

BG-101

Selecting carrots with increased resistance to cavity spot

M. R. McDonald¹ K. Vander Kooi¹ and P. W. Simon²

¹ Department of Plant Agriculture, University of Guelph, Guelph ON, Canada N1G 2W1.

² USDA- ARS, University of Wisconsin, Madison, WI, USA

Cavity spot of carrot is caused by several species of *Pythium*, especially *P. violae* and *P. sulcatum*. The disease can be very difficult to control with fungicides. The most effective management method is the use of resistant cultivars. Carrot breeding lines were screened to identify differences in susceptibility to cavity spot in order to support the carrot breeding program of the USDA. Trials were conducted on high organic matter soil (organic matter ~ 72%, pH 5.7 – 6.0) in the Holland Marsh, Ontario, Canada (44°15` N, 79°35` W). Cavity spot occurs regularly at this site. A total of 56 breeding lines and several commercial cultivars were grown each year. Carrots were assessed for cavity spot incidence and severity in August (mid-season) and after harvest in October. Carrots were also assessed for forking, as a symptom of *Pythium* root dieback, in 2016, and for leaf blight severity and for bolting in 2015-2016. Cavity spot incidence ranged from a maximum of 30 -97% over the four years of the trial. Several lines with purple (anthocyanin) pigments and cv. Purple Haze had consistently low incidence of cavity spot. Cultivar Atomic Red was highly susceptible all years. Four orange breeding lines were identified that had consistently low cavity spot. These have been incorporated into the breeding program.

BG-102

The Search for Salinity Tolerance in Diverse Carrot Germplasm

Adam Bolton¹ and Phil Simon^{1,2}

¹ Department of Horticulture, Plant Breeding and Plant Genetics Program, University of Wisconsin, Madison; ² Vegetable Crops Research Unit, USDA, Agricultural Research Service, Department of Horticulture, University of Wisconsin Madison, WI

Carrot is a widely grown and economically important vegetable worldwide that provides a rich dietary source of vitamin A, but production is restricted by salt-affected soil in many parts of the world. There is evidence that carrots are especially salt sensitive relative to other crops, but little research has been devoted to evaluating genetic variation and breeding for salt tolerance in carrot. A promising source of genetic diversity for salt tolerance is the USDA Plant Introduction (PI) Collection, many of which grow natively in areas with relatively high levels of salt. In a preliminary study, we have evaluated 292 carrot accessions at seed germination and found evidence for a low incidence of salt tolerance. Salt tolerance will also be evaluated during plant growth and carrot populations, to map the inheritance and combine multiple genetic sources of resistance, will be developed.

BG-103

Characterization of a genomic region under selection in cultivated carrot (*Daucus carota* subsp. *sativus*) reveals a candidate domestication gene

Alicja Macko-Podgórn¹, Gabriela Machaj¹, Katarzyna Stelmach¹, Douglas Senalik², Ewa Grzebelus¹, Massimo Iorizzo³, Philipp W. Simon², Dariusz Grzebelus¹

¹*Institute of Plant Biology and Biotechnology, Faculty of Biotechnology and Horticulture, University of Agriculture in Krakow, Krakow, Poland*

²*Vegetable Crops Research Unit, United States Department of Agriculture-Agricultural Research Service, Department of Horticulture, University of Wisconsin–Madison, Madison, WI, USA*

³*Plants for Human Health Institute, Department of Horticultural Science, North Carolina State University, Kannapolis, NC, USA*

No systematic knowledge about the molecular mechanisms involved in the domestication syndrome in carrot are available, however, the ability to form a storage root is the essential transition from the wild *Daucus carota* to the cultivated carrot. We mapped a previously identified region under selection to the distal portion of the long arm of carrot chromosome 2, confirmed that it had been selected, as reflected in both the lower nucleotide diversity in the cultivated gene pool, as compared to the wild and high F_{ST} . We delimited the region to ca. 37 kb and identified a candidate domestication syndrome gene carrying three non-synonymous single nucleotide polymorphisms and one indel systematically differentiating the wild and the cultivated accessions. This gene, *DcAHLc1*, belongs to the AT-hook motif nuclear localized (AHL) family of plant regulatory genes which are involved in the regulation of organ development, including root tissue patterning. AHL genes work through direct interactions with other AHL family proteins and a range of other proteins that require intercellular protein movement. Based on QTL data, we speculate that *DcAHLc1* might be involved in the development of the carrot storage root, as the localization of the gene overlapped with one of the QTLs. We propose that the 'cultivated' variant of *DcAHLc1* has been selected from wild Central Asian carrot populations upon domestication. However, some primitive eastern landraces and the derived B7262 purple inbred line still carry the 'wild' variant, reflecting complexity of the genetic determination of the formation of carrot storage roots.

BG-104

New carrot germplasm from Spain and its use in breeding, genetic, and taxonomic studies

David M. Spooner¹, Philipp W. Simon¹, and Fernando Martínez-Flores²

¹*USDA-ARS, Vegetable Crops Research Unit, Department of Horticulture, University of Wisconsin, USA.*

²*Universidad de Alicante, P. O. Box 99, ES-03080 Alicante, Spain*

The Apiaceae (Umbelliferae) family contains 455 genera and over 3500 species, and is one of the largest families of seed plants. The genus *Daucus* contains carrot (*Daucus carota* L. subsp. *sativus* Hoffm.), the economically most important cultivated member of Apiaceae in terms of economic importance and nutrition. The latest genus-level treatment of *Daucus* by Sáenz Laín (1981) used morphological and anatomical data and recognized 20 species. Rubatzky et al. (1999) later estimated 25 species of *Daucus*, and Banasiak et al. (2016), using DNA sequences from nuclear ribosomal ITS and the three plastid markers redefined and expanded the genus *Daucus* to include representatives of nine other genera and now containing 53 species and winged fruits in addition to its traditionally recognized spiny fruits. The genus *Daucus* has a center of endemism in the Mediterranean Region, with several species occurring in North America, South America, and Australia. We have been expanding the available germplasm collections strategically, with Spain of critical importance because of its many species not available as germplasm. We conducted three expeditions to Spain in 2016, including the Balearic Islands (June 5-18, Aug 23-Sept 6, and Oct 7-10), designed to collect mature fruits of species differing in phenology. We collected over 120 accessions of *Daucus* (*Pseudorlaya pumila*, *D. (Pseudorlaya) miniscula*, *D. arcanus*, *D. aureus*, *D. carota* subsp. *carota*, *D. carota* subsp. *gummifer*, *D. carota* subsp. *maximus*, *D. crinitus*, *D. durieua*, and *D. setifolius*). These new germplasm resources, in concert with existing germplasm, are allowing much more comprehensive studies of the breeding and genetic value of these taxa, and taxonomic relationships, to be reviewed in this presentation.

BG-105

The influence of organic and conventional production environments on breeding for carrot top size

Charlene Grahn¹, Erin Silva², Philip Simon^{1, 3}

1. Graduate Research Assistant, Department of Horticulture, University of Wisconsin- Madison

2. Assistant Professor, Department of Plant Pathology, University of Wisconsin- Madison

3. Professor and Plant Breeder, USDA- Agricultural Research Service, Vegetable Crops Research Unit, University of Wisconsin- Madison

Carrot top morphology influences crop weed competitiveness and ease of mechanical harvesting; however, top morphology traits are seldom the focus of carrot breeding projects and research. In addition to genetic influences, carrot top size is influenced by environmental conditions and management practices. These GxExM interactions make carrot top size an ideal model trait for studying the impacts of selection under organic and conventional management. This study seeks to elucidate the heritability of carrot top size while answering the question: "Is selection for carrot top size in organic production systems effective in a conventional environment, or must selection be made in an organic environment if it is to be relevant to organic growers?" To accomplish this goal, four diverse F2 and F3 segregating carrot populations were evaluated in 2015 and 2016, respectively, in adjacent certified organic and conventionally managed fields at the University of Wisconsin- Madison West Madison Agricultural Research Station. Trait heritability and response to selection were compared between the two environments by selecting individual F2 plants within different top size categories in 2015 and evaluating the top size of their F3 progeny in 2016. F3 progeny were also evaluated in El Centro, CA in 2017 to determine the relevance of carrot top size evaluation in Wisconsin to California carrot growers. The results of this research will inform breeders about the heritability of carrot top size in organic and conventional environments and the need to manage breeding trials organically when developing new cultivars for organic growers.

BG-106

Elicitation of anthocyanins in hairy root cultures of black carrots

Shih-Ti Chen¹, Gregorio Barba Espin¹, Trine Bundgaard Andersen¹, Bjarne Jørnsgård², Renate Müller¹, Henrik Lütken¹

¹University of Copenhagen, Faculty of Science Department of Plant and Environmental Sciences, Crop Sciences Section Højbakkegård Allé 9-13, DK-2630 Taastrup, Denmark

²Chr. Hansen Natural Colors A/S, Natural Colors Division
Agern Allé 24, DK-2970 Hørsholm, Denmark

Anthocyanins are water-soluble flavonoid pigments occurring in several tissues of higher plants. There is increasing demand for natural food colorants that can substitute synthetic colors due consumer concerns. Highly stable acylated anthocyanins may impart desirable color and stability for commercial food products. To date, over 600 different anthocyanins have been identified from plant sources comprising aglycones and various glycosylated and acylated compounds. Suitable sources of acylated anthocyanins are radishes, red cabbage, purple sweet potatoes and black carrots. Black carrots (*Daucus carota* ssp. *sativus* var. *atrorubens* Alef.) have particularly high anthocyanin levels in the taproot.

A promising approach to further increase the content of naturally present anthocyanins in black carrots is natural transformation by *Agrobacterium rhizogenes*. During *A. rhizogenes*-mediated transformation *root oncogenic loci (rol)*-genes are transferred from the T-DNA of the root-inducing plasmid. The stable introgression of the T-DNA causes hairy roots (HRs) to develop from the site of infection. HRs often produce increased levels of secondary metabolites compared to untransformed

roots and *in vitro* cell cultures. The first aim of this study is to obtain HR cultures for black carrots containing *rol*-genes as a platform for increased anthocyanin concentration per biomass.

Anthocyanins are regarded as secondary metabolites. The accumulation of secondary metabolites often requires elicitors, which usually act as signalling molecules of plant stress responses. The second aim is to use the HR cultures in elicitation experiments to further elevate the anthocyanin levels. Collectively, these approaches will potentially lead to future sustainable production of anthocyanins.

BG-107

Phenotypic, Genotypic, and Freedom to Operate Variation in US Carrot Cultivars

Claire Luby, Julie Dawson, Irwin Goldman
Department of Horticulture, University of Wisconsin-Madison

Increased use of intellectual property rights over plant germplasm has led to a complicated landscape for exchange among plant breeders. Our goal was to examine phenotypic and genotypic diversity present in commercially available carrot (*Daucus carota* L. var. *sativus*) germplasm in relation to the freedom to operate—the ability for plant breeders to access and use crop genetic diversity. A collection of 140 commercially available carrot cultivars were grown in replicated field trials in the Madison, WI area in 2013 and 2014. Phenotypic measurements were recorded for leaf and root characteristics. Illumina sequencing was used to conduct genotyping by sequencing analysis on all cultivars to understand the range of genetic diversity present. Additionally, the intellectual property rights associated with each cultivar was noted to determine the freedom to operate. We found that although one-third of the commercially available US carrot cultivars in our study are restricted through some form of intellectual property rights, the genetic and phenotypic variability of the protected cultivars does not represent a completely separate group from the available material. Phenotypic analyses including ANOVA and principal components analysis, suggest that many of the traits differed significantly based on market class, but not by whether the cultivar had freedom to operate. The principal components and Fst analyses on the genotyping by sequencing data revealed that carrot market classes (Fst = 0.065) and freedom to operate classes (Fst = 0.023) were not genetically distinct, and that principle components 1 and 2 account for only 10.1% of the total genotypic variation, implying that cultivated carrot germplasm in the US forms an unstructured population. Our findings suggest that the genetic diversity present in carrot cultivars that have freedom to operate is potentially large enough to support carrot breeding efforts in most market classes given present levels of intellectual property protection.

BG-108

Genetic Analysis of Carrot Root Shape and Top Size Measured by Image Analysis

Sarah Turner¹, Nathan Miller², Edgar Spalding², Phil Simon^{1, 3}

¹ Department of Horticulture, Plant Breeding and Plant Genetics Program, University of Wisconsin, Madison; ² Department of Botany, University of Wisconsin, Madison; ³; Vegetable Crops Research Unit, USDA, Agricultural Research Service, Department of Horticulture, University of Wisconsin Madison, WI,

Many quantitative phenotypes of interest to carrot breeders remain difficult and time intensive to measure. These include storage root shape, which has been used to categorize orange carrot cultivars since the 1600s, and top size, which influences weed competitive ability and management costs. While genetic variation for carrot root shape and top size has been widely observed, models for the genetic control of these traits have not been reported due to limitations in phenotyping methods. To address this bottleneck, an image-based phenotyping platform was created to perform morphometric analysis

on harvested carrots. Image-extracted traits included digital root and shoot biomass, leaf number, petiole length, and root shape. Digital estimates were five times more efficient to collect and were well correlated with hand measurements. Additionally, image-extracted data is being used in subsequent genetic studies, which include diallel analysis and quantitative trait loci (QTL) mapping. Continued advances are being pursued through the development of field-based imaging systems. These improvements will allow the incorporation of non-genetic variables, such as developmental variation and planting density, which complicate genetic analyses.

BG-109

Marker Assisted Recurrent selection (MARS) for development of nutritionally rich, nematode resistant Carrot (*Daucus carota* L.) suitable to tropical region

Sarvamangala S. Cholin* Chaitra A. Poleshi, Manikanta D. S and Jagadeesha R. C.
University of Horticultural Sciences, Bagalkot-587103, Karnataka, India

Carrot (*Daucus carota* L.), a highly out crossing vegetable belonging Apiaceae family is known for its principle nutrient component carotenoids and also has incredible antioxidant and detoxifying properties. Despite, its importance as nutritionally rich vegetable, least efforts are made for the development of tropical varieties due to its biennial nature and high vernalization requirement. Nematode is another major disease which spoils the quality and productivity of roots; hence, resistance to nematodes is another major objective in development of varieties to warmer climates. Recent availability of whole genome sequence of carrot and gene specific markers for economic traits such as carotenoids, sugar type, nematode resistance, and other stress responsive genes will help a molecular breeder in precise selection of superior plants. MARS is one of the best approaches in carrot for rapid development of superior varieties by enriching the population with desirable alleles at multiple loci within few cycles of selection than by traditional breeding alone. A simple PCR can detect the plants carrying desirable alleles at different loci in early seedling stage in a large segregating population to ease in selection and crossing. Already available gene specific and tightly linked markers will be explored for development of varieties rich in sugar (*Invertase Isozyme II*), carotenoids (*Y locus*), nematode resistance (*Mi* and *Mj*), vernalization (*VRN*) and better stress tolerance (*AOX*). Two to three cycles' recurrent selection will be done for the allelic enrichment in the population. The new variety would help a farmer of the tropical region to produce nutritionally rich roots as well as to maintain the seeds for the next generations.

BG-110

Utilizing 2D Imaging to Map Root System Architecture QTL in Carrot (*Daucus carota* L.)

Shelby Ellison, *University of Wisconsin-Madison Department of Horticulture* and Philipp Simon,
University of Wisconsin-Madison Department of Horticulture, USDA Vegetable Crops Research Unit

Effective phenotyping in carrot is complicated by the fact that the agronomically valuable portion of the crop is underground. To better understand the genetics of carrot root architecture, novel approaches must be conceived and applied in the field of high resolution, high throughput phenotyping. One such approach is to scan roots and use 2D image analysis software to extract traits of interest. We have used the programs RootNav and SmartRoot to measure carrot root architecture traits in an F₂ mapping population between wild and cultivated carrot. Phenotypic measurements have been used in conjunction with genotypic information to better understand the genetic basis of lateral root formation and root shape in carrot. We have identified several QTL controlling the number of lateral roots and carrot root shape. Estimates of heritability and further QTL mapping are being conducted in F₃ families. Establishing a protocol for 2D image analysis in carrot, as a model root crop, will facilitate the application of these technologies to other root and tuber crops such as sugar and

table beet, potato, and cassava. Finally, increased knowledge pertaining to carrot root architecture can be used to design cultivars to better meet farmer and consumer needs.

BG-111

Sources of Genetic Variation for Early Plant Growth in Diverse Carrot Germplasm

Adam Bolton¹ and Phil Simon^{1,2}

¹ Department of Horticulture, Plant Breeding and Plant Genetics Program, University of Wisconsin, Madison; ²Vegetable Crops Research Unit, USDA, Agricultural Research Service, Department of Horticulture, University of Wisconsin Madison, WI

Carrot seed germination is often uneven for a given seed lot, sometimes occurring over a course of several days or more. This leads to variation in seedling emergence, early plant growth, and stand establishment, and may even account for variation in storage root size at harvest. Many non-genetic variables can account for variation in carrot seed germination and stand establishment including variation in seed maturity and cleaning, dormancy, disease attack, planting depth, soil conditions, weed competition, and microclimate, to name a few. Genetic variation has also been implicated in accounting for phenotypic variation in these early phases of plant growth, but is not well-documented. To begin to assess the genetic basis of this complex of traits, 736 carrot Plant Introductions (PIs) from the germplasm collection in Ames, Iowa, were evaluated for variation in seedling emergence in Hancock, WI. Emergence was preliminarily screened in the field and 20 PIs with uniform emergence of small plants (cotyledons only), and 20 PIs with uniform emergence but larger plants (2-3 true leaves) were evaluated in the lab. Seeds from both groups were germinated, transplanted to the greenhouse when radicles emerged, and growth measured for 56 days after transplanting. PIs with smaller seedlings in the field germinated slower in the lab, and the early plant growth rate of slower-germinating seed lots was slower for young plants in the greenhouse. Early plant growth in progeny will be evaluated and breeding pools will be developed.

BG-112

Deploying *Meloidogyne incognita* Nematode Resistance in Carrot

Phil Simon¹, Joe Nunez², William Matthews³, Phil Roberts³

¹USDA-ARS, Vegetable Crops Unit, University of Wisconsin-Madison Department of Horticulture;

²University of California Cooperative Extension, Farm and Home, Bakersfield CA; ³University of California-Riverside Department of Nematology

Root knot nematodes (*Meloidogyne* spp.) are a major pest attacking carrots (*Daucus carota*) worldwide. Root knot nematodes cause galling and forking of the carrot root, rendering an infected carrot unfit for market. The current management practices of applying broad spectrum soil fumigants works well, but is coming under continuously restricted regulations, is costly for growers, and is considered damaging to the environment. Genetic resistance to nematodes would be an ideal solution to eliminate or strongly reduce the use of broad spectrum soil fumigants in carrot production. Resistance to *M. javanica* has already been discovered and mapped to the *Mj-1* locus on chromosome 8 in a 'Brasilia' cultivar. Beyond *M. javanica* resistance, genetic resistance to *M. incognita* was discovered in three diverse sources of resistance, from Syria, Europe and South America, and resistance genes mapped. A consensus genetic map of the three populations revealed five non-overlapping QTLs for *M. incognita* resistance. Resistance was high in the original genetic backgrounds in which it was discovered and in mapping populations, but introgression of resistance genes into carrots with horticultural quality suitable for US commercial production has not yet been reported. In recent field trials new inbreds with *M. incognita* resistance genes from multiple genetic sources were

observed to have been a high level of resistance combined with long, smooth root shape and excellent horticultural quality. Steps to deploy resistance will be discussed.

BG-113

Marker development for genes of the carrot terpene biosynthesis

Thomas Nothnagel, Holger Budahn, Detlef Ulrich, Jens Keilwagen, Thomas Berner, Heike Lehnert and Frank Dunemann

Julius Kuehn-Institute, D-06484 Quedlinburg, Germany

Terpenes are an important group of compounds in carrot influencing significantly taste and aroma. Additionally, terpenoids play a considerable physiological role as phytohormones and photosynthesis pigments as well as for communication and defense of the plants. So it has been shown that terpenoids help to attract pollinators or predators of herbivores. Terpenoid secondary metabolites are abundant in many essential oils, resins and floral scents among them some with pharmaceutical relevance.

Aim of our research is the development of functional molecular markers for some important genes of the terpene metabolism of carrot on the basis of associations between candidate genes and the content of individual volatile organic compounds (VOCs). The availability of the assembled whole carrot genome sequence (Iorizzo et al., 2016) and some other plant genomes provided the possibility for a genome wide inventory of the carrot terpene synthase (TPS) gene family. Homology-based gene prediction (Keilwagen et al., 2016) utilizing RNAseq data (Iorizzo et al., 2016) resulted in 65 putative functional TPS candidate genes belonging to the known TPS subfamilies of angiosperms. In parallel the volatile profile was analyzed for individual carrot genotypes using a semi-quantitative headspace SPME gas chromatography. For the association of SNPs of selected TPS candidate genes to the VOCs in carrot leaves and roots we pursued two approaches i) a QTL based mapping approach by using a bi-parental F₂ mapping population and ii) a GBS based genome-wide association study (GWAS) by using a diversity set of 96 carrot genotypes. Preliminary results of our research will be discussed.

CP-101

Effects of biotic and abiotic stress on carotenoid content in carrot

Geoffriau Emmanuel, Perrin Florent, Dubois-Laurent Cécile, Huet Sébastien, Suel Anita, Le Clerc Valérie, Briard Mathilde, Peltier Didier
IRHS, Agrocampus Ouest, INRA, Université Angers, SFR 4207 QUASAV F-49045 Angers, France

Synthesized by plants, carotenoids are key pigments as photoprotective compounds in chlorophyll organs and help attract pollinators and dispersers for non-chlorophyll organs such as flowers and fruits. However, in underground organs, such as roots or tubers, their role is not clearly determined. Carotenoids also represent an important class of human health metabolites as precursors of vitamin A. The carrot root, an important vegetable consumed worldwide, contains high concentrations of carotenoids, and therefore represents an interesting model to understand the accumulation in these pigments.

If some knowledge about genetic determinism exists, a few studies have highlighted the impact of environmental factors on the accumulation of carotenoids in carrots. This work thus aims to (i) determine whether environmental factors modulate the accumulation of carotenoids in carrot roots and leaves, and (ii) identify the regulation levels of the carotenoid accumulation.

In this work, two studies were conducted on a panel of genotypes with various root color. The first study was to highlight the impact of two contrasted growing periods for temperature and global radiation on the carotenoid accumulation and the expression level of biosynthetic pathway genes. The second study aimed to determine more precisely the impact of individual and combined stress (water restriction, *Alternaria dauci* inoculation) on the carotenoid accumulation.

CP-102

Cover crops effects on nitrogen and weeds in MI processing carrots

D. Corey Noyes¹, Zachary D. Hayden¹, Dean Baas², Haddish Melakeberhan¹, Ben Werling² and Daniel C. Brainard¹,

1. *Department of Horticulture, Michigan State University, East Lansing, MI, USA.*
2. *Michigan State University Extension*

Cover crops are gaining popularity as potentially valuable tools for managing soils and pests in processing carrot production in Michigan. We hypothesized that cover crops—sown in late summer the season before carrot production—would suppress weeds, improve N availability, and increase crop quality and yield. Four on-farm trials were conducted during the 2014-15 (sites 1 and 2) and 2015-16 (sites 3 and 4) growing seasons to evaluate the effects of a range of cover crops including: 1) oats 2) oilseed radish (OSR) “Defender”; 3) Dwarf Essex Rape (DER); and 4) an oats+OSR mix. A cover crop free control treatment was included for comparison. Cover crop biomass ranged from 2-9 T/ha, with greatest productivity occurring at site 3, likely due to an earlier planting date and higher soil fertility. Carrot yields were greater following cover crops compared to the no cover crop control in 4 out of 16 cases, and unaffected in the remaining 12 cases. At site 3, carrot marketable yields were increased by 14-30%, and the percentage of forked carrots reduced by 50% or more in treatments containing cover crops in the mustard family (OSR, DER, and oats+OSR); these treatments also had higher soil N and lower densities of winter annual weeds in early spring compared to the oats and no cover crop control. Ongoing research is aimed at evaluating the impact of these cover crops on nematode community as an indicator of soil health, and fungal pathogens that may influence carrot productivity.

PM-101

Distribution of *Xanthomonas hortorum* pv. *carotae* in Commercial Carrot Seed Lots

Jeremiah Dung, *Central Oregon Agricultural Research Center, Oregon State University, 850 NW Dogwood Lane, Madras, Oregon 97741*

Bulk samples of carrot seed are tested for *Xanthomonas hortorum* pv. *carotae* (*Xhc*) using a seed wash dilution plating assay. Testing protocols for seed-borne pathogens usually assume that infested seeds are fairly uniform with regards to bacterial populations on individual seeds and the assay will detect the average number of bacteria for infested seed present in the sample. However, previous studies have demonstrated that bacterial populations on individual seeds may vary and be non-normal in distribution. Sixteen commercial carrot seed lots were tested using a bulk seed wash assay and contained *Xhc* at populations between 10^5 and 10^9 CFU/g seed. Individual seeds from these seed lots were assayed to determine *Xhc* populations on individual seeds. The incidence of *Xhc*-infested seed varied among the seed lots, ranging from 7.7 to 94.3% infested seed. Seven of the 16 lots harbored <20% infested seed, while four lots contained infested seed at an incidence of 23 to 39%. Populations of *Xhc* ranged from 2 CFU/seed (the limit of detection of the assay) to 6.4×10^6 CFU/seed; three seed lots contained individual seeds with populations $>10^5$ CFU/seed. Most of the *Xhc* populations were not adequately described by a normal distribution and were highly and positively skewed. The incidence of *Xhc*-infested seed in carrot seed lots and the populations on individual seeds may be important factors influencing seed-borne transmission of *Xhc* and the efficacy of seed treatment, but the epidemiological implications of a relatively few, highly infested seeds in seed lots are not well-understood.

PM-102

Pythium diseases of carrots

Joe Nunez¹ and Mike Davis²

¹*University of California Cooperative Extension, Bakersfield Ca 93307*

²*University of California, Department of Plant Pathology, Davis, CA 95616*

Cavity spot of carrots caused by *Pythium* species has been studied extensively by University of California researchers for over 30 years. In California *Pythium violae* and *P. sulcatum* are the main causes of cavity spot. However other *Pythium* species such as *P. ultimum* and *P. irregulare* have been isolated from diseased tissue. The host range of *P. violae* and *P. sulcatum* is broad with some hosts being symptomatic hosts while others are asymptomatic hosts. This host range can affect the choice of crop rotations if the desired effect is to reduce the incidence of cavity spot or *Pythium* root dieback. Many soil factors, including salinity, EC, pH, OM and soil temperature, have been studied to determine what, if any, effect they have on the development of cavity spot. Many chemical and organic fungicides have been evaluated over the course of 30 years of research. Several fungicides are now registered for use in California that have efficacy on the management of cavity spot. However, biologicals have not shown sufficient efficacy to be recommended options for the control of cavity spot. Increasing microbial activity by the addition of organic matter has resulted in the development of suppressive soils. These and other cavity spot studies conducted by various UC researchers will be presented.

PM-103

Carrots Viruses in the UK – an Agronomic Challenge

Howard Hinds

Root Crop Consultancy Limited, 8 Ridgeway, Southwell, Nottinghamshire, NG25 0DU

Historically there are two carrot virus complexes which occur in the UK, Carrot Motley Dwarf Complex (CMD) and *Parsnip yellow fleck virus* (PYFV). Virus symptoms in the foliage show mottled, yellow, brown and red leaves. In roots they cause black spotting, cracking, kipping and excess hairiness. Heavy infection will significantly reduce plant stands and yields. In 2015 carrot virus accounted for around £19 million crop losses. Recently research by scientists at FERA Science Ltd, UK, discovered novel and unexpected viruses infecting carrots, one *Carrot yellow leaf virus* (CYLV) is linked to internal root browning.

These viruses are aphid transmitted, with the main vector being willow-carrot aphid (*Cavariella aegopodii*). Parsnip aphids (*Cavariella pastinacae*) and peach-potato aphid (*Myzus persicae*) may also be significant virus transmitters in carrots. CMD is transmitted relatively slowly in a persistent manner, however PYFV and CYLV are transmitted quickly in a semi-persistent manner. These aphids migrate into crops in late spring and usually numbers peak in June and July, however populations show large variations annually and regionally. Warmer winters, due to climate change, are thought to be a reason why populations are on the increase.

There are several sources of the carrot viruses in the UK. Apiaceous weeds are a source of PYFV, with cow parsley (*Anthriscus sylvestris*) the main UK weed host. Carrots are a source of CMD, which allows circular transmission from carrot to carrot in the crop. In-field storage of carrots in the UK could be creating a bridge for carrot to carrot transmission between seasons. Seed may also be an important virus source.

The distribution of carrot growing areas in the UK means that isolation of crops, or breaks in growing, are not an option to reduce exposure to virus infection. Removal of weed hosts is not possible as they are found so widespread. Therefore management of carrot viruses relies mainly on insecticide control. Timing of sprays is generally linked to regional and local aphid trapping. Seed treatment with Thiamethoxan is proving effective for the early season control. Thereafter there is a shortage of foliar aphicide sprays to cover the mid to late season period. The loss of pirimicarb in 2017 is another depletion of chemical options. Further research is required to identify the most damaging carrot viruses and understand the key periods when aphids infect them, to better target chemical applications and sowing timings.

PM-104

Understanding the ecology and epidemiology of *Pythium violae* causing cavity spot on carrot.

Kathryn Hales¹, Gary Bending², Tim Pettitt³, John Clarkson¹

¹Warwick Crop Centre, University of Warwick, UK, ²Life Sciences, University of Warwick, UK, ³NPARU, University of Worcester, UK.

Cavity spot is a major disease of carrot, which in the UK is caused primarily by the soilborne oomycete *Pythium violae*. Infection results in small black lesions and an unmarketable crop with high-value losses occurring every year. Disease management is challenging due to variable fungicide efficacy and difficulty in implementing long rotations. A lack of effective research tools including diagnostics for *P. violae* and the absence of a reproducible inoculation procedure for carrot has hampered research to understand the factors conducive to disease.

Initially, the identity of *Pythium* spp. associated with cavity spot was determined using a collection of 127 isolates from diseased carrots. Following ITS sequencing, 60% were identified as *P. violae*, 15% as *P. intermedium* and 14% as *P. sulcatum*. Further characterisation through sequencing of additional

housekeeping genes and pathogenicity tests is being carried out to understand variation in the pathogen. Furthermore, an amplicon sequencing approach will be used to investigate *Pythium* communities and their interaction with other microbiota.

In order to quantify *P. violae* in soil and roots, a specific PCR test has been developed which, in combination with an oospore capture procedure, potentially allows testing of larger soil samples. Initial results suggest that detection of less than 10 oospores in 10 g may be possible. Testing of qPCR is currently underway.

Inoculum production and plant assay methods are also being developed for *P. violae*. Results have indicated that the pathogen can cause damping-off symptoms on seedlings while root stunting and small numbers of lesions have been observed on mature roots.

PM-105

California Carrot IPM from 1995 to 2014.

Jim Farrar, *UC IPM Program*

California is the largest producer of fresh market of carrots in the United States. Carrot production, pest management, and marketing have undergone significant changes in the last 20 years. California is also the only state with 100% pesticide use reporting in agriculture. Based on the Department of Pesticide Regulation database, pesticide use in carrots has also changed over the last 20 years. Soilborne pests are the primary problems since carrot root need to be straight and free of blemishes for the fresh market. Pre-plant fumigation continues to be a major method of soilborne pest management and there has been a shift from metam-sodium to metam potassium. Foliar diseases are a concern since health tops are needed for harvest. Current fungicides applied are narrower spectrum and lower risk to human health than 20 years ago. Insects are relatively minor pests of carrots in California and current insecticides applied are less toxic than 20 years ago. Organophosphate use has declined significantly, organochlorines are no longer used; while neonicotinoid use has increased. Biological pesticide use increased significantly from 2012 to 2014 but is a relatively small proportion of pesticides applied to carrots. Changes in carrot IPM practices and pesticide use will be discussed.

PM-106

Evaluation of Flea Beetle Phenology and Damage to Carrot Production in California

Joe Nunez, *UCCE, 1031 South Mount Vernon Ave., Bakersfield California 93307*
David Haviland, *UCCE, 1031 South Mount Vernon Ave., Bakersfield California 93307*

For the past few years carrot growers in the lower San Joaquin and Antelope Valleys have been reporting an unknown injury to the taproot of carrots. Superficially the damage looks like cavity spot

(*Pythium* sp.), a fungal disease that causes depressed lesions oriented across the taproot. However, upon closer inspection it became evident that damage was being caused by insect feeding, coupled with secondary infections that enhanced the injury's appearance as cavity spot. This damage is now attributed to feeding by flea beetle larvae. The principal concern with flea damage is that it can be confused with cavity spot.. This may trigger the use of fungicides for a problem caused by insects, or vice versa. The result is a lack of control, a waste of money, and continued economic damage to the crop. Currently very little is known about the best approach to flea beetle management in carrots in California. In this study we tested several different monitoring techniques to understand flea beetle phenology in California as a first step towards developing management guidelines for carrot growers.

PM-107

Managing root-knot nematodes in organic carrot production – an overview of California studies

A. Ploeg¹, J.O. Becker¹, and J. Nunez².

¹Department of Nematology, University of California, Riverside, CA 92521, and ²University of California Cooperative Extension Kern County, Bakersfield, CA 93307.

Carrots are grown organically on about 11,500 acres in California, which represents approximately 14% of the total California carrot acreage. In 2006, carrots surpassed tomatoes as the most sold organically grown vegetable. Although there is a price premium for organically grown carrots, there are also major challenges. One of these is the occurrence of root-knot nematodes (rkn, *Meloidogyne* spp.). The nematodes are particularly damaging on lighter sandier soils, which are the favored soil types for carrot production. Two damaging species: *M. incognita* and *M. javanica* are frequently found in California carrot fields. The nematodes cause de carrot to form galls or bumps on the surface, resulting in an unmarketable product. In a conventional production system, soil fumigants or, more recently, non-fumigant synthetic nematicides can be used to effectively control the nematodes, but these products are not available to organic growers. Promising new carrot varieties with sufficient levels of resistance against rkn are under development, but even when available they should be used judiciously to avoid the risk of rapid appearance of virulent nematode strains that can break through the resistance. Thus, few options are available in organic production systems. Since the introduction of the DiTera in 1996 as the first biological nematicide, a range of biologically-based strategies and nematicidal products have been developed and have been evaluated in California field trials by us and by others. A summary of results from various field trials on methods and products suitable for organic production systems will be presented.

PM-108

Evaluation of new nematicides for control of nematodes in carrots, in Ontario, Canada

K. Vander Kooi¹, D. Van Dyk², and M. R. McDonald¹

¹ Department of Plant Agriculture, University of Guelph, Guelph ON, Canada

²Ontario Ministry of Agriculture, Food and Rural Affairs, Guelph ON, Canada

Carrots are particularly sensitive to nematodes especially during taproot formation. Root-knot nematode (*Meloidogyne hapla* Chitwood) and carrot cyst nematode (*Heterodera carotae* Jones) are the major nematode pests of carrots in Ontario. There is zero tolerance for root-knot nematodes in carrot production so the presence alone is enough to recommend control measures. Soil fumigation is the primary management option used by carrot growers. Fumigants PicPlus (chloropicrin 86%) and Busan/Vapam (metam sodium 42.5%) are registered on carrots for nematode control. Finding alternative nematicides is vital to provide Ontario carrot growers with the management tools they

need. Two non-fumigant nematicides have potential for nematode control: Nimitz (fluensulfone 480 g/L) and Velum Prime (fluopyram 50%). Field trials in commercial carrot fields with a history of nematode damage were conducted in 2014 – 2016 on high organic matter soils (60-80%). Various treatments were evaluated, included PicPlus, PicPlus + Vapam, PicPlus + Nimitz, Vapam, Nimitz, and Velum Prime. Carrots were harvested and assessed for nematode damage, forking, stunting and yield. Nematode damage was rated on a scale of 0-5. No significant differences in yield or percent marketable were found in 2016. In all years, PicPlus reduced nematode damage compared the check and increased yield in 2014 and 2015. In 2014, Vapam, Nimitz, and combinations of these products increased carrot yield and percent marketable carrots and reduced damage severity. Combining applications of PicPlus at seeding and pre-plant applications of Vapam or Nimitz did not significantly increase efficacy over a separate application of these products.

PM-109

New nematicides provide effective protection against root-knot nematodes

J. Ole Becker¹, Antoon Ploeg¹, and Joe Nunez².

¹Department of Nematology, University of California, Riverside, CA 92521, and ²University of California Cooperative Extension Kern County, Bakersfield, CA 93307

Root-knot nematodes (rkn), particularly *Meloidogyne incognita* and *M. javanica* are the economically most important pathogens in California's fresh market carrot production. They reduce the quality of the harvested product primarily by inducing galling and forking of the main root. Galled feeder roots are also less able to supply the plant with water and nutrients which causes yield reduction. The rkn's wide host range, absence of commercially available rkn-resistant carrot cultivars, and the lack of effective non-fumigant nematicides, biocontrol products or cultural practices have resulted in reliance on pre-plant soil fumigants such as Telone II (a.i. 1,3-dichloropropene) and metam sodium or metam potassium. Often substantial parts of fields need to be excluded from fumigation because of buffer zone requirements. Other restrictions address emissions of volatile organic compounds associated with fumigant use. During the past four years we have evaluated development products with novel nematicidal ingredients in several *M. incognita*-infested field trials. At medium to high rkn population density pressure both DPX-Q8U80 (a.i. fluazaindolizine, DuPont) and Nimitz (a.i. fluensulfone, Adama) mitigated rkn disease symptoms and increased marketable yield compared to the non-treated control. With effective new modes-of action, lower mammalian toxicity, and lesser environmental impacts than previous generations of nematicides, these products are expected to considerably reduce soil fumigant use in California's carrot production.

PM-110

Variation among *Meloidogyne* spp. isolates on a panel of resistant carrot genotypes

Philip A. Roberts, ¹, William C. Matthews¹, Philipp W. Simon² and Tra T. Duong¹

¹Department of Nematology, University of California, Riverside, CA 92521, USA

²USDA ARS, Vegetable Crops Research Unit, Department of Horticulture, University of Wisconsin, Madison, WI 53706, USA.

A collection of 49 isolates of *Meloidogyne arenaria*, *M. hapla*, *M. incognita* and *M. javanica* were compared for their infection potential on a panel of 11 diverse sources of resistant carrots (*Daucus carota*). The resistant genotypes were sources from 'Brasilia,' 'Homs,' 'Ping Ding' and 'Western Red' or combinations of these sources. They are known to contain genes for resistance to *M. incognita* and *M. javanica*. The goal was to determine the breadth of utility of resistance traits available in carrot germplasm and whether nematode virulence to the resistance is present. A susceptible carrot,

Imperator 58, was included as a control. All nematode isolates were cultured on greenhouse-grown susceptible tomato host plants. One month after seeding into sand-filled pots, each plant at the 3- to 5-leaf stage was inoculated in the root-zone with 50,000 freshly extracted eggs. Carrot root systems were assayed for root-galling (scale 0 – 8) and egg production 70 days after inoculation. Each isolate x carrot genotype combination was replicated four times and the test was conducted twice. The most resistant genotypes across isolates were derived from Brasilia 1252 and HxB, a cross between Homs and Brasilia. Ping Ding and Western Red also exhibited effective resistance across isolates. Of 29 *M. incognita* isolates, three were slightly more aggressive on Homs and Ping Ding, whereas the Brasilia sources were unaffected by those more aggressive isolates. The *M. incognita* isolates included ones known to be virulent on the tomato *Mi-1* gene or the cowpea *Rk* gene, but there was no correlation between virulence on the *Mi-1* and *Rk* genes and ability to parasitize resistant carrot genotypes. Two isolates of *M. arenaria* and seven isolates of *M. javanica* were avirulent on the carrot resistance sources, whereas variation in ability to parasitize resistant carrots was found among 11 *M. hapla* isolates.