. However, we also detected NLRs in Challenger tissues that were not part of our host-pathogen study. As a result of both the pathogen and celery development studies, we have full length gene models of 402 of the predicted 477 NLRs. Based on our TagSeq expression data, 428 of the 477 predicted NLRs are expressed in celery crowns under at least one condition. Clearly, Challenger is not NLR-deficient, and might even serve as a NLR germplasm resource for celery breeding.

We next compared the NLRs in the *Foa* race 2-resistant Challenger with those in the *Foa* race 2-susceptible Ventura (Table 5). Song et al. (2021) reported cv. Ventura, which is susceptible to *Foa* race 2, only has 62 NBS, which can be a more encompassing category than NLRs. However, our BLASTs indicate that Ventura has a similar number of NLRs, but that the Ventura's DNA sequence differs, and is consequently possibly non-functional in a relatively high percentage. The two sub-categories of NLRs that are most likely to be R genes for resistance are called TNLs and CNLs: Ventura has less than 75% DNA similarity in ¼ of Challenger's 135 TNLs and 1/5 of Challenger's CNLs. More specifically, near what's shown as the bottom of chromosome 4 in Fig. 6, there is a 0.4 Mb region (approximately 0.1% of the entire chromosome) that has 16 TNL NLRs that are highly dissimilar in Challenger and Ventura. As described later in this report, our Genotype-by-Sequencing data (Fig. 10, on the right side of Chromosome 4) indicates that this region was inherited from Challenger's race 2-resistant parent.

Fig. 7 shows a Principal Component Analysis of a total of 40,464 genes that were **expressed** in Challenger crowns from plants that were either in mock-infested pots or were exposed to either *Foa* race 2 or *Foa* race 4 at multiple time points. The results show that are relatively few differences in Challenger when exposed to race 2, i.e., the resistant interaction.

Fig. 5. Maps of the 11 chromosomes of *Apium graveolens.* A) The density of genes in celery cv. Challenger. B) The recombination frequency based on a genetic map of *A. graveolens*. C) The density of transposable elements (TE), long terminal repeat retroviral elements (LTR), and Copia and Gypsy retroviral elements.



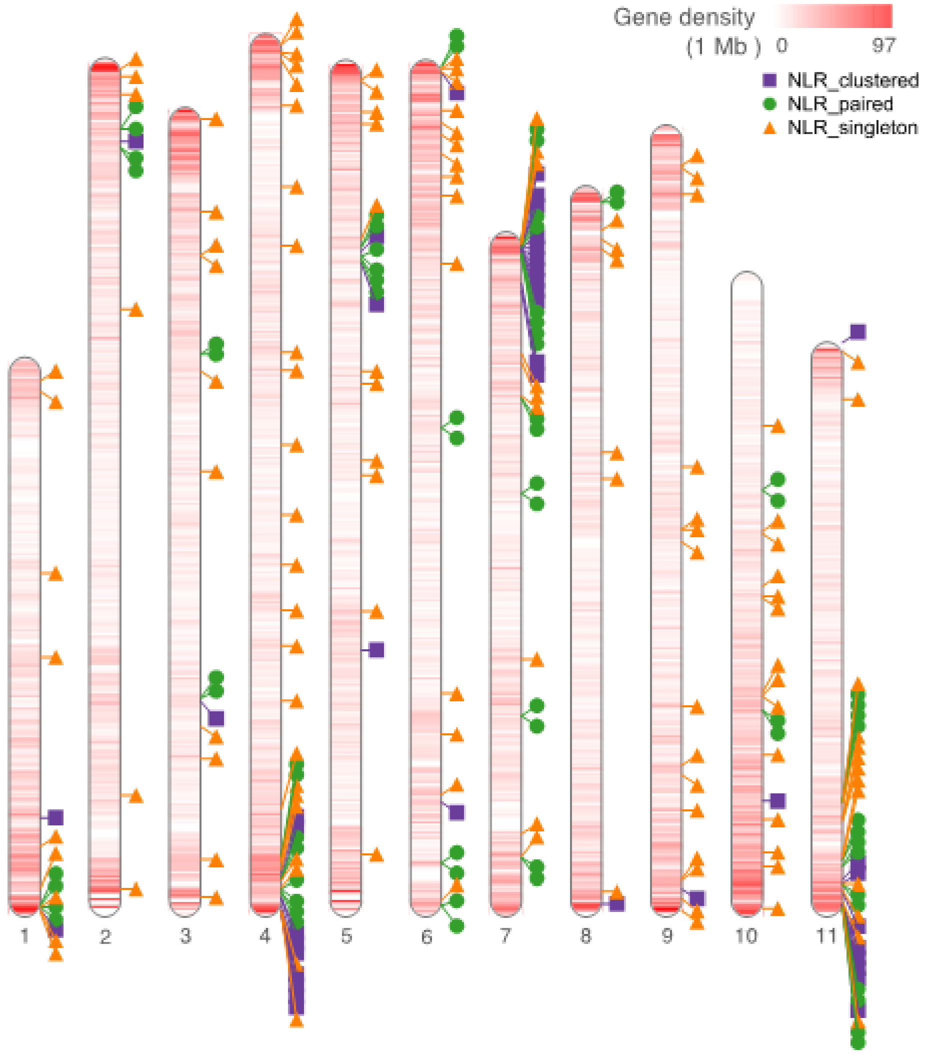


Fig. 6. Inside the 11 chromosomes, the density of 40,464 expressed genes in cv. Challenger are shown in a red scale from white (0 genes/Mb) to red (high density of genes, 97 genes/Mb). The symbols outside the chromosomes indicate the locations of a common type of resistance gene to *F. oxysporum* in other hosts, called NLRs (Nucleotide-binding domain and Leucine-rich Repeat–containing family (Adachi and Kamoun 2022). NLRs are frequently found in clusters, and the purple squares indicate NLR clusters of 3 or more with no more than two non-NLR genes within the cluster. Here, we show the locations of 477 NLRs that were first detected by the NLR Annotator algorithm, and then manually examined to make sure that the NLR domains are within either an annotated gene or an "open reading frame" (ORFs). As indicated in the text, we have evidence of expression in celery crowns of 428 (90%) of the 477 predicted NLRs and full-length gene models of 402 (84%) of the predicted NLRs.

Table 5. A comparison of the similarity of NLRs in Challenger, which is *Foa* race 2-resistant and Ventura, which is susceptible.

	Criterion for category: identity and alignment required, %	No. of NLR loci in each category	No. of the 135 TNLs in each category	No. of the 110 CNLs in each category
Identical	100	239	70	53
Highly similar	≥98<100	95	24	16
Somewhat similar	≥75<98	52	**7**	**19**
Highly dissimilar	<75	90	**34**	**22**
Absent in Ventura	-	1	0	0
Total		477	135	110

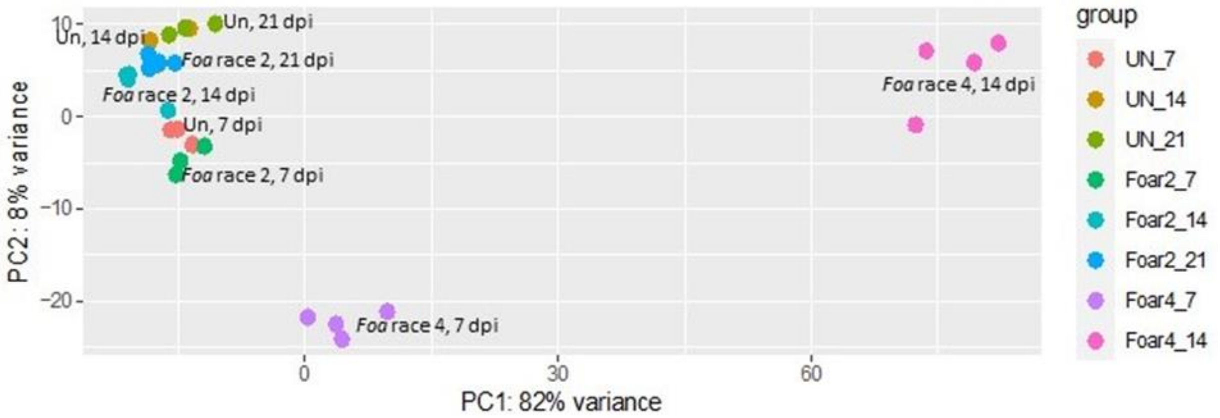


Fig. 7. Principal Component Analysis of the Tag-Seq dataset in Challenger crowns 7, 14 or 21 days post infestation (dpi) with either *Foa* race 2 (*Foar2*), *Foa* race 4 (*Foar4*) or a mock control (UN); no data were collected from the *Foar4* after 21 days because the plants were too debilitated. The data are based on the expression of the 40,464 genes that were detected in any of the crown (Tag-Seq) samples. Not surprisingly, the data show that there are many more differences in gene expression between the uninoculated Challenger and the highly virulent *Foa* race 4, than there are between the uninoculated Challenger and the avirulent *Foa* race 2. (Note that differences on the x-axis (PC1) are much more important than differences in the y-axis (PC2). However, there are some statistical differences in gene expression with *Foa* race 2-infested versus the uninfested controls, particularly between *Foa* race 2-infested and uninoculated Challenger at day 14 (325 significantly up-regulated in *Foa* race 2-infested and 557 down-regulated in the infested. There were also 95 significantly up-regulated genes at day 7 and 264 significantly up-regulated expressed genes at day 21 in the *Foa* race 2-infested compared to the mock-infested control.

As indicated above, genotyping-by-Sequencing (GBS) is a low-cost tool for characterizing celery and other *Apium graveolens* accessions. Using 12 *A. graveolens* accessions that we selected because they either might have been a parent of Challenger and/or because they had different responses to *Foa* race 2, we documented over a million single nucleotide polymorphisms (SNPs) amongst the 12 accessions. The data confirm that the resistant parent of Challenger was the celeriac A0112 and indicate that the main celery parent was probably Tendercrisp (Fig. 9); we are still completing this analysis.

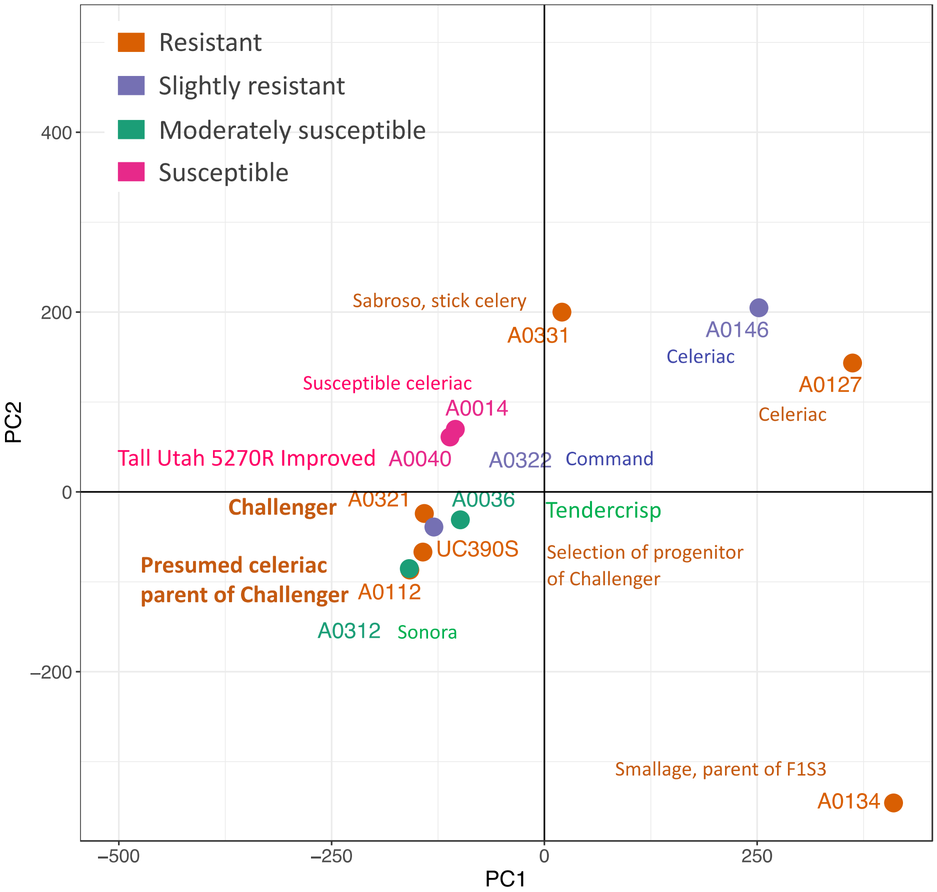
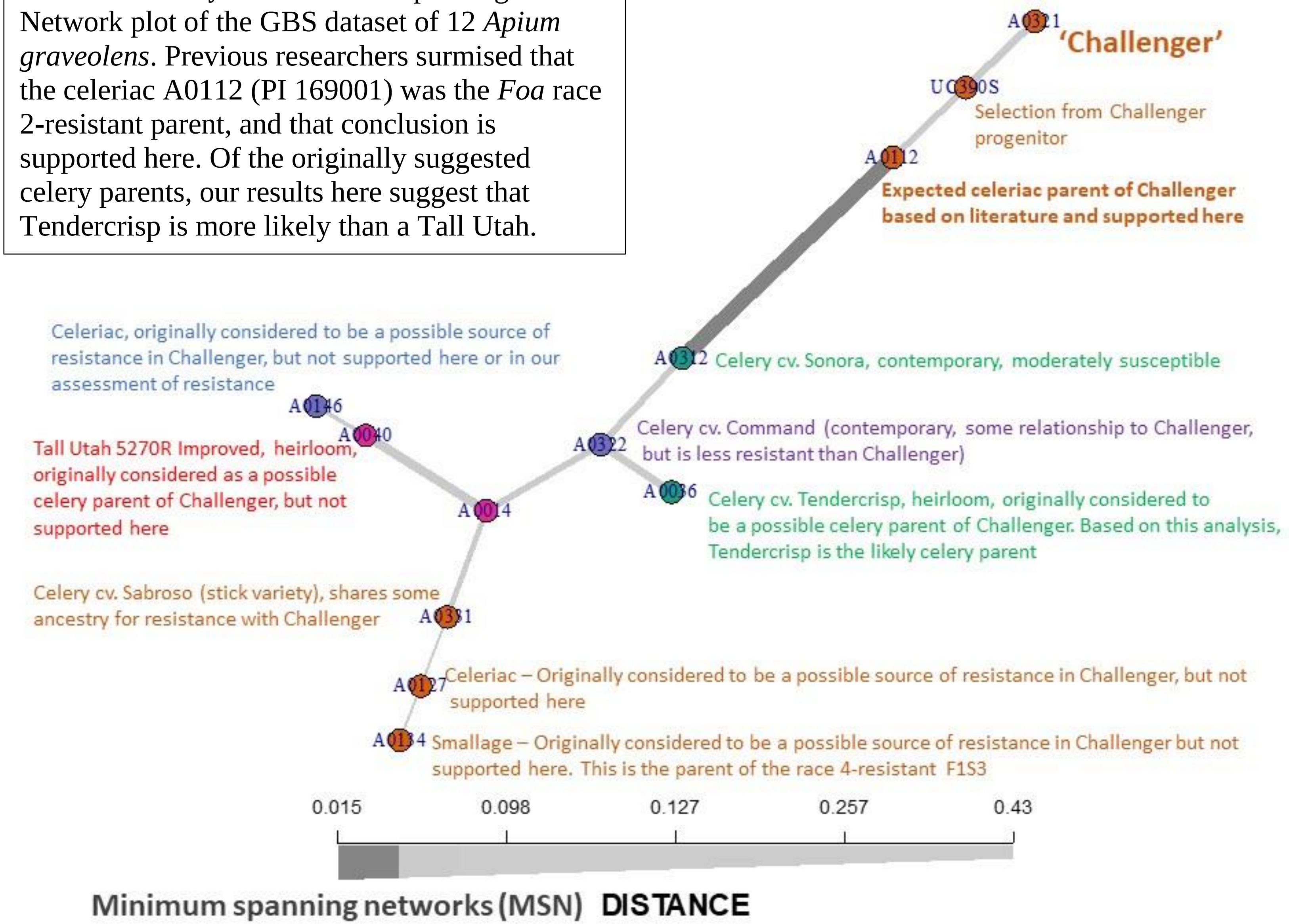


Figure 8. Use of a Genotype-by-Sequencing (GBS) Protocol for celery. Principle component analysis (PCA) of 12 *A. graveolens* accessions using **1,211,111** single nucleotide polymorphism **(SNP) markers (!)**. In this figure, the further apart two points are to each other, the less DNA they have in common; differences in points on the x-axis (PC1) are a much more sensitive indicator of differences than differences in points on the y-axis (PC2). Resistance or susceptibility to *Foa* race 2 are shown in the legend. The accessions include 1 smallage (A0134, parent of the F1S3, in the lower right corner), 3 celeriac (A0112, A0127, and A0146) and the rest are celery. The PCA supports the conclusion that the F1S3 parent PI 181714 is the most diverse of the 12 accessions, and that accessions do not cluster by resistance to *Foa* race 2.

Fig. 9. Use of a Genotype-by-Sequencing (GBS) Protocol for celery. A Minimum Spanning Network plot of the GBS dataset of 12 *Apium graveolens*. Previous researchers surmised that the celeriac A0112 (PI 169001) was the *Foa* race 2-resistant parent, and that conclusion is supported here. Of the originally suggested celery parents, our results here suggest that Tendercrisp is more likely than a Tall Utah.



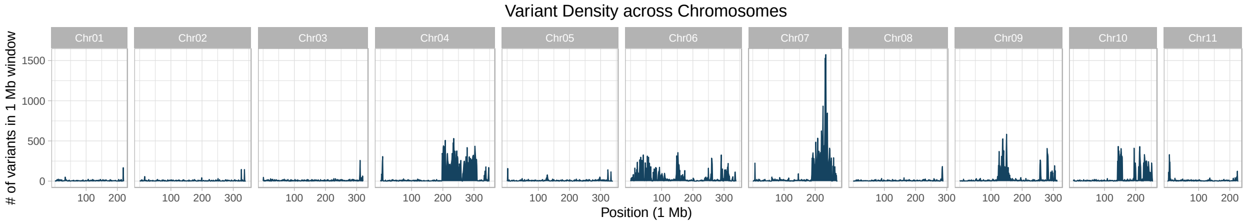


Fig. 10. Use of a Genotype-by-Sequencing (GBS) Protocol for celery: Zones of introgression of the race 2-resistant celeriac parent into celery. GBS data of 116,381 differential SNPs were "mapped" onto the Challenger full genome sequence. The y axis shows the number of SNPs in each 1 Mb window that are shared by Challenger and the race 2-resistant celeriac parent PI 169001, and that differ from Tendercrisp. Because we have good SNP coverage across the genome (Fig. 11 lower panel), the race 2-resistance gene(s) are likely in the regions of the chromosomes above with peaks.

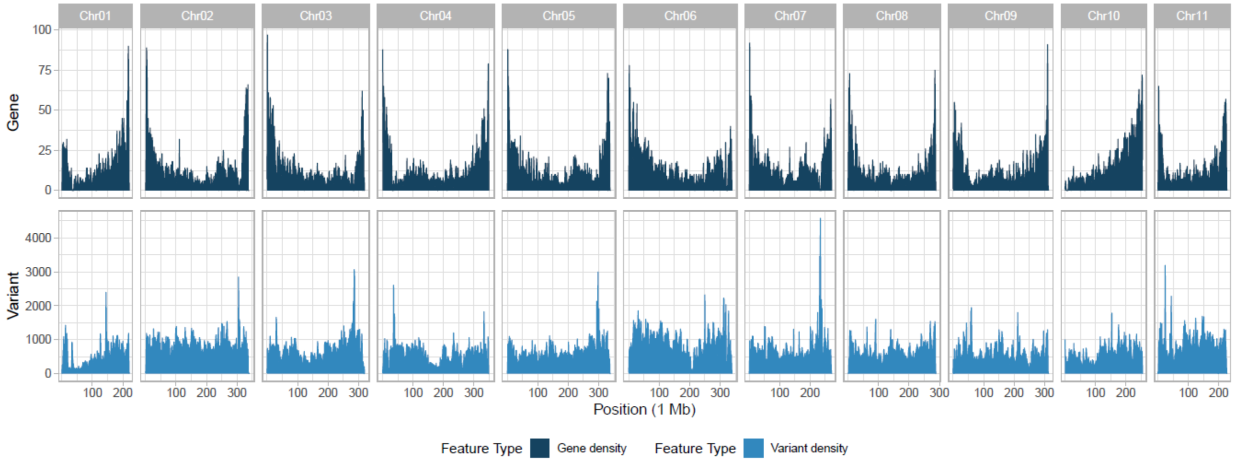


Fig. 11. Upper panel, a histogram of the number of genes in each 1 Mb window across each Challenger chromosome. Lower panel, a histogram of the number of GBS variants in the 12 accessions in each 1 Mb window across each Challenger chromosome. The 12 accessions are shown in Fig. 8 and described in Fig. 9.

While we have focused on selecting R gene candidates, we have also used the TagSeq data to characterize the differentially expressed "downstream" response genes in Challenger to *Foa* race 2 and to *Foa* race 4. In the susceptible interaction, Challenger expresses a greater quantity of the typical downstream genes associated with resistance than occur in the resistant interaction with *Foa* race 2. However, without the appropriate R gene (which is present in the F1S3 but not in Challenger), Challenger's response to *Foa* race 4 is apparently either too little, too late, or in the wrong location to save itself.

As one example of how we are putting together all of the information to identify R gene candidates in Challenger to *Foa* race 2, NLR gene Ap04_NLR65 is a TIR-NBARC-LRR. It is expressed significantly more in crowns from plants that were infested with *Foa* race 2 than when Challenger was infested with *Foa* race 4 at 7 dpi, which would be consistent with a race 4 effector suppressing the ability of the host to detect the pathogen. Based on the location of Ap04_NLR65, the "allele"/form of Ap04_NLR65 was inherited from the race 2-resistant parent; the form of Ap04_NLR65 in the susceptible celery host Ventura has less than 75% identity with the resistant form. We also have an older TagSeq dataset from crowns of Tall Utah 5270R Improved plants, which are closely-related to cv. Ventura, that were either uninfested, or infested with *Foa* race 2 or race 4; mapping of these data onto the Challenger assembly should help to either confirm or deny that Ap04_NLR65 is an R gene candidate (and a probable marker) for race 2 resistance.

To summarize our results with Challenger for Objective 5, to date, we have assembled the cv. Challenger genome to chromosome level, anchored the contigs to a genetic map, and can provide full-length annotation of 24,064 gene models and RNA support for expression of an additional 16,400 genes. We are currently using bioinformatic algorithms that predict R genes (NLRs and PRRs), transcriptomics, genomic comparisons to the *Foa* race 2-susceptible cv. Ventura, and Genotype-by-sequencing (GBS) introgression-zone data to assemble gene candidates for the resistance gene to *Foa* race 2. Finally, we developed a GBS protocol for celery for scoring different accessions (Fig. 8) and used it to both confirm the parentage of Challenger (Fig. 9) and to identify those regions of the genome that are likely or unlikely to have the race 2-resistance gene(s).

Acknowledgements. The *A. graveolens* recombination frequencies for the genetic map data were generously provided by Bejo Zaden BV, Netherlands. We are grateful for the CCRAB support.

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ERI-23 (unsubmitted)

Project Title:

“Year 2: Celery Breeding for Resistance to Fusarium Oxysporum f. sp. apii Race 2 and Race 4”

Renee Eriksen, USDA ARS Salinas

Oleg Daugovish, UCCE Ventura County

Christopher Greer, UCCE San Luis Obispo County

Alexander Putman, UC Riverside

Due to continuing re-evaluation of the data for 2022-23, as of February 2, 2026, a final report of this work has not yet been submitted. The researchers are aware of the need to complete the data evaluation and will submit as soon as it is available.

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&
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California Celery Research Advisory Board
Annual Report for 2022-2023
Management and Economics of Insect Pests on Celery

Principal Investigator: Dr. Thomas Perring, Department of Entomology
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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", was transplanted on 20 Oct 2022 at Agricultural Operations, University of California, Riverside, California (Figure 1A). The plots were three beds wide (two rows per bed on 60" centers) by 25 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, three separate drench treatments consisted of Beleaf 50 SG, Movento 240 SC, and Verimark 200 SC. The remaining treatments were foliar applications of Beleaf 50 SG, Exirel 100 SE, Mustang Maxx, VST exp. (3 rates with Vader as an adjuvant), an organic rotation, and a low input IPM rotation. The organic rotation included Aza-direct, Entrust SC, Pyganic 5.0 EC, Trilogy EC, Dipel DF, Grandevo WDG, and Venerate XC along with Oroboost as an adjuvant. The low input treatment consisted of Exirel 100SE, Beleaf 50 SG, Radiant 1.0 SC, and Dipel DF (Table 1). All of the foliar treatments used Dyne-amic as an adjuvant at 0.25% with the exception of the VST exp. and organic applications. Mustang Maxx was used as the chemical standard. 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 (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- Beleaf – drench (12/22, 1/20, 2/10, 3/3)	50 SG	2.8 oz	9C	FMC
3- Movento - drench (12/22,1/20, 2/10,3/3)	240 SC	5.0 oz	23	Bayer
4- Verimark - drench (12/22, 1/20, 2/10, 3/3)	200 SC	10.0 oz	28	FMC
5- Beleaf – foliar	50 SG	2.8 oz	9C	FMC
Dyne-amic		0.25%		Loveland
(12/22,1/9, 2/10, 3/3)				
6- Exirel – foliar	100 SE	20.5 oz	28	FMC
Dyne-amic		0.25%		Loveland
(12/22, 1/9, 2/10)				
7- Mustang Maxx - foliar	0.8 EC	4.0 oz	3A	FMC
Dyne-amic		0.25%		Loveland
(12/22, 1/9, 1/20, 1/27, 2/2, 2/10)				
8- VST-Exp. +		32 oz		Vestaron
Leprotec	Btk	16 oz	11	Vestaron
Vader		0.125%		Loveland
(12/22,1/9,1/20,1/27, 2/2, 2/10, 3/6)				
9- VST-Exp. +		64 oz		Vestaron
Leprotec	Btk	16 oz	11	Vestaron
Vader		0.125%		Loveland
(12/22, 1/9, 1/20, 1/27, 2/2, 2/10, 3/6)				
10- VST-Exp. +		128 oz		Vestaron
Leprotec	Btk	16 oz	11	Vestaron
(12/22, 1/9, 1/20, 1/27, 2/2, 2/10, 3/6)				
11- Organic IPM				
a-Aza-direct		32 oz	UN	Gowan
b-Entrust	SC	8.0 oz	UNB	Corteva
c-Pyganic +	5.0EC	17.0 oz	3A	MGK
Trilogy	EC (1%)	128.0 oz	UN	Certis
d-Dipel	DF	1 lb	11	Valent
e-Grandevo	WDG	3 lb	UNB	Marrone Bio

f-Venerate	XC	128.0 oz	UNB	Marrone Bio
Oroboost		0.25%		Oro-Agri
(a=12/22, b=1/9, c=1/20, d+e=1/27, c=2/2, d+f=2/10, d+f=3/6)				
12- IPM				
a-Exirel	100 SE	13.5 oz	28	FMC
+ Beleaf	50 SG	2.8 oz	9C	Bayer
b-Radiant	SC	8.0 oz	5	Corteva
+ Beleaf	50 SG	2.8 oz	9C	Bayer
c-Exirel	100 SE	13.5 oz	28	FMC
d-Dipel	DF	1 lb	11	Valent
Dyne-amic		0.25%		Loveland
(a=12/22, b=1/9, c=1/27, d=2/10, d=3/6)				

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

Figure 1. A is a celery field plot at UCR Agricultural Operations in 2022-2023. 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 19 January 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, earwigs, and beet armyworm, in numbers sufficient to analyze. Statistical differences between treatments were seen for beet armyworm (Leps) on 19 January (Figure 3). The best performing lepidopteran treatment was Exirel-foliar, which had zero percent damage. The Beleaf-foliar and VST-Exp products had the highest levels of lepidopteran infestation. Aphid numbers were highest in the untreated plots and there was low insect pressure for lygus and earwigs. Heavy periods of rain were present throughout the growing season.

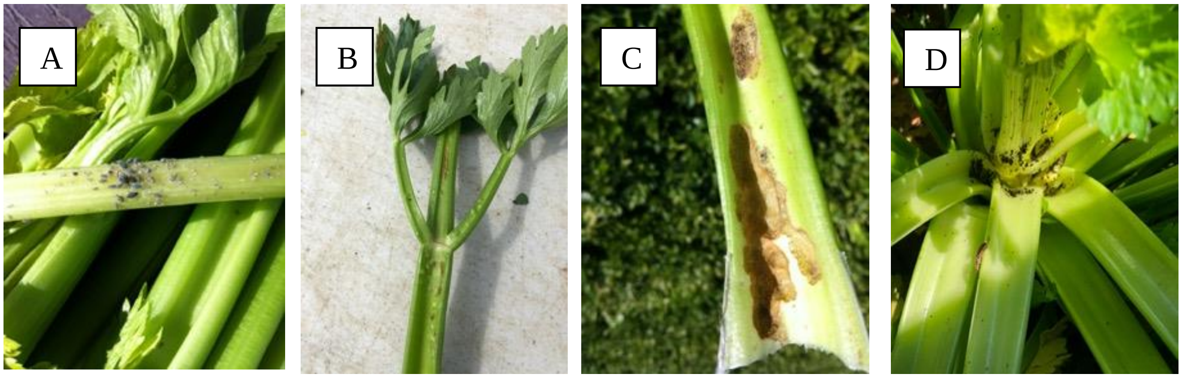
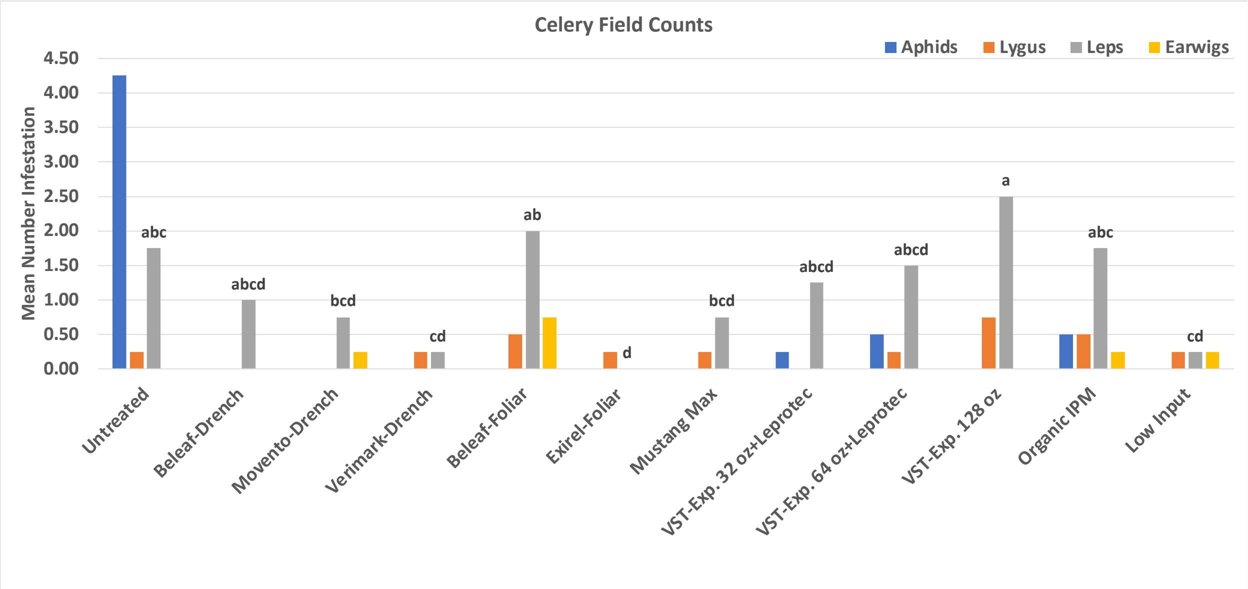


Figure 2. Insects and damage seen in the Celery IPM Trials at the UCR Agricultural Operations research study. A. Aphids; B. Lygus bug damage; C. Beet armyworm damage; D. Earwig damage.

Figure 3. Field counts level of infestation on 19 January (insects plus damage)



Harvest Evaluations:

The field was evaluated at harvest on 17 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 12% (3.0/25 plants) damage (Table 2). There were significant differences between the treatments for worm control. Verimark, Exirel, Mustang Maxx, Movento, and the IPM rotation were the better performing products with 4% or less damage. The drench treatment of Verimark sustained 0% lepidopteran damage. The foliar treatments of Exirel, Mustang Maxx, and the low input rotation, all sustained 2% or less of lepidopteran damage. Cutworm pressure was very low this season. Leafminers and whiteflies have not been included because of low pest pressure. Similarly, while a few earwigs and lygus were seen in our field counts, there was very little damage on the plants at harvest. Cabbage aphid was present in the field this year, but no significant differences were seen between treatments. 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	--	8.00	3.00 ab	0.50
2- Beleaf – drench (12/22, 1/20, 2/10, 3/3)	2.8 oz	5.25	2.00 abcde	0.00
3- Movento - drench (12/22,1/20, 2/10,3/3)	5.0 oz	5.75	1.00 bcde	0.00
4- Verimark - drench (12/22, 1/20, 2/10, 3/3)	10.0 oz	2.00	0.00 e	0.25
5- Beleaf – foliar Dyne-amic (12/22,1/9, 2/10, 3/3)	2.8 oz 0.25%	6.00	2.75 ab	0.50
6- Exirel – foliar Dyne-amic (12/22, 1/9, 2/10)	20.5 oz 0.25%	4.25	0.50 cde	0.00
7- Mustang Maxx -foliar Dyne-amic (12/22, 1/9, 1/20, 1/27, 2/2, 2/10)	4.0 oz 0.25%	4.00	0.25 de	0.00
8- VST-Exp. + Leprotec Vader (12/22,1/9,1/20,1/27, 2/2, 2/10, 3/6)	32 oz 16 oz 0.125%	5.50	3.50 a	0.25
9- VST-Exp. + Leprotec Vader (12/22, 1/9, 1/20, 1/27, 2/2, 2/10, 3/6)	64 oz 16 oz 0.125%	6.75	1.25 bcde	0
10- VST-Exp. + Leprotec (12/22, 1/9, 1/20, 1/27, 2/2, 2/10, 3/6)	128 oz 16 oz	3.75	2.5 abc	0
11- Organic IPM a-Aza-direct b-Entrust c-Pyganic + Trilogy d-Dipel e-Grandevo f-Venerate Oroboost (a=12/22, b=1/9, c=1/20, d+e=1/27,	 32 oz 8.0 oz 17.0 oz 128.0 oz 1 lb 3 lb 128.0 oz 0.25%	4.75	2.25 abcd	0

c=2/2, d+f=2/10, d+f=3/6)				
12- IPM a-Exirel + Beleaf b-Radiant + Beleaf c-Exirel d-Dipel Dyne-amic (a=12/22, b=1/9, c=1/27, d=2/10, d=3/6)	13.5 oz 2.8 oz 8.0 oz 2.8 oz 13.5 oz 1 lb 0.25%	0.75	0.5 cde	0
ANOVA F_{value}		1.431	2.455	0.764
ANOVA P value		0.202	0.021	0.672

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

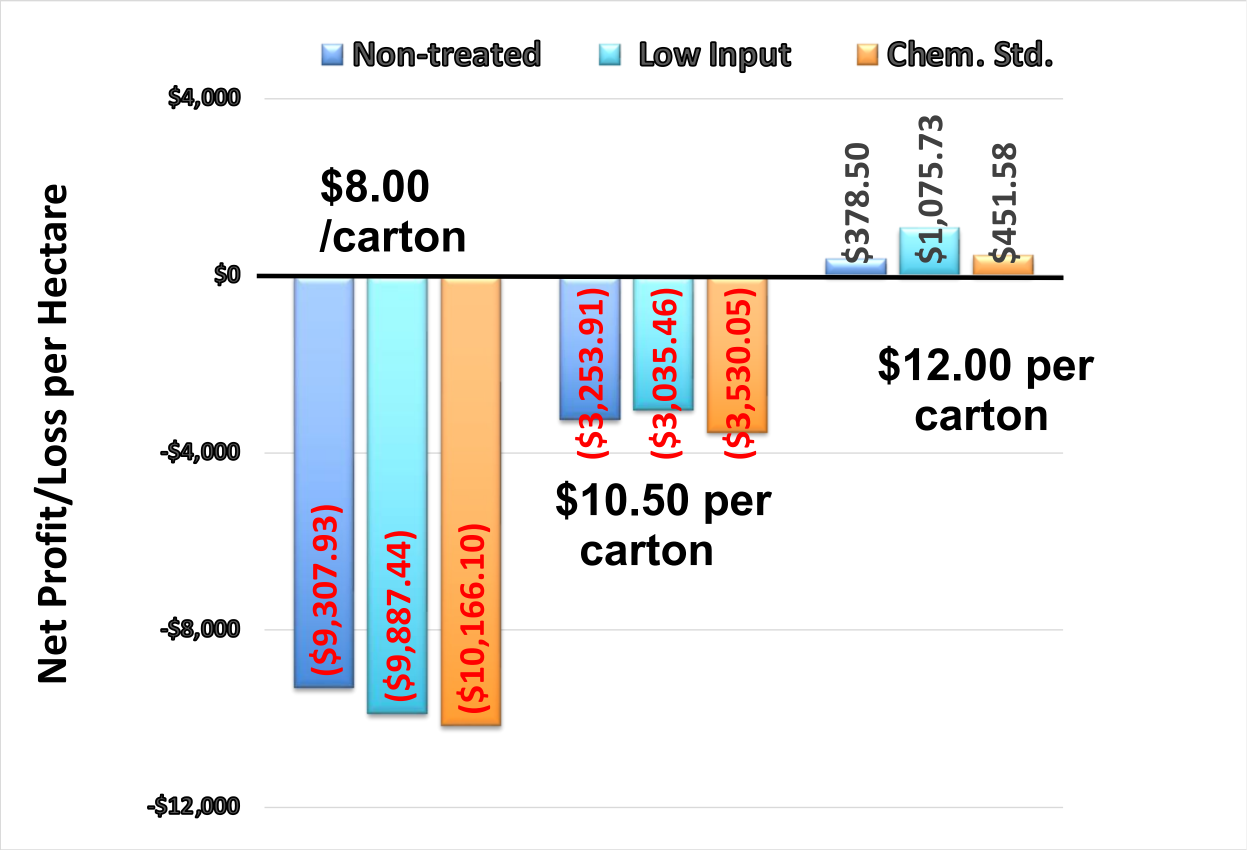
Objective II. Economic Analyses of an IPM and Chemical Standard Trial.

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) Mustang Maxx®. In the IPM plots chemicals were applied 5 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 2022. 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.

Lygus Bug Resistance Research

We are continuing to develop quick and effective tools that can be used to determine levels of resistance of insects in field populations. Based on feedback from the Celery Research Advisory Board (CRAB), our initial efforts have been focused on the lygus bug. Lygus bug is also a pest for strawberry growers, and Dr. Perring had contacts within the Cal Poly Strawberry Center who were willing to assist us in our efforts to develop the biochemical tests necessary to detect resistance in field populations of lygus bugs. Kiley Jensen, a graduate student of the Strawberry Center, provided a susceptible lygus bug colony to do baseline resistance testing. The lygus bug colony has been established successfully and we are ready to start testing.

Kiley had also done some toxicity profiles of Bifenthrin, which is a pyrethroid. His results indicated that there was widespread resistance in several field collected populations in the Santa

Maria, CA region. Pyrethroids are commonly used in many agricultural regions that celery is grown, and the next step will be to establish toxicity profiles for the susceptible lygus colony and other field collected populations. Once the resistant populations have been identified, development of biochemical assays to identify the resistance mechanisms in the resistant insect populations will be done.

Success in this project will provide improved guidance toward making better decisions when choosing an insecticide.

Future Research

In our 2023 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. 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 an additional season in our organic IPM treatment rotation to determine if these products are viable options.