



Monona Terrace Community and Convention Center, designed by Frank Lloyd Wright

39th INTERNATIONAL CARROT CONFERENCE

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**39th International Carrot Conference Program
Madison, Wisconsin
August 21-24, 2018**

Tuesday, August 21

Opening reception, 6-8 pm Community Terrace, Monona Terrace Community and
Convention Center

Wednesday, August 22

Community Terrace, Monona Terrace Community and
Convention Center

- 8:00 am Registration, Coffee and Continental Breakfast**
- 9:00 am **Conference welcome and overview** — Irwin Goldman and Phil Simon,
Department of Horticulture and USDA-ARS, UW-Madison
- 9:15 am **Welcome** — Associate Dean Bill Barker, Dean, College of Agricultural and Life
Sciences, UW-Madison
- 9:25 am **Overview of Wisconsin’s Agricultural Economy** — Jeremy Beach, Renk
Agribusiness Institute, UW-Madison
- 9:45 am **From apples to zucchini: Wisconsin specialty crop production**— Jed
Colquhoun, Department of Horticulture, UW-Madison
- 10:05 am Break sponsored by Wisconsin Potato and Vegetable Grower’s Association**



- 10:45 am **Carrot cyst nematode survey in the Holland Marsh, Ontario, Canada and surrounding carrot growing regions, 2017** — Dennis Van Dyk, Kevin Vander Kooi, Mary Ruth McDonald, Qing Yu, Ekaterina Ponomareva, Fengcheng Sun
[ABSTRACT 201](#)
- 11:05 am **Integrated weed management without linuron herbicide in carrot** — Jed B Colquhoun, Richard A Rittmeyer, Daniel J Heider [ABSTRACT 202](#)
- 11:25 am **Stacked in-row cultivation tools improve weed management and tool selectivity in carrots** — Daniel C Brainard, Sam F Hitchcock Tilton, Chun-Lung Lee [ABSTRACT 203](#)
- 11:45 am **In-row mechanical cultivation in carrots: Can “cultivation-tolerant” varieties improve selectivity?** — Sam Hitchcock Tilton, Chun-Lung Lee, Daniel C Brainard
[ABSTRACT 204](#)

12:05 pm Lunch sponsored by Seminis – Monsanto



- 1:30 pm **Historical and modern trends in vegetable processing** — Nick George, Midwest Food Products Association, Madison, Wisconsin [ABSTRACT 301](#)
- 2:00 pm **The Organic Carrot Landscape** — Micaella Colley, Organic Seed Alliance and Wageningen University, Netherlands [ABSTRACT 302](#)

2:30 pm Break sponsored by Vilmorin, View Posters



- 3:30 pm **Seasonal and spatial patterns of Aster Yellows phytoplasma infectivity and pathogen diversity in Wisconsin carrots** — Russell Groves, Justin Clements, Marjorie Garcia, Linda Crubaugh, Emily Duerr, Agnieska Zwolinska, Richard Immink, Stan Maree, Saskia Hogenhout [ABSTRACT 401](#)

- 3:50 pm **Yields of carrot cultivars grown on organic soils in Ontario, Canada in relation to seasonal climate** — Kevin D Vander Kooi, Shawn Janse, Mary Ruth McDonald [ABSTRACT 402](#)
- 4:10 pm **Trends in Carrot IPM in Central Ontario, Canada** — Zachariah Telfer, Mary Ruth McDonald [ABSTRACT 403](#)
- 4:30 pm **Carrot endophytes: influence of genotype and management system on abundance, diversity and potential functional roles** — Sahar Abdelrazek, Lori Hoagland, Philipp Simon [ABSTRACT 404](#)
- 4:50 pm **Evaluation of carrot germplasm under abiotic stressful conditions in Bangladesh** — M.A. Rahim [ABSTRACT 405](#)
- 5:10 pm **Integrating induced mutagenesis in carrot breeding programs; harnessing the advantages of radiation breeding** — P. Huzar Fatty Beejan [ABSTRACT 406](#)
- 5:30 pm **New nematicides for the management of root-knot nematodes in carrots** — Joe Nunez [ABSTRACT 407](#)
- 6:00 pm *Reception*
- 6:30 pm *Banquet dinner*
After dinner speakers: Steve Pincus and Beth Kazmar, Tipi Produce, Evansville, Wisconsin
[Carrot Production on a Diversified Organic Farm in Wisconsin](#)



Thursday, August 23

- 8:00 am** **Coffee and Continental Breakfast**, Community Terrace, Monona Terrace
Community and Convention Center
- 9:00 am **The QTL mapping of carrot root traits with a high resolution bin map
based on backcross inbred lines** — Tingting Sun, Chenggang Ou,
Chengjiang Li, Huaifu Ren, Zhiwei Zhao, Feiyun Zhuang [ABSTRACT 502](#)
- 9:20 am **Extended studies of subspecies variation of *Daucus carota* using
genotyping-by-sequencing** — David M. Spooner, Philipp W. Simon, Holly
Ruess, Emmanuel Geoffriau, Charlotte Allender, Najla Mezghani,
Fernando Martínez Flores [ABSTRACT 501](#)
- 9:40 am **Parentage analysis in carrot lines characterized by SSR markers** —
Sabine Karin Clausen, Steffen Dahlke, Søren K. Rasmussen [ABSTRACT 503](#)

10:00 am **Break sponsored by Vilmorin**



- 11:00 am **Improving the carrot genome assembly and gene prediction: strategies
to overcome challenges from short read genome assemblies** — Massimo
Iorizzo, Hamed Bostan, Su Liu, Shelby Ellison, Douglas Senalik, Philipp
Simon [ABSTRACT 601](#)
- 11:20 am **Epistatic interactions contributing to carotenoid presence in carrot
(*Daucus carota* L.)** — S.L. Ellison, K. Coe, D. Senalik, and P.W. Simon
[ABSTRACT 602](#)
- 11:40 am **New sources of root-knot nematode (*Meloidogyne* spp.) resistance in
carrot germplasm** — Philip A. Roberts, William C. Matthews, Tra T.
Duong, Philipp W. Simon [ABSTRACT 603](#)
- 12:00 pm** **Lunch sponsored by Bejo Seeds, Inc.**
Lunchtime Presentation: Professor Lew Friedland
Political Communications and Discourse in Wisconsin



- 1:15 pm **Development of genomic-prediction strategies for top height and flavor in a carrot (*Daucus carota*) germplasm collection** — Keo Corak, Shelby Ellison, Claire Luby, Doug Senalik, Massimo Iorizzo, David Spooner, Irwin Goldman, Phil Simon, Julie Dawson [ABSTRACT 701](#)
- 1:35 pm **Root and shoot phenotypes quantified by computational image analysis**— Edgar Spalding [ABSTRACT 702](#)
- 1:55 pm **Using digital image-based phenotyping to investigating the genetic bases of root shape and market class in carrot** — Scott Brainard, Julie Dawson, and Irwin Goldman [ABSTRACT 703](#)
- 2:15 pm **Analysis of the *Or* gene and its role in carotenoid accumulation in carrot** — Kevin Coe, Shelby Ellison, Doug Senalik, Julie Dawson, and Philipp Simon [ABSTRACT 704](#)
- 2:35 pm Afternoon Break**
- 3:15 pm **Mapping QTL for carrot shoot traits in diverse crop management systems** — Charlene Grahn, Erin Silva², Shelby Ellison³, Philipp Simon [ABSTRACT 801](#)
- 3:35 pm **Utilizing ionomic analysis in carrot** — Adam Bolton, Charlene Grahn, Morgan Pettit, Ivan Baxter, Lori Hoagland, Micaela Colley, Erin Silva, and Philipp Simon [ABSTRACT 802](#)
- 3:55 pm **Discussion of 40th International Carrot Conference Meeting Site**
- 4:00 pm Carrot tasting and flavor workshop (Julie Dawson); Poster session**
- 6:30 pm *Dinner on your own*

Friday, August 24 *Breakfast on your own*

8:00 am Buses leave from Park Hotel on Capitol Square for field trial at Paul Miller Farm, Hancock, Wisconsin and demonstration plots at Hancock Agricultural Research Station

Box lunch provided at Hancock Agricultural Research Station

1:30 pm First bus departs Hancock for Madison, estimated return time, 3 pm

ABSTRACTS

ABSTRACT 201 Carrot cyst nematode survey in the Holland Marsh, Ontario, Canada and surrounding carrot growing regions, 2017

Dennis Van Dyk¹, Kevin Vander Kooi², Mary Ruth McDonald², Qing Yu³, Ekaterina Ponomareva³, Fengcheng Sun⁴

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²*Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada*

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The carrot cyst nematode *Heterodera carotae* Jones is a recently discovered pest in the Holland Marsh, region of Ontario, Canada, where carrots are grown on muck soils. This nematode was previously only reported in Europe and Michigan. In recent years, patches of carrots in commercial fields in the Holland Marsh were found with poor growth, stunting, forking with a proliferation of secondary roots, and cysts associated with the damage. Thirty carrot fields in this region were sampled in November 2016 and then sampled again following a rotational crop in November 2017. An additional 28 samples were taken in 2017 in surrounding carrot growing regions of both muck and mineral soils. Soil samples from the top 20 cm of soil were sampled in an X pattern in each field. Samples were analyzed for the presence of carrot cyst nematode. Veriform nematodes were extracted using a Baermann funnel and the Fenwick method was used for cysts. Second stage juveniles, males, and cysts were recovered. The species was confirmed as *H. carotae* using morphological and molecular methods. On average, cyst counts in 2017 were higher and juvenile counts lower than in 2016. Ninety four percent of fields sampled within the Holland Marsh contained some level of carrot cyst nematode but only one field outside of the Holland Marsh was positive for this nematode. No carrot cyst nematode was found in any mineral soil carrot fields, which is consistent with what has been reported in Michigan. Carrot cyst nematode cyst counts increased from 2016 to 2017 in most fields, regardless of rotational crop. There appears to be a maturation process in which all of the potential cysts do not mature and detach from carrot roots in time to be extracted in a fall soil sample after carrots are grown.

ABSTRACT 202 Integrated weed management without linuron herbicide in carrot

Jed B Colquhoun¹, Richard A Rittmeyer¹, Daniel J Heider¹

¹University of Wisconsin-Madison, Madison, WI, USA

Carrot weed management is challenging given variable crop emergence, slow early-season growth and few viable control options. Linuron herbicide has been a mainstay for conventional growers but is limited in use on coarse-textured, low organic matter soils and where resistant weeds have become common. With this in mind, studies were conducted to: 1) identify herbicide programs that provide season-long control; 2) evaluate pre-emergent herbicides on cereal nurse crops interseeded among carrots for wind erosion control; 3) identify carrot varieties that suppress weeds with rapid emergence and establishment; and, 4) investigate gibberellic acid applications to enhance vegetative top growth. In the carrot herbicide evaluation, pendimethalin applied pre-emergence followed by prometryn at the three- and five-carrot leaf stage resulted in the most consistent weed control and crop yield among the commercially-available programs without linuron. S-metolachlor, pendimethalin and prometryn were evaluated at multiple rates relative to barley, oat and wheat growth as nurse crops interseeded with carrots. By 14 days after treatment, 1.12, 1.68 and 2.24 kg ai/ha prometryn and 1.0 kg ai/ha s-metolachlor resulted in greater barley, oat and wheat injury than in the non-treated nurse crops or where pendimethalin was applied. Several carrot varieties were also evaluated for their ability to tolerate and suppress weeds. For example, 'Bolero' established a broad crop canopy sooner than most other varieties and maintained 95% of the weed-free carrot yield when weeds were present. In contrast, 'SFF' variety established slowly and never achieved full ground cover in canopy development. As a result, weed biomass was greater than in any other variety and the yield of the weedy carrots was only 72% of the weed-free yield. Carrot competitive ability was further enhanced with two 200 mg/L gibberellic acid applications at the 3- and 5-leaf crop growth stage without compromising root yield. In our current research we're integrating these strategies with dense seeding configurations and strip-tillage for a more holistic and less herbicide-intensive approach.

ABSTRACT 203 Stacked in-row cultivation tools improve weed management and tool selectivity in carrots

Sam F Hitchcock Tilton¹, Chun-Lung Lee¹, Daniel C Brainard¹

¹Michigan State University, East Lansing, Michigan, United States

In a series of field experiments we evaluated the impact of four in-row mechanical weeding tools on carrots (*Daucus carota*) and two surrogate weed species: yellow mustard (*Sinapis alba*), and German millet (*Setaria italic*). Finger weeders (F), torsion weeders (T), flexline harrows (X), and Duo hilling discs (HD) were applied to carrots and weeds individually and in combination (tool 'stacking') when the carrots had 1 true leaf, approximately 25 days after planting. Tool combinations gave greater weed control and selectivity than single tools. The F+HD combination particularly resulted in the greatest selectivity and reduction in the time required for subsequent hand weeding. No tool effects were detected on carrot quality or yield. However, across all tools, lower final carrot densities were associated with lower yields. The finger weeder controlled more weeds as soil moisture increased or when more soil was moved into the carrot row. Whereas the torsion weeder did not appear to kill weeds through hilling and its efficacy was greater under drier soil conditions. In many cases, yellow mustard was more susceptible to death by burial than German millet.

ABSTRACT 204 In-row mechanical cultivation in carrots: Can “cultivation-tolerant” varieties improve selectivity?

Sam Hitchcock Tilton¹, Chun-Lung Lee¹, Daniel C Brainard¹

¹*Michigan State University, East Lansing, Michigan, United States*

One approach to improving the selectivity of mechanical cultivation tools in carrots is to identify varieties that are most tolerant to those tools. Identification of such “cultivation-tolerant” varieties and their associated traits may also be helpful for breeding efforts aimed at reducing costs associated with weed control. Field trials were conducted on sandy soils in central Michigan to compare cultivar response to each of four types of in-row weeding tools (finger weeder, torsion weeder, hilling discs, flextine harrow). Tools were applied to eight different cultivars of commercially available carrots at three sites in 2016 and 2017. Characterization of root vs shoot partitioning for each cultivar was evaluated based on the area of fresh root and shoot tissue at the time of cultivation. Differences in the survival rate of carrot cultivars were observed for the torsion weeder at all three sites and for the flextine harrow in one of three sites, but not for the finger weeder or hilling discs. At the time of cultivation, carrot cultivars varied in their root size at all three sites, but varied in shoot size at only 1 of 3 sites. Over all sites, there was a positive relationship between carrot shoot size and tolerance to the finger weeder, and a positive relationship between carrot root size and tolerance to the torsion weeder, although both relationships were only marginally significant ($p=0.095$; $p=0.061$). These results demonstrate that commercially available carrot cultivars vary in their tolerance to cultivation tools, and suggest that early partitioning to root tissue confers tolerance to tools that uproot (torsion weeder), while early partitioning to shoot tissue confers tolerance to tools that bury (finger weeder). A relationship was also observed between cultivar seed size and plant size at the cotyledon and 1st true-leaf stage, suggesting that screening of carrot cultivars or seed-lots for large seed size may be a useful strategy for improving carrot tolerance to cultivation tools, thereby improving the selectivity of those tools.

ABSTRACT 301 Historical and modern trends in vegetable processing

Nick George¹

¹*Midwest Food Products Association, Madison, Wisconsin*

NO ABSTRACT

ABSTRACT 302 The Organic Carrot Landscape

Micaela Colley¹

¹*Organic Seed Alliance and Wageningen University*

Organic consumers are commonly driven by nutrition, flavour and fresh eating qualities in vegetables, and carrots are widely known for all of these benefits. US organic carrot production reached \$88 million dollar sales value in 2016, and accounted for 11.7% of total carrot production acreage, down from 14.7% peak in 2011, but much higher than 5.8% in 2005 (USDA-NASS, 2016). This represents a greater percentage of the total market compared with other vegetable crops and over 5% of total organic vegetable sales. Popularity for nutritional health benefits, and ease of fresh raw consumption of carrots, particularly favourable for children, may be a key reason why organic carrots hold a significant portion of the total carrot market. In recent years the organic market has also led the trend of introduction of novel colour carrots, including purple, yellow, red, and white, growing in popularity as “rainbow carrots”, among chefs and organic grocers.

Carrot production challenges overlap between organic and conventional systems including major pests and disease, but the management practices and prioritization of cultivar traits often differs between the two systems. Organic carrot producers rely on an integrated pest management approach with an emphasis on cultural methods including use of cover crops, crop rotations, mechanical weed management, and selection of crop cultivar. Public and private research efforts and Extension programs are striving to address production challenges in response to expansion in organic carrot production (Seaman, 2016; Simon et al., 2017). In particular weed competitiveness is of primary interest in organic carrot breeding and cultivar choice as weed management through flaming, cultivation and hand weeding is a significant labor cost input and weed tolerance can vary by variety (Peruzzi et al., 2007, Seaman, A., 2016, Colquhoun et al., 2017). Root knot nematodes, (*Meloidogyne spp.*) are a key pest in both organic and conventional production, particularly in California, the lead state in carrot acreage, and organic producers rely on field selection, crop rotations and practices to boost soil health rather than application of soil fumigants. Recent release of nematode-resistant breeding lines for key species, *M. incognita* and *M. javanica*, holds promise for helping address this pest (USDA ARS, 2015; Parsons et al., 2015). Insect pests and disease pressures including leaf Blights, root rots, rust fly, and lygus, are also generally common to both organic and conventional systems and in some cases organic pesticide and fungicide treatments are employed in addition to cultural methods (Seaman, 2015).

Bibliography:

- Colquhoun, J. B, R. A Rittmeyer, D. J Heider. 2017. Tolerance and Suppression of Weeds Varies among Carrot Varieties. *Weed Technology* 31(06):1-6.
- Parsons, J., W. Matthews, M. Iorizzo, P. Roberts, and P.W. Simon. 2015. QTL for *Meloidogyne incognita* nematode resistance in carrot. *Molec. Breeding* 35:114.
- Peruzzi, A., Ginanni, M., Fontanelli, M., , Raffaelli, M., and P. Bàrberi. 2007. Innovative strategies for on-farm weed management in organic carrot. *Renewable Agriculture and Food Systems*. 22(4); 246–259
- Seaman, A. (ed). 2016. Organic Production and IPM guide for carrots. Cornell University, New York State Department of Agriculture and Markets. NYS Publication No. 133. (accessed April 12, 2018) <https://ecommons.cornell.edu/bitstream/handle/1813/42892/2016-org-carrots-NYSIPM.pdf?sequence=5>
- Simon, P.W, J.P Navazio, M Colley, C McCluskey, J Zystro, L Hoagland, P.A Roberts. 2017. “The Cioa (Carrot Improvement for Organic Agriculture) Project: Location, Cropping System and Genetic Background Influence Carrot Performance Including Top Height and Flavour.” *Acta Horticulturae* 1153 (1153): 1–8.
- USDA, National Agricultural Statistics Service (NASS). 2017. Certified Organic Survey 2016 Summary. (accessed August, 2018) http://usda.mannlib.cornell.edu/usda/current/OrganicProduction/OrganicProduction-09-20-2017_correction.pdf
- USDA, National Agricultural Statistics Service (NASS). 2017. Vegetables, 2016 Summary. ISSN: 0884-6413. (accessed, August, 2018) https://www.nass.usda.gov/Publications/Todays_Reports/reports/vegean17.pdf
- USDA, ARS and University of California Riverside. 2014. Notice of release of NH2168 Carrot. (accessed August, 2018) <https://www.ars.usda.gov/ARSUserFiles/50901000/files/simon/publications/Simon%20Release%20Nh2168.pdf>

ABSTRACT 401 Seasonal and spatial patterns of Aster Yellows phytoplasma infectivity and pathogen diversity in Wisconsin carrots

Russell Groves¹, Justin Clements¹, Marjorie Garcia¹, Linda Crubaugh¹, Emily Duerr¹, Agnieszka Zwolinska², Richard Immink³, Stan Maree⁴, Saskia Hogenhout⁴

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Few studies link mechanistic aspects of gene function to the ecological niche of an organism and the environment. In the current investigation, we hope to gain a better understanding of how specific genes drive epidemics of insect-vectored parasites. Aster yellows phytoplasma (AYp) excel at controlling their hosts. These bacterial parasites are colonizers of two Kingdoms, where they propagate intracellularly inside the vascular phloem cells and throughout the body of their insect vectors. AYPs are obligate colonizers requiring both their plant and insect hosts for survival and spread in nature, and specific virulence proteins (effectors) interact with and degrade plant transcription factors conserved among plant species. Thus, AYP effector genes have a long reach whereby they have the potential to drive AYP epidemics by interacting with conserved plant transcription factors, alter plant development, and increase plant susceptibility to polyphagous insect vectors. The goal of this project is to quantify the presence and prevalence of single effector genes in relation to parasite fitness and the broader environment. The overall hypothesis is that a set of core effectors may affect AYP fitness in Wisconsin carrot, where AYP outbreaks have been prevalent in recent years. Thus, the presence or absence of a specific effector gene in an AYP population may provide an accurate predictor of the severity of an approaching AYP outbreak in a region.

ABSTRACT 402 Yields of carrot cultivars grown on organic soils in Ontario, Canada in relation to seasonal climate

Kevin D Vander Kooi¹, Shawn Janse¹, Mary Ruth McDonald¹

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Carrots are among the highest value field vegetable grown in Ontario. Approximately one third of the carrots produced in Ontario are grown in the Bradford/Holland Marsh area where soil conditions are ideal for carrot production: organic peat soils (pH 5.5-6.5), organic matter 50-75%. Seed companies are continually breeding new carrot cultivars that require testing under Ontario conditions. For the past forty years the University of Guelph's Muck Crops Research Station (MCRS), in the Holland/Bradford Marsh (44° 5' N, 79° 35' W), has conducted cultivar trials for seed companies that submit cultivars from around the world to be evaluated on organic muck soil.

Cultivars were assessed for total yield, marketable yield, quality parameters and disease ratings. Carrots are typically stored in cold storage at 1-3°C and 85-95% RH for up to eight months. Storability is important because the majority of carrots produced are stored and marketed through the winter months. Stored carrots are evaluated for percent of marketable carrots, percent decay and weight loss.

It is important to have cultivars that will yield well from year to year regardless of the weather. This was investigated using data from 2013-2017 on cultivars Cellobunch, Envy, Belgrado, Bastia, Berlin and SV2384. These cultivars performed consistently in harvest evaluations and in storage, and Cellobunch and Envy are benchmark cultivars that have been in the trials for over 20 years. Cultivars Belgrado and Berlin have been developed to produce oversized carrots. These had the highest mean marketable yields (101 t/ha and 99.5 t/ha) compared to the average (82.0 t/ha). Yield of cultivars varied over the years but the ranking was consistent. The variability was related to weather. Marketable yield of carrots was positively correlated with mean temperatures in June ($r = 0.97$, range (18.2- 19.4)).

ABSTRACT 403 Trends in Carrot IPM in Central Ontario, Canada

Zachariah Telfer¹, Mary Ruth McDonald¹

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An integrated pest management program for carrots has been running for the past 12 years in the Holland Marsh, which is a major carrot production region in central Ontario, Canada. The program is delivered through the University of Guelph Muck Crops Research Station. Between 300 and 400 acres of carrots have been scouted each year since 2012. Cavity spot and Pythium root dieback are the most prevalent diseases in the marsh, often occurring in 100% of scouted fields with an average of 20% of roots affected by these diseases each year. Fusarium dry rot occurs every year in 5-15% of fields, although overall a low proportion of roots (<5%) are infected. Sclerotinia white mold was not observed at harvest any of the years. Aster yellows has not been a problem in the past five years, with no affected roots in 2015 and 2017 and no more than 1% of roots with symptoms, on average, in scouted fields. This corresponds with aster leafhopper monitoring, where populations were typically low and well managed over the season. Carrot rust fly populations have also been low. In only 3 of the past 6 years have the average trap counts exceeded the threshold of 0.1 flies/trap/day for fresh market carrots. On average the counts never exceeded the 0.2 flies/trap/day threshold for processing carrots. This is consistent with damage; average rust fly damage was never over 1% in the past six years. The carrot weevil is the most important insect pest in the marsh, with the highest damage and population counts. Average damage across scouted fields was around 5%. Overall, scouting confirms most pests and diseases are being managed appropriately and continued scouting ensures that future problems will be detected.

ABSTRACT 404 Carrot endophytes: influence of genotype and management system on abundance, diversity and potential functional roles

Sahar Abdelrazek¹, Lori Hoagland, Philipp Simon

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Carrot is a nutritious and high-value crop, but it is subject to several agronomic challenges and many growers lack access to chemical inputs to help overcome them. The plant microbiome more specifically endophytes has recently emerged as a key factor in the health and productivity of plants and there is much interest in determining whether these communities can be manipulated to enhance crop performance. Soil is generally the primary factor affecting microbiome composition, though genotype has been shown to have a smaller effect in some crops indicating that it may be possible to select for microbial relationships in breeding programs. For this to occur in carrot, differences in the composition, heritability and potential functional role of microbes among genotypes must be determined. The goal of this study was to begin to address these knowledge gaps by investigating these relationships in nine carrot genotypes with diverse genetic backgrounds and agronomic characteristics. Specifically, we determined the antagonistic potential of endophytes isolated from carrots grown under organic and conventional management, identified fungal endophyte communities in a subset of genotypes grown in these crop systems using next-generation sequencing and identified endophytes in seeds and seedlings grown under axenic conditions and determined their potential to fix nitrogen, solubilize phosphorous, produce siderophores and IAA. Results of these studies provide evidence that carrot taproots are colonized by a diverse assortment of bacterial and fungal endophytes. Endophyte communities in carrots grown in organic systems were more diverse and had greater antagonistic activity, though smaller yet significant differences among genotypes were apparent supporting the hypothesis that endophyte composition is least in part, under genetic control. A wide variety of endophytic microbial taxa with plant growth promoting properties (PGPRP) were present in seeds providing evidence that these microbes could be part of a core microbiome. Differences in endophyte communities among carrot developmental stage and genotypes were apparent, providing further support that these microbial relationships are under genetic control. Results of these studies provide evidence that endophytes play a critical role in helping carrots acquire nutrients and withstand pathogen stress, and someday it may be possible to begin selecting for these beneficial relationships in breeding programs. In the meantime, management practices that improve soil health will aid in colonizing carrot roots with beneficial microbes that can enhance crop performance. Moreover, microbes with PGPRP isolated in this study could be used as inoculants to further improve carrot performance, especially in degraded soils.

ABSTRACT 405 Evaluation of carrot germplasm under abiotic stressful conditions in Bangladesh

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An ongoing study evaluated carrot wild relatives (CWR) and cultivars adapted to warmer climates in warm, dry, and saline field conditions to initiate intercrossing of climate-resilient traits from carrot wild relatives to adapted, nutritious cultivated germplasm, and to field trial CWR x carrot intercrosses and their derivatives. A series of experiments were conducted in drought area (extremely northern), saline (southern part) and warm (north western) parts of Bangladesh during 2014 to 2017. About 175 wild carrot genotypes were tested for root and seed production. In the saline areas only 13 genotypes formed storage roots but among them 7 produced seeds. The salinity level was about 28ds. In the drought areas, among 100 germplasm accessions only 26 accessions formed storage roots and 16 accessions produced seeds. In the warm area, out of 116 accession tested, 16 accessions produced seeds. Seed germination ranges from 30-80%. In summary, over the three years trial, the accessions PI652410 produced roots and seeds under all stressful conditions. Moreover, the cultivated Brazilian varieties (Brasilia Agroflore and Prima Agorflore) also performed better under warm and drought conditions but not well under saline conditions.

Keywords: Carrot, *Daucus carota*, drought, salinity, abiotic stress, root, seed

ABSTRACT 406 Integrating induced mutagenesis in carrot breeding programs; harnessing the advantages of radiation breeding

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In an era of advanced plant breeding using recombinant DNA technologies, the century old tried and tested method of induced mutagenesis as applied to carrot improvement is of interest as it is both safe and relatively less expensive, making the technique ideal for niche market needs and for developing countries. A project on induced mutation using gamma irradiation has been started in the developing country of Mauritius. With a production of 4152.7 tons harvested from an area of 292.6 ha in 2017, carrot is an important crop for the island. This production is solely from seeds imported from major seed companies. The seeds account for a growing part of the farmers' production costs due to the high seed prices. The local carrot seeds have fallen into disuse and are not cultivated by the growers. The radiation breeding project aims at ensuring food and nutritional security and decreasing reliance on seed imports. It involves the use of gamma rays for inducing mutation as a means of introducing genetic variations. From the large number of ensuing mutated populations, putative mutants with characteristics of interest in terms of disease resistance, yield and improved nutritive value, will be selected. Modern molecular techniques, by increasing the efficacy of screening and selection, help eliminate chimeras and the large populations that previously deterred from induced mutagenesis in crop breeding programs. The broadening of carrot cultivar diversity for developing countries can enlarge the gamut available to researchers and plant breeders and enable diverse carrot production possibilities. Combined with optimized quality seed multiplication, the locally bred carrot seeds selected for local production will help decrease production costs while more nutritious carrots will benefit the health and quality of life of inhabitants.

Keywords: Carrot breeding, induced mutagenesis, gamma irradiation, food security

ABSTRACT 407 New nematicides for the management of root-knot nematodes in carrots

Joe Nunez¹

¹University of California Cooperative Extension Kern County, Bakersfield, CA 93307.

Root-knot nematodes (RKN) are the economically the most important pathogens in California's fresh market carrot production. They reduce the quality and yield of the harvested roots by inducing galling and forking of the main root. The galled feeder roots are less able to supply the plant with water and nutrients which results in yield reduction. Currently the California carrot industry relies on pre-plant soil fumigants such as Telone II (a.i. 1,3-dichloropropene) and metam sodium or metam potassium. However due to severe restrictions and regulations for human and environmental safety often substantial parts of fields need to be excluded from fumigation because of buffer zone requirements. New novel nematicides have emerged from major agriculture chemical companies in the last four years that have shown excellent efficacy in the control of RKN. Fluazaindolizine (DuPont-Dow), fluensulfone (Adama) and fluopyram (Bayer) have shown excellent nematicide properties in field trials conduct in moderate to high RKN infested soils. These new chemistries have effective new modes-of action, lower mammalian toxicity, and lesser environmental impacts than previous generations of nematicides.

ABSTRACT 501 Extended studies of subspecies variation of *Daucus carota* using genotyping-by-sequencing

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Daucus carota is widely distributed worldwide. Its taxonomy is complex with quite the variant interpretations of the number of subspecies and varieties and, in total, more than 60 taxa have been proposed for the phenotypic variants observed within the highly variable “*D. carota* complex”, here interpreted to include all taxa with $2n = 18$ chromosomes. Genotyping-by-sequencing (GBS) is a recently developed DNA technique that identifies genome-wide single nucleotide polymorphisms (SNPs) through next-generation sequencing technology, producing a powerful and cost-effective genotyping procedure. It has been particularly useful to investigate diversity and taxonomy at the species level, including two recent studies in *Daucus carota* (Arbizu et al. 2016. BMC Evol. Biol. 16: 234; Mezghani et al. 2018, [Genet. Resour. Crop Evol., 65: 1359–1368](#)). The present study extends these two studies by adding germplasm from areas not examined before and new taxa, obtained from (1) the Agrocampus Ouest – IRHS, France, (2) the Warwick Crop Centre, England, and (3) an expedition in Spain in 2016 of inland and coastal environments, including the four main Balearic Islands of Mallorca, Menorca, Ibiza, and Formentera. In total, 297 accessions were examined, with 188 as placeholders from the above two studies, and 109 new accessions from the three new sources. GBS identified 29,041 filtered SNPs used in the analyses. Maximum Likelihood phylogenetic analysis and Structure analysis identified nine taxonomically and geographically associated major groups. Most notably, the series of forms growing along the Mediterranean and Atlantic coasts referred to broadly as *D. carota* subspecies *gummifer* co-occur with members of subspecies *carota* in four of these groups (Western Europe, Southern Europe and Balearic Islands, Iberian Peninsula and Morocco, North Africa), suggesting parallel evolution of the former in maritime environments. The 18-chromosome species *D. gracilis* (N Africa) and *Tornabenea annua* and *T. tenuissima* from Cape Verde fall firmly within the *D. carota* clade, forcing a reconsideration of their classification as subspecies of *D. carota*.

ABSTRACT 502 The QTL mapping of carrot root traits with a high resolution bin map based on backcross inbred lines

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Cultivated carrot is considered as the cross of eastern cultivar and wild carrot and developed various shape types by means of selection and introgression during several centuries. Root shape and size determined the yield and appearance quality to meet the demands for both fresh and processing market. However, there were few studies on QTL mapping of traits associated with root shape and size due to lacking a high resolution genetic map with large amounts of molecular markers distributed around whole genome. A backcross inbred lines (BILs) derived from a crossing between wild species ‘Songzi’ and European orange cultivar ‘Amsterdam’ were developed to establish a bin map. Parental lines and each individual BIL were resequenced at approximately 10× and 1.8× fold coverage, respectively. A total of 3,223,700 SNPs were detected, and 13,445 Bin markers were generated using a sliding window approach. Finally, the genetic map was consisted of 2,027 Bins contained 154,776 SNPs; the total genetic distance of map was 1,436.43 cM with an average interval of 0.71 cM between Bin markers. A total of 37 QTLs associated with 14 agronomic traits were detected and explained 10.09% ~ 66.92% of phenotypic variation. Especially, four QTLs including one for root length, one for root shoulder width and two for root shoulder width/root middle width, were stably detected in both two years; three of them were located at 44.9cM on chromosome 2. According to the physical position, 21 predicted genes with function annotations were selected as candidate genes for all QTLs. In this study, the construction of the high resolution map based on low-coverage re-sequencing technology help with QTL mapping for agronomic traits of carrot. Furthermore, the detection of QTLs also helps to discover and clone function genes controlled root shape and size.

Note: The authors of this presentation were unable to attend the conference

ABSTRACT 503 Parentage analysis in carrot lines characterized by SSR markers

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Food coloring is widely used to influence the perceived flavor of food and make them more attractive to consumers. However, due to concerns over food safety over recent years, there has been an increasing interest among both consumers and manufacturers to replace the synthetic dyes with natural colors. Development of crop varieties with high concentration of pigments, therefore, has a huge economic potential as raw materials in the production of natural food colorants. This project aims to develop new varieties of carrot with a high concentration of pigments (beta-carotene and anthocyanins). The carrots are developed through selection within existing varieties over several generations. To compare the pigment concentration in the roots, a new color screening method has been developed for the rapid determination of carotene content in orange carrots using Raman spectroscopy. The polycross approach has been used to maximize the number of cross combinations that can be represented among the progeny. The polycross, however, lacks genetic control with complete loss of paternity information among the progeny. Simple sequence repeat (SSR) marker-based paternity analysis is proposed as an effective molecular tool for identifying paternity. Progeny from each polycross family has been genotyped along with the parents, using 14 previously described SSR markers. The objective of this study is to demonstrate that the paternity of polycross progeny from carrot can be determined by using polymorphic SSR markers and to assess potential linkage of the markers to pigment concentration. The ability to identify paternity information allow for a rapid assessment of diversity at the genome level and for a targeted selection of parental plants in carrot breeding programs.

ABSTRACT 601 Improving the carrot genome assembly and gene prediction: strategies to overcome challenges from short read genome assemblies

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The release of the carrot genome sequence in 2016 and its gene prediction and annotation have rapidly enhanced molecular and genomic research for this species, changing the nature of research in carrot biology. Research is shifting more towards extensive genetic screening for genome-wide association analysis and functional genomics. However, despite the high-quality of the current carrot genome assembly v2.0 release, improvements are needed due to the multiple challenges associated with short read sequencing data used to develop it. In this work, we aim to i) increase the contiguity of the current carrot genome assembly, ii) anchor a higher proportion of the genome to genetic maps, and iii) improve gene prediction and annotation. Aided by the advancement of new technologies and the availability of long-read sequencing techniques, here we present a preliminary PacBio Sequel genome assembly using FALCON and CANU assemblers in which the contiguity of the assembly (N50) was improved ≈ 108 fold, compared to the Illumina based published version. In addition, preliminary data to integrate Nanopore and existing paired-end sequences to improve the quality of the genome assembly are presented here. Using an integrated genetic linkage map including over 1,008 markers associated with the nine carrot linkage groups and the BAC-end sequence data, we were able to anchor and scaffold around 400Mb of the assembled genome to the nine carrot chromosomes. This fraction includes about 40Mb extra as compared with the publically available chromosome scale carrot genome assembly. Finally, a comparison between two currently available sets of gene predictions developed with different pipelines (DCAR v2 using maker and NCBI RefSeq) indicated that over 6000 gene models have no overlap and only 1,064 genes overlap completely. This motivates the improvement of carrot gene predictions, since a large proportion of gene models are missing or miss-predicted in either one of the sets.

ABSTRACT 602 Epistatic interactions contributing to carotenoid presence in carrot (*Daucus carota* L.)

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Carrots (*Daucus carota* ssp. *sativus*), particularly dark orange carrots, are an important source of provitamin A carotenoids, dissimilar from their wild progenitor *D. carota* ssp. *carota*. Two previously described genes, *Y* and *Y2*, are known to affect carotenoid prevalence in carrot taproot. We have recently identified a third gene, *Or*, using a genome-wide association analysis in 154 wild and 520 domesticated carrot accessions based on presence or absence of orange pigmentation. The genomic region containing *Or* displayed patterns associated with a selective sweep including reduced nucleotide diversity, high *FST*, and elevated linkage disequilibrium. In other plants, *Or* homologs function to differentiate non-colored plastids into chromoplasts, which provide a sink for carotenoids. Additionally, *Or* post-transcriptionally regulates Phytoene Synthase (PSY), the most important regulatory enzyme in the carotenoid pathway. To explore the epistatic interactions between *Or*, *Y* and *Y2* and how these genes contribute to both carotene and lutein accumulation in the carrot tap root we have phenotyped and genotyped ~ 500 F₂ individuals (493B x QAL_{Uzbek}) segregating for all three genes. We have also conducted a haplotype analysis to better understand the selection history of carotenoid accumulation. To do this we have sequenced the genic space of the three fine-mapped regions for *Or*, *Y* and *Y2* in 288 individuals with varying degrees of pigmentation. The results pave the way for creating a robust marker-assisted selection strategy for various pigmentation schemes in carrot breeding programs.

ABSTRACT 603 New sources of root-knot nematode (*Meloidogyne* spp.) resistance in carrot germplasm

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Using a collection of isolates of *Meloidogyne arenaria*, *M. hapla*, *M. incognita* and *M. javanica*, we have used a combination of greenhouse and field screening assays to identify and characterize sources of resistance and their genetic control among diverse sources of carrot (*Daucus carota*). Further selections of single resistance sources or combinations of resistance sources from ‘Brasilia,’ ‘Homs,’ ‘Ping Ding’ and ‘Western Red’ backgrounds were made, from which we have identified resistance effective against some or all root-knot species. A primary focus is resistance to *M. incognita*, which is typically also effective against *M. arenaria* and *M. javanica*. A second focus has been to characterize selections from ‘Homs’ which express high levels of resistance to *M. hapla*. Segregating populations derived from some of these resistance sources are being used for QTL mapping of resistance trait determinants. In parallel, a field screening of the USDA carrot germplasm collection was made in a field infested with *M. incognita*. The screened accessions comprised 694 wild carrot and unadapted cultivated carrot germplasm entries, of which 73 entries (10.5%) were identified as having putative partial to high levels of resistance. A subset of 13 (1.9%) entries had very high *M. incognita* resistance responses based on the level of galling symptoms on taproots. Taproots of all putative resistant entries were collected for crossing and seed production. About 80 entries of these putative resistance sources were assayed in greenhouse pots inoculated with *M. incognita* three weeks after emergence, for validation of resistance phenotypes based on root-galling and nematode egg production.

ABSTRACT 701 Development of genomic-prediction strategies for top height and flavor in a carrot (*Daucus carota*) germplasm collection

Keo Corak, Shelby Ellison, Claire Luby, Doug Senalik, Massimo Iorizzo, David Spooner, Irwin Goldman, Phil Simon, Julie Dawson

NO ABSTRACT

ABSTRACT 702 Root and shoot phenotypes quantified by computational image analysis

Edgar Spalding

NO ABSTRACT

ABSTRACT 703 Using digital image-based phenotyping to investigating the genetic bases of root shape and market class in carrot

Scott Brainard, Julie Dawson, and Irwin Goldman

Surprisingly little is known about the genetic control of root shape-related traits in carrot, despite their importance in determining the eventual end use, and thereby the so-termed “market class” of carrot varieties. This gap in our current understanding can limit the range of market classes included in breeding programs that focus on specific root shapes, as well as the efficiency and accuracy with which desired shapes can be bred. These limitations can be most apparent when attempting to incorporate exotic germplasm in the development of varieties adapted to novel biotic or abiotic conditions (e.g., those encountered in organic production systems).

My research utilizes a diverse array of inbred breeding lines in order to identify and characterize the genetic basis of root shape characteristics. I am creating biparental QTL mapping populations to identify loci contributing to a variety of morphological traits determinative of market class (e.g., degree of shouldering and tip fill, length, aspect ratio). Additionally, I am performing a half-diallel cross to characterize heritability of these traits, as well as the combining ability of the inbred parents.

Underlying both of these experiments is the development and implementation of a high-throughput method for phenotyping carrot roots using digital imaging, which could be integrated into any breeding program interested in the morphological aspects of root shape. My talk will detail my work in developing this pipeline so far, from image acquisition, to processing algorithms, to data management.

ABSTRACT 704 Analysis of the *Or* gene and its Role in Carotenoid Accumulation in Carrot

Kevin Coe, Shelby Ellison, Doug Senalik, Julie Dawson, and Philipp Simon

Carrot (*Daucus carota*) is one of the richest sources of the vitamin A precursor β -carotene in the human diet. Two genes, Y and Y_2 have been previously identified to be responsible for the majority of carotenoid accumulation in carrot roots. Y conditions all carotenoid accumulation in carrot roots, and the allele present in orange and yellow carrots harbors a 212 bp insertion in the gene. Y_2 is known to condition the accumulation of β - and α -carotene in carrot roots. The identity of Y_2 is unknown, but Y_2 has been fine-mapped to a 650-kb region on Chromosome 7. Recently, the *Or* gene was identified by a genome-wide association study (GWAS) to also be significantly associated with carotenoid accumulation in carrots roots. During plant growth, *Or* stimulates chromoplast biogenesis, thereby creating a sink for carotenoids to accumulate. Additionally, *OR* has been shown to stabilize PHYTOENE SYNTHASE (PSY), the rate limited enzyme in the carotenoid biosynthetic pathway. Molecular studies of *Or* in other plants, such as Arabidopsis, melon, and cauliflower have revealed mutations that result in increased sequestration of β -carotene in tissues that are normally non-photosynthetic. It is our hypothesis that during carrot domestication, a mutated *Or* allele was selected, alongside Y and Y_2 , for its unique ability to increase carotenoid accumulation in root tissue. Causal mutations in *Or* are currently being identified using a panel of wild and domesticated resequenced plant introductions (PIs). Additionally, patterns of *Or* expression will be analyzed in a mapping population of carrots identified to be fixed for Y and Y_2 but still segregating for orange, yellow, and white root color.

ABSTRACT 801 Mapping QTL for carrot shoot traits in diverse crop management systems

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Carrot shoot morphology affects crop harvestability, weed competitiveness, foliar disease tolerance, and fresh market consumer appeal. The genetic contribution to phenotypic variation in carrot shoots remains poorly understood despite this impact on crop growth and quality. Carrot shoot morphology is also heavily influenced by non-genetic factors such as planting density, nutrient availability, and intra- and inter-species competition. These non-genetic variables complicate breeding efforts to improve shoot morphology in carrot with accuracy. The goal of this study was to detect QTL associated with carrot shoot morphology to enable marker-assisted selection efforts for these traits while selecting for shoot traits in conventional and organic management conditions. To accomplish this, high-density linkage maps of four diverse F2 carrot populations were constructed using genotyping by sequencing (GBS) to discover single nucleotide polymorphism (SNP) markers that were then compared to the carrot reference genome. QTL markers were identified in these four populations for seedling vigor, midseason shoot height, harvest shoot height, and harvest shoot biomass. These QTL can be used to exploit the heritable variation in these traits in marker-assisted carrot breeding efforts.

ABSTRACT 802 Utilizing Ionomic Analysis in Carrot

Adam Bolton, Charlene Grahn, Morgan Pettit, Ivan Baxter, Lori Hoagland, Micaela Colley, Erin Silva, and Philipp Simon

The “ionome” is defined as all the essential and nonessential mineral elements found in an organism. Ionomic analysis utilizes high-throughput inductively coupled plasma mass spectrometry (ICP-MS) and has been applied extensively in many plant species, but not in carrot. Ionomic analysis gives us the ability to measure the concentration of nutrients crucial to plant health (N, P, K, Mg, Ca, Zn, etc.) as well as heavy metals potentially harmful to human health such as arsenic, selenium, cobalt, and cadmium. Ionomic analysis has been applied to evaluate diversity in the ionomic profile of diverse germplasm, characterize the genetic basis of that diversity, and study the physiological mechanisms of ion accumulation in abiotic stress. We have established a foundation for ionomic analysis in carrot and will present some applications for understanding sodium transport under salt stress, differential partitioning of mineral nutrients, and evidence for genotype specific heavy metal uptake.

POSTER ABSTRACTS

ABSTRACT 901 Displaying, interpreting, and exploring carrot population performance in multi-environment field trials

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Many phenotypic traits in carrot display high genotype by environment interaction (GxE). This complicates cultivar development efforts aiming to achieve consistently high performance across diverse growing environments. An understanding of what causes this GxE can help identify traits that contribute to better regional crop performance and environments that facilitate accurate evaluation of breeding material. Principle component analysis (PCA) coupled with GGE and AMMI biplot analysis can help to achieve this understanding by visualizing GxE in a way that facilitates meaningful cultivar evaluation and mega-environment identification from even highly complex and unbalanced datasets. We applied these techniques to conventionally and organically managed carrot breeding trials conducted in California and Wisconsin from 2015 to 2017. The results identify primary sources of GxE within the trials, types of phenotypic variation most relevant to crop performance, and environmental variables that have the greatest effect on phenotypic selection efficiency in a carrot breeding program.

ABSTRACT 902 Selecting carrots with increased resistance to cavity spot

Kevin Vander Kooi¹, Mary R McDonald¹, Phil W. Simon²

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NO ABSTRACT

ABSTRACT 903 Why We Should Carrot All About Stand Establishment in *Daucus carota*

Jenyne S. Loarca, Julie Dawson, Philipp W. Simon

Carrot seedlings are notorious amongst growers for having uneven, variable stand establishment – an early season trait, characterized by varying time to emergence, stand count, and plant maturity among plants in a population. Cotyledons emerge at irregular intervals and plants grow and mature at different rates, even among genetically uniform lines. This sporadic tendency has far-reaching consequences for end-of-season marketable root yield. To evaluate the genetic basis for stand establishment, carrot plant introductions (P.I.) from the USDA collection will be evaluated in the field, and broad-sense heritability will be calculated for stand establishment's core traits: early emergence timing, high stand-count, and uniform early plant development (measured by number of true leaves). In addition to field measurements, a subset of P.I.s will be measured using machine imaging in the Biotron under controlled conditions in order to reduce environmental variation. An association analysis with the P.I.s, and genetic mapping in biparental F₂ populations, will be used to better characterize the genetic architecture of the core traits. These studies will set the stage for the development of breeding pools and field-based machine imaging, with the long-term goal of developing improved carrot cultivars for breeders, growers, and consumers.

ABSTRACT 904 Bioproducts for the suppression of carrot leaf blights caused by *Alternaria dauci* and *Cercospora carotae*.

Mary Ruth McDonald¹, Laura Riches¹, Kevin Vander Kooi¹

¹*University Of Guelph, Guelph, Ontario, Canada*

Two types of bioproducts were evaluated for the suppression of carrot leaf blights, caused by *Alternaria dauci* and *Cercospora carotae*. One group was a food grade oil, applied in conjunction with various adjuvants (FGO+A), the second was Stella Maris, an extract of the aquatic plant, *Ascophyllum nodosum*. These were evaluated in replicated field trials in the Holland Marsh, Ontario, Canada (44°02' N, 75° 35' W) with carrot cv. Belgardo seeded on high organic matter soils (pH ~6.3, organic matter 73%). Trials were conducted from 2013 to 2017. The food grade oil products were applied 4 or 5 times a season beginning when blight symptoms were first observed. The standard fungicides boscalid was included in 2013, azoxystobin + difenoconazole (Quadris Top) in other years, and both fungicides in 2014. Stella Maris was applied as a drench followed by foliar sprays alone, or alternated with Quadris Top. Incidence and severity of leaf blight and percent of dead leaves were recorded. Severity was rated on a scale of 0-5 and a disease severity index (DSI) was calculated. The DSI of the carrot leaf blights ranged from 20 - 52 in the untreated check and incidence was from 57% to over 90%. DSI was reduced to 35- 36% in years of high disease pressure by the FGO+A. In 2015, the FGO alone reduced DSI to 24%. The FGO+A also reduced the percent of dead leaves in 2013 and 2015. Disease suppression was equivalent to that of fungicide boscalid. There was no advantage to combining the FGO+A with a fungicide, or doubling the rate. Quadris Top was more effective than FGO+A in reducing leaf blight incidence and severity. Stella Maris alone did not reduce leaf blight but Stella Maris alternated with Quadris Top provided similar efficacy to the fungicide. These bioproducts show some promise for the management of carrot leaf blights in commercial carrot production.

ABSTRACT 905 Halo-priming of carrot seeds at supra-optimal temperature

Muhammad Mahmood Ur Rehman¹, Muhammad Amjad¹, Khurram Ziaf¹, Philipp Simon², Aneela Nijabat², Anam Noor¹

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Carrot is a winter crop and getting popularity due to its high nutritional value with various health benefits. Global warming and high temperature have catastrophic effects on plant growth and yield. Pakistan situated in sub-tropical to tropical region with extreme summer and continuously shrinking winter. Particularly, during early cropping season (Aug-Sep), carrot production is practiced in Punjab-Pakistan due to its high profitability (early crop) but prominent reduction in carrot yield have been observed due to exposure of high temperature at germination stage that leads to very low plant density. Therefore, a study had been planned to cope with this issue. Seed priming is extensively used to improve seed germination under both optimum and adverse environments and benefits have also been found for following growth. Halo-priming with KNO₃ is employed for seed invigoration of many crops as a priming tool. For this purpose, carrot seeds (cultivar T-29) were primed with various concentration of KNO₃ (ranged from 50 mM to 300 mM with eight treatments including hydro-priming and unprimed control) for 12 h at room temperature. After drying, seeds were placed in Petri dishes with four replications for evaluation of germination at supra-optimal temperature (35±2 °C) in the incubator. Seed priming significantly improved the germination and related attributes of carrot seeds as compared to unprimed seeds. Maximum germination (79%) was attained with 50 mM KNO₃ and unprimed seeds showed least germination (58%), while electrical conductivity of seed leachates was reduced by all the seed priming treatments. Priming with lowest KNO₃ concentration exhibited higher phenolic contents in the seedlings and improved enzymatic activities in term of peroxidase, superoxide dismutase, catalase, and lower the malondialdehyde contents. These alterations could be possible reasons of improvement in carrot seeds. Moreover, two best performing priming treatments (from the laboratory experiment) along with hydro-priming and unprimed seeds were evaluated for field trials during 2015 and 2016. Higher root yield was also observed from lower KNO₃ priming treatment. Thus, it was revealed that carrot halo-priming with KNO₃ (lower concentration) could enhance germination potential and enzymatic activities that resulted in higher root yield.

ABSTRACT 906 Identifying the best approach to characterize bacterial endophyte diversity in carrots (*Daucus carota*)

Narda Jimena Trivino Silva¹

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Increasing evidence supports the important role of the plant microbiome in supporting plant health and productivity. Endophytes, which are microbes that spend at least some portion of their life cycling living inside plants, are likely to be particularly important because they are able to evade plant immune systems. Recent evidence has shown that endophytes can enhance plant growth, as well as act as antagonists against pathogens. Because they often cause no symptoms in their hosts, and are notoriously difficult to isolate and culture, endophytes have been understudied. Previous studies using culture-based approaches indicate that carrot roots host bacterial endophytes from several genera including *Bacillus*, *Pseudomonas*, *Xanthomonas*, *Pantoea* among others. However, culture-independent surveys based on genomic tools in other crops indicate that the diversity of bacterial endophytes in carrot roots is likely to be much higher. We recently determined that existing primer sets commonly used to characterize bacterial community structure are ineffective in carrot roots, due to excessive amplification of chloroplast and mitochondrial DNA from carrot. Blocking primers, which have proved successful in blocking amplification of these organs in other plant species to characterize endophytes, were also ineffective. Thus, the aim of this study was determine if pretreatment of carrot root cores with microfiltration, with or without enzymatic digestion to remove plant tissues, could aid in endophyte recovery and amplification. Each of these three pretreatment options were combined with one of three amplification protocols designed to target different hypervariable regions of 16S rRNA, to identify the most optimal approach to characterize carrot bacterial endophyte community structure. This included the standard approach using primers targeting V3-V4, blocking primers followed by primers targeting V5-V6, and mismatch primers targeting V5-V7. Sequencing of amplification products from these treatments are underway using Illumina MiSeq.

ABSTRACT 907 Field assessment for abiotic stress resilience in carrot under drought, salt and heat stressed environments of Pakistan

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Carrot (*Daucus carota* subsp. *carota* L.) is a root crop well-known due to its fresh consumption, juices, pigments, throughout the world. This short duration crop is sensitive to environmental stresses such as drought, salinity and heat. Three independent trials were performed at drought, salt and heat stressed environments of Pakistan. Thirty, thirty and fifty seven diverse carrot accessions were selected for drought, salt and heat stress evaluation respectively for two years. Root diameter (RD), root weight (RW), root length (RL), protein contents and total sugars (TS) were measured in salt and drought stressed environments. Germination, leaf per plant, leaf area, leaf length, plant fresh weight, plant dry weight, root weight, total sugars and protein contents were recorded at heat stressed conditions. Under each stress, on the basis of response exhibited, the accessions were classified as tolerant, moderately tolerant and susceptible. Pearson's Correlation coefficient (r) remained significantly positive among RD, RL, RW and TS in all stressed conditions. First two Principal components analysis (PCs) explained 77%, 62% and 32 % variation in salinity, drought and heat trials. On the basis of studied traits, agglomerative hierarchical clustering (AHC) inferred three classes in all stressed conditions. Stress tolerant best performing accessions will be utilized by breeding programs to develop elite lines with required traits.

ABSTRACT 908 Genomic and Transcriptomic Analysis of Salt and Heat Stress in Carrot Seed Germination

Adam Bolton, Mahmood Rehman, Aneela Nijabat, Amir Ali, Majharul Mannan, M. A. Rahim, Shelby Ellison, and Philipp Simon

Carrot is a widely grown and economically important vegetable that provides a rich dietary source of vitamin A to much of the world. Carrot has long been observed to be one of the most salt and heat sensitive vegetable crops, and production is restricted in many parts of the world due to these abiotic stresses. To date there have been few phenotypic and genetic evaluations for traits related to salt and heat tolerance in carrot. Screening for tolerance at the germination stage is the first step in the identification of tolerant genotypes as it is a critical stage for crop development. The development of molecular markers would be a useful tool to select genetically tolerant lines for breeding improved carrot tolerance to abiotic stress at the germination stage. In order to identify regions of the genome associated with abiotic stress at the seed germination stage we have utilized a combination of RNA sequencing and genome-wide association analysis on a subset of 294 previously phenotyped diverse germplasm accessions for both salt and heat stress. We have identified a wide range of phenotypic diversity for these traits and potential candidate genes that warrant further investigation.

ABSTRACT 909 Genetic mapping of anthocyanin pigment traits from specific tissues of the carrot root and leaves

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Purple carrots can accumulate large quantities of anthocyanins in their roots, as well as in other plant tissues and organs. The consumption of these water-soluble pigments is associated with reduced risk of cardiovascular disease, diabetes, arthritis and cancer, mainly due to their anti-oxidant and anti-inflammatory activities. In this study, we explored the genetic basis of anthocyanin pigmentation in different carrot root and leaf tissues. An F₂ population (N=254) segregating for anthocyanin accumulation was used. Phenotypic data was obtained by scoring visually anthocyanin pigmentation in the root phloem and xylem, and in leaf petioles. Additionally, the content of the 5 major anthocyanin pigments in the root phloem and xylem, independently, was estimated by HPLC analysis. A linkage map was constructed using 1013 genotyping-by-sequencing (GBS) markers, which were distributed across the 9 carrot chromosomes. The entire map covered 911.9 cM, with an average marker spacing of 0.9 cM. Loci related to anthocyanin content in the different tissues were mapped using R/qtl. Mapping of traits with parametric distribution revealed 18 significant QTL for phloem anthocyanins on chromosomes 3, 4, 6 and 7, and 8 QTL for xylem anthocyanins mapped on chromosomes 3 and 7. Co-localized anthocyanin QTL with highest phenotypic explanatory power mapped to two regions of chromosome 3. These regions correspond to those of *P1* and *P3*, the anthocyanin loci previously described. Leaf petiole pigmentation was mapped as a binary trait, and its map position co-localized with the region of *P3*. Ongoing transcriptome analysis (RNA-Seq) in purple and non-purple phloem tissues is expected to aid in delimiting the chromosome regions associated with phloem pigmentation and finding candidate genes for this trait.

ABSTRACT 910 Characterization of the Tendency for Bolting among Wild and Unadapted Carrot Accessions

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Modern carrot cultivars are biennials, requiring exposure to cold temperatures in order to flower. Initiation of flowering, referred to as bolting, is an undesirable trait for growers and consumers as it stimulates fiber development in the root, rendering the crop unmarketable. Wild accessions and cultivars adapted to warm climates are an invaluable source of genetic diversity which can provide traits that address critical needs of the carrot industry such as resistance to biotic and abiotic stress, reliable stand establishment, and improved consumer quality. However, the wild carrot and unadapted cultivated germplasm includes early flowering, annual plants that are unsuitable for commercial cultivation. Understanding the genetic basis of bolting in carrot will enable breeding strategies that leverage the full range of carrot diversity. We have characterized bolting frequencies within the first season of cultivation for 695 accessions, representing the breadth of carrot genetic diversity. Bolting was scored in diverse environments including the desert Coachella Valley of Southern California and, in the north-central United States, the Central Sands region of Wisconsin. Thus far, only 292 accessions had no bolting plants across all trials. Among bolting accessions, one half were environment-specific and bolting frequency had a continuous distribution indicating quantitative genetics with a strong environmental interaction. A single gene has been identified as having a major role in controlling carrot floral induction in a mapping population. This study of diverse accessions indicated additional genes underlie the trait. A genome wide association study will be carried out to identify quantitative trait loci and candidate genes affecting bolting in carrot.

ABSTRACT 911 Documenting changes in carrot weevil activity and behaviour in Canada.

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The carrot weevil, *Listronotus oregonensis* (LeConte), is a major carrot pest in Canada. Carrot weevil larvae feed on the carrot root, rendering the root unmarketable due to tunneling damage. According to past research, the carrot weevil has a single generation in Canada, oviposits through May to early July, and only oviposits on plants that have reached the 4th true leaf stage or older. Recent issues in carrot weevil control are: high (>10%) damage despite insecticide application, mortality of young carrots due to larval feeding, and a new, second generation of the weevil. Trials were conducted at the University of Guelph - Muck Crops Research Station, from 2016 to 2018 to assess weevil activity and damage through seeding date trials and weevil monitoring. Carrots were seeded at 6 dates, from early May to late June. Oviposition on plants younger than the 2nd true leaf stage was observed, and early seeded plots had significantly more dead carrots and carrot weevil damage. In 2016, carrot weevil damage also increased between late July and October, meaning late season oviposition which is indicative of a second generation. Carrot root baits were used to track carrot weevil oviposition and some oviposition was detected in July and October in 2016 and 2017. However, as the carrots grow, the root sections are less attractive to weevils. Hence the root sections likely underestimate carrot weevil oviposition as the season progresses. These trials are being repeated in 2018. Future research should examine if insecticide applications can protect seedlings from mortality caused by carrot weevil and investigate alternate attractants or monitoring techniques for carrot weevil. With the potential second generation, mid to late season insecticide applications may also be required, however the dense carrot canopy may complicate the efficacy of these treatments.

ABSTRACT 912 Improving the carrot genome assembly and gene prediction: strategies to overcome challenges from short read genome assemblies

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The release of the carrot genome sequence in 2016 and its gene prediction and annotation have rapidly enhanced molecular and genomic research for this species, changing the nature of research in carrot biology. Research is shifting more towards extensive genetic screening for genome-wide association analysis and functional genomics. However, despite the high-quality of the current carrot genome assembly v2.0 release, improvements are needed due to the multiple challenges associated with short read sequencing data used to develop it. In this work, we aim to i) increase the contiguity of the current carrot genome assembly, ii) anchor a higher proportion of the genome to genetic maps, and iii) improve gene prediction and annotation. Aided by the advancement of new technologies and the availability of long-read sequencing techniques, here we present a preliminary PacBio Sequel genome assembly using FALCON and CANU assemblers in which the contiguity of the assembly (N50) was improved ≈ 108 fold, compared to the Illumina based published version. In addition, preliminary data to integrate Nanopore and existing paired-end sequences to improve the quality of the genome assembly are presented here. Using an integrated genetic linkage map including over 1,008 markers associated with the nine carrot linkage groups and the BAC-end sequence data, we were able to anchor and scaffold around 400Mb of the assembled genome to the nine carrot chromosomes. This fraction includes about 40Mb extra as compared with the publically available chromosome scale carrot genome assembly. Finally, a comparison between two currently available sets of gene predictions developed with different pipelines (DCAR v2 using maker and NCBI RefSeq) indicated that over 6000 gene models have no overlap and only 1,064 genes overlap completely. This motivates the improvement of carrot gene predictions, since a large proportion of gene models are missing or miss-predicted in either one of the sets.

ABSTRACT 913 Variation in anthocyanin pigmentation in the purple carrot germplasm as affected by genotype and plant tissue

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The consumption of anthocyanin-rich fruits and vegetables is associated with reduced risk of cardiovascular disease, diabetes, arthritis and cancer, mainly due to anthocyanin's antioxidant and anti-inflammatory activities. Some purple carrots accumulate large quantities of anthocyanins in their roots and, therefore, they represent excellent dietary sources of these pigments. Anthocyanin pigmentation varies among organs and tissues of the carrot plant, and among carrot genetic stocks.

In this study we characterized total anthocyanin content and anthocyanin composition, by HPLC analysis, in different root and above-ground plant tissues of 26 carrot accessions, including open-pollinated (OP) and hybrid cultivars. Phenotypic variation for presence and intensity of purple pigmentation varied broadly among different plant tissues and among accessions. Significant variation ($p < 0.05$) for concentration of total anthocyanins (TA), total acylated (TAA) and non-acylated anthocyanins (TNAA), and for individual pigments (IP), was found for each plant tissue/organ among the carrot accessions evaluated. Likewise, significant variation for TA, TAA, TNAA and IP was found across different plant tissues of some accessions. In general, TA content in the root phloem was higher than in the xylem. Intra and inter-accession comparative analysis of anthocyanin composition in the root phloem and xylem, and in above-ground plant tissues (leaf petiole and lamina, flower stalk, inflorescence, and fruit), was performed. These data will contribute to the understanding of genetic and biochemical aspects of carrot anthocyanin pigmentation.

ABSTRACT 914 Genome-wide comparative analysis of carrot *DcSTO* MITEs reveals high diversity and recent bursts of activity

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Recently, owing to the availability of the reference carrot genome assembly and high throughput genotyping technologies, SNP polymorphisms have been extensively used to characterize genetic diversity and to identify genes governing important traits. However, genetic variation resulting from the activity of transposable elements (TEs) remains largely unexplored. In other plant species, it has been shown that more than half of alleles resulting from TE insertions are not in linkage disequilibrium with adjacent SNPs, which makes these variants interesting to study genetic diversity. Miniature Inverted-Repeat Transposable Elements (MITEs), small, non-autonomous DNA transposons, are usually the most abundant and polymorphic fraction of mobile elements associated with genic regions in plants. Here, we evaluated the extent of structural variation resulting from past activity of *DcSTO* (*Daucus carota* *Stowaway*-like MITEs) in 31 wild and cultivated carrot accessions using available sequencing data. In total, we identified 18,812 insertion sites of 14 *DcSTO* families, all of them being polymorphic. Genetic diversity analysis based on *DcSTO* insertion polymorphism reflected the history of carrot domestication. Interestingly, we observed an exceptionally high rate (66,2%) of insertion sites present only in a single accession. Insertion sites of one family, *DcSTO7b*, were much more diverse than all other families, likely indicating that it may currently be mobile. 1.5% of insertion sites shared parallel, unrelated insertions of different *DcSTO* MITEs in the same genomic localization in different accessions, indicating the presence of insertion hotspots. We selected 722 and 407 insertion sites residing in introns of the western and eastern carrot gene pools, respectively, and converted them into simple PCR-based markers. Our results provide insight into understanding the evolutionary dynamics of carrot *Stowaway* MITEs and their importance in shaping the carrot genome.

ABSTRACT 915 A cluster of MYB transcription factor regulate anthocyanin biosynthesis in carrot (*Daucus carota* L.) root and leaf

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Purple carrots, which accumulate large quantities of anthocyanins in their roots and leaves, represent an excellent dietary source of antioxidant phytonutrients. In a previous study, by linkage analysis in a carrot F₂ mapping population segregating for root and leaf anthocyanin pigmentation, we identified two regions in chromosome 3 with co-localized QTL for all anthocyanin pigments of the carrot root, whereas leaf pigmentation segregated as a single dominant gene and mapped to one of these “root pigmentation” regions. In the present study we performed fine mapping combined with gene expression analyses (RNA-Seq) to identify candidate genes controlling anthocyanin pigmentation in carrot root and leaves. By linkage mapping, the chromosome region controlling root and leaf pigmentation was delimited to 541 kb and 535 kb, respectively. Genome wide prediction coupled with phylogenetic analyses allowed the identification -in this region- of a cluster of six MYB transcription factors associated with anthocyanin biosynthesis regulation. Comparative transcriptome analysis in pigmented and non-pigmented root and leaf tissues indicated that expression of MYB1 was associated with anthocyanin pigmentation in both root and leaf tissues, whereas MYB3 was only associated with leaf pigmentation. MYB2, a gene that has been previously suggested to be a key regulator of the anthocyanin pathway in carrot was not consistently associated with neither tissues. These results strongly suggest that MYB1 plays a major role in the regulation of anthocyanin biosynthesis in carrot, while MYB3 seems to modulate pigmentation only in leaves.

ABSTRACT 916 Extended studies of interspecific relationships of *Daucus* using DNA sequences from ten nuclear orthologs

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The latest comprehensive taxonomic monograph of *Daucus* by Sáenz (1981) recognized 21 species; Rubatzky et al. (1999) later estimated 25 species. Recent molecular studies using a variety of plastid and nuclear DNA sequences, however, have been drastically changing our understanding of the ingroup and outgroup relationships of *Daucus* (e.g., Spalik and Downie, 2007, *J. Biogeogr.* 34: 2039-2054; Banasiak et al., 2016, *Taxon* 65: 563-585; Spooner et al., 2017, *Amer. J. Bot.* 104: 296-312). Banasiak et al. (2016) used DNA sequences from nuclear ribosomal ITS and the three plastid markers (*rps16* intron, *rpoC1* intron, and *rpoB-trnC* intergenic spacer) to redefine and expand the genus *Daucus* to include the following genera and species into its synonymy: *Agrocharis* Hochst. (4 species), *Melanoselinum* Hoffm. (1 species), *Monizia* Lowe (1 species), *Pachyctenium* Maire & Pamp. (1 species), *Pseudorlaya* (Murb.) Murb. (2 species), *Rouya* Coincy (1 species), *Tornabenea* Parl. (6 species), *Athamanta dellacellae* E.A.Durand & Barratte, and *Cryptotaenia elegans* Webb ex Bolle. They made the relevant nomenclatural transfers into *Daucus*, expanding the genus to contain over 50 species. Arbizu et al. (2014) identified 94 nuclear orthologs in *Daucus*, constructed a phylogeny, and determined 10 of them to provide essentially the same phylogeny as all 94, paving the way for additional nuclear ortholog studies in carrot. These 10 nuclear orthologs were then successfully used in a focused study of the species boundaries of the *D. guttatus* complex (Arbizu et al. 2016, *Syst. Bot.* 41:479-492), which, in concert with data from type specimens (Martínez Flores et al., 2016, *Syst. Bot.* 41:464-478) determined the species boundaries and proper nomenclature of the species in this group. The focus of the present study is to further expand these studies by adding taxa from areas not examined with these ten nuclear orthologs before; obtained from (1) the Agrocampus Ouest – IRHS, France, (2) the Warwick Crop Centre, England, and (3) an expedition in Spain in 2016. These include *D. arcanus*, *D. durieua*, *D. gracilis*, *D. montanus*, *D. setifolius*, *Melanoselinum decipiens*, *Monizia edulis*, *Pseudorlaya miniscula*, *Tornabenea annua*, and *T. tenuissima*. Relative to prior studies using these markers, *D. arcanus* is sister to *D. pusillus*, *D. durieua* to *D. guttatus*, *D. gracilis*, *Tornabenea annua*, and *T. tenuissima* (along with *D. sahariensis*) sister to *D. carota*, *Melanoselinum decipiens* and *Monizia edulis* sister to each other and these to a clade containing *Pseudorlaya miniscula*, *P. pumila*, and other species containing 2n = 18 chromosomes, *D. setifolius* to *D. crinitus*, and *D. montanus* (a hexaploid) as a possible allopolyploid between *D. pusillus* and *D. glochidiatus*.

ABSTRACT 917 Genome-Wide Association of Volatile Flavor Compounds in Carrot (*Daucus carota* L.)

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Carrot is one of the most widely consumed vegetables due to its culinary characteristics and health benefits. Carrot breeders have devoted most of their efforts to improve field traits necessary to ensure marketability and market acceptance by consumers is strongly influenced by appearance. Differences in culinary quality among carrots are also important for consumers and one of the most prominent breeding goals is flavor, but few studies have evaluated the genetics of carrot flavor. The objective of this study is to evaluate carrot flavor in 700 open-pollinated carrots from around the world and several mapping populations. Flavor volatiles will be evaluated with GC (gas chromatography) and flavor notes will be sampled organoleptically. Information on chromatographic analysis will be presented.

Additional index words: *Daucus carota*, flavor, genome-wide association, GC (gas chromatography)

ABSTRACT 918 Genome Wide Association Mapping of Lycopene Accumulation in Carrot Root with a Genotyping-by-Sequencing Approach

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Red carrot originates from Asia and is still very popular there. Lycopene is the red-colored carotenoid predominantly found in red carrot and one of the important carotenoids with respect to its antioxidant activity associated with human health. However, the genetic and molecular basis of lycopene accumulation in red carrot is not well understood. In this study, we conducted a two-year and two-environment Mendelian and genome-wide association mapping of lycopene content using 96 F₂ plants and a 285-plant combination of F₂ plants, F₂-derived F₃ plants and F₃-derived F₄ plants from crosses among five carrot lines. Phenotypic data evaluated included visual scores and HPLC data. Genome-wide association and Mendelian mapping revealed three consistent and distinct QTLs significantly associated with lycopene content. The results of this study provide a foundation to unravel genetic mechanism of lycopene accumulation in red carrot and the significant SNP markers identified will be used in marker-assisted selection.

ABSTRACT 919 Identifying phenotypes, markers, and genes in carrot germplasm to deliver improved carrots to growers and consumers

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A survey of U.S. carrot growers and seed industry stakeholders was conducted and a meeting was held in 2015 to identify key traits important for improved carrot quality and productivity anticipated to meet future market demands. The feedback revealed that the carrot industry needs breeding stocks and genomic tools that can be used to develop carrots with improved field performance, including disease and pest resistance, and abiotic stress tolerance; and improved flavor and nutritional quality to better meet consumer needs. Given this critical stakeholder input, the goals of this project are to: 1) phenotype diverse carrot germplasm and breeding stocks to discover and characterize variation for traits important for improving carrots for the U.S. market; 2) develop an expanded carrot genomic and phenotypic database for breeders to catalogue genomic variation and track genes underlying important traits; 3) initiate the development of breeding pools from diverse germplasm and breeding stocks that include alleles for improved crop production and consumer quality traits, and test them on-farm with growers, including for flavor and nutritional value for consumers; and 4) assess the market value and impacts of carrot traits on grower and consumer decisions. A timeline of activities has been developed, with evaluation of approximately 750 modern and heirloom open-pollinated cultivars; landraces from the Middle East, Asia, Africa, Europe, and South America; and breeding lines from public sector carrot improvement programs initiated. To date, new sources of resistance to *Alternaria* leaf blight and root-knot nematodes, reduced incidence of bolting, and improved stand establishment, flavor, and nutritional quality have been identified preliminarily. The development of breeding pools has been initiated to capture enriched sources of allelic variation useful for carrot breeders, and an expanded carrot database that includes both genomic and phenotypic data is being created.

ABSTRACT 920 Utilization of Carrot CWRs for Carrot Pre-breeding in Bangladesh and Pakistan

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Carrot is a very widely grown vegetable that is not only a valuable cash crop, but also an excellent source of Vitamin A derived from the orange pigments familiar to consumers. Carrot production has historically been in cooler climates, but with the development of carrot cultivars for subtropical regions of Brazil in the last 40 years, carrot production has expanded dramatically in warmer climates around the world. For example, carrot production in Bangladesh has risen significantly in recent years. Since most of the global incidence of Vitamin A deficiency is in warmer regions of the world, the development of carrot cultivars adapted to subtropical climates takes on even greater potential importance. Cultivated carrot germplasm is genetically and phenotypically diverse, and crossable wild relatives are a reservoir of even more genetic diversity. Wild carrot germplasm has been collected in very warm, dry, and, in some cases, very saline sites, and this germplasm is available in the USDA carrot germplasm collection. This project evaluated carrot wild relatives and cultivated carrots in warm, dry, saline field conditions, intercrossed climate-tolerance from wild relatives to adapted, nutritious cultivated germplasm, and evaluated intercrosses among carrots and their derivatives in hot, dry, saline field sites in Bangladesh and Pakistan. Exposure to heat and salinity in field trials was effective in limiting growth for most of the germplasm entries evaluated, whereas exposure to drought did not limit carrot growth as dramatically as heat or salt. Of particular interest, a few entries demonstrated heat, drought, and salinity tolerance in both Bangladesh and Pakistan. Intercrosses involving plants with novel abiotic stress resilience traits of carrot crop wild relatives (CWRs) with highly nutritious, good flavor, widely-grown carrot types were initiated in both Bangladesh and Pakistan, and seed production was successful in subsequent generations. Tolerance for heat, salinity, and drought was discovered among carrot germplasm accessions evaluated and, for selected entries, was reliably demonstrated across both locations and across several years. Interestingly, among tolerant germplasm accessions, many were cultivated carrot. While wild carrot relatives also demonstrated repeatable tolerance, the incidence of tolerant cultivated carrots suggests that genes in cultivated background can be tapped to develop breeding populations with good horticultural quality favorable to both farmers and consumers. The inheritance of tolerance is being evaluated and germplasm is being developed.

ABSTRACT 921 CIOA 2 - Carrot Improvement for Organic Agriculture with Added Grower and Consumer Value

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Carrot Improvement for Organic Agriculture 2 (CIOA 2) builds upon accomplishments of the CIOA 1 project funded by the USDA OREI. Plant breeding is long-term work and the proposed project will maximize impacts of the CIOA 1 research by delivering new, improved carrot cultivars and breeding lines to the organic seed trade; developing new breeding populations that combine critical traits identified during CIOA 1; expanding the screening of diverse carrot germplasm and field testing of finished cultivars and advanced materials in diverse organic environments; and advancing our understanding of positive genetic-soil microbial interactions, thereby expanding the potential to breed for nutrient use efficiency, disease resistance, and drought tolerance. The long-term goals are to: 1) deliver carrot cultivars with improved disease and nematode resistance, improved nutrient acquisition, seedling vigor and weed competitive traits, increased marketable yield, superior nutritional value, flavor and other culinary qualities, and storage quality for organic production; 2) determine how carrot genotypes interact with, or influence, the root microbiome to access key nutrients under limiting environments, and limit heavy metal uptake; 3) inform growers about cultivar performance to maximize organic carrot production, markets, and organic seed usage; 4) inform consumers about the positive environmental impacts of organic production systems and about carrot nutritional quality, flavor and culinary attributes; and 5) train undergraduate, graduate, and post-doctorate students in critical organic agriculture issues. A timeline for project activities was developed and on-farm field trials have been initiated in six states to identify promising carrot breeding stocks with stakeholder involvement. New genetic sources of improved flavor, nutritional value and novel colors with promising production characteristics have been identified, and major differences in susceptibility to foliar diseases such as carrot red leaf, *Cercospora* leaf spot, and bacterial blight have been identified. Fine mapping of resistance genes conditioning root-knot nematode resistance is underway to accelerate the incorporation of resistance into new breeding stocks. In addition, marker-assisted selection was initiated for major pigmentation genes.
