American Phytopathological Society, Pacific Division

Annual Meeting

Maple Hall
La Conner, Washington
June 29-30, 2016
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CONFERENCE OVERVIEW

Welcome to the 2016 meeting of the Pacific Division of the American Phytopathological Society. The Pacific Division is the regional representation of APS. Eligible members are those members of APS who live in the geographical region of the Pacific Division which includes: Alaska, Arizona, California, Colorado, Hawaii, Idaho, Montana, Nevada, New Mexico, Oregon, Utah, Washington, Wyoming and contiguous provinces in Canada (British Columbia, Alberta and Saskatchewan).

LOCAL ARRANGEMENTS COMMITTEE

Lindsey DuToit, Washington State University
Debra Inglis, Washington State University
Tobin Peever, Washington State University

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President – David Gent, USDA-ARS
President-Elect – Soumaila Sanogo, New Mexico State University
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Secretary-Treasurer – Inga Zasada, USDA-ARS
Divisional Forum Representative – Natalie Goldberg, New Mexico State University
2016 AWARD WINNERS

GRADUATE STUDENT TRAVEL AWARD

Daniel Farber, Oregon State University
Zachary Frederick, Washington State University
Leslie Holland, University of California-Davis
Lauri Lutes, Oregon State University
Lindani Moyo, Washington State University
Cristian Olaya, Washington State University
Sowmya Ramachandran, Washington State University
Hannah Rivedal, Oregon State University
Xuefei Wang, Washington State University

EARLY CAREER AWARD

Jeremiah Dung, Oregon State University

LIFETIME ACHIEVEMENT AWARD

Jim Adaskaveg, University of California Riverside
Debbie Inglis, Washington State University
2016 GRADUATE STUDENT ORAL PRESENTATION COMPETITION

Christian Aguilar, Washington State University
Iqbal Aujla, Washington State University
Shannon Carmody, Washington State University
Sahar Dabirian, Washington State University
Binod Pandey, Washington State University
Daniel Farber, Oregon State University
Zachary Frederick, Washington State University
Gretchen Freed, Washington State University
Cassandra Funke, University of Idaho
Leslie Holland, University of California, Davis
Lauri Lutes, Oregon State University
Lindani Moyo, Washington State University
Cristian Olaya, Washington State University
Sowmya Ramachandran, Washington State University
Hannah Rivedal, Oregon State University
Rachel Rudolph, Oregon State University
Javier Tabima, Oregon State University
Yvonne Thompson, Washington State University
Lisa Tran, University of Idaho
Moying Wang, Washington State University
Xuefei Wang, Washington State University
David Wheeler, Washington State University
ACKNOWLEDGEMENTS

We thank the following individuals for their generous gift of their time and financial support of the meeting.

APS CAREER ADVANCEMENT, DEVELOPMENT RESOURCES, AND EDUCATION COMMITTEE PROFESSIONAL DEVELOPMENT WORKSHOP

Rachel Bomberger, Washington State University

STUDENT TRAVEL AWARD COMMITTEE

Jeremiah Dung, Oregon State University

Alan Dyer, Montana State University

Isolde Francis, California State University Bakersfield

Steve Hanson, New Mexico State University

Claudia Nischwitz, Utah State University

GRADUATE STUDENT ORAL COMPETITION AND UNDERGRADUATE POSTER COMPETITION JUDGING TEAM

Jeremiah Dung, Oregon State University

Alan Dyer, Montana State University

Isolde Francis, California State University

Alex Karasev, University of Idaho

Zamir Punja, Simon Frasier University, British Colombia
OTHER LOCAL ARRANGEMENT VOLUNTEERS

Shannon Carmondy, Washington State University
Mike Derie, Washington State University
Zachary Frederick, Washington State University
Babette Gundersen, Washington State University
Dalphy Harteveld, Washington State University
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INFORMATION

- **Addresses and contact information.**

  **Maple Hall**
  104 Commercial Street
  La Conner, WA 98257

  **Washington State University Mt. Vernon Research and Extension Center**
  16650 WA-536
  Mt Vernon, WA 98273
  Phone: 360-848-6120

  **La Conner Country Inn**
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  La Conner, WA 98257
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  **La Conner Channel Lodge**
  205 N 1st Street
  La Conner, WA 98257
  Phone: 360-466-1500

  **Emergency contact:**
  David Gent
  Email: gentd@onid.orst.edu
  Mobile: 541-206-9307

- **Oral presentations.** Oral presentations, unless otherwise noted, are 15 minutes including questions. The agenda is very full and the time limits will be enforced to ensure the meeting stays on schedule. A PC computer, digital projector, laser point, and audio system will be available. Presentations will need to be loaded prior to the morning session on the day a talk will be presented.

- **Poster guidelines.** Guidelines for posters will follow the general guidance given for the APS Annual Meeting (see online). However, the maximum poster dimensions for the Pacific Division meeting are **36" wide x 48" in length.** Poster set-up will occur Wednesday, June 29 between 7:30 and 8:30 AM. Each poster will be assigned a number corresponding to the associated abstract (see program below). Pins will be available at each poster board for hanging.
• **Parking logistics.** You will need a parking permit good for Maple Hall on June 29 and 30. These are only good for the La Conner Town owned parking lot on Second Street (to the east of Maple Hall). The parking lot along the channel in front of Maple Center (west side of Maple Hall) is a paid lot. The parking passes do NOT apply for Tuesday, June 28 therefore participants should park along one of the side streets or pay to park in the Town owned parking lot. The walk from the Channel Inn to Maple Hall is about ¼ mile. Parking permits have been sent by email and also are available at the registration desk.

• Wifi is available at Maple Hall, Password: maple20ten01

**REGISTRATION AND INFORMATION DESK**

The Registration and Information Desk, located at the entrance of Maple Hall, 104 Commercial Street, La Conner, Washington 98257

- Wednesday, June 28 7:30 to noon
- Thursday, June 29 7:30 to noon
PROGRAM SCHEDULE

Tuesday June 28:
10:00 - 11:30 am  APS Career Advancement, Development Resources, and Education Professional Development Workshop (Washington State University Mt. Vernon Research and Extension Center)
12 PM - late afternoon  Field tour of Skagit Valley agriculture (meet at Maple Hall)

Wednesday June 29:
7:30 – 8:30 AM  Load presentations; hang posters
8:30 – 9:00 AM  Opening and Welcome
   8:40 AM  Tim Murray, APS President – Science to practice – Update from APS council
9:00 – 12:00 PM  Opening Symposium “The future climate of the Western U.S.: Implications for forest health and plant disease management” – Moderator: David Gent
   9:00 AM  David Gent – Introduction
   9:05 AM  David Peterson, US Forest Service – Reshaping nature: Climate change and forest ecosystems in the western U.S.
   9:35 AM  Susan Frankel, U.S. Forest Service – Forest pathogens and climate change: Observations and prediction
10:05 – 10:20 AM  Break
   10:20 AM  Sanford Eigenbrode, University of Idaho – Aphids, plant viruses, and climate change in the Pacific Northwest
   10:50 AM  Kendra Baumgartner, USDA-ARS - Water stress exacerbates the severity of Botryosphaeria dieback in grapevines infected by Neofusicoccum parvum
   11:10 AM  Gabrielle Roesch-McNally, Iowa State University – Farmers’ climate change beliefs and adaptation and mitigation strategies: Highlighting findings from a survey and in-depth interviews with corn belt farms
11:40 AM  Discussion

12:00 – 1:30 PM  Business meeting and working lunch

1:30 – 5:30 PM  Graduate Student Presentations – Moderator: Jerry Weiland

1:30 PM  **Zack Frederick** - *Susceptibility of weedy hosts to Verticillium dahliae isolates*

1:45 PM  **Christian Aguilar** - *Bull’s-eye rot management: Understanding the disease cycle of Neofabraea spp. occurring on apples grown in the US Pacific Northwest*

2:00 PM  **Hannah Rivedal** - *Utilizing field surveys, variety trials and indicator species analysis to diagnose a soil borne disease complex in winter squash*

2:15 PM  **Iqbal Aujla** - *Surprising revelations in the biology of crown and root rot pathogens of wheat*

2:30 PM  **Xuefei Wang** - *Grape berry colonization and biological control of Botrytis cinerea by indigenous vineyard yeasts*

2:45 PM  **Leslie Holland** - *Diversity of Cytospora species associated with fruit and nut crop canker diseases in California*

3:00 PM  **Cristian Olaya** - *Predictive models for tospoviral proteins involved in virion assembly and host defense suppression*

3:15 PM  **Daniel Farber** - *Scaling up: the effect of plot size and initial inoculum on dispersal gradients of Puccinia striiformis f.sp. tritici*

3:30 – 3:45 PM  **Break**

3:45 PM  **Cassandra Funke** - *Strain specific resistance to Potato virus Y (PVY) in potato efficiently reduces the prevalence of the PVY∅ strain under semi-field conditions*

4:00 PM  **Lisa Tran** - *Composition of Potato virus Y strains in Idaho seed potato between 2012 and 2015*

4:15 PM  **David Wheeler** - *Evidence that specific rotation crops infected by Verticillium dahliae in Washington State do not serve as reservoirs for the mating type, MAT1-1*
4:30 PM  **Binod Pandey** - *Diverse mycoviral sequences in the sweet cherry powdery mildew fungus (Podosphaera prunicola) revealed by next-generation sequencing*

4:45 PM  **Lauri Lutes** - *Historical survey of cherry viruses in Oregon*

5:00 PM  **Lindani Moyo** - *Transcriptome-wide mining of potato genes targeted by Potato virus Y-derived viral small interfering RNAs*

5:15 PM  **Rachel Rudolph** - *Alternative management practices of Pratylenchus penetrans in red raspberry in the Pacific Northwest*

5:30 - 7:00 PM  **Posters, including student poster highlight, social time**

7:00 - 9:00 PM  **Awards banquet**

**Thursday June 30**

8:00 – 9:15 AM  **Student Presentations (continued) - Moderator: Jerry Weiland**

8:00 AM  **Moying Wang** - *Stability and fitness advantages of metalaxyl-resistant isolates of Pythium ultimum*

8:15 AM  **Sahar Dabirian** - *Grafting watermelon to control Verticillium wilt caused by Verticillium dahliae in Washington*

8:30 AM  **Sowmya Ramachandran** - *Effectors from Puccinia suppress plant host defense response*

8:45 AM  **Gretchen Freed** - *Effect of temperature on virulence of fungal isolates collected in mycofloristic survey of Camassia quamash*

9:00 AM  **Shannon Carmody** - *Potential seed transmission of Pyrenopeziza brassicae and Mycosphaerella capsellae in brassicas in the Pacific Northwest USA*

9:15 AM  **Javier Tabima** - *Effect of read depth, missing data, imputation and variant callers on genotyping-by-sequencing for population genetic analysis*

9:30 AM  **Yvonne Thompson** - *Identifying genetic resistance to the cereal cyst nematode Heterodera filipjevi in Pacific Northwest spring wheat*

9:45 – 10:00 AM  **Break; Graduate Student Competition Judges Meeting**
10:00 - 12:00 PM  Oral Presentations – Moderator: Natalie Goldberg

10:00 AM  Le Thanh Tam - Classification powdery mildew fungi in Viet Nam and potential in bio-control by indigenously endophyte bacteria Bacillus amyloliquefaciens BA1

10:15 AM Richard Smiley - Using DNA extracted from soil to quantify inoculum densities of multiple soilborne pathogens in long-term cropping systems trials

10:30 AM Jeremiah Dung - Development and validation of a quantitative PCR assay for the detection of Claviceps purpurea sensu lato ascospores

10:45 AM Jose Urbez-Torres - Young vine decline DNA-macroarray: a fast, specific, sensitive, and multiplexing diagnostics tool to assess the health status of grapevine nursery propagation material

11:00 AM Robin Ludy - Diversity of mycelial compatibility groups of Sclerotium cepivorum causing white rot in Oregon

11:15 AM Melanie Kalischuk - Monitoring Phytophthora infestans sporangia using volumetric trapping

11:30 AM Helga Forster - Reduced sensitivity to potassium phosphite in Phytophthora species and its implication for the management of Phytophthora brown rot of citrus

11:45 AM Chao Xiang - Molecular mapping of stripe rust resistance genes in spring wheat line W18

12:00 – 1:30 PM  Lunch with awards presented to winning students

1:30 - 5:00 PM  Oral Presentations – Moderator: Soumaila Sanogo

1:30 PM Yu Lei - Characterization of somatic recombinant isolates of Puccinia striiformis, the stripe rust pathogen

1:45 PM Mostafa Abugrain - Development of products for management of broad host-range gall forming phytopathogens

2:00 PM Michael Gordon - Testing the efficacy of commercially-available compounds for managing Agrobacterium tumefaciens

2:15 PM Evan Thompson - Dynamics of colonization of pome flowers by biocontrol strains of Aureobasidium pullulans, a yeast that effectively suppresses fire blight
2:30 PM  Bill Schneider - Identification of toxin production pathways by genomic sequencing of Rathayibacter toxicus and the associated phage

2:45 – 3:00 PM  Break

3:00 PM  Alexander Karasev - Changing epidemiology of Potato virus Y in potato, and the role of strain specific resistance in facilitating the spread of recombinant strains

3:15 PM  Kelsie Green - Mapping the conformational epitope for a monoclonal antibody recognizing tuber necrotic strains of Potato virus Y

3:30 PM  Xue Feng - Strain composition of Bean common mosaic virus and Bean common mosaic necrosis virus isolates from field samples of common bean

3:45 PM  Marjo Ala-Poikela - A novel strain of Beet curly top virus from Mexico

3:45 – 4:00 PM  Break

4:00 PM  Stephanie Szostek - Western flower thrips can transmit Tomato spotted wilt virus from infected tomato fruits

4:15 PM  Chinnaraja Chinnadurai - Complete genome sequencing of Zucchini yellow mosaic virus causing mosaic in cucurbits in Trinidad

4:30 PM  Jose Urbez-Torres - Prevalence of Grapevine red blotch-associated virus in British Columbia

4:45 PM  Naga Teja Natra - The current status of nepoviruses in Washington vineyards

5:00 PM  Jim Farrar - Impact of integrated pest management (IPM) in California

5:15 PM  Concluding Remarks - Soumaila Sanogo, President, APS Pacific Division

5:30 - 7:00 PM  Poster viewing/take-down
POSTERS AND PRESENTING AUTHOR

** Participant in student poster competition

1. A novel Fusarium pathogenic to common rose mallow (Hibiscus moscheutos) is a sister taxon to Fusarium buharicum – Frank Dugan

2. Exploration of wheat root phenotyping for Rhizoctonia resistance – Patricia Okubara

3. Impacts on plant health of complex pathogen communities - Erin Gunnink Troth

4. Identification and pathogenicity of fungal species associated with canker diseases of pistachio in California – Mohamed Nouri

5. Flavonoid biosynthetic pathway components contribute to the resistance of mature Arabidopsis thaliana seeds to Aspergillus infection – Teresa De Sitter

6. Effect of culture filtrates from four Trichoderma species on sporangia and zoospore production, and mycelial growth by Phytophthora capsici - Soum Sanogo

7. Emerging root-infecting pathogens of marihuana (Cannabis sativa) - Zamir Punja

8. Clonality within disease foci and field populations of Sclerotinia sclerotiorum causing basal stalk rot in sunflower seed crops in central Washington - John Weber

9. Identification and pathogenicity of Fusarium species associated with crown rot of pistachio in California – Maria Crespo

10. Pomegranate dieback in California caused by Lasiodiplodia gilanensis - Jose Urbez-Torres

11. First report of Urocystis camassiae causing smut of Camas (Camassia quamash) in Idaho, United States - Kyrylo Savchenko

12. Apple anthracnose canker life cycle and disease cycle – Whitney Garton

13. Extracellular alkalinization assay: a fast and reliable method to detect the defense response in potato – Natalia Moroz

14. **Chokecherry and sweet cherry are infected by two host-specific Podosphaera species – Swarnalatha Moparthi
15. Adaptation to qualitative and quantitative host resistance by *Podosphaera macularis* in the Pacific Northwest – Sierra Wolfenbarger

16. **Nitrogen fertilization increases powdery mildew, arthropod pests, and nitrate accumulation in hops** – Anne Iskra

17. Relative abundance of potato psyllid haplotypes in potato fields during 2012 to 2015, and incidence of *Candidatus Liberibacter solanacearum* - Jennifer Dahan

18. First occurrence of *Pseudomonas syringae* pv. *syringae* causing lesions on pumpkin fruit in WA, U.S. - Lydia Tymon

19. Protein expression in *Rathayibacter toxicus* FH79 analyzed by mass spectrometry - Christine Fennessey

20. Analysis of toxin gene transcription in *Rathayibacter toxicus* infected with bacteriophage – Aaron Sechler

21. **Investigating motility and persistence of PBTS *Rhodococcus* spp. – Paul Lambert

22. Potential seed transmission of *Pyrenopeziza brassicae* and *Mycosphaerella capsellae* in brassicas in the Pacific Northwest USA – Shannon Carmody

23. Towards construction of genetic linkages for mapping virulence genes in *Puccinia striiformis* f. sp. *tritici*, the wheat stripe rust pathogen - Congying Yuan

24. Pyramiding stripe rust resistance genes on wheat chromosomes 2B, 4B, and 7B - Meinan Wang

25. Expression profiling of pathogenesis-related protein genes in wheat resistance to the stripe rust pathogen (*Puccinia striiformis* f. sp. *tritici*) – Sumaira Farrakh

26. Virulence characterization of *Puccinia striiformis* f. sp. *tritici* in the US for the past 48 years using the Yr single-gene differentials - Tinglan Liu

27. Developing a wheat germplasm with linked genes Yr64 and Yr65 for resistance to stripe rust - Yanmin Qie

28. **Development of *Puccinia striiformis* f. sp. *tritici* mutants for avirulence characterization** - Yuxiang Li

29. Seedling reactions of Mexican wheat varieties and advanced lines to four races of *Puccinia striiformis* f.sp. *tritici*, the stripe rust pathogen - Pedro Figueroa-Lopez
30. Variation of telial formation in the Puccinia striiformis f. sp. tritici population – Anmin Wan

31. Suppressor of RNA silencing from wheat stem rust fungus, Puccinia graminis - Chuntao Yin

32. Development of an infectious clone of the Worland strain of Beet curly top virus – Alan Poplawsky

33. Evidence that tuber cracking in potato can be caused by Potato virus Y - Debra Inglis

34. Discovery of grapevine Pinot Gris Virus and current status of other less-common grapevine viruses in British Columbia – Jose Urbez-Torres

35. Assessing the sanitary status of certified grapevine mother blocks in Washington State – Basavaraj Bagewadi

36. Recombination analysis of the whole genomes for three isolates of Beet curly top virus from beet leafhoppers collected in Oregon – Kelsie Green

37. Presence of Citrus psorosis virus with watermelon ‘moon rings’ in Washington State – Ying Zhai

38. Double Nickel biofungicide efficacy on root health for young grape in the San Joaquin Valley - Eric Flora

2016 APS PACIFIC DIVISION BUSINESS MEETING AGENDA

1. Call to order: Welcome; Announcements on division activities; new officer (David Gent)

2. Retiree and Necrology report (David Gent)
   a. Bruce Kirkpatrick, UC Davis

3. Reading of minutes of previous business meeting (Inga Zasada)

4. Secretary – Treasurer’s report (Inga Zasada)

5. Division Forum report (Natalie Goldberg)

6. Future meeting sites, dates - proposals (David Gent)
   a. Review of results from 2015 membership survey
   b. 2017 suggestions and site nominations
   c. 2018: Potential for joint meeting with Pacific Branch of the Entomological Society of America, mid-June, Tahoe

7. Acknowledgements of volunteers and sponsors (David Gent)
   a. Officers
   b. Local arrangement committee
   c. Other local arrangement volunteers
   d. Professional Development Workshop
   e. Judges for Graduate Oral Presentation Competition:
   f. Judges for Student Poster Competition
   g. Invited presenters and special guests
   h. Financial sponsors

8. Discussion and vote on raising Pacific Division membership dues (David Gent)

9. Other topics from the membership (David Gent)

10. Handing of the gavel to incoming President Soum Sanogo

11. Adjournment (Soum Sanogo)
ABSTRACTS

Development of products for management of broad host-range gall forming phytopathogens. M. ABUGRAIN, M. Putnam, and T. Mahmud. Oregon State University, Corvallis, OR, USA.

Crown gall and leafy gall disease caused by phytopathogenic Agrobacterium tumefaciens and Rhodococcus, respectively, are a significant, costly, and chronic problem in the ornamentals nursery industry. Crown gall has been particularly troublesome in crops that are clonally propagated. Losses are due to the lack of effective chemicals for control of diseases caused by these bacteria. In an attempt to provide growers with viable options for disease prevention, we embarked upon a program to test various botanical extracts for use against A. tumefaciens and Rhodococcus. We investigated the antibacterial activity Achillea millfolium (yarrow), Withania somnifera (ashwagandha), Artemisia absinthium (wormwood), Centaurea cyanus (bachelor's button), Matricaria recuita (chamomile), Taraxacum officinale (dandelion), Celtis boninensis and Strobilauthes cusia. Extracts of these plants were prepared and tested using agar diffusion and micro-dilution assays. We found that a number of extracts from these plants have good antimicrobial activity against R. fascians, indicating their potentials to be used as green alternatives to synthetic agrochemicals for treating plants. The present results encourage further effort to investigate plant-derived bioactive compounds that may possess good antibacterial properties against these gall-forming plant pathogens.

Bull’s-eye rot management: understanding the disease cycle of Neofabraea spp. occurring on apples grown in the US Pacific Northwest. C. AGUILAR (1), M. Mazzola (2), and C. Xiao (3). (1) Washington State University Tree Fruit Research and Extension Center, Wenatchee, WA, USA; (2) USDA-ARS Tree Fruit Research Laboratory, Wenatchee, WA, USA; (3) USDA-ARS Commodity Protection and Quality, Parlier, CA, USA.

In the US Pacific Northwest, bull’s-eye rot of pome fruit, caused by Neofabraea spp., is a major quarantine concern. Of the four fungi causing this disease, Neofabraea perennans and Neofabraea kienholzii are common in north central Washington. In addition to fruit decay, N. perennans causes perennial canker and dieback of apple trees. Currently the over-seasoning strategies of N. kienholzii have not been elucidated. The objectives of this research were to determine the relative capacity of N. kienholzii to induce cankers in comparison with N. perennans, determine the timing of canker induction and fruit infection by either fungus, and to evaluate the efficacy of various fungicides for control of bull’s-eye rot. Based on the findings from this research, N. kienholzii is capable of inducing cankers however, cankers were generally smaller than those induced by N. perennans. Canker induction by both species was prevalent in October compared to other inoculation periods (p < 0.01). Fruit infection was observed at each inoculation period, however disease incidence was greatest near the end of the fruit growing season (October, P < 0.0001). Among those examined, thiophanate-methyl, thiabendazole and pyrimethanil where the only chemicals found to provide effective bull’s-eye control (P < 0.0001), yet due to modes of action and current use by industry, resistance to these fungicides is considered high risk.

An isolate of the Beet curly top virus (BCTV) collected from pepper in Chihuahua, Mexico, was subjected to molecular and biological characterization. The complete genome of BCTV-Mex was sequenced after cloning, and found to be 2,912-nt long. The genome of BCTV-Mex represented a recombinant with BCTV-Worland and BCTV-CFH being the most likely parents. Two full-length, infectious clones of BCTV-Mex (1.47 and 1.53 genomes) were assembled in a binary construct for delivery into plants via agroinoculation. Infectivity of BCTV-Mex clones was monitored through a combination of symptom observations and ELISA. The infectivity was confirmed for sugar beet, tomato, and Nicotiana benthamiana. Symptoms caused by BCTV-Mex were milder in all infected hosts compared to symptoms caused by two other infectious constructs, BCTV-CFH and BCTV-Logan.

Baseline sensitivity of Phacidiopycnis piri from pear to six pre and postharvest fungicides. A. AMIRI, and K. Mulvaney. Washington State University, Wenatchee, WA, USA.

Phacidiopycnis piri (teleomorph Potebniamycles pyri) was first reported in 2004 on pear fruit in Washington. P. piri is a quarantine pathogen in many countries which has limited access to WA fruit packers. Fungicides are commonly applied preharvest to protect pears from inoculum that survives on bark and cankers and at harvest to protect fruit during storage. In this study we established the baseline sensitivities of 106 P. piri isolates never exposed to the preharvest fungicides boscalid and pyraclostrobin and to the postharvest fungicides fludioxonil, difenoconazole and pyrimethanil. The isolates used in this study were not exposed to thiabendazole in the season of isolation. The effective concentrations inhibiting mycelial growth by 50% (EC$_{50}$) were calculated by plotting the log fungicide concentration to Probit of measured inhibition. Mean EC$_{50}$ values were 0.24, 0.38, 0.61, 1.09, 1.56 and 1.81 µg/ml for fludioxonil, pyraclostrobin, pyrimethanil, difenoconazole, thiabendazole, and boscalid, respectively. Variation factors were lower than 100, except for pyraclostrobin, indicating lower intrinsic variability in sensitivity between isolates within the baseline population. Positive correlations were observed between in vitro EC$_{50}$ values and the efficacy of the aforementioned fungicides in controlling P. piri on detached apples. Baseline values from this study will be valuable in detecting potential shifts in sensitivity occurring in P. piri populations.

Surprising revelations in the biology of crown and root rot pathogens of wheat. I. AUJLA (1), and T. Paulitz (2). (1) Washington State University, Pullman, WA, USA; (2) USDA-ARS, Wheat Health, Genetics and Quality Research Unit, Pullman, WA, USA.

Temperature and moisture have profound influences on the activity of Fusarium culmorum, F. pseudograminearum, Rhizoctonia solani AG-8 and R. oryzae causing crown and root rots of wheat respectively, in the dryland wheat production area of the Pacific Northwest region of the United States. This study determined the effects of temperature and water potential (a measure of soil moisture) on the mycelial growth, dry weight and spore germination of these wheat pathogens on potato dextrose agar and broth adjusted to different osmotic and matric potentials (-0.13 to -10 MPa) with sodium
chloride, potassium chloride, and polyethylene glycol (PEG-8000), and incubated at temperatures ranging from 4 to 35°C. Linear mycelial growth of both Fusarium spp. was optimal at 20 - 25°C and -1 to -3 MPa. Dry weight gain showed similar trends in F. culmorum, but F. pseudograminearum showed variation in optimum temperature in response to shift in water potential. Optimum temperature for spore germination ranged from 10-30°C for F. culmorum and 15-30°C for F. pseudograminearum with some decline at extreme temperature and drier ranges. Rhizoctonia solani AG-8 was more restricted for optimal growth, while growth rate of R. oryzae declined less compared to AG-8 with lower water potential and higher temperature. This study contributes to the knowledge of the biology and epidemiology of these pathogens, and will be used in predicting their potential distribution under future climate scenarios.

Assessing the sanitary status of certified grapevine mother blocks in Washington State. B. BAGEWADI (1), C. Ocampo (2), A. Movva (1), D. Hottell (2), M. Garza (2), N. Natra (1), and N. Rayapati (1). (1) Department of Plant Pathology, Washington State University-IAREC, Prosser, WA, USA; (2) Undergraduate student in V&E Program, WSU-Tri-Cities, Richland, WA, USA.

Maintaining virus-tested grapevines in certified nurseries is recognized as the first line of defense in preventing the spread of viruses through the planting stock. Towards this objective, a collaborative project between Washington State University, WSDA Plant Services Program and grapevine nurseries was initiated to systematically examine the sanitary status of certified mother blocks in Washington State. In 2015, we tested samples from white-fruited cultivars of Vitis vinifera, since these cultivars do not express visual symptoms. A composite sampling strategy was adopted to collect and process grapevine samples for virus indexing. A total of 1,226 composite samples, representing 4,919 individual grapevines, from seven white-fruited cultivars were tested by RT-PCR/PCR for the presence of Grapevine leafroll-associated virus 3 (GLRaV-3) and Grapevine red blotch-associated virus (GRBaV). The results indicated that nearly 12% of composite samples were positive for GLRaV-3. None of the 1,226 composite samples tested positive for GRBaV. Total RNA isolated from about 10% of composite samples were analyzed by next-generation sequencing (NGS). The NGS data revealed the presence of sequences aligning with GLRaV-3, Grapevine rupestris vein feathering virus, Grapevine Rupestris stem pitting-associated virus and two viroid species (Hop stunt viroid and Grapevine yellow speckle viroid 1), and the absence of sequences specific to GRBaV.

Potential seed transmission of Pyrenopeziza brassicae and Mycosphaerella capsellae in brassicas in the Pacific Northwest USA. S. CARMODY (1), C. Ocampo (2), and L. du Toit (1). (1) Department of Plant Pathology, Washington State University, Mount Vernon, WA, USA; (2) Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, USA.

Pyrenopeziza brassicae and Mycosphaerella capsellae are new pathogens to the Pacific Northwest USA that cause light leaf spot and white leaf spot, respectively, on many species in Brassicaceae. Cabbage (Brassica oleracea) and mustard (B. juncea) plants were inoculated separately at pod set with P. brassicae and M. capsellae to produce naturally infested seed lots. Symptoms developed on the leaves and pods of

-1-
plants inoculated with *P. brassicae*, and only on the leaves of plants inoculated with *M. capsellae*. Incubating infested seed on NP-10 agar medium for 3 weeks at 4°C followed by 3 weekly microscopic examinations resulted in detection of *P. brassicae* on 12.5 ± 2.3% of the mustard seed and 0.4 ± 0.5% of the cabbage seed. *M. capsellae* was not detected on seed. When the *P. brassicae*-infested mustard seeds were planted under misters in a greenhouse, 1.6% of 1,000 seedlings developed light leaf spot (20% seed transmission rate from the 12.5% infested seeds). In April 2016, *P. brassicae* was found on wild *B. rapa* (bird’s rape mustard) plants and *B. juncea* cover crops in Skagit, Snohomish, and Whatcom Counties in Washington; and *M. capsellae* was detected on wild *B. rapa* in Skagit and Whatcom Counties. Koch’s postulates confirmed pathogenicity of the *P. brassicae* isolates, and β-tubulin DNA sequencing confirmed the species identification. This is the first report of *P. brassicae* and *M. capsellae* in Washington State, a critical region of brassica seed production.

**Complete genome sequencing of Zucchini yellow mosaic virus causing mosaic in cucurbits in Trinidad.** C. CHINNADURAI (1), A. Ramsubhag (1), and J. Jayaraman (1). (1) Department of Life Sciences, Faculty of Science and Technology, The University of the West Indies, St Augustine, Trinidad and Tobago.

*Zucchini yellow mosaic virus* (*ZYMV*) was recently noticed in pumpkin and squash in Trinidad with severe mosaic and yellowing symptoms in leaves and deformation and color alterations in the fruits. The symptoms were noticed at all growth stages of the crop and a maximum disease incidence of 74% was recorded in the dry season during 2014 and 2015. Leaf samples were collected from pumpkin (5 sample) and squash (5 sample) showing severe symptoms from farmer’s fields representing different cropping zones of Trinidad. Total RNAs were extracted from all the leaf samples. cDNA was synthesized with 1 μg of RNA and PCR was carried out with coat protein primers ZYMVCP-F1/ZYMVCP-R1 to confirm the presence of virus. For sequencing of the whole genome, 10 pairs of overlapping primers targeting the entire genome of ZYMV was designed and PCR conditions were optimized. PCR amplifications were performed and the resulting amplicons were cloned into pGEM®-T vector and sequenced by Sanger sequencing. All the sequences were analyzed using various different bioinformatics tools including blast, Clustal W and Mega 6 software and complete genome of ZYMV (~ 9590 bp) was obtained for the Trinidad isolates. The blast analyses proved that the Trinidad isolate is a new strain of ZYMV since which showed more than 6.0 % variability with other reported isolates. The closest relationship of Trinidad isolate was found with NAT isolate (EF062582) from Israel with 94.1 % nucleotide identities followed by 94.0 % identities with SEO4T (Slovakia), AG (Israel) and H (Czech republic) isolates. The lowest nucleotide identities of 80.6 % was obtained with ZYMV13PREP from Reunion Island. From this study a new strain of ZYMV causing severe mosaic in cucurbits was identified in Trinidad.

**Identification and pathogenicity of Fusarium species associated with crown rot of pistachio in California.** M. CRESPO (1), M. Nouri (1), D. Doll (2), and F. Trouillas (1). (1) Department of Plant Pathology, University of California, Davis, Kearney Agricultural Research and Extension Center, Parlier, CA, USA; (2) University of California Cooperative Extension Merced County, Merced, CA, USA.
Only a few Fusarium species are known to cause crown and root rot diseases in woody plants. During recent surveys in California, crown rot symptoms and decline of pistachio (Pistacia vera) trees were observed in orchards located in Merced and Fresno Counties. Twenty-seven Fusarium isolates were isolated in culture medium from symptomatic bark and wood tissues. Fungi were identified based on morphological characteristics and comparison of DNA sequences of the internal transcriber spacer region (ITS) of the rDNA, translation elongation factor 1-α (TEF), and the second largest subunit of the RNA polymerase 2 (RPB2) with reference sequences. Phylogenetic analyses using maximum parsimony of the various sequence data sets allowed the identification of Fusarium solani, F. oxysporum, F. equiseti and F. proliferatum. Two separate lineages were also detected within each of the F. solani and F. oxysporum clade. To determine the pathogenicity of the various Fusarium isolates, 1-year-old detached twigs of P. vera cv. ‘Kerman’ as well as ‘UCB-1’ (P. atlantica × P. integerrima) and P. integerrima rootstocks were inoculated with representative isolates of the four Fusarium species. After one month incubation in the laboratory, lesions produced in twigs inoculated with the different Fusarium isolates were significantly longer than those formed in the agar-only inoculated control. This study suggests that Fusarium species may act as crown rot pathogens of pistachio in California.

**Grafting watermelon to control Verticillium wilt caused by Verticillium dahliae in Washington.** S. DABIRIAN (1), C. Miles (1), and D. Inglis (1). (1) Washington State University, Mount Vernon, WA, USA.

Verticillium wilt (VW), caused by Verticillium dahliae (Vd), decreases watermelon yield 25-75% in WA. A field study conducted in 2015 at three locations in WA investigated the use of grafted plants and plastic mulch for reducing VW in watermelon. Cv. TriX Palomar non-grafted (control) and grafted with rootstocks Super Shintosa, Tetsukabuto and Just were grown with black and clear plastic mulch. Area Under Disease Progress Curve (AUDPC) was greater for non-grafted (765) than for grafted TriX Palomar (Ave. 166). At Mount Vernon, where VW pressure was highest, yield (kg/plant) of non-grafted TriX Palomar was lower (7 kg) than grafted treatments (Ave. 13 kg), whereas at Othello and Eltopia, there were no differences. At season’s end, Vd was greatest in stems of non-grafted plants at Mount Vernon and Eltopia (87 % and 89 %, respectively), and there was no difference at Othello (Ave. 22 %). AUDPC was greater for plants grown with black mulch (385) than for plants grown with clear mulch (237). AUDPC was greatest at Mount Vernon (680), and lowest at Eltopia (84). After harvest Vd density under black mulch increased to 4, 4.5 and 55 cfu g⁻¹ of soil at Eltopia, Othello, and Mount Vernon, respectively (before planting levels were < 1 cfu g⁻¹ of soil Vd at Eltopia and Othello and 28 cfu g⁻¹ of soil at Mount Vernon). In contrast Vd under clear mulch was similar to the level at planting at each location. Grafting and clear plastic mulch may provide adequate control for Vd.

**Relative abundance of potato psyllid haplotypes in potato fields during 2012 to 2015, and incidence of Candidatus Liberibacter solanacearum.** J. DAHAN (1), E. Wenninger (2), N. Olsen (2), and A. Karasev (1). (1) University of Idaho, Moscow, ID, USA; (2) University of Idaho, Kimberly, ID, USA.

The potato disease Zebra Chip (ZC) has been linked to infection of plants by the
bacterium *Candidatus Liberibacter solanacearum* (Lso). Five haplotypes (hapA to hapE) of Lso have been described so far in different crops, with only hapA and hapB being associated with ZC in potato. Both haplotypes are vectored and transmitted to a variety of solanaceaeous plants by the tomato/potato psyllid, *Bactericera cockerelli* (Šulc). Four psyllid haplotypes have been identified: Northwestern, Central, Western and Southwestern. Here, psyllid samples collected in Idaho potato fields from 2012 to 2015 were used to clarify spatial and temporal patterns in distribution and abundance of psyllid and Lso haplotypes. A shift from hapA toward hapB of Lso was revealed during these four seasons, indicating possible evolution of Lso populations in Idaho fields. Although we confirmed that Western psyllids were the most abundant by far during the four seasons of observation, we also observed changes in abundance of other haplotypes, including increased diversity of psyllid haplotypes during 2015. South-central Idaho exhibited more diversity in psyllid haplotypes than Southwestern Idaho. Seasonal changes observed for the Northwestern and Central haplotypes could potentially be linked to psyllid migration and/or habitat changes.

**Flavonoid biosynthetic pathway components contribute to the resistance of mature *Arabidopsis thaliana* seeds to *Aspergillus* infection.** T. DE SITTER (1), M. Brodhagen (1), and J. Young (1). (1) Western Washington University, Bellingham, WA, USA.

*Aspergillus flavus* and *Aspergillus parasiticus* are ubiquitous, filamentous, saprophytic fungi that infect the mature seeds of oil-containing crops, contaminating them with aflatoxins. We are using a two-model pathosystem to identify the genetic and molecular components that confer seeds with resistance to *Aspergillus*. While seeds of the model plant *Arabidopsis thaliana* are only mildly infectible, we have identified *A. thaliana* lines mutant in flavonoid biosynthetic genes that are highly susceptible to *Aspergillus flavus* as well as the model fungus *Aspergillus nidulans*. By systematically inoculating seeds of *A. thaliana* mutants with *A. nidulans*, we revealed that flavonoid biosynthetic pathway enzymes from chalcone synthase to dihydroflavonol reductase are important for conferring resistance to *Aspergillus*, while the branches responsible for producing flavanols and oxidized proanthocyanidins are not required. Additionally, we revealed that oxidation by at least one laccase-like enzyme is necessary for resistance. Finally, flavonoid molecules in *A. thaliana* only contribute to *Aspergillus* resistance in older mature seeds, indicating that younger mature seeds rely on another form of resistance.

**Development and validation of a quantitative PCR assay for the detection of *Claviceps purpurea sensu lato* ascospores.** J. DUNG (1), J. Scott (1), S. Alderman (2), N. Kaur (3), D. Walenta (4), K. Frost (3), and P. Hamm (3). (1) Oregon State University, Madras, OR, USA; (2) USDA-ARS, Corvallis, OR, USA; (3) Oregon State University, Hermiston, OR, USA; (4) Oregon State University, La Grande, OR, USA.

*Claviceps purpurea sensu lato* is an important seed replacement pathogen of grasses grown for seed. Microscopic methods that are used to detect and quantify *Claviceps* ascospores captured by spore traps are usually not rapid enough to inform fungicide application decisions within an ergot IPM program. The objectives of this project were to develop and validate a quantitative PCR (qPCR) procedure to detect
and quantify *C. purpurea sensu lato* ascospores caught by spore traps. A SYBR Green qPCR assay was developed that amplified a 96 bp region of the *C. purpurea sensu lato* genome. Specificity of the primers was confirmed against 41 *C. purpurea sensu lato* isolates collected from perennial ryegrass, Kentucky bluegrass, barley, rye, smooth brome, and cordgrass and 11 isolates of six other *Claviceps* species. The qPCR reactions were >97% efficient and melt curve analysis confirmed that the primers generated a single product. Ct values were significantly related to DNA quantity ($R^2=0.99; P=0.0002$) and the number of spores ($R^2=0.99; P=0.0004$). The assay was applicable for samples containing 1 pg to 10 ng of DNA or 4 to 40,000 spores. Results from qPCR and microscopic examination of 34 spore trap samples were correlated ($r=-0.68; P<0.0001$) and the qPCR assay detected spores on four samples from which they were not observed using microscopy. This assay provides a rapid and sensitive means for detecting and monitoring *C. purpurea sensu lato* ascospores captured by spore traps.

**Scaling up: the effect of plot size and initial inoculum on dispersal gradients of *Puccinia striiformis f.sp. tritici*.** D. FARBER (1), and C. Mundt (1). (1) Oregon State University, Corvallis, OR, USA.

How the spatial scale of dispersal studies affects the measured dispersal gradient has been a question of great importance in disease ecology. This question can help address the appropriateness of extrapolating an observed dispersal gradient beyond the scope of plots used in an empirical study, which is of great interest for modelers of dispersal and epidemic spread. To address this question, we combined a small-scale dataset (up to 1.5 m) and a field-wide dataset (up to 103.6 m) of the primary disease gradients of *Puccinia striiformis f.sp. tritici*, the causal agent of wheat stripe rust. The small- and large-scale dispersal studies were conducted from 2012 to 2014, and 2002 to 2003, respectively, under similar growing conditions. The two datasets were each normalized by the number of lesions at a common observation distance, 0.914 m from the source. The two datasets were then merged, log-transformed, and fit by the modified inverse-power distribution $y=a+(x+c)^b$, with a best-fit $c$ found by iteration, resulting in a slope of $y = 0.22 + (x + 0.12 \text{ m})^{-2.32}$, with a $b$ within the 95% prediction interval of those fit to local and field-wide dispersal gradients of *P. striiformis* separately, as well as the dispersal gradients of several other aerially dispersed organisms. Additionally, the proportion of small- and large-scale lesions as a function of distance in m were fit by maximum likelihood estimation of the Modified Pareto probability mass function, a discrete form of the associated probability density function: $y=7.51(1+x/0.41)^{-4.08}$. These results suggest it is possible to extrapolate the results of a dispersal study to better understand dispersal at a larger scale, given that the study systems remain constant.

**Expression profiling of pathogenesis-related protein genes in wheat resistance to the stripe rust pathogen (*Puccinia striiformis f. sp. tritici*).** S. FARRAKH (1), M. Wang (1), and X. Chen (2). (1) Department of Plant Pathology, Washington State University, Pullman, WA, USA; (2) USDA-ARS, Wheat Health, Genetics, and Quality Research Unit and Department of Plant Pathology, Washington State University, Pullman, WA, USA.
Interactions of the stripe rust pathogen (*Puccinia striiformis* f. sp. *tritici*) with wheat plants activate a wide range of host responses. Among different defense responses associated with termination of a pathogen is the expression of particular pathogenesis-related (PR) protein genes. The objective of this study was to identify PR protein genes involved in wheat resistance to stripe rust. The expression levels of eight PR protein genes were quantitatively evaluated at 0, 24, and 48 hours post inoculation (hpi) and 7 and 14 days post inoculation (dpi) in near isogenic line of wheat with resistance gene *YrTr1* and a recombinant inbred line with *YrExp2* using races PSTv-4 (incompatible) and PSTv-37 (compatible). Analysis of quantitative real time PCR (qRT-PCR) revealed that PR protein genes appear to be upregulated and downregulated differently at different time points during the infection process between the wheat lines. Majority of the PR protein genes, *PR1.2* (2.1), *PR2* (5.8), *PR3* (10.25), and *PR5* (16.18) were upregulated at 48 hpi in the incompatible reaction of *YrExp2*, whereas in the *YrTr1* line, *PR1.2* (9.5), *PR2* (7.5), *PR3* (8.0), *PR9* (5.2), and *PR10* (6.4) were upregulated at 24 hpi. *PR4* was upregulated at all time points in *YrExp2*. The PR protein genes were significantly (*P* >0.05) higher in the incompatible interactions than the compatible interactions for both lines. The results provide useful information for understanding wheat resistance against stripe rust.

**Pest Management Strategic Plans improve investment in integrated pest management in Pacific Northwest hops.** J. FARRAR (1), M. Baur (2), K. Murray (3), S. Elliott (2), and A. Crump (2). (1) Statewide Integrated Pest Management Program, University of California Division of Agriculture and Natural Resources, Davis, CA, USA; (2) Western Integrated Pest Management Center, Davis, CA, USA; (3) Oregon State University, Corvallis, OR, USA.

Pest Management Strategic Plans (or PMSPs) identify pest-management practices and needs in a crop or setting. Developed by researchers, extension specialists and growers, they document pest-management research, regulation and education priorities. Plans are then used several ways. State and federal agencies use them to understand pest management practices and needs, and as evidence of stakeholder involvement and priorities. Researchers, extension specialists and growers use them to direct research, promote best pest-management practices and leverage funding. On average, a dollar invested in a PMSP generates $20 in additional funding. The Western Integrated Pest Management Center compared PMSPs for Pacific Northwest hops published in 2008 and 2015 as a case study to show the impact and changes that PMSPs can make. The 2008 PMSP identified disease and other pest research, regulatory and educational needs, and generated over $3 million for researchers and extension specialists to address those priorities. The 2015 PMSP documented improvements that funding helped bring about: broadened use of mechanical control of mildews and the targeted control of powdery mildew during the early stages of cone development (resulting in an estimated yield increase worth $2 million.) PMSPs can be developed for other crops to prioritize research and leverage funding to address diseases and pests in Western agriculture, and expand IPM practices that protect human and environmental health.
Impact of integrated pest management (IPM) in California. J. FARRAR (1), M. Baur (1), and S. Elliott (1). (1) University of California, Davis, CA, USA.

Integrated pest management (IPM) is sometimes described as a method to reduce pesticide use. This has resulted in questions about the success of IPM in relation to continued use of pesticides in agriculture. IPM is more correctly described as a method to reduce economic, human health and environmental risks from pests and pest management strategies. Therefore, total pounds of pesticide applied is a mis-measure of IPM impact. Instead, IPM should be evaluated in regards to economic, human health and environmental risks from pests and pest management strategies. In California from 1995 to 2014, total pounds of pesticides declined by 8% but the value of agricultural productivity increased by 142%. The reduction in pesticide application has not been uniform. From 2000 to 2014 there were significant declines in the use of pesticides known to cause reproductive toxicity (71% decrease), cholinesterase-inhibiting pesticides (60% decrease), potential ground water pollutants (72% decrease) but there were increases in the use of potential carcinogens (18% increase) and toxic air contaminants (15% increase). Pesticide residue data indicates the percentage of food samples with pesticides residues that exceed tolerances are 1.0% or less. USGS data indicates that pesticide in agricultural watersheds are decreasing. California air monitoring data documents no or low concentrations of pesticides, except for one sample which exceeded target screening levels for 1,3-dichloropropene.

Strain composition of Bean common mosaic virus and Bean common mosaic necrosis virus isolates from field samples of common bean. X. FENG (1), and A. Karasev (1). (1) University of Idaho, Moscow, ID, USA.

Between 2013 and 2016, over 30 samples were submitted to the Plant Virology Laboratory representing heirloom cultivars of common bean with symptoms of mosaic, leaf distortion, and stunting. All samples came from California or Oregon, and were subjected to species-specific serotyping suggesting that samples were infected with Bean common mosaic virus ( BCMV) or Bean common mosaic necrosis virus ( BCMNV). These field isolates of BCMV and BCMNV were typed using a panel of bean differentials to determine their pathotype, and subjected to partial sequencing. BCMNV isolates were grouped in pathogroups (PGs) III and VI, while BCMV isolates were grouped in PG-I, III, IV, and VI. PG-VI isolates of BCMV were found to have sequences closely related to the RU-1 strain of BCMV. This data confirms a wide presence of the RU-1 related isolates of BCMV in heirloom cultivars of common bean. Several BCMV field isolates represented mixtures between different PGs, which were successfully separated using bean differentials. In at least two cases, field samples contained both BCMV and BCMNV.

Protein expression in Rathayibacter toxicus FH79 analyzed by mass spectrometry. C. FENNESSEY (1), A. Sechler (1), M. McMahon (1), W. Garrett (2), D. Luster (1), W. Schneider (1), and E. Rogers (1). (1) USDA-ARS-FDWSRU, Ft. Detrick, MD, USA; (2) USDA-ARS-ABBL, Beltsville, MD, USA.

*Rathayibacter toxicus* is a gram-positive bacterium that is the causative agent of annual ryegrass toxicity ( ARGT), a disease that causes devastating losses to the Australian livestock industry. *R. toxicus* exhibits a complex life cycle, using the
nematode *Anguina funesta* as a physical vector to carry it up to the seed head of annual ryegrass (*Lolium rigidum*), a grass commonly used as livestock feed. Infected grass seed contains both nematode and bacterial galls; bacterial galls may contain tunicamycin, a highly toxic corynetoxin. Although *R. toxicus* is not known to be present in the US, there are several other species of *Rathayibacter* that are not known to produce tunicamycin and are endemic to areas outside Australia, including parts of the US. Therefore, diagnostic tools are needed that are that can accurately and precisely discriminate among *Rathayibacter* species. Using SDS-PAGE and mass spectrometry, we analyzed the protein expression of *R. toxicus* under stationary growth phase conditions to identify unique proteins for immunoassay development and obtain a more complete understanding of the biology of *R. toxicus* strain FH79. A total of 333 individual proteins were identified. Some of the more abundant proteins appear to be good candidates for genus-specific or species-specific antibodies; polyclonal antibodies are currently under development.

Seedling reactions of Mexican wheat varieties and advanced lines to four races of *Puccinia striiformis* f.sp. *tritici*, the stripe rust pathogen. P. FIGUEROA-LOPEZ (1), X. Chen (2), and A. Wan (2). (1) INIFAP-CIRNO-CENEB, Obregon, Mexico; (2) Department of Plant Pathology, Washington State University, Pullman, WA, USA.

Stripe rust of wheat is a disease that during the 21 century has increased in importance in many regions of the world, including Mexico. Because selection for stripe rust resistance was not an important criterion in Mexico, little is known about resistance in most of its commercial varieties. The objective of this work was to evaluate stripe rust resistance in a historical series of 188 bread wheat varieties (BWV) and 28 durum wheat varieties (DWV) released in Mexico between 1950 and 2009, and 29 bread-wheat advanced lines (BWAL). Seedling tests were performed by inoculating the wheat genotypes with races PSTv-4, PSTv-14, PSTv-37, and PSTv-40. Results showed that 41 genotypes (16.7%) were resistant to PSTv-37, 63 (25.7%) resistant to PSTv-40, 98 genotypes (40%) resistant to PSTv-4, and 127 genotypes (51.8%) resistant to PSTv-14. Among different wheat genotypes, DWV had the highest percentage (17.9%) of resistant genotypes to the four races, followed by BWAL (13.8%) and BWV (1.06%). Trigal F2012 and Don Carlos “s” were the only BWV with resistance to all four races, whereas in DWV Ovachiú C65, Yavaro C79, Aconchi C89, CEVY OROC2008, and Anatoly C2011 were resistant to all races. Of the BWAL group, Colibri and one line each from the following crosses were also resistant to the four races: Colibri/Finsi, Colibri/Kronstad, and Colibri/Berkut.

Double Nickel biofungicide efficacy on root health for young grape in the San Joaquin Valley. E. FLORA (1), S. Ockey (2), O. Cuevas (1), and D. Kloeppep (1). (1) Pacific Ag Research, San Luis Obispo, CA, USA; (2) Certis USA, LLC, Yakima, WA, USA.

Double Nickel LC™, a broad spectrum biofungicide containing *Bacillus amyloliquefaciens* D747, was tested in a three-year longitudinal study on newly planted Primitivo variety wine grapes. Root Knot Nematode (*Meloidogyne* sp.) related damage did negatively affect newly established vines that were untreated when planted into medium textured soil artificially infested above threshold. Double Nickel injected into
drip irrigation at 1 qt/a in spring and 2 qt/a in fall applications resulted in significantly fewer Root Knot Nematode counts in soil compared to the untreated plots. A reproduction factor was calculated for the population increase between spring and fall counts, and control based on this population response to treatment was 74% compared to the untreated in year 3, and 30% improvement over standard of Telone II® applied PPI. Trunk girth, soluble sugar in juice and canopy senescence were all positively affected by Double Nickel treatments. Trunk diameters were nearly 2mm wider on treated vines compared to the untreated, and after three years, Double Nickel treated vines had 15% larger diameter trunks than untreated. Leaf senescence was significantly more advanced in Double Nickel treated vines in year 1 and 2, but juice had a lower sugar content compared to other treatments. When fruit was produced in years 2 and 3, fruit production trended higher from vines treated with Double Nickel compared to the untreated and standard.

Reduced sensitivity to potassium phosphite in Phytophthora species and its implication for the management of Phytophthora brown rot of citrus. H. FORSTER (1), W. Hao (1), and J. Adaskaveg (1). (1) University of California, Riverside, CA, USA.

Phytophthora citrophthora (Pc) and P. syringae (Ps) are the major species causing brown rot of citrus fruit in California. Potassium phosphite (PP) is used as a preharvest treatment and is the only registered postharvest fungicide to manage this disease. We evaluated in vitro toxicity of PP against 40 isolates each of Pc and Ps from 29 orchards. The majority of isolates (77.5% of Pc and 90% of Ps) were sensitive to PP with mean EC50 values for mycelial growth of 7.8 and 18.6 µg/ml, respectively. The remaining isolates had mean EC50 values of 92.0 (range 50.8 to 251.8 µg/ml) and 120.8 µg/ml (range 97.9 to 141.6 µg/ml), respectively. Preharvest applications with labeled rates of PP were not effective in reducing brown rot of orange when inoculated with a less sensitive isolate (EC50 = 69 µg/ml) of Pc, but reduced decay by 88% as compared to the control when a sensitive isolate was used. In postharvest studies, 10-s in-line drench applications at 54°C with 4,000 µg/ml PP reduced brown rot of orange fruit inoculated with sensitive or resistant (EC50 = 186 µg/ml) Pc isolates by 90% or 0%, respectively. Dip treatments for 5 s at 54°C were more effective and resulted in a 100% or 90% reduction in decay for the two isolates, respectively. Therefore, postharvest PP can still be very effective in reducing brown rot caused by less-sensitive isolates when applied in heated solutions. New, highly effective preharvest fungicides with different modes of action are in development.

Susceptibility of weedy hosts to Verticillium dahliae isolates. Z. FREDERICK (1), T. Cummings (1), and D. Johnson (1). (1) Washington State University, Pullman, WA, USA.

Verticillium wilt, caused by Verticillium dahliae, is a persistent disease of dicotyledonous crops due to a wide host range and survival in soil. Some V. dahliae isolates exhibit increased aggressiveness on a specific plant host while retaining a wide host range. It is known that weeds serve as hosts for V. dahliae, but unknown if weeds could serve as inoculum sources for aggressive V. dahliae isolates from crop hosts. The goal of this research was to quantify V. dahliae microsclerotia from twelve weeds grown in potting mix infested with one of eight aggressive V. dahliae isolates from crop hosts.
All twelve weedy hosts were infected by at least one *V. dahliae* isolate, although the number of microsclerotia from some infections was low (< 5 microsclerotia/g dry plant). Black nightshade and litchi tomato provided greater inoculum density of the *V. dahliae* potato isolate than any other isolate (*P* ≤ 0.0055) in each of two years. Interestingly, a *V. dahliae* isolate from tomato was observed to have greater inoculum density in large crabgrass and wild oats (*P* < 0.0055) in one year. These observations indicate that black nightshade growing during and in-between potato crop rotations may increase the inoculum density of the potato-aggressive isolates of *V. dahliae*.

**Effect of temperature on virulence of fungal isolates collected in mycofloristic survey of *Camassia quamash***. G. FREED (1). (1) Washington State University, Pullman, WA, USA.

Populations of *Camassia quamash*, an herbaceous perennial, often dominate native wetlands, and the bulb is transplanted into mitigation sites. Refrigeration may reduce bulb losses due to storage rot. Objectives of this work were to determine the fungi in *C. quamash* bulbs and seed; and to test for pathogenic fungal taxa at two temperatures among the isolates recovered. *Camassia quamash* seeds were obtained from GRIN W6 45020 (USDA-ARS National Plant Germplasm System). Fungal isolates were obtained from bulbs at three locations: a forest wetland meadow, a garden and a wetland prairie. Bulb tissue was excised from the apical tip, basal plate, leaf scale and terminal bud then plated onto agar, as were seeds. Candidate isolates for pathogenicity testing on *C. quamash* bulbs were selected: three *Penicillium* spp., two *Fusarium* spp., one *Trichoderma* sp. and one *Botrytis* sp. Bulbs were surface disinfested and wounded (1 mm x 4 mm). Inoculum (1.5 x 10^5/1 ml) was pipetted into the wound. Mock-inoculated controls with water agar were used. Prepared bulbs were incubated at either 5C or 23C. Rate of lesion expansion (mm/wk) was recorded at the end of the incubation period. *Botrytis* Cq23 exhibited significantly higher (*p* < 0.001) virulence among all isolates tested. Temperature effect was highly significant (*p* < 0.001) for *Botrytis* Cq23, *Fusarium* Ta9C and *Trichoderma* Tr25D. Prior reports of these taxa on *C. quamash* bulbs appear lacking. *Trichoderma* is rarely reported as a pathogen.

**Strain specific resistance to *Potato virus Y* (PVY) in potato efficiently reduces the prevalence of the PVYO strain under semi-field conditions**. C. FUNKE (1), K. Frost (2), N. Olsen (3), and A. Karasev (1). (1) University of Idaho, Moscow, ID, USA; (2) Oregon State University, Hermiston, OR, USA; (3) University of Idaho, Kimberly, ID, USA.

*Potato virus Y* (PVY) is a serious threat to potato production due to the negative effects it has on tuber yield and quality, in particular, due to induction of potato tuber necrotic ringspot disease (PTNRD), typically associated with recombinant strains of PVY. Recombinant strains have spread in the U.S. for the past several years, although the reasons for their continued spread remain unclear. To address the shift in strain abundance, screen-house experiments were conducted and revealed that three of the four most popular potato cultivars grown in the Columbia Basin of Washington and Oregon, Russet Burbank, Ranger Russet, Alturas, and Umatilla Russet, exhibited strain-specific resistance against PVYO, which resulted in selective multiplication of recombinant strains of PVY under semi-field conditions. Five weeks after inoculation,
the recombinant strains PVY\textsuperscript{N-Wi} and PVY\textsuperscript{NTN} were significantly more prevalent than the non-recombinant strain PVY\textsuperscript{O}. The negative selection against the non-recombinant PVY\textsuperscript{O} strain is likely caused by the presence of the Ny\textsubscript{Ibr} gene identified in potato cultivars in laboratory experiments.

**Apple anthracnose canker life cycle and disease cycle.** W. GARTON (1), M. Mazzola (2), and C. Miles (1). (1) Department of Horticulture, Washington State University, Northwestern Research and Extension Center, Mount Vernon, WA, USA; (2) Department of Plant Pathology, USDA-Agriculture Research Service, Wenatchee, WA, USA.

In the maritime Pacific Northwest, *Neofabraea malicorticis* (H.S. Jacks) anamorph *Cryptosporiopsis curvispora* (Peck) produces cankers on trees and ‘Bull’s-eye rot’ on fruit. Growers in western Washington have reported removing 2-5% of trees and in some cases entire orchard blocks due to apple anthracnose. Research on apple anthracnose is limited because it is not a severe problem in other regions. In order to create an effective management plan, a controlled inoculation study was conducted in a screen house at WSU Mount Vernon NWREC, WA to better understand canker development. The five treatments: 1) Bordeaux mixture, wounding, inoculation; 2) Bordeaux mixture, no wounding, inoculation; 3) wounding, inoculation; 4) inoculation only; 5) control (non-inoculated). The treatments were designed to elucidate the necessity of wounding for infection and if Bordeaux mixture [copper sulfate (CuSO\textsubscript{4}) and calcium hydroxide (Ca (OH)\textsubscript{2})] can prevent infection with or without wounding. A canker was first observed 9 weeks after inoculation on 27 Jan. 2016, in treatments 1 and 2 and 13 weeks after inoculation, a canker appeared in all treatments excluding the control. Canker area size ranged from 0.02 to 0.24 cm and infection occurred regardless of wounding and Bordeaux mixture application. Small streaks of diseased tissue expanding from the wounded/inoculated area were observed only in treatment 3, suggesting that Bordeaux mixture may prevent disease progression when wounding occurs.

**Testing the efficacy of commercially-available compounds for managing Agrobacterium tumefaciens.** M. GORDON (1), M. Wiseman (1), and M. Putnam (1). (1) Oregon State University, Corvallis, OR, USA.

Crown gall disease, caused by *Agrobacterium tumefaciens*, remains a costly problem for growers of plants used for ornamental purposes. *Agrobacterium* requires a wound for infection and spreads easily through common pruning and propagation practices. Currently there are no known treatments—biological or chemical—that effectively prevent infection by *A. tumefaciens* throughout its host range. The objective of this study was to test commercially available products for their ability to challenge symptom development in gall-prone plants, with the ultimate goal of helping the nursery industry to better manage the spread of crown gall. Selection of products for *in planta* assays was guided through *in vitro* growth inhibition assays using the Kirby-Bauer disk-diffusion method. Active ingredients with *in vitro* efficacy included phosphorus acids, peroxides, benzoic acid, and oxytetracycline. Biocontrols were also selected for *in planta* assays and included *Bacillus subtilis*, *Streptomyces lydicus*, and extract of *Reynoutria sachalinensis*. *Rosa* and *Leucanthemum* were wounded and inoculated with
a mix of *A. tumefaciens* isolates. Biocontrols were applied three days prior to inoculation, and chemical treatments were applied immediately after inoculation. All treatments were continually applied at weekly intervals until development of symptoms. Preliminary results suggest none of the trialed products are effective in preventing infection.

**Mapping the conformational epitope for a monoclonal antibody recognizing tuber necrotic strains of *Potato virus Y*.** K. GREEN (1), and A. Karasev (1). (1) University of Idaho, Moscow, ID, USA.

*Potato virus Y* (PVY) is a serious threat to potato production worldwide, due to effects on tuber yield and quality. Recombinant strains of PVY associated with tuber necrotic ringspot disease (PTNRD) typically have an N serotype recognized by several commercial monoclonal antibodies (MAbs). This N serotype, thus, serves as a valuable trait for quarantine screening against PTNRD-inducing strains of PVY, and respective MAbs are extensively used in the international potato trade. One of these MAbs, 1F5, marketed by Agdia (Elkhart, IN), was previously shown to have a conformational epitope, with the amino acid residue 98 of the capsid protein (CP) of PVY involved in the interaction. However, no other regions of the CP were known to be involved in the 1F5-specific epitope. In January 2016, a PVY-positive field sample was identified as having a 1F5-binding capacity, although the residue 98 in its CP appeared to be O-specific rather than N-specific. Several PVY isolates exhibiting 1F5-binding and non-binding behavior were subjected to immuno-capture PCR and partial sequencing, to identify other regions of the CP involved in binding of the 1F5 MAb. One additional position close to the N-terminus of the CP was identified as likely involved in the interaction with 1F5.

**Recombination analysis of the whole genomes for three isolates of *Beet curly top virus* from beet leafhoppers collected in Oregon.** K. GREEN (1), S. Rondon (2), J. Crosslin (1), and A. Karasev (1). (1) University of Idaho, Moscow, ID, USA; (2) Oregon State University, Hermiston, OR, USA.

The beet leafhopper, *Circulifer tenellus*, transmits the *Beet curly top virus* (BCTV) to multiple crops, including bean, tomato, and pepper. Over 800 insects were collected between 2007 and 2009 in northwestern Oregon and tested for BCTV. One hundred-fifty-one (18.9%) were found positive for the virus. The complete virus genomes from one virus-positive insect collected in each of the three years were determined. BLAST analysis of the BCTV whole genome sequences from 2007, 2008, and 2009 insects showed 98, 94, and 96% identities with the BCTV “Worland” sequence (AY134867), respectively. The BCTV_2008 sequence showed the greatest identity (96%) with another BCTV genomic sequence (JN817383), and was found to be a recombinant between BCTV-Worland type representing the majority of the genome (ca. 2.2-kb) and BCTV-CFH type that provided a ca. 0.8-kb fragment spanning replication-related genes C1 and C2. This area of the BCTV genome, between the C1 and C2 genes, was previously found to carry symptom determinants of the virus, and the data may suggest more severe effects of BCTV during the 2008 season. BCTV appears to be common and widespread in *C. tenellus* in eastern Oregon and that there is substantial genetic
diversity among the virus strains present in this important field and vegetable crop-growing region.

**Impacts on plant health of complex pathogen communities.** E. GUNNINK TROTH (1), A. Dyer (1), and J. Johnston (1). (1) Montana State University, Bozeman, MT, USA.

Root pathogen communities are often a complex collection of agents whose interactions with regards to plant health are little understood. To explore the impacts of these interactions on plant health, a study was conducted to document the interactions among five rhizosphere-inhabiting pathogens in-field: *Cochliobolus sativus*, *Fusarium pseudograminearum*, *Rhizoctonia solani*, *Pythium ultimum*, and *Penicillium claviforme*. Interactions among pathogens were observed by their effect on plant health. Plant health was measured as seedling emergence, mid-season vigor, plant height, and yield, and was observed in response to inoculations with all single, pairwise, four-pathogen and five-pathogen combinations. Four significant antagonistic relationships were observed among all pairwise combinations of *C. sativus*, *P. claviforme*, and *P. ultimum*, affecting emergence and vigor (*P* < 0.05, all). Conversely, synergism was observed between *F. pseudograminearum* and *R. solani* that significantly reduced seedling emergence (*P* = 0.002). This synergism was also apparent in the community inoculations (emergence *P* = 0.017, vigor *P* = 0.005). Interactions within complex root pathogen communities of wheat involve dynamic processes that largely favor antagonism and improved plant health. All interactions among pathogens were measured through indirect effects (i.e., plant health). Work is ongoing to establish whether these interactions are reflected in changes in pathogen populations.

**Diversity of Cytospora species associated with fruit and nut crop canker diseases in California.** L. HOLLAND (1), M. Nouri (2), and F. Trouillas (2). (1) Department of Plant Pathology, University of California, Davis, Davis, CA, USA; (2) Department of Plant Pathology, University of California, Davis, Kearney Agricultural Research and Extension Center, Parlier, CA, USA.

*Cytospora* species are important pathogens of many hardwood tree species causing severe canker and dieback symptoms. In the fruit and nut crops, *Cytospora* infections have often been considered secondary to freeze, sunburn and other injuries. Identification of *Cytospora* to the species level is made difficult by limited taxonomic studies and sequence data availability. While morphological and phylogenetic studies have been conducted on important host such as *Eucalyptus*, little work has been done to address the diversity and pathogenicity of *Cytospora* species associated with the fruit and nut crops in California. This study aims to identify the principal species associated with canker diseases in woody perennial crops, and investigate their distribution and host range. Isolates were collected from cankers in almond, pistachio, cherry, plum, peach, olive, quaking aspen and various cottonwoods. Multi-locus sequence analyses of the ITS and β-tubulin genes combined with morphological analyses revealed several new species of *Cytospora*. Similarities between isolates from riparian areas (cottonwoods) and from agricultural hosts (*Pistacia vera*) suggest that riparian areas may serve as a source of inoculum of these pathogens as they spread in wet weather conditions. Pathogenicity tests were performed on almond and pistachio to assess the ability of the isolates to cause disease in these hosts.
Evidence that tuber cracking in potato can be caused by Potato virus Y. D. INGLIS (1), B. Gundersen (1), and A. Beissinger (1). (1) WSU Mount Vernon NWREC, Mount Vernon, WA, USA.

Specialty potatoes for fresh market must meet high quality standards. “Cracking” is a defect that occurs when tubers split while growing, and sometimes can be caused by fluctuating soil moisture. To determine if an association exists between cracked tubers and Potato virus Y (PVY), the following was done using cv. Chieftain. Field-grown plants were flagged for mosaic. At harvest, healthy plants had significantly fewer \((P=0.05)\) cracked tubers than plants mildly or highly symptomatic. During the subsequent winter grow-out of progeny from the PVY negative and positive plants, 0% and 22-32% of tubers, respectively, were cracked. Tuber cracking in screenhouse and field trials planted to both cracked and certified virus-free nuclear tubers was not altered by either constant or alternating, nor high or low irrigations. Instead, the main factor leading to cracked progeny tubers was planting cracked seed tubers from PVY positive plants. Sampling at seasonal time points in a field trial yielded cracked tubers 63 days after planting. When cracked tubers from PVY\textsuperscript{N-Wi} positive plants were cut with a sterile knife at sprouted eyes to obtain sap, 25% of plants grown from recipient nuclear seed tubers cut with the same knife had mosaic symptoms, tested positive for PVY\textsuperscript{N-Wi}, and averaged 3.8% cracked tubers—the control source and recipient tubers remained healthy and PVY negative. PVY needs to be among the disease differentials when diagnosing cracked potato tubers.

Nitrogen fertilization increases powdery mildew, arthropod pests, and nitrate accumulation in hops. A. ISKRA (1), S. Lafontaine (2), C. Phillips (3), T. Shellhammer (2), K. Trippe (4), M. Twomey (1), J. Woods (1), and D. Gent (5). (1) Oregon State University, Dept. of Botany and Plant Pathology, Corvallis, OR, USA; (2) Oregon State University, Dept. of Food Science and Technology, Corvallis, OR, USA; (3) US Department of Agriculture, Agriculture Research Service, Corvallis, OR, USA; (4) US Department of Agriculture, Agricultural Research Services, Corvallis, OR, USA; (5) Oregon State University, Dept. of Botany and Plant Pathology/ US Department of Agriculture, Agricultural Research Services, Corvallis, OR, USA.

Nitrogen fertilization may exacerbate or suppress various plant diseases depending on the pathosystem and form of nitrogen applied. Studies were conducted during 2014 and 2015 to quantify how nitrogen fertilization rate influences powdery mildew on hop (caused by Podosphaera macularis), as well as arthropod pests, yield, and nitrate accumulation in cones. In a commercial hop yard in Washington State in 2015, the incidence of leaves and cones with powdery mildew in plots that received 90 to 270 kg nitrogen per hectare was increased 15% and 30%, respectively, late in the season with the highest fertilization rate. Powdery mildew did not develop in plots in Oregon in either year, but the abundance of two spotted spider mites and defoliation from hop looper increased with increasing nitrogen fertilization. In both Washington and Oregon, yield of cones and bittering acids was maximal with intermediate rates of nitrogen. Nitrate levels in cones, a negative quality factor in hops, increased concomitantly with nitrogen fertilization rate. These early results indicate it may be possible to moderate powdery mildew, multiple arthropod pests, and nitrate accumulation in cones without negatively impacting yield, by avoiding excessively high
rates of nitrogen fertilizer.

**Monitoring Phytophthora infestans sporangia using volumetric trapping.** M. KALISCHUK (1), S. Watson (1), L. Steward (1), M. Harding (2), R. Howard (3), and L. Kawchuk (4). (1) Lethbridge College, Lethbridge, AB, Canada; (2) Alberta Agriculture and Forestry, Brooks, AB, Canada; (3) Ag Research Solutions Ltd., Brooks, AB, Canada; (4) Agriculture and Agri-Food Canada, Lethbridge, Canada.

Late blight, caused by the oomycete Phytophthora infestans (Mont.) de Bary, is a devastating disease in potato and tomato and causes yield and quality losses worldwide. The US-23 strain appears to tolerate warmer and dryer climates and consequently threatens the Canadian Prairie commercial and seed potato industries. The best management practice for controlling this pathogen relies on proactive fungicide application on a regular basis. A volumetric spore trap network was established during the growing seasons of 2014 and 2015 in Alberta and real-time data provided growers with a 10-14 day advanced warning that the pathogen was present in the environment in advance of late blight development. A density of 1-10 sporangia per cubic meter of air for three consecutive days was the threshold that predicted an infection in the field. Volumetric air sampling combined with spore sticky traps mounted onto an unmanned aerial vehicle (UAV) was successfully used to triangulate late blight hotspots. This enabled rouging and pretreatment to reduce pathogen pressures and eradicate the late blight pathogen from fields. The P. infestans genotype US-23 dominated late blight pathogen populations in Alberta and was usually observed first on tomatoes. The prevailing westerly winds and decomposing compost piles of backyard gardeners influence the dispersal of P. infestans sporangia near commercial potato growing regions in Alberta, Canada. This volumetric spore trapping network may be used for risk-based decision making in order to reduce the number of proactive fungicide treatments required during the growing season and provide economical and environmental benefits.

**Changing epidemiology of Potato virus Y in potato, and the role of strain specific resistance in facilitating the spread of recombinant strains.** A. KARASEV (1). (1) University of Idaho, Moscow, ID, USA.

Since 2002, recombinant strains of Potato virus Y (PVY) spread throughout the potato production areas in the U.S. Some of these recombinant strains are associated with tuber quality losses, in addition to the yield reduction. The driving forces behind the emergence and spread of these recombinant strains of PVY are not completely understood at the moment. Resistance to non-recombinant and some recombinant strains can be found in commercial cultivars grown in the U.S. However, certain recombinants can overcome most of the resistance genes in potato known today, and these are the ones the most prevalent in potato at the moment. Field studies and model experiments suggest that the currently observed prevalence of specific recombinant strains of PVY may be related to strain specific resistance to PVY exhibited in the most popular potato cultivars. More interactions between breeding programs and plant virologists involved in PVY studies are needed to control PVY in potato.
Investigating motility and persistence of PBTS *Rhodococcus* spp. P. LAMBERT (1), E. Molina (1), R. Stampler (1), E. Fichtner (2), D. Vereecke (3), and J. Randall (4). (1) NMSU, Las Cruces, NM, USA; (2) UCANR, Tulare, CA, USA; (3) Ghent University, Ghent, Belgium; (4) NMSU, Las Cruces, USA.

*Rhodococcus fascians* is a bacterial phytopathogen with a large host range consisting of both monocot and dicot plants. It can exist as an epiphyte or gain entry into the host at which point it may cause economically significant damage in crops. Symptoms of *R. fascians* include stunting, shortened internodes, leafy galls, leaf deformation, and altered root morphology. A disease outbreak named Pistachio Bushy Top Syndrome (PBTS) in the US was caused by two *Rhodococcus* spp. related to *R. fascians*. Research on these isolates includes understanding the mechanisms of motility and their persistence in soil. Experiments involving PBTS isolates include in vitro assays combined with microscopic imaging to examine the growth and potential movement of the bacteria. The PBTS *Rhodococcus* isolates were also used in plant assays on both ‘UCB-1’ trees and Nicotiana benthamiana plants. Both plant species developed symptoms that included stunting and leaf malformations and bacterial colonization and movement was assessed by microscopy. Survival of the pathogen in soilless potting medium was assessed under greenhouse conditions. Overall the data from these assays suggest that *R. fascians* persists at least three months in potting medium under greenhouse conditions. This information will help both growers and researchers better understand how to manage diseases caused by these pathogens.

Water stress exacerbates the severity of Botryosphaeria dieback in grapevines infected by *Neofusicoccum parvum*. D. LAWRENCE (1), E. Galarneau (1), R. Travadon (1), and K. Baumgartner (1). (1) United States Department of Agriculture-Agricultural Research Service, Davis, CA, USA.

Botryosphaeria dieback (causal fungus *Neofusicoccum parvum*) is a detrimental grapevine trunk disease, causing internal wood degradation, killing shoots, and reducing yields. We examined the interactive effects of drought and *N. parvum* infection, common vineyard stresses, on wood-lesion development. Woody stems of potted *Vitis vinifera* ‘Cabernet Sauvignon’ were inoculated after wounding (IW). Control plants were either non-inoculated-wounded (NIW) or non-inoculated-non-wounded (NINW). At 2 weeks post-inoculation (WPI), water stress was imposed on half of the plants. Leaf water potential was maintained, through weekly monitoring, at > -8 bars for non-stressed and < -13 bars for stressed plants. To test the specificity of host-based markers of infection, developed previously for *N. parvum* in non-stressed plants, asymptomatic leaves were collected for RNA extraction at 2 WPI (before water stress), and at 8 and 12 WPI (6 and 10 weeks post-stress, respectively). IW-stressed plants had the most severe levels of wood lesions. At 2 WPI, none of the markers were differentially expressed among treatments. By 12 WPI, seven markers showed higher expression, but only in stressed plants, regardless of inoculation treatment. Two markers showed consistent overexpression at 8 WPI in IW plants that were stressed and non-stressed, suggesting their specificity to *N. parvum* infection.

Characterization of somatic recombinant isolates of *Puccinia striiformis*, the
stripe rust pathogen. Y. LEI (1), M. Wang (1), A. Wan (1), C. Xia (1), D. See (2), and X. Chen (2). (1) Department of Plant Pathology, Washington State University, Pullman, WA, USA; (2) USDA-ARS Wheat Health, Genetics, and Quality Research Unit and Department of Plant Pathology, Washington State University, Pullman, WA, USA.

Natural population studies of *Puccinia striiformis* (the causal agent of stripe rust on wheat, barley, and grasses) have indicated that somatic recombination plays a possible role in the pathogen variation. To study somatic recombination, susceptible wheat or barley plants were inoculated with mixed urediniospores of paired isolates of *P. striiformis*. Possible recombinants were isolated from progeny spores through a series of inoculations of wheat or barley genotypes. They were compared with the parental isolates on the set of 18 wheat and/or 12 barley genotypes used to differentiate races of the wheat and barley stripe rust pathogens, respectively, for virulence changes. The isolates were tested with 51 simple sequence repeat and 144 single-nucleotide polymorphism markers for genotype changes. From 68 possible recombinant isolates obtained from nine combinations of isolates based on virulence tests, 53 were proven by markers. Various types of recombinants were determined, including lost virulence from both virulent parental isolates, gained virulence from both avirulent isolates, combined virulences from both parents, and inherited virulence from one parent and avirulence from another. Marker data indicate that most recombinants were produced through chromosome re-assortment and cross-over after the hybridization of two parental isolates. The results demonstrate that somatic recombination is a mechanism by which new variants can be generated in the fungus.

Development of *Puccinia striiformis* f. sp. tritici mutants for avirulence characterization. Y. LI (1), M. Wang (1), A. Wan (1), and X. Chen (2). (1) Department of Plant Pathology, Washington State University, Pullman, WA, USA; (2) USDA-ARS Wheat Health, Genetics, and Quality Research Unit and Department of Plant Pathology, Washington State University, Pullman, WA, USA.

*Puccinia striiformis* f. sp. *tritici* (*Pst*) is an obligate biotrophic fungus causing stripe rust of wheat. Mutation is considered as a major mechanism of the pathogen variation, but has not been experimentally determined. The objectives of this study were to develop and characterize *Pst* mutants generated by mutagenesis. Urediniospores produced from a single-uredinium isolate of race PSTv-18, which has the highest number of avirulence genes, were treated with ethyl methanesulfonate (EMS) at concentrations of 0.02M and 0.03M for 6, 7, and 8 minutes. The treated spores were grown on wheat genotypes susceptible to the wild type isolate and screened on 50 genotypes of wheat and barley with various genes for resistance to stripe rust. Potential mutants isolated from the screening experiment were tested for virulence patterns on the set of 18 wheat *Yr* single-gene lines and 18 simple sequence repeat (SSR) markers. Virulence tests showed that 20 mutant isolates were different from the wild type. Changes of avirulence to virulence were observed for resistance genes *Yr1*, *Yr2*, *Yr6*, *Yr8*, *Yr9*, *Yr10*, *Yr31*, *Yr43*, *Yr44*, *YrSP*, *YrTr1*, *YrTye*, and genotypes Paha and those with *YrA*+ and *Yr39*+. SSR markers showed that 18 of the 20 mutants were different from the wild type. Both virulence and SSR marker data showed that EMS mutagenesis was able to generate multiple-site mutants. These mutants are useful for further characterizing avirulence genes and understanding the pathogen evolution.
Virulence characterization of *Puccinia striiformis* f. sp. *tritici* in the US for the past 48 years using the *Yr* single-gene differentials. T. Liu (1), A. Wan (1), and X. Chen (2). (1) Department of Plant Pathology, Washington State University, Pullman, WA, USA; (2) USDA-ARS, Wheat Health, Genetics, and Quality Research Unit and Department of Plant Pathology, Washington State University, Pullman, WA, USA.

*Puccinia striiformis* f. sp. *tritici* causes wheat stripe rust, an important disease in the US. Races of the pathogen were identified using various numbers of wheat differential cultivars from 1968 to 2009 and using a set of 18 *Yr* single-gene lines since 2010. To characterize races and identify virulence changes of the pathogen, 908 isolates were randomly selected from the collections of 1968-2009 in the US and tested on the new differential set. The virulence patterns were compared with races identified with the new differential set in 2010-15. A total of 184 races were identified, including 96 races detected in 1968-2009 but not in 2010-15 and 13 races detected only after 2010. The number of races identified in each year had a trend of increasing, ranging from 5 in 1986 to 41 in 2010, and the number of virulences per race also increased over the years. Most races developed from previously existing races through single-step mutation, but some races formed through virulence recombination. Multiple introductions of races were detected. Virulences to *Yr1*, *Yr6*, *Yr7*, *Yr17*, *Yr32*, *Yr44*, and *YrExp2* were detected throughout the 48 years. Virulences to *Yr10* and *Yr24* were first detected in 1970, *Yr27* in 1971, *Yr43* in 1974, *YrSP* and *YrTye* in 1972, *YrTr1* in 1975, and *Yr8* and *Yr9* in 1999. No virulences were detected for *Yr5* and *Yr15*. The results are useful in understanding the pathogen evolution in virulence and utilization of effective resistance genes for control of the disease.

A novel *Fusarium* pathogenic to common rose mallow (*Hibiscus moscheutos*) is a sister taxon to *Fusarium buharicum*. S. Lupien (1), F. Dugan (1), K. Ward (2), and K. O'Donnell (3). (1) USDA-ARS Western Regional Plant Introduction Station, Pullman, WA, USA; (2) Department of Plant Pathology, Washington State University, Pullman, WA, USA; (3) USDA-ARS Mycotoxin Prevention and Applied Microbiology Research, Peoria, IL, USA.

*Hibiscus moscheutos* cultivars are highly desirable ornamentals. First detected in 2012, a novel *Fusarium* species was diagnosed as causing crown rot on several cultivars of *H. moscheutos* in Washington State. To complete Koch’s postulates, pathogenicity trials were conducted on *H. moscheutos* cultivar Luna Rose in a greenhouse in the winter of 2014-2015, using two isolates recovered from symptomatic crowns (NRRL 66179, NRRL 66182) and one isolate from a symptomatic root (NRRL 66184). Negative controls were mock-inoculated with sterile water. Trials were repeated in a growth room in the summer of 2015. Crown rot developed at the point of inoculation in each treatment plant; the negative controls remained healthy. Isolates recovered from symptomatic crown tissue, but never from controls, were identified as the novel *Fusarium* sp. employing morphological data and partial translation elongation factor 1-alpha (*TEF1*) sequences, thus completing Koch’s postulates. Phylogenetic analyses of partial *TEF1*, DNA-directed RNA polymerase II largest (*RPB1*) and second largest subunit (*RPB2*) nucleotide sequences placed the novel *Fusarium* sp. within the *F. buharicum* species complex and sister to *F. buharicum*. The latter species was reported to cause stem lesions on kenaf (*H. cannabinus*) in Iran and crown rot of cotton.
in Uzbekistan and Russia. Therefore, the available data suggests these pathogens might specialize on members of the Malvaceae.

**Historical survey of cherry viruses in Oregon.** L. LUTES (1), and J. Pscheidt (1). (1) Oregon State University, Dept. of Botany & Plant Pathology, Corvallis, OR, USA.

Sweet cherries (*Prunus avium*) rank in the top three fresh market fruit commodities in Oregon. Despite a major focus on sweet cherry viruses in Washington state, a low priority ranking was given to virus diseases by cherry growers in Oregon. Due to potential economic harm, an investigation was initiated to determine viral presence in Oregon cherry production areas. Published data was compared to digital and physical queries for viral diagnoses of *P. avium* samples assessed at the Oregon State University (OSU) Plant Clinic from 1956 – present. Additionally, the OSU Herbarium *Prunus sp.* collection (oldest sample dated 1882) was visually inspected for commonly associated viral symptoms, such as mosaics, ringspots, line patterns or enations. *Cherry twisted leaf-associated virus* was diagnosed by the OSU Plant Clinic in cherry samples from the Willamette Valley and The Dalles regions. *Cherry green ring mottle virus* was diagnosed in cherry samples from the Willamette Valley and *Tobacco ringspot virus* (TRSV) was found in cherry samples from the Grand Ronde Valley. Each of these viruses were previously unpublished as occurring in Oregon. OSU Plant Clinic records allowed for specific cherry growing regions to be identified, as opposed to only state or Pacific Northwest designations. Of the 373 *Prunus sp.* vouchers surveyed in the OSU Herbarium, one, *Prunus emarginata* from Douglas County, OR, displayed possible leaf mosaic symptoms. Finding the presence of viruses, such as TRSV and the others, allows for more effective disease management of existing orchards or establishment of new orchards in specific cherry growing regions.

**Diversity of mycelial compatibility groups of Sclerotium cepivorum causing white rot in Oregon.** S. MENG (1), R. Ludy (1), M. Hoover (1), and N. Osterbauer (1). (1) Oregon Department of Agriculture, Salem, OR, USA.

White rot, caused by the fungal pathogen *Sclerotium cepivorum*, is one of the most important diseases of Allium crops worldwide. Significant economic losses occur when *S. cepivorum* infests an *Allium*-growing area, partially because the pathogen can survive for >20 years in an infested field. The Oregon Department of Agriculture certifies *Allium* crops as free from white rot by inspecting 100% of the plants in each field. From 2007 to 2015, 92 isolates of *S. cepivorum* were collected from 72 infested fields (2,519 acres) in five counties from a total of 458 garlic fields (12,804 acres) in ten counties around the state. Genetic diversity of the *S. cepivorum* isolates was examined by identifying the isolates’ mycelial compatibility groups (MCG). Four MCG (MCG1, MCG2, MCG3, and MCG4) were identified among isolates. The majority of isolates (88%) belonged to MCG3, followed by MCG1 (6%), MCG4 (5%), and MCG2 (2%). The greatest diversity was observed in Jefferson County, where 3 MCG groups were detected. These results indicate that there is little genetic diversity in Oregon’s *S. cepivorum* population.

**Chokecherry and sweet cherry are infected by two host-specific Podosphaera species.** S. MOPARTHI (1), and G. Grove (1). (1) Washington State University,
Irrigated Agriculture and Extension Center, Prosser, WA, USA.

Powdery mildew of sweet cherry caused by *Podosphaera prunicola*, is a major problem in the cherry growing regions of Washington State. It is not known whether the powdery mildew that infects sweet cherry is same species as the one that infects chokecherry. Morphological features of both powdery mildew species were compared, the chasmothecial appendages of the sweet cherry powdery mildew were arranged equatorially, whereas the chasmothecial appendages of the chokecherry powdery mildew were fasciculate. Based on this major difference, it was determined that the powdery mildew that infects chokecherry is *Podosphaera tridactyla* and the powdery mildew that infects sweet cherry is *Podosphaera prunicola*. Isolates of *P. tridactyla* and isolates of *P. prunicola* formed separated clades, in a phylogenetic tree generated with ITS and 28S rDNA sequences. In cross inoculation experiments, *P. tridactyla* did not infect sweet cherry and *P. prunicola* did not infect chokecherry, supporting the presence of host specificity among species. Morphological, phylogenetic and pathological evidence support the presence of two different species of *Podosphaera* that infect chokecherry and sweet cherry in Washington State.

**Extracellular alkalinization assay: a fast and reliable method to detect the defense response in potato.** N. MOROZ (1), D. Tripathi (1), and K. Tanaka (1). (1) Washington State University, Pullman, WA, USA.

A quantitative and robust bioassay to assess defense response is important to study plant disease resistance, but also useful for early identification of disease during pre- or non-symptomatic phases. The increase in extracellular pH is known as one of the early defense responses. In this study, we established a fast and reliable alkalinization assay to monitor plant defense response in potato. Using potato suspension cell culture, we observed alkalinization response against various pathogen- and plant-derived elicitors in dose- and time-dependent manners. We also assessed the defense response against a variety of potato pathogens, such as protists (*Phytophthora infestans* and *Spongospora subterranea*), fungi (*Verticillium dahliae* and *Colletotrichum coccodes*) and bacteria (*Pseudomonas syringae*). Our results showed that extracellular pH was increased within 30 min in proportion to the number of pathogen spores. Based on our data, we suggest that alkalinization assay is one of the effective tools to study disease resistance response against multiple pathogens.

**Transcriptome-wide mining of potato genes targeted by Potato virus Y- derived viral small interfering RNAs.** L. MOYO (1), S. Ramesh (2), S. Williams (3), N. Mitter (3), V. Sathuvalli (4), and H. Pappu (1). (1) Washington State University, Pullman, WA, USA; (2) ICAR-Directorate of Soybean Research, Indore Madhya Pradesh, UNK, USA; (3) University of Queensland, St. Lucia, UNK, Australia; (4) Oregon State University, Hermiston, OR, USA.

*Potato virus Y* (PVY) is an economically important pathogen of potato. The existence of biologically distinct strains that differ in their symptoms in potato complicates disease management efforts. The molecular mechanisms underlying the potato-PVY interactions are largely unknown. Plants respond to viral infection by accumulating small RNAs that mediate targeted degradation of the viral RNAs. We previously characterized virus-specific, small interfering (vsi) RNAs for PVY-N, PVY-
NTN and PVY-O in potato cv. Russet Burbank. The three strains exhibited diversity in absolute number, copy number and hotspots for vsiRNA in their respective genomes. To elucidate the silencing effect of the vsiRNAs on host genes, we mined, in silico, the potato transcriptome and identified transcripts for their propensity for strain-specific vsiRNAs. Target transcripts represented KEGG pathways in plant hormone signaling, plant-pathogen interaction, RNA transport and, the GO terms in defense response and response to stress and were validated by qRT-PCR. These findings suggest that the virus targets and perturbs host plant defenses. Differential targeting of host genes was exhibited by the three strains and may partly account for their differential behaviour in potato. These clues on virus-host interactions can be applied in developing novel strategies for disease management.

The current status of nepoviruses in Washington vineyards. N. NATRA (1), S. Akinbade (2), B. Bagewadi (3), P. Swamy (3), A. Schultz (4), and R. Naidu (1). (1) Department of Plant Pathology, Washington State University, Irrigated Agriculture Research and Extension Center, Prosser, WA, USA; (2) Nematology Lab, WSDA Plant Services Program, WSU-IAREC, Prosser, WA, USA; (3) Washington State University, Irrigated Agriculture Research and Extension Center, Prosser, WA, USA; (4) Hattrup Farms Inc., Wapato, WA, USA.

Diseases caused by nematode-transmitted viruses (nepoviruses) are recognized as one of the serious impediments to the long-term sustainability of vineyards in Washington State. Previous studies have shown the presence of Grapevine fanleaf virus (GFLV) and absence of its nematode vector (Xiphinema index) in Washington vineyards. However, the significance of nepoviruses has been elevated with a recent report of the occurrence of Tobacco ring spot virus (TRSV) in a grower vineyard. In 2015 season, a limited survey of vineyards using virus-specific diagnostic assays revealed the presence of GFLV and TRSV in three wine grape (Vitis vinifera) cultivars in geographically separate vineyards. RNA1 and RNA 2 of TRSV was determined to be 7,519 and 3,927 nucleotides, respectively, and showed maximum similarity with corresponding sequences of TRSV-SK strain from South Korea. Using cucumber baiting assays, the spread of TRSV from symptomatic grapevines to healthy cucumbers by soil-inhabiting nematodes was demonstrated. Using morphological characteristics and molecular analysis of genomic DNA, X. rivesi was identified in soils collected from TRSV-affected vineyard. The detection of TRSV by RT-PCR in nematodes suggested the potential of X. rivesi as a vector of the virus. Studies on impacts of TRSV on fruit yield and quality in a wine grape cultivar showed that symptomatic grapevines produced significantly less fruit with low amounts of sugars compared to non-symptomatic vines.

Identification and pathogenicity of fungal species associated with canker diseases of pistachio in California. M. NOURI (1), L. Holland (2), D. Doll (3), C. Kallsen (4), E. Fichtner (5), T. Michailides (1), and F. Trouillas (1). (1) Department of Plant Pathology, University of California, Davis, Kearney Agricultural Research and Extension Center, Parlier, CA, USA; (2) Department of Plant Pathology, University of California, Davis, Davis, CA, USA; (3) University of California Cooperative Extension Merced County, Merced, CA, USA; (4) University of California Cooperative Extension
To date, only a few diseases are known to affect pistachio in California. Nevertheless, recent changes in weather patterns and prolonged drought have increased plant stress, thus potentially reducing plant tolerance to diseases. During the year 2015, we conducted surveys in California to detect possible new or emerging diseases of pistachio. Cankers in trunks and branches as well as dieback symptoms of mature pistachio trees were observed in several orchards of the San Joaquin Valley. Canker symptoms consisted of brown to dark brown vascular discoloration, from which isolation of putative fungal pathogens was attempted. Isolated fungi were identified by sequencing and NCBI BLAST of the partial internal transcribed spacer region (ITS). Preliminary sequence analyses revealed species of *Cytospora*, *Colletotrichum*, and *Phoma*, *Diaporthe ambigua*, *Neofusicoccum mediterraneum*, *Phaeoacremonium mortoniae*, and *Schizophyllum commune* in cankers. Pathogenicity tests on detached pistachio twigs were conducted in the laboratory to determine the ability of the various fungal species to cause diseases. Results indicated that all these species were pathogenic to pistachio, producing typical cankers. Among all, *Cytospora* species appeared to be the most virulent. Further detailed studies are being conducted to complete the identification of these fungal pathogens and better understand their biology and distribution in California pistachio.

**Exploration of wheat root phenotyping for Rhizoctonia resistance.** P. OKUBARA (1), A. Mahoney (2), N. Leston (3), S. Hulbert (3), and K. Sanguinet (4). (1) USDA-ARS Wheat Health, Genetics and Quality, Pullman, WA, USA; (2) Molecular Plant Sciences, Washington State University, Pullman, WA, USA; (3) Department of Plant Pathology, Washington State University, Pullman, WA, USA; (4) Department of Crop and Soil Science, Washington State University, Pullman, WA, USA.

Current screens for *Rhizoctonia* resistant wheat incorporate both field trials and greenhouse assays, but pathogen populations in the field are difficult to reproduce from year to year. Using three wheat genotypes having enhanced root growth in the presence of *R. solani* AG-8, we are exploring endogenous early seedling root growth phenotypes as predictors of *Rhizoctonia* resistance in Pacific Northwest wheat lines. One genotype is the ethyl methanesulfonate mutant Scarlet-Rz1, in which resistance is inherited as a single dominant or co-dominant allele; two other genotypes, SYN 172 and SPCB 3104, are synthetic or synthetic-derived wheats in which resistance is conferred by multiple quantitative trait loci. In all genotypes, resistance was correlated to higher total root length relative to that in the corresponding susceptible genotypes Scarlet and Louise (WinRHIZO, Regents Instruments). However, other root growth traits that can be monitored within 14 days at low cost are also of interest. Preliminary experiments with susceptible Scarlet and resistant Scarlet-Rz1 indicate that resistant roots emerge more slowly but grow more quickly after emergence than susceptible roots. This trend is not observed in resistant and susceptible synthetic genotypes. Other preliminary experiments indicate that wheat seedling roots grow well in the gellan gum-based clear medium GelZan (Phytotech Labs). When combined with 360° imaging (Ortery Technologies), seedling root architecture can be assessed in three dimensions and quantified using GiaRoots software. Three pathogen-based approaches will enable a
comparison of resistant and susceptible genotypes with and without pathogen: 1) browning of seedling roots after exposure to the pathogen in a ground oat substrate; 2) seminal root angle of seedling roots grown against the walls of transparent pots; and 3) architectural traits of mature roots in soil, including lateral root number, branching angle and root hair number, quantified using the CI-600 in situ root imaging system.

**Predictive models for tospoviral proteins involved in virion assembly and host defense suppression.** C. OLAYA (1), B. Adhikari (2), G. Raikhy (1), J. Cheng (2), and H. Pappu (3). (1) Washington State University, Pullman, WA, USA; (2) University of Missouri, Columbia, Columbia, MO, USA; (3) Washington State University, Pullman, WA, USA.

Tospoviruses (*Tospovirus: Bunyaviridae*) cause significant losses to a wide range of agronomic and horticultural crops worldwide. To engineering virus resistance, target proteins and motifs with critical functions have to be characterized. *Tomato spotted wilt virus* was used to understand the structure of the nucleocapsid (N) and silencing suppressor (NSs) proteins coded by the viral small RNA. We used several state of the art 3D modeling algorithms, MULTICOM, ITASSER, ROBETTA and CONFOLD to predict the tertiary structures, and pairwise ranking method APOLLO and TM-SCORE to rank the resulting models. A total of 31 and 27 complete sequences of the N and NSs genes, respectively, of all known tospoviruses were aligned. At least 8 conserved residues of the N protein and 9 in the NSs protein were identified. The N protein models predicted were built based on the Orthobunyavirus templates. All models showed β-sheets, consistently located near the amino terminus, and several α-helices. For the NSs protein, no *Bunyaviridae*-based proteins were available. The modelers selected several unrelated templates to build the NSs protein predictions. The predictions made by all three servers were similar to the N protein, whereas, it was less so for the NSs protein. This is the first attempt to predict the 3D structure of any tospoviral NSs protein. Our results form the basis for further work on structure-function relationships of tospoviral proteins.

**Diverse mycoviral sequences in the sweet cherry powdery mildew fungus (*Podosphaera prunicola*) revealed by next-generation sequencing.** B. PANDEY (1), N. Rayapati (1), and G. Grove (1). (1) Washington State University, Irrigated Agriculture Research and Extension Center, Prosser, WA, USA.

Fungal viruses (mycoviruses) are frequently found in several plant pathogenic fungi. This study was undertaken to examine mycoviral sequences in the fungus *Podosphaera prunicola*, the causal agent of powdery mildew disease in sweet cherry. Double-stranded RNA preparations of the fungal conidia and mycelium scraped from the infected cherry leaves were analyzed by next-generation sequencing (NGS). The quality filtered NGS reads were assembled de novo into contigs using the CLC Genomics workbench 8.5.1 software and subjected to BLASTn and BLASTx analyses against sequences available in public databases. The results showed the presence of distinct mycovirus-like sequences. Four of these sequence contigs, ranging in size between 1,915 and 2,334 nucleotides (nt), contained a single open reading frame (ORF), potentially encoding a protein with similarity to the RNA-dependent RNA polymerase of viruses in the family *Partitiviridae*. Three additional sequence contigs,
ranging in size between 1,736 and 2,104 nt, contained a single ORF encoding a putative protein similar to the capsid protein of viruses in the family *Partitiviridae*. Another contig of 11,449 nt containing four putative ORFs showed similarity to the genome of an unclassified mycovirus, *Macrophomina phaseolina tobamo-like virus*, in the family *Virgaviridae*. These preliminary results suggest that the fungus causing powdery mildews in cherries may contain diverse mycovirus populations.

**Prevalence of Grapevine red blotch-associated virus in British Columbia.** S. POOJARI (1), T. Lowery (1), A. Schmidt (2), M. Rott (3), and J. Urbez-Torres (4). (1) Summerland Research and Development Centre - Agriculture and Agri-Food Canada, Summerland, BC, Canada; (2) Centre for Plant Health - Canadian Food Inspection Agency, North Saanich, BC, Canada; (3) Centre for Plant Health - Canadian Food Inspection Agency, North Saanich, BC, Canada; (4) Summerland research and Development Centre - Agriculture and Agri-Food Canada, Summerland, BC, Canada.

Grapevine (*Vitis vinifera L.*) is an important crop in British Columbia (BC) contributing over CAD $2.1 billion into the Canadian economy. BC, with over 10,000 acres, is the second largest grape-growing region in Canada with the majority of commercial vineyards located in the Okanagan Valley. Grapevine red blotch-associated virus (GRBaV) was first observed in New York in 2012. Since then, it has been reported to occur in wine-grape cultivars as well as free-living *Vitis* spp. from several grape-growing regions in the USA. Negative impacts associated with GRBaV infection in wine-grapes, including reduced yield and poor fruit quality could pose a threat to the sustainability of the grape and wine-industry. To determine the current status of GRBaV in BC vineyards, field surveys were conducted during both 2014 and 2015 growing seasons. In total, 205 vineyard blocks were surveyed in BC. Overall, 2,196 random composite samples (10,980 vines) and 229 single targeted vines were tested for the presence of GRBaV by PCR using virus specific primers. GRBaV was detected from 34 (1.5%) and 26 (11.3%) composite and targeted samples, respectively, indicating a low incidence of this virus in BC vineyards. Phylogenetic analysis based on the full-length genome of eight representative isolates from BC indicated the presence of mixed genetic variants in BC vineyards. This work provides the foundation for further studies to investigate the role played by GRBaV on grapevine health and will assist the development of management strategies in BC.

**Discovery of grapevine Pinot Gris Virus and current status of other less-common grapevine viruses in British Columbia.** S. POOJARI (1), T. Lowery (1), A. Schmidt (2), and J. Urbez-Torres (1). (1) Summerland Research and Development Centre - Agriculture and Agri-Food Canada, Summerland, BC, Canada; (2) Centre for Plant Health - Canadian Food Inspection Agency, North Saanich, BC, Canada.

Grapevine (*Vitis vinifera L.*) hosts the widest variety of pathogens of any woody perennial crop and at least over 70 different viruses have been found to infect grapes. Among them, less-common viruses, including *Grapevine fanleaf virus* (GFLV), *Grapevine fleck virus* (GFkV), *Arabis mosaic virus* (ArMV), and/or the recently discovered Grapevine Pinot gris virus (GPGV) have been shown to affect vine health by reducing vine growth and fruit quality. To understand the current status of these grapevine viruses in British Columbia (BC), surveys were conducted between 2013 and
2015 growing seasons. Both random-composite samples and single-targeted vines were collected in different grape-growing regions of BC and tested for the presence of GFLV, GFkV, and ArMV by DAS-ELISA and/or RT-PCR. GFLV was detected in 17 out of 188 (9%) blocks surveyed and in 25 out of 1,220 composite samples (2%). GFkV was detected in 231 out of 788 (29.7%) of the composite samples collected and no positives were detected for ArMV from 998 composite samples. Additionally, single tube RT-PCR using specific primers to the coat protein (CP) gene detected GPGV in one sample showing severe chlorotic mottling and deformation of the leaves. GPGV isolate from BC was confirmed by completing the full genome sequence. This study represent the first report of GPGV in BC, which underscores the importance of rigorous virus testing for monitoring the occurrence and/or introduction of less-common viruses in commercial vineyards.

**Development of an infectious clone of the Worland strain of *Beet curly top virus***

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Strain Worland of the *Beet curly top virus* (BCTV) is one of three BCTV strains affecting beans and sugar beet in the dry desert climate of the western U.S. BCTV is a type member of the genus Curtovirus, family Geminiviridae. It is transmitted by leafhoppers, and has a ca. 3.0-kb single-stranded, circular DNA genome. To create a tool for the screening of curly top-resistant common bean and sugar beet germplasm, we generated a full-length, infectious clone of BCTV-Worland (1.1 genome) in a binary construct for delivery into plants via agroinoculation. The infectivity of this BCTV-Worland clone was monitored through a combination of symptom observations, ELISA, and PCR tests. The infectivity was confirmed for sugar beet, tomato, common bean, and *Nicotiana benthamiana*. The time-course of BCTV-Worland symptom development was compared to symptoms caused by two other infectious constructs, BCTV-CFH and BCTV-Logan.

**Developing a wheat germplasm with linked genes Yr64 and Yr65 for resistance to stripe rust.**

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Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is one of the most important wheat diseases worldwide, and resistance is the best control strategy. In a previous study, two genes, Yr64 and Yr65 originally from durum wheat conferring resistance to all tested *Pst* races, were mapped to different loci, but linked in the short arm of chromosome 1B. The objective of this study was to pyramiding Yr64 and Yr65 into a single common wheat line. A cross was made between common wheat lines of Yr64 and Yr65 selected from previous studies. A line was selected from the F4 progenies to make a cross with ‘Avocet S’ based on its infection type (IT) 0 that was different from IT 2 on both Yr64 and Yr65 lines. Among 336 F2 plants from the new cross tested with race PSTv-11 in the greenhouse, 5 plants were susceptible and the remaining 331 plants were resistant. Testing 100 F3 lines in the greenhouse with the same race resulted in homozygous susceptible lines from susceptible F2 plants and separated homozygous resistant lines from segregating lines derived from resistant F2 plants. The
results confirmed the linkage of the two genes and indicated that the selected line had two genes. Genotyping the F₄ line, Yr64 and Yr65 lines, and Avocet S with molecular markers flanking the two genes supported the presence of both genes in the selected line. The new line with linked Yr64 and Yr65 should be useful for developing wheat cultivars with durable resistance to stripe rust.

**Effectors from *Puccinia* suppress plant host defense responses.** S. RAMACHANDRAN (1), C. Yin (1), J. Kud (2), K. Tanaka (1), A. Mahoney (1), F. Xiao (3), and S. Hulbert (4). (1) Washington State University, Pullman, WA, USA; (2) University of Idaho, Moscow, WA, USA; (3) University of Idaho, Moscow, ID, USA; (4) Washington State University, Pullman, WA, USA.

Plants employ several defense systems to guard against infection. In order to successfully infect the host, pathogens secrete a number of proteins that attenuate host defenses. Here we report nine effector proteins from cereal rust pathogens, *Puccinia graminis* and *Puccinia striiformis* that suppress the plant hypersensitive response (HR) when expressed transiently in *Nicotiana benthamiana*. Of the twenty putative effector proteins selected and expressed in *N. benthamiana* using *Agrobacterium*-mediated transient transformation, nine proteins, *Shr1* – *Shr9* (Suppressors of Hypersensitive Response), were found to suppress R gene mediated hypersensitive response. These proteins differentially interfere with R gene Pto(Y207D), and effector-R gene combination GPA/RBP-1 and ATR13/RPP13 mediated HR. Expression analysis of these nine suppressors showed that they may be required at all stages of rust infection. In addition, *Shr7* reduced production of reactive oxygen species (ROS) triggered by flg22, a common PAMP elicitor. Furthermore, delivery of *Shr7* into wheat leaves via *Pseudomonas* type-III secretion system suppresses non-specific HR induced by *Pseudomonas syringae* pv. *syringae* DC3000. To our knowledge the present report constitutes the first evidence for the presence of plant defense suppressors in *Puccinia*. Overall, these studies reveal that fungi, much like bacteria and oomycetes, use suppression of host defenses as a strategy to infect plants.

**Utilizing field surveys, variety trials and indicator species analysis to diagnose a soil borne disease complex in winter squash.** H. RIVEDAL (1), A. Stone (1), and K. Johnson (1). (1) Oregon State University, Corvallis, OR, USA.

A novel late-onset, soil borne disease is threatening winter squash produced in Oregon’s Willamette Valley. Anecdotal evidence from growers and extension personnel suggest that total winter squash yield has fallen by 50% due to this disease. In 2014 and 2015, field surveys were conducted to determine the presence and diversity of fungi associated with commercial squash plants. A total of 2300 fungal isolates were subjected to DNA extraction and sequencing of ITS and TEF1 alpha genes. *Fusarium oxysporum* (26% of isolates) and *Plectosphaerella cucumerina* (21% of isolates) were consistently associated with diseased plants, as well as *Fusarium solani* and *Setophoma spp*. Cucurbit variety trials also were conducted and rated (1 to 4) for disease severity in roots, crowns and vascular tissue. Disease was most severe on winter squash (average rating 2.4) followed by watermelon, pumpkin and cucumber (ratings of 2.0, 1.9 and 1.3, respectively). Utilizing indicator species analysis, comparisons of isolated fungal communities confirmed *F. oxysporum* to be more
prevalent in diseased fields compared to healthy fields ($P \leq 0.001$); however, *P. cucumerina* and *F. solani* were significantly associated ($P \leq 0.001$) with diseased fields on smaller-sized organic farms. Additional experiments on pathogenicity and host range of collected fungi are underway to better understand this disease complex.

**Emerging root-infecting pathogens of marihuana (*Cannabis sativa*).** G. RODRIGUEZ (1), P. Campbell (1), and Z. Punja (2). (1) Agrima Botanicals, Maple Ridge, BC, Canada; (2) Simon Fraser University, Burnaby, BC, Canada.

Legalized cultivation of marihuana is encouraging the development of previously unreported plant diseases, of which root rot pathogens are an emerging threat to the industry. During 2013-2015, plants with symptoms of stunted growth, wilting and yellowing of foliage were sampled. Affected plants had brown discolored roots and evidence of root rot. Isolations from surface-sterilized tissues on various agar media revealed the following which were identified from ITS1-ITS4 rDNA sequence comparisons: *Pythium dissotocum* and *P. myriotylum*, and *Fusarium solani* and *F. oxysporum*. Pathogenicity tests were conducted on rooted cuttings grown in a hydroponic nutrient solution by adding pathogen inoculum (agar plugs or spore suspensions) and maintaining plants in a growth chamber set at 25°C and a 16-hr photoperiod for 10 days. Alternatively, rooted cuttings were inoculated directly with a mycelial plug placed on the main root and incubated in a moist environment for 7 days. Roots were examined for discoloration and root rot symptoms and rated on a scale of 1 (no symptoms) – 4 (extensive browning and rot). Re-isolations were made from diseased roots. All four pathogens caused symptoms of root discoloration and rotting to varying degrees. The most aggressive species were *P. dissotocum* and *P. myriotylum*, followed by *F. solani* and *F. oxysporum*. These root-infecting pathogens have the potential to spread extensively once introduced into a commercial growing facility.

**Alternative management practices of *Pratylenchus penetrans* in red raspberry in the Pacific Northwest.** R. RUDOLPH (1), I. Zasada (2), and L. DeVetter (1). (1) WSU, Mount Vernon, WA, USA; (2) USDA-ARS, Corvallis, OR, USA.

In recent years, red raspberry (*Rubus idaeus*) planting longevity in the Pacific Northwest has declined significantly. This decline has been partially attributed to severe pressure from the plant-parasitic nematode, *Pratylenchus penetrans*, which has been shown to contribute to reduced raspberry plant vigor, yield, and economic returns. Several commercial fumigant products are effective at suppressing *P. penetrans* populations, but efficacy is short-lived compared to the potential longevity of a perennial production system like floricane red raspberry. This research was designed to test alternatives to chemical fumigation that have potential to suppress *P. penetrans* and enhance soil quality in red raspberry field production, in addition to maintaining commercial fruit yields. In one experiment, a two-year study was established in fall of 2014 evaluating the effects of nine cover crops planted in the alleyways of an established raspberry field in northwest, Washington. In the spring of 2015, *P. penetrans* populations in raspberry roots were highest in plots seeded with a perennial ryegrass mix, although this ground cover supported the lowest *P. penetrans* numbers in its own roots. A similar trend was observed in the fall of 2015. There were no significant differences in raspberry fruit yield among treatments the first summer after
establishment. In a second experiment, a two-year study was established evaluating pre-plant treatments of brassicaceous seed meal (BSM) and chemical fumigation with or without root inoculum removal in a commercial red raspberry field in northwest Washington. The treatments were BSM + inoculum removal, full rate metam sodium, full rate metam sodium + inoculum removal, and half rate metam sodium; all were applied once at the beginning of the study. The first summer after planting, no significant differences in vegetative growth were observed among treatments. In the fall, *P. penetrans* populations were highest in raspberry roots planted in soil treated with BSM.

**Effect of culture filtrates from four *Trichoderma* species on sporangia and zoospore production, and mycelial growth by *Phytophthora capsici***. S. SANOGO (1), P. Lujan (1), Y. Zhu (1), M. Lytle (1), and B. Bailey (2). (1) New Mexico State University, Las Cruces, NM, USA; (2) USDA-ARS, Beltsville, Beltsville, MD, USA.

Sporangia and zoospores are important for the dispersal of *Phytophthora capsici* and other species of *Phytophthora*. Reduction in the production of these propagules, and in the vegetative growth of *P. capsici*, may lead to a reduction in inoculum potential and thereby result into a decrease in the incidence and severity of Phytophthora blight. Research was conducted to assess the effect of four species of *Trichoderma* (*T. asperellum*, *T. atroviride*, *T. harzianum*, and *T. virens*) on asexual reproduction and vegetative growth of *Phytophthora capsici*. Sporangia production and zoospore release were monitored on 1-cm mycelium plugs from a 5-7 day-old culture of an isolate of *P. capsici* placed in 25 ml conidia suspension (105 conidia/ml) of *Trichoderma*, and incubated at 27°C for 72 h. Additionally, mycelial growth of *P. capsici* was evaluated on 1-cm mycelium plugs placed in filter-sterilized (0.22 µm) culture filtrate of *Trichoderma* grown in potato dextrose broth (PDB) or in PDB amended with casamino acid for 5 days under agitation on a rotary shaker at room temperature (22-25 °C). Sporangia production was abundant in the presence of all *Trichoderma* species, with 75 to 100% of the plugs showing sporangia production greater than 100 sporangia per microscopic view. However, with *T. virens*, 75 to 100% of plugs showed sporangia production at less than 50 sporangia per microscopic view. Zoospores were released in the presence of all *Trichoderma* species. There was a drastic reduction in growth of *P. capsici* in culture filtrate of *T. virens* on potato dextrose broth amended with casamino acids. Sporangia production and zoospore release were not negatively affected by the *Trichoderma* species examined in this study. Results also suggest that culture filtrates of *Trichoderma* contain factors that may affect the growth of *P. capsici*.

**First report of *Urocystis camassiae* causing smut of Camas (*Camassia quamash*) in Idaho, United States**. K. SAVCHENKO (1), and L. Carris (1). (1) Washington State University, Pullman, WA, USA.

Camas (*Camassia leichtlinii* and *C. quamash*; Asparagaceae) is a traditional native root vegetable important to the Native American tribes in western North America. Smutted stems and leaves of camas were observed and collected in Nez Perce County, Idaho, USA, in June of 2015 in a wet meadow located at 46.1597 N, 116.7982 W. Only several plants in a population of more than a hundred were infected (less than 5% incidence). Lead colored, blister-like sori covered by the epidermis developed on
infected stems and leaves, and gradually ruptured exposing the blackish brown, powdery mass of spore balls. Spore balls were subglobose, to ovoid, 22–30 x 20–50 μm, brown, composed of (1) 2–5 spores completely surrounded by a layer of smooth, hyaline-yellowish sterile cells. Teliospores were subglobose or ovoid, 11–15 x 12–17.5 μm diam., reddish brown with smooth ca. 1 μm thick walls. To confirm the morphological identification, specimens of *Urocystis on Camassia* from the United States National Fungus Collection (Herbarium BPI), including the type specimen on *C. quamash* from British Columbia, were examined and compared with the one from Idaho. Since there are no sequences of *U. camassiae* deposited in GenBank, the specimen from Idaho was used for the DNA extraction. NL1 and NL4 primers were used to amplify the large subunit ribosomal RNA gene region (LSU). The LSU sequence of *U. camassiae* showed 99.7–99.8% similarity with three other species of *Urocystis* (*U. carcinodes*, *U. ficariae*, *U. floccosa*) previously deposited in GenBank. A representative specimen was deposited in the WSU Mycological Herbarium. Camas smut is quite rare and has previously been reported only from British Columbia, Indiana, and Oregon. This is the first report of *U. camassiae* causing smut of camas in Idaho.

**Analysis of toxin gene transcription in Rathayibacter toxicus infected with bacteriophage.** A. SECHLER (1), B. Atha III (2), J. King (3), E. Rogers (1), and W. Schneider (1). (1) USDA-ARS-FDWSRU, Ft. Detrick, MD, USA; (2) Dept of Biological Sciences, Towson University, Towson, MD, USA; (3) Dept of Biochemistry, Mississippi State Univ, Mississippi State, MS, USA.

The USDA-APHIS Select Agent *Rathayibacter toxicus* is a gram-positive bacterium that produces a tunicamycin-like toxin in many species of forage grass. This toxin causes a poisoning (often fatal) in livestock that consume it (LD50 3-5 μg/kg). The mechanism and trigger for toxin production is largely unknown. Toxin production has been associated with the presence of an *R. toxicus* specific bacteriophage, CS14Φ, but its role in nature is unclear. In the laboratory, infection of *R. toxicus* by the CS14Φ has been shown to induce toxin production in culture. A close inspection of the *R. toxicus* genome found a single putative tunicamycin gene cluster (TGC) composed of 14 genes organized into two likely transcriptional units. Using four specific qPCR primers and probes for the putative genes within the TGC, two genes per transcriptional unit, transcription was measured during log growth of *R. toxicus* (day 2), and early, mid, and late infection of *R. toxicus* by CS14Φ cultures (days 3, 5, and 14). Evidence of toxin production was observed only for the late infection culture as tested by growth on an indicator lawn of toxin-sensitive bacteria. TGC genes were transcribed at all four time points, suggesting that control of toxin production may occur through a non-transcriptional mechanism.

**Identification of toxin production pathways by genomic sequencing of Rathayibacter toxicus and the associated phage.** A. SECHLER (1), D. Schneider (2), B. Schroeder (3), T. Murray (4), E. Rogers (1), D. Luster (1), and W. Schneider (1). (1) USDA-ARS FDWSRU, Fort Detrick, MD, USA; (2) USDA-ARS Holley Center for Plant Microbe Interactions Research, Ithaca, NY, USA; (3) University of Idaho, Moscow, ID, USA; (4) Washington State University, Pullman, WA, USA.

*Rathayibacter toxicus* (RT) is a gram-positive bacteria that affects multiple forage
grass species. RT is listed as a USDA-APHIS select agent because of the production of a lethal toxin (tunicamycin) that kills livestock, a disease known as Annual Ryegrass Toxicity (ARGT). ARGT is a frequent issue in Australia, the only known location where RT is found. Not all members of the Rathayibacter genus produce toxin, and the exact mechanisms of toxin production and control were previously unknown. In most cases, RT toxin production is associated with the presence of phage CS14Φ. To identify the genetic elements involved in RT toxin production, the complete genomes of RT and CS14Φ were sequenced. The RT genome is a single chromosome 2.5Mb in size, which is relatively small for the genus. Approximately 2340 hypothetical open reading frames (ORFs) were identified. The genome of CS14Φ is 44,000 nt in size with 73 hypothetical ORFs. A cluster of genes with similarity to a tunicamycin production gene clusters from Streptomyces spp. was found in the genome of RT. The tunicamycin gene cluster (TGC) had a significantly lower GC content (54%) than the rest of the RT genome (61%), suggesting that the TGC may have originated as a mobile element. In addition, the TGC has the same GC content as CS14Φ and there are regions of shared sequence between CS14Φ and the TGC, suggesting a possible role for the phage in control of TGC expression and toxin production.

Using DNA extracted from soil to quantify inoculum densities of multiple soilborne pathogens in long-term cropping systems trials. R. SMILEY (1). (1) Oregon State University, Pendleton, OR, USA.

Root pathogens in rainfed field crops are typically studied in short-term trials having a focus on only a few pathogens. Studies rarely compare treatments in long-term trials where pathogens may have attained a state of equilibrium. Four experiments at the Columbia Basin Agricultural Research Center near Pendleton, OR are among the oldest field trials in North America; annual cereals (84 yr), wheat-fallow rotations with either residue and fertilizer treatments (84 yr) or tillage and fertilizer treatments (75 yr), and a wheat-pea rotation with tillage treatments (52 yr). Inoculum densities of 17 fungal and nematode pathogens were quantified during two years using DNA extracted from 500 g soil samples. Treatments strongly affected DNA concentrations (pg/g of soil) of Bipolaris sorokiniana, Drechslera tritici-repentis, Fusarium culmorum, F. pseudograminearum, Gaeumannomyces graminis var. tritici, Helgardia spp., Phoma pinodella, Pratylenchus neglectus, P. thornei, Pythium spp., and Rhizoctonia solani AG-8. Two of the pathogens had not been previously detected at this location. Positive and negative correlations occurred between species of Pratylenchus, between Fusarium and Gaeumannomyces, and between Pratylenchus and either Fusarium, Gaeumannomyces, Pythium, or Rhizoctonia. The paper at http://dx.doi.org/10.1094/PDIS-09-15-1020-RE describes this research and proposes that disease management can be improved by using DNA technologies to study pathogen dynamics in soil.

Western flower thrips can transmit Tomato spotted wilt virus from infected tomato fruits. S. SZOSTEK (1), P. Rodriguez (2), J. Sanchez (2), S. Adkins (3), and R. Naidu (1). (1) Department of Plant Pathology, Washington State University Irrigated Agriculture Research and Extension Center, Prosser, WA, USA; (2) Heritage University,
Tomato spotted wilt virus (TSWV) and other thrips-vectored tospoviruses have long been known to spread via plant propagation material. Global dissemination of tospoviruses has also been linked to transport of thrips-infested and virus-infected horticultural products through trade. The role of tomato fruits transported across state and national borders has not previously been examined as a means of virus spread or as a source for thrips acquisition of virus. Tomato fruits displaying symptoms consisting of chlorotic and necrotic rings, irregular blotches, fruit deformation and discoloration were observed for sale in several grocery stores in eastern Washington State. Many of these symptomatic fruits tested positive for TSWV in lateral flow immunoassays. First instar western flower thrips (Frankliniella occidentalis) larvae acquired TSWV from infected tomato fruits and transmitted the virus as adults to Emilia sonchifolia plants. Symptomatic E. sonchifolia plants were confirmed positive for TSWV by lateral flow immunoassays and sequence analysis of a portion of the nucleocapsid gene. These results have important implications in the dissemination of TSWV (and likely other tospoviruses) to new geographic areas by human-assisted transport of infected tomato fruits. Additionally, infected tomato fruits discarded by grocery stores could serve as a virus source for local thrips vectors to spread extrinsic virus isolates to susceptible plant species in the vicinity.

Effect of read depth, missing data, imputation and variant callers on genotyping-by-sequencing for population genetic analysis. J. TABIMA (1), B. Knaus (2), and N. Grünwald (2). (1) Oregon State University, Corvallis, OR, USA; (2) USDA-ARS, Corvallis, OR, USA.

Genotyping by sequencing (GBS) is becoming one of the most popular techniques to obtain a high number of single nucleotide polymorphisms (SNP) while being cost effective; but this technique is not flawless. GBS reduces the complexity of the genome to fragments cut by restriction enzymes, obtaining high numbers of SNPs for a large number of samples in an affordable manner. Nonetheless, the GBS technique presents some issues that are not commonly addressed: Plates with an uneven number of reads per sample, low read depths in each variant, a high proportion of missing data per dataset, and a high abundance of rare SNPs. If these issues are not comprehensively addressed, the SNPs obtained by GBS can lead to errors and misrepresentation of the population dynamics in the dataset of interest. We present here an evaluation of the influence of read depth, variant callers, missing data, and imputation on GBS datasets to create a briefing on how to process these datasets, with an emphasis on oomycete plant pathogens of the genus Phytophthora. We observe that filtering by read depth quartiles and by the maximum values of mapping quality results in a reduced dataset after removing rare alleles, as well as low-coverage and low-quality SNPs. We also show that different variant callers obtain different numbers of SNPs for the same dataset, and that genotype imputation does not result in better variant panels due to misrepresentation of the number of heterozygote SNPs in a dataset. We recommend a strict and careful post-processing of GBS data. We conclude that these filtering processes will overcome the innate issues of GBS, and will lead to high quality datasets for use in population genetic approaches.
Classification powdery mildew fungi in Viet Nam and potential in bio-control by indigenously endophyte bacteria *Bacillus amyloliquefaciens* BA1. L. THANH TAM (1), N. Minh Khue (2), N. Tuyen (1), L. Thao (1), N. Hanh (1), L. Thao (1), P. Dung (1), and N. Liem (1). (1) Plant Protection Research Institute, Ha Noi, Vietnam; (2) Plant Protection Department of Lai Chau province, Lai Chau, Vietnam.

Studies from the Viet Nam-Japan co-operation project funded by Ministry of Science and Technology (MOST) of Viet Nam in years 2013-2015 on classification powdery mildew fungi have already showed that there are 4 genus powdery mildews fungi (*Erysiphe*, *Golovinomyces*, *Podosphaera*, *Microidium*) with 9 species damaging in 11 host plant families with total of 27 main crops and other sub-host plants in Viet Nam. Improved management methods are needed to prevent yield losses and reduced agricultural product exports. Especially, the objection on finding out the new bio-product for prevention and suppression powdery mildew has priority over conventionally chemical methods due to its safety to animal, environment and human health as well. End of year 2013, endophyte bacteria *Bacillus amyloliquefaciens* BA1 was isolated from leaves of para-rubber tree. This endophyte has high activity in catalyzing chitin, beta-glucan and cellulose but its antagonistic activity against powdery mildew fungi is unknown. After tests in laboratory, it is suggested that antibiotic compounds possibly found in cultured solution of *B. amyloliquefaciens* as inturin and surfactin may play a role in inhibition the germination of powdery mildew conidia. Later, it is asked whether bio-product BA1 made from this endophyte with 3.7 x 10^8 CFU/ml may have effect in bio-control powdery mildew fungi on several main crops in natural conditions of Viet Nam. As being expected, results from field trials with twice treatments by BA1 at 7 % concentration in a period of 7 days proved a significant decrement in severity index of powdery mildew on mandarin and soybean obtained after spraying 14 days being 62.1 % and 60.0 %, respectively. Consequently, indigenously endophyte bacteria *B. amyloliquefaciens* BA1 may be used for making a bio-product with potential in control powdery mildew fungi disease on several main crops and plants in Viet Nam.

Dynamics of colonization of pome flowers by biocontrol strains of *Aureobasidium pullulans*, a yeast that effectively suppresses fire blight. E. THOMPSON (1), T. Temple (1), R. Elkins (2), and K. Johnson (1). (1) Oregon State University, Corvallis, OR, USA; (2) University of California, Lakeport, CA, USA.

*Aureobasidium pullulans* is used as a biocontrol for fire blight protection in apple and pear. We assessed floral colonization of *A. pullulans* in orchards near Lakeport CA, and Medford and Corvallis OR. Blossom Protect, a mix of *A. pullulans* strains CF10 and CF40, and its acidic companion, Buffer Protect, were sprayed at 80% bloom. In late bloom, flowers were sampled, washed individually and dilution-plated onto potato dextrose agar. Filamentous yeasts resembling *A. pullulans* were selected and isolated into pure culture. *ITS*, *Bt2*, and *Elo2* PCR-primers were used to confirm *A. pullulans*, while strain specific primers, SCAR6 and SCH3 RAPD, were used to distinguish CF10 and CF40 from environmental strains. Overall, 1273 of 1414 isolates (90%) were *A. pullulans*, but only 28% were confirmed as CF10 or CF40. Incidence of CF10 or CF40 was higher after Blossom Protect treatment (46% of flowers) compared to no treatment (22%). On non-treated trees, most *A. pullulans* isolates (77%) were apparently environmental. Questions arise after contrasting the outstanding biocontrol efficacy of Blossom Protect with results of this
effort: e.g., is *A. pullulans*’ ability to suppress fire blight strain specific?, and does the acidic buffer recruit environmental *A. pullulans* to flowers? This study also is the basis of the recommendation to treat every row with Blossom Protect as the secondary flower-to-flower movement of CF10 and CF40 appears limited.

**Identifying genetic resistance to the cereal cyst nematode *Heterodera filipjevi* in Pacific Northwest spring wheat.** Y. THOMPSON (1), R. Smiley (2), T. Paulitz (3), and K. Garland-Campbell (3). (1) Washington State University, Pullman, WA, USA; (2) Oregon State University, Pendleton, OR, USA; (3) USDA-ARS, Washington State University, Pullman, WA, USA.

The cereal cyst nematode, *Heterodera filipjevi*, is an invasive root pathogen of wheat in many regions of the world, causing significant economic damage. Crop rotations, long fallows, or nematicide applications reduce cereal cyst nematode damage; however, they are not profitable in rain-fed wheat producing areas of the Pacific Northwest. Genetic resistance is the most cost-effective, environmentally friendly, and easily adopted method to suppress this pathogen. The purpose of this research was to determine if resistance to *H. filipjevi* exists in locally-adapted wheat germplasm. A field naturally infested with *H. filipjevi* near Colton, WA was selected to screen cultivars and breeding lines from the Western Regional Spring Wheat Nursery in 2013, 2014, and 2015. The Washington Extension Spring Variety Trials were also screened in 2013 and 2015. The experimental design was a replicated complete block design with five replications in 2013 and three replications in 2014 and 2015. Five plants from each sample were pooled and the number of white females visible on roots were assessed using a 0-5 rating scale. The cultivar “SY Steelhead” had the lowest mean rating (0.62), and the cultivar “Kelse” had the highest mean rating (5.00). “SY 605CL”， “Ouyen”， UC1741， “Chara”， and “SY Steelhead” had the lowest mean ratings (0.62 to 2.18) and were rated moderately resistant to resistant. These results will provide regional breeders and growers with adapted sources of resistance to *H. filipjevi*.

**Composition of *Potato virus Y* strains in Idaho seed potato between 2012 and 2015.** L. TRAN (1), K. Green (1), C. Funke (1), O. Nikolaeva (1), M. Chikh-Ali (1), and A. Karasev (1). (1) University of Idaho, Moscow, ID, USA.

*Potato virus Y* (PVY) is the most serious threat to seed potato production in Idaho, as the main reason for seed lot rejections in the last 10-15 years. PVY exists as a complex of strains and variants, many of which are recombinants. Between 2013 and 2016, all seed potato lots from Idaho subjected to winter grow-out testing were investigated for the presence of PVY and for the relative abundance of PVY strains in virus-positive seed lots. During this time period, the trends in the PVY strain composition changed reflected the national trends, with the non-recombinant strain PVY<sup>O</sup> decreasing eight-fold in prevalence, to less than 4% of all PVY-positives. Currently, recombinant strains PVY<sup>N-Wi</sup>, PVY<sup>NTN</sup>, PVY<sup>N-O</sup>, and PVY-NE11 make up more than 90% of all PVY-positive samples found in the Idaho winter grow-out tests. Prevalence of the PVY<sup>NTN</sup> strain associated with tuber quality effects remained relatively stable, over the period of observation, at around 20%. Further monitoring of the PVY strain composition would be needed to understand the driving forces of these changes in prevalence of the PVY strains in potato production areas.
First occurrence of *Pseudomonas syringae* pv. *syringae* causing lesions on pumpkin fruit in WA, U.S..  L. Tymon (1), and D. Inglis (1). (1) Vegetable Pathology Program, WSU-Mount Vernon, Mount Vernon, WA, USA.

In Summer 2015, ‘Cinnamon Girl’ pumpkin grown in the Skagit Valley of western WA exhibited sunken lesions. Small sections of fruit tissue were excised, macerated with sterile distilled water, and the macerate was plated onto NBY agar. Two colonies from fruit were purified in culture. DNA was extracted from each isolate, and the 16S rDNA region amplified and sequenced. Sequences exhibited 96-99% similarity with *Pseudomonas syringae* sequences (PS) in GenBank. Four-mo-old fruit were injected with a suspension of bacterial cells at a concentration of approximately $1 \times 10^8$ CFU/mL. Sunken lesions were observed after 4 days on fruit. To assess the PS pathovar, three housekeeping genes, *rpoD*, *gyrB*, and *gltA* were amplified and sequenced. Sequences were aligned with reference isolate sequences acquired from the PAMDB database, and an NJ analysis was conducted. The three pumpkin isolates clustered with sequences from *PSS* and *P. syringae* pv. aptata (PSA) isolates. Pathogenicity testing on ‘Red Ace’ beet seedlings, a host of PSA, revealed that none of the three WA isolates caused lesions on the beet seedling leaves, thus the pumpkin isolates were not PSA. *PSS* previously has been isolated from cucurbits. However, this is the first time *PSS* has been reported on pumpkin in WA.

Young vine decline DNA-macroarray: a fast, specific, sensitive, and multiplexing diagnostics tool to assess the health status of grapevine nursery propagation material.  J. Uribez-Torres (1), and D. O’Gorman (1). (1) Summerland Research and Development Centre - Agriculture and Agri-Food Canada, Summerland, BC, Canada.

The young vine decline complex (YVD), associated with the grapevine trunk diseases black foot and Petri disease, is caused by a wide range of taxonomical unrelated fungi and it is responsible for substantial untenable economic losses to the grapevine industry worldwide. YVD fungi are known to occur in nursery propagated material and thus, detection prior to planting is critical to assure longevity of newly established vineyards. A YVD-DNA-macroarray based on the reverse dot-blot hybridization and with capability to simultaneously detect 34 YVD fungi has been recently developed. The objectives of this study were i) to implement this diagnostic tool to evaluate the health status of grapevine propagated material and ii) to compare this technique against currently used detection tools for fungal pathogens at the nursery level. Two hundred ready to plant vines (grafted and self-rooted) were provided by two nurseries. For each plant, total DNA was obtained from roots, rootstock basal end, graft-union, and scion and processed with the DNA-macroarray. The DNA-macroarray successfully detected and identified several YVD fungi and showed *Phaeomoniella chlamydospora* to be the most prevalent YVD pathogen followed by *Cadophora luteo-olivacea*, *Phaeoacremonium minimum*, and *Ilyonectria* spp. Among all different plant parts, YVD pathogens were detected primarily in the basal end of the rootstock. The DNA-macroarray was shown to be a much faster and a more accurate, and sensitive detection tool than other techniques used in the nursery such as traditional plating or single PCR.
Pomegranate dieback in California caused by *Lasiodiplodia gilanensis*. J. URBEZ-TORRES (1), F. Peduto Hand (2), F. Trouillas (3), and W. Gubler (4). (1) Summerland Research and Development Centre - Agriculture and Agri-Food Canada, Summerland, BC, Canada; (2) Department of Plant Pathology - Ohio State University, Columbus, BC, Canada; (3) Department of Plant Pathology, University of California Davis, Parlier, CA, USA; (4) Department of Plant Pathology, University of California Davis, Davis, CA, USA.

The fruit and juice of Pomegranate (*Punica granatum* L.) have been shown to be an important source of nutrients and antioxidants, which has increased its popularity among consumers in the past few years. Pomegranate production in California has significantly increased during the last decade and over 33,000 acres are currently planted primarily in the Southern San Joaquin Valley. During the summer of 2009, decline of young pomegranate trees was observed in several orchards in Riverside County. Symptoms were characterized by lack of spring growth and overall dieback expressing throughout the entire tree or in one to several branches. Sunken areas were observed on trunks and branches of diseased trees and cross sections revealed cankers in the wood. A total of 25 symptomatic young trees (3- to 5-year-old) cv. ‘Wonderful’ were collected from five different orchards to determine the canker causal agent/s. White fluffy and fast-growing fungal colonies that became dark-green with age were consistently isolated from the cankered tissue. Morphological characters along with DNA sequence analyses of three gene regions (ITS1-5.8S-ITS2, β-tubulin and TEF-1α) allowed the identification of *Lasiodiplodia gilanensis*. Koch’s postulates were completed in 2 year-old pomegranate trees cv. ‘Wonderful’ planted at the UC Davis Plant Pathology Field Station. Twelve months after inoculation, *L. gilanensis* isolates showed to be highly virulent producing cankers of up to 21 cm in length. This study reports for the first time the botryosphaeriaceous fungus *L. gilanensis* as the causal agent of cankers and consequent dieback of pomegranate trees in California.

Variation of telial formation in the *Puccinia striiformis* f. sp. *tritici* population. A. WAN (1), and X. Chen (2). (1) Department of Plant Pathology, Washington State University, Pullman, WA, USA; (2) USDA-ARS, Wheat Health, Genetics, and Quality Research Unit and Department of Plant Pathology, Washington State University, Pullman, WA, USA.

The wheat stripe rust pathogen, *Puccinia striiformis* f. sp. *tritici*, produces uredinia and telia on wheat plants. Telial formation after urediniospore production may contribute to the aggressiveness and fitness, and therefore affect the pathogen survival and disease epidemics. Significant increase in telial quantity and earliness of formation has been observed in fields. To determine differences in telial formation among the pathogen populations, percentage of telial formation (proportion changed from uredinia) were observed on susceptible wheat plants 40 days after inoculation with urediniospores for 1002 isolates collected from 2013 to 2015 throughout the US under controlled greenhouse conditions. Overall, 76% of the isolates were able to produce telia, ranging from 1 to 90% with an average of 20%. For different years, 79%, 52%, and 94% of the isolates produced telia with an average of 25%, 7% and 33% telia formation in 2013, 2014, and 2015, respectively. Differences in telial formation were observed among race groups, regions of collection, and months of sampling. Telial formation was more related to specific races than the numbers of virulence factors. Generally, isolates
from the western US produced few telia than those from the eastern US. Isolates collected in earlier season had low telial formation than those collected in the later season. The results may be useful for predicting the relative aggressiveness and fitness of races in the pathogen population.

**Grape berry colonization and biological control of *Botrytis cinerea* by indigenous vineyard yeasts.** X. WANG (1), E. Kramer (1), D. Giawe (1), and P. Okubara (2). (1) Department of Plant Pathology, Washington State University, Pullman, WA, USA; (2) United States Department of Agriculture, Agricultural Research Service, Wheat Health, Genetics and Quality Research Unit, Pullman, WA, USA.

Botrytis bunch rot, caused by *Botrytis cinerea*, is one of the most important grape diseases in wet environments. Our specific objectives were to evaluate indigenous yeast strains for colonization ability of grape berries and antagonistic activity against *B. cinerea in vitro* and on wounded berries. In a previous study, fifty indigenous yeasts strains of 16 genera, isolated from Washington vineyards, were tested for suppressive activity. In the current study, colonization of eleven strains of *Aureobasidium pullulans*, *Candida saitoana*, *Curvibasidium pallidicorallinum*, *Metschnikowia chrysoperlae*, *Metsch. pulcherrima*, *Meyerozyma guilliermondii*, *Saccharomyces cerevisiae* and *Wickerhamomyces anomalus* was quantified. Rapid and stable growth was observed for all yeast strains from 2 to 10 days after inoculation, with mild to moderate discoloration of the skin and internal tissues around the wound. *Aureobasidium pullulans* P01A006 showed effective inhibitory against nine *B. cinerea* isolates *in vitro*. The most extensive antagonism *in vivo* was shown by seven yeast strains, which consistently reduced symptom development and sporulation of *B. cinerea*. Strains of *Mets. pulcherrima* significantly controlled Botrytis bunch rot *in vivo*. Our findings indicate that indigenous yeasts that might contribute to the unique flavors of Washington wine could provide effective control against *B. cinerea*.

**Pyramiding stripe rust resistance genes on wheat chromosomes 2B, 4B, and 7B.** M. WANG (1), and X. Chen (2). (1) Department of Plant Pathology, Washington State University, Pullman, WA, USA; (2) USDA-ARS, Wheat Heath, Genetics, and Quality Research Unit and Department of Plant Pathology, Washington State University, Pullman, WA, USA.

Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is one of the most damaging diseases of wheat. The disease can be controlled by developing resistant cultivars. To develop wheat lines with two resistance genes on same chromosomes, crosses were made with wheat lines carrying linked resistance genes. Progeny lines with potentially pyramided resistance genes were selected through screening 165 to 726 F2 plants and F2:3 lines in each bi-parental cross for resistance to stripe rust, and the selected lines were further screened using molecular markers flanking each gene. F6 lines advanced through single seed descent were developed and evaluated in fields in consecutive 4-5 years for confirming resistance and further selected based on desirable plant types. A total of 14 new wheat germplasm lines were developed, including 2 winter and 12 spring wheat lines, each carrying two linked resistance genes. The pyramid genes and their genetic distances (cM) in the spring lines are *Yr5/Yr53* (35.6) on chromosomal arm 2BL; *Yr50+Yr62* (27.1) on 4BL; and *Yr52+Yr59* (5.4),
Yr59+YrPl182103 (5.8), Yr59+YrZh84 (6.0), YrZh84+YrPl182103 (6.4),
Yr39+YrPl182103 (9.6), Yr67+YrPl182103 (7.5), Yr52+YrZh84 (12.2), Yr39+Yr52
(31.2), Yr39+Yr59 (41.1), and Yr52+YrPl182103 (6.1) on chromosome 7BL. The two
winter lines have resistance genes YrZh84+YrPl182103 and Yr50+Yr62. These lines
are useful for facilitating incorporation of pyramided resistance genes in linkage into
wheat cultivars.

**Stability and fitness advantages of metalaxyl-resistant isolates of Pythium ultimum.** M. Wang (1), and W. Chen (2). (1) Washington State University, Pullman,
WA, USA; (2) USDA ARS, Washington State University, Pullman, WA, USA.

Pythium damping-off of chickpea is an important disease, and has been
traditionally managed through seed treatment using the fungicide metalaxyl. However,
Pythium populations in the US Pacific Northwest have developed resistance to this
fungicide and metalaxyl is no longer effective. Conventional approach to managing
fungicide resistance is to stop using the fungicide to let the resistant population
disappear due to resistance-associated fitness cost. To evaluate this approach for
managing the metalaxyl-resistant Pythium, we investigated the stability and saprophytic
fitness of metalaxyl-resistant Pythium isolates. The stability of the metalaxyl-resistance
trait was studied over 10 generations, and the relative competitiveness of the metalaxyl-
resistant isolates was compared with that of metalaxyl-sensitive isolates for growth rate.
Results showed that metalaxyl-resistant isolates consistently grew faster in terms of
colony diameter (4.9 cm/day) and mycelia dry weight (24 mg/day) than metalaxyl-
sensitive isolates (3.6 cm and 19 mg/day, respectively). The metalaxyl-resistant isolates
remained resistant after 10 generations of sub-culturing in the absence of metalaxyl, as
indicated by ED50 values. Because of the fast growth rate and stable resistance trait of
the resistant isolates, simply stopping using metalaxyl is not a viable solution. More
active management approaches such as using alternative fungicides are required to
manage the metalaxyl-resistant Pythium.

**Clonality within disease foci and field populations of Sclerotinia sclerotiorum causing basal stalk rot in sunflower seed crops in central Washington.** J. Weber
(1), T. Chen (2), W. Chen (2), and L. du Toit (1). (1) Washington State University Mount
Vernon NWREC, Mount Vernon, WA, USA; (2) USDA ARS, Grain Legume Genetics
and Physiology Research Unit, Pullman, WA, USA.

Sunflower seed production in the Columbia Basin of central Washington has
grown from 20 ha in 2008 to >2,000 ha in 2015. White mold, caused by Sclerotinia
sclerotiorum, is the main disease affecting this crop. Basal stalk rots are caused by
direct infection from soilborne sclerotia, whereas mid-stalk and head rots are caused by
ascospores. To assess the genetic diversity and population structure of S. sclerotiorum
in sunflower seed crops, the fungus was isolated from basal stalk infections of
sequentially infected plants (disease foci) in a field near Ephrata, WA (92 isolates from
26 foci) and a field near Odessa, WA (73 isolates from 26 foci). Genotyping the isolates
with 8 simple sequence repeat markers revealed 28 and 19 multilocus haplotypes in the
Ephrata (EP) and Odessa (OD) populations, respectively, with 7 common to both fields.
A chi-square test of the observed frequency of isolate pairs from adjacent plants with
the same haplotype compared to the expected frequency at random revealed that the
spatial aggregation of haplotypes within disease foci was highly significant ($P = 10^{-34}$ and $10^{-32}$ for the EP and OD populations, respectively). Both populations were highly clonal, and analysis of molecular variance indicated no genetic differentiation between the populations ($P = 0.98$). The results suggest infection of adjacent plants within white mold foci in sunflower seed crops is likely from sclerotia of the same isolate or mycelium from the same sclerotium.

Evidence that specific rotation crops infected by *Verticillium dahliae* in Washington State do not serve as reservoirs for the mating type, MAT1-1. D. WHEELER (1), and D. Johnson (1). (1) Washington State University, Pullman, WA, USA.

*Verticillium dahliae* causes yield losses of a wide range of economically valuable wild and domesticated plants worldwide. The clonal reproductive model used to explain *V. dahliae* population structure has been challenged by evidence of recombination; however, both mating types requisite for typical recombination are not detected in the 1:1 ratio expected for a sexually reproducing organism. We tested the hypothesis that asymptomatic rotation crops serve as reservoirs for the underrepresented mating type, MAT1-1. Fourteen rotation crops of potato and mint were collected from 21 fields in the Columbia Basin of Washington State. *Verticillium* spp. were detected from rotation crop stems sampled from 8 of 21 (38%) fields and the incidence of infected stems ranged from 1 to 63%. Recovered isolates were identified as *V. dahliae* and *V. isaacii* with morphological criteria and, for 2 isolates from each field, multilocus sequence typing using actin (*ACT*), elongation factor 1 alpha (*EF1-a*), glyceraldehyde-3-phosphate dehydrogenase (*GPD*), and tryptophan synthase (*TS*) sequence data. Consistent with the predominantly clonal reproductive model proposed for *V. dahliae*, the mating types of all isolates from rotation crops were MAT1-2. The absence of MAT1-1 in rotation crops together with accumulating evidence of recombination support the presence of nonmeiotic forms of recombination or other, not yet sampled, hosts in ancestral and or contemporaneous cryptic sexual recombination.

Adaptation to qualitative and quantitative host resistance by *Podosphaera macularis* in the Pacific Northwest. S. WOLFENBARGER (1), G. Grove (2), M. Nelson (2), C. Ocamb (1), C. Probst (2), M. Twomey (1), and D. Gent (3). (1) Oregon State University, Department of Botany and Plant Pathology, Corvallis, OR, USA; (2) Washington State University, Irrigated Agriculture Research and Extension Center, Prosser, WA, USA; (3) US Department of Agriculture-Agricultural Research Service, Forage Seed and Cereal Research Unit, Corvallis, OR, USA.

Hop powdery mildew (caused by *Podosphaera macularis*) is an important disease of hop. Disease management is achieved with a variety of tactics, with host resistance being a favored method. However, durable resistance is challenging to identify because of the continuous adaptation of *P. macularis*. In 2012, powdery mildew developed in fields containing cultivars with the resistance factor R6 in Washington and Idaho. By 2013, R6-virulent strains of the fungus were reported in Oregon, becoming widespread in 2014. Concurrently, reports of powdery mildew on the cultivar Cascade, which is believed to possess quantitative resistance, have increased since 2012. Both
R6-virulent and Cascade-derived strains of \textit{P. macularis} are positive for the mating type \textit{MAT1-1} and are able to overcome resistance genes \textit{Rb}, \textit{R3}, \textit{R5}. R6-virulent strains also infect cultivars reported to possess \textit{R4} and \textit{R6}, whereas virulence on \textit{R4} and \textit{R6} is rare in Cascade adapted strains. However, the latter demonstrate specialization to Cascade unlike R6-virulent strains. Surveys of commercial hop yards during 2012 to 2015 document that powdery mildew is now prevalent on cultivars possessing \textit{R6} resistance through-out the Pacific Northwest while powdery mildew on Cascade appears to be limited to Washington and Idaho at present. While resistance genes \textit{R1} and \textit{R2} remain effective in the Pacific Northwest, new sources of resistance and strategies for deployment are needed for the future.

\textbf{Molecular mapping of stripe rust resistance genes in spring wheat line W18.} C. XIANG (1), M. Wang (1), T. Wang (2), D. See (3), and X. Chen (3). (1) Department of Plant Pathology, Washington State University, Pullman, WA, USA; (2) Chengdu Institute of Biology, Chinese Academy of Sciences, Chengdu, China; (3) USDA-ARS Wheat Health, Genetics, and Quality Research Unit and Department of Plant Pathology, Washington State University, Pullman, WA, USA.

Stripe rust, caused by \textit{Puccinia striiformis} f. sp. \textit{tritici}, is one of the most important diseases of wheat worldwide, and is best controlled by growing resistant cultivars. Spring wheat line W18 is highly resistant to stripe rust. To map the resistance gene(s), W18 was crossed with Chuanyu 12, and 189 \textit{F\textsubscript{10}} recombinant inbred lines (RILs) were developed. The tests of the RILs with races PSTv-37 and PSTv-40 at seedling stage under controlled greenhouse conditions indicated that W18 had two different genes for resistance to these races, respectively. The parents and RILs were also phenotyped in randomized field experiments at Chengdu, China from 2011 to 2013, and at Pullman and Mount Vernon, Washington in 2014. The RILs were genotyped with 700 simple sequence repeat (SSR) markers. The phenotype and genotype data mapped two major genes for stripe rust resistance, one in chromosome 1B near the centromere and the other in the long arm of chromosome 5D. The 1B gene was detected with race PSTv-37 in the greenhouse seedling test and the field tests in Chengdu and Mount Vernon, whereas the 5D gene was detected with race PSTv-40 in the greenhouse seedling test and in the fields at Pullman and Mount Vernon. The 1B gene is likely \textit{Yr26}, whereas the 5D gene is new because its chromosomal location is different from previously reported \textit{Yr} genes. The genes and closely linked markers identified in this study are useful for developing wheat cultivars with stripe rust resistance.

\textbf{Suppressor of RNA silencing from wheat stem rust fungus, \textit{Puccinia graminis}.} C. YIN (1), S. Ramachandran (1), Y. Zhai (1), C. Bu (2), H. Pappu (1), and S. Hulbert (1). (1) Plant Pathology, WSU, Pullman, WA, USA; (2) College of Biological Science and Engineering, Beijing University of Agriculture, Beijing, China.

Plants use RNA silencing to defend against viral infections. To successfully infect plants, viruses encode proteins, called silencing suppressors (VSRs), which suppress RNA silencing as counter-defense strategies. Like viruses, bacteria and oomycete plant pathogens also have evolved to suppress RNA silencing to cause disease. Here, we report that one gene encoded effector-like protein from wheat pathogen \textit{Puccinia graminis} suppresses RNA silencing in plants. This gene was induced in infected wheat
leaves and includes two alleles which display 5 bp difference. The proteins encoded by
the two alleles were found to partially suppress cell death caused by Pto (Y207D) when
inoculated 24 hours prior to the Agrobacterium strain carrying Pto (Y207D).
Furthermore, transient expression of this gene in Nicotiana benthamiana enhances
plant susceptibility to a virus, Impatiens Necrotic Spot Virus (INSV). Our results suggest
that pathogens use RNA silencing suppression as a universal strategy to cause
disease.

Towards construction of genetic linkages for mapping virulence genes in
Puccinia striiformis f. sp. tritici, the wheat stripe rust pathogen. C. YUAN (1), M.
Wang (1), D. See (2), and X. Chen (2). (1) Department of Plant Pathology, Washington
State University, Pullman, WA, USA; (2) USDA-ARS Wheat Health, Genetics, and
Quality Research Unit and Department of Plant Pathology, Washington State University,
Pullman, WA, USA.

Puccinia striiformis f. sp. tritici, the wheat stripe rust pathogen, is a dikaryotic,
biotrophic, and macrocyclic fungus. To determine the genetics of virulence and
construct linkages for mapping and cloning virulence genes, we developed a
segregating population of 120 isolates by selfing isolate 08-220 on barberry under
controlled greenhouse conditions. The progeny isolates were phenotyped on a set of 32
wheat Yr single-gene lines and genotyped with 30 simple sequence repeat (SSR) and
23 single nucleotide polymorphism (SNP) markers. The progeny isolates were all
avirulent to resistance genes Yr5, Yr10, Yr15, Yr24, YrSP, YrTr1, YrCV, Yr45, Yr53,
and Yr32; and virulent to Yr29 and Yr41, indicating that these avirulence or virulence
loci were homozygous. Segregation of the 1:3 (avirulence : virulence) ratio was
observed for the virulence loci corresponding to YrAvS, YrA, Yr1, Yr6, Yr7, Yr8, Yr9,
Yr25, Yr26, Yr27, Yr28, and Yr35; the 1:15 ratio for Yr21, YrTye, Yr44, Yr43, and Yr31;
the 7:9 ratio for Yr17 and YrExp2; and the 9:7 ratio for Yr2. The ratios indicated that
virulence can be controlled by one or two genes with different modes of inheritance and
interactions. Linkages were found among virulence loci corresponding to YrA, Yr1, Yr6,
Yr7, Yr8, and Yr9 and marker SNP340. More markers are being identified for
constructing more linkage maps. The results are useful for studying the host-pathogen
interaction and improving control strategies using host resistance.

Presence of Citrus psorosis virus with watermelon ‘moon rings’ in Washington
State. Y. ZHAI (1), D. Villamor (2), C. Miles (3), K. Eastwell (2), and H. Pappu (1). (1)
Washington State University, Pullman, WA, USA; (2) Irrigated Agriculture Research &
Extension Center (IAREC), Prosser, WA, USA; (3) Washington State University Mt
Vernon Research & Ext, Mount Vernon, WA, USA.

Watermelon fruit with concentric ringspots, referred to as ‘moon rings’, have been
observed in many parts of the world. While suspected of viral etiology, especially of a
tospovirus or a potyvirus, none of them could be detected. In western Washington
State, watermelon fruit with ring spots on the rind have been observed for at least 15
years. Symptoms appear late in the season as fruit start maturing. Recent testing for
several tospoviruses and potyviruses by serological methods did not provide evidence
of the presence of any of the tested viruses. We used next generation sequencing of the
total RNA extracted from the symptomatic portions of the rind followed by de novo
assembly of the resulting sequences. BLASTX analysis to the non-redundant protein sequence NCBI database showed a major class of contigs representing the genome of Citrus psorosis virus (CPsV, genus Ophiovirus, family Ophioviridae). Several minor contigs had sequences representing a wide range of other virus families. CPsV is an important pathogen of citrus worldwide. The host range of CPsV is relatively narrow and is believed to be limited to Citrus species and their hybrids such as grapefruit, mandarin, orange and tangerine, lemon, pomelo and lime. The role of CPsV in the induction of ‘moon rings’ symptoms in watermelon remains to be investigated. Further research is underway to test additional samples and perform transmission experiments.
Dr. James Adaskaveg – University of California – Riverside

James E. Adaskaveg received his B.S. degree in agronomy in 1982 at the University of Connecticut, Storrs, and his M.S. and Ph.D. degrees in plant pathology in 1984 and 1986, respectively, at the University of Arizona, Tucson. He was a post-doctorate researcher and subsequently a research plant pathologist/lecturer in the Department of Plant Pathology at the University of California, Davis, before he joined the faculty of the Department of Plant Pathology at the University of California, Riverside, in 1995. There, he is currently a professor of plant pathology with statewide responsibilities in tree fruit and nut pathology. With his enthusiasm and success in solving disease problems, he is highly respected by the California agricultural community, and he is recognized nationally and internationally for his outstanding contributions on the biology, epidemiology, and management of tree pathogens, including postharvest fruit decays. He has been invited to numerous national and international meetings and workshops where he enthusiastically shares his knowledge. He was the recipient of the Almond Research Appreciation Award in 1997 for his research on almond anthracnose; the Cherry Man of the Year award of the sweet cherry industry of California in 2003 for his pre- and postharvest research on brown rot; the Albert G. Salter Memorial award in 2006 for his research on Septoria spot and postharvest decays of citrus; the APS Lee M. Hutchins Award in 2008; the Congreso Argentino de Citriculture Appreciation Award in 2010 for international contributions in citriculture; and he became APS Fellow in 2014. Since 2004, Adaskaveg is a scientific advisor for USDA-APHIS and has been involved in trade negotiations on diseases of citrus, pomegranate, pome fruit, stone fruit, and strawberry where his research and negotiation skills helped to overcome trade barriers and kept international trade markets open. Adaskaveg is an outstanding scientist and his diverse program effectively combines applied and basic research on fungal and bacterial pre- and postharvest diseases in tree fruit and nut production. He has successfully studied peach rust, demonstrated the presence of visible quiescent infections by *Monilinia fructicola* and *Botrytis cinerea* in sweet cherry fruit, identified and characterized the causal pathogen of almond anthracnose as *Colletotrichum acutatum* and designed effective management strategies, and he worked on numerous other important diseases of fruit and nut crops. Throughout his career, Adaskaveg has been pivotal in the development and registration of many new pre- and postharvest fungicide treatments for numerous crops in collaboration with regulatory agencies, the IR-4 program, the chemical industries, as well as the agricultural community. More recently, Adaskaveg has been instrumentally involved in the registration of the highly effective postharvest biofungicides potassium phosphite (for management of citrus brown rot) and pimaricin (for management of decays of citrus, stone, and pome fruit crops). His program also includes various aspects of bacterial diseases. He has been very influential in the first registration in over 50 years of the agricultural antibiotic kasugamycin that will be available for pome fruit, walnuts, cherries, and other crops where currently few treatment options are offered. He characterized the mechanism of streptomycin resistance in California isolates of *Erwinia amylovora* and found it to be
distinct from that of strains from other pome fruit growing areas. For olives, he helped to register a new equipment sanitation treatment that will reduce the spread of olive knot (caused by Pseudomonas savastanoi pv. savastanoi) in orchards. Over the years, Adaskaveg’s research program adapted rapidly to the changing needs of the fruit and nut industries. New or recurring diseases, are studied promptly and Adaskaveg is known for communicating his results effectively to the industry. In addition to his effort on registration of new fungicides, Adaskaveg also promotes the responsible use of these compounds to prevent overuse and to minimize resistance development. Adaskaveg is also an effective, popular, and dedicated instructor to his undergraduate and graduate students where he teaches general mycology and selected fields in plant pathology (e.g., epidemiology, postharvest disease management, and disease diagnosis). In his service to APS, he was an Associate Editor of Phytopathology from 2005 to 2007. He was the APS Pacific Division President (2002 to 2003), Pacific Division Councilor (2009 to 2010), the first Divisional Forum Representative (2010 to 2012, chair in 2012), he served on the APS Financial Advisory Committee, and he has organized or co-organized three well-attended field trips on California fruit diseases during APS annual or divisional meetings. In summary, Adaskaveg’s contributions to agricultural research and APS are extraordinary and he well deserves recognition in a Pacific Division Lifetime Achievement award.

**Dr. Debra Inglis – Washington State University**

Dr. Inglis’ independent academic career started as a Postdoctoral Research Associate at the University of Wisconsin, followed by an Adjunct Assistant Professor position in plant pathology at Montana State University. After four years working part-time in plant pathology while bringing two children into the world, Dr. Inglis returned to full-time academia in 1993 as an Assistant Plant Pathologist at Washington State University, located at the WSU Mount Vernon Research & Extension Unit (REU). She received tenure in 1999 after establishing a successful research and extension program on diseases of fresh market and processing vegetables. The extraordinary depth of Dr. Inglis’ professional and academic leadership skills came to light when she was invited in 2004 by Dr. James Cook, Dean of the WSU College of Agricultural, Human, & Natural Resource Sciences (CAHNRS), to serve as Interim Director of the WSU Mount Vernon REU and Assistant Dean for WSU CAHNRS. During the five years in this position, Dr. Inglis led the WSU Mount Vernon REU through a major renovation that upgraded the facility to a Research & Extension Center. She spearheaded development of a comprehensive strategic plan, provided on-site coordination for the $8 million Agricultural Research & Technology Building (ARTB), and implemented a vision to convert the 59 year-old unit into a modern, full-service research and extension center. Of the $8 million required for the project, Dr. Inglis helped raise >$2 million in public appropriations and gifts. Under her leadership, the number of faculty located at the NWREC doubled to eight by 2008, and now has 10 faculty and has outgrown the facilities. The major growth coordinated by Dr. Inglis served as a model for revitalizing agricultural R&E Centers throughout the U.S., particularly during the economic recession. For this effort, Dr. Inglis received the WSU CAHNRS Achievement Award for
“Extraordinary Initiative in the Development of the ARTB at the WSU Mount Vernon NWREC”, as well as the Distinguished Service Award from the Western Washington Horticultural Association in 2006; the WSU CAHNRS’ National Women’s History Month Award for Professional and Academic Leadership in 2009; and was inducted into the WSU CAHNRS’ Hall of Honored Alumni and Friends in 2009. Dr. Inglis has engaged extensively in academic service and leadership as a plant pathologist. She has served on multiple federal and regional USDA grant review panels, as Associate Editor (2002-04) and Senior Editor (2008-10) of Plant Disease, as ad hoc reviewer for many other journals, and as President of the APS Pacific Division (2013). Dr. Inglis has chaired or served as a member on numerous WSU search committees. She has published >65 plant pathology research manuscripts in peer-reviewed journals, >20 refereed extension bulletins or manuals, 6 book chapters, >50 technical peer reviewed articles, 20 conference proceedings, and ~90 conference abstracts. Dr. Inglis has given 40 invited presentations at regional, national, and international meetings, literally hundreds of research-based extension and outreach presentations to the regional and national vegetable community, and successfully procured millions of dollars in funding for research and extension activities over 23 years since starting a tenure track position at WSU. Her exemplary leadership as PI of a large USDA Specialty Crop Block Grant resulted in the team receiving the 2013 NIFA Partnership Award for Innovative Programs and Projects. Dr. Inglis has chaired 8 graduate students’ committees, served as member of an additional 16 graduate students’ committees, and mentored 4 postdoctoral research associates. She started the WSU Vegetable Pathology Team in 2000, which expanded into the Pacific Northwest Vegetable Extension Group with ~25 participants in multiple disciplines from Idaho, Oregon, and Washington. The team received the WSU CAHNRS Interdisciplinary Team Award in 2011. In 2014, Dr. Inglis received the WSU Sahlin Faculty Excellent Award for Leadership. An exemplary characteristic of Dr. Inglis is her sense of ‘ownership’ for all, i.e., that it is a privilege and responsibility to contribute to the success of individual scientists and programs as well as the greater scientific body.

Biography of Early Career Award Recipient

Dr. Jeremiah Dung – Oregon State University

Dr. Dung, a native of Spokane, WA, received his Ph.D. in plant pathology from Washington State University in 2012 followed by a post doc at Oregon State University in Hermiston, OR. He is currently an assistant professor in the Department of Botany and Plant Pathology at Oregon State University and is located at the Central Oregon Agricultural Research Center, Madras, OR. Research contributions include the characterization of Verticillium wilt epidemiology in potato and mint and the development of integrated pest management approaches for ergot in grass seed. Dr. Dung is currently developing methods to detect, quantify, and identify Verticillium dahliae in soil and collaborating with scientists to understand the molecular genetic basis of mint susceptibility to Verticillium wilt. Dr. Dung has been an exceptionally
productive young scientist with numerous journal publications and technical reports. Dr. Dung has an extension appointment and had produced several extension publications and has extended his research findings to growers through extension oral presentations.

Biographies of Graduate Student Travel Award Recipients

Daniel Farber – Oregon State University

Since I declared politics as my major at University of California at Santa Cruz I have been interested in reducing the negative impacts of human activities on our environment. This has involved several shifts away from the social side towards the sciences, beginning with switching majors to environmental studies, with a focus on sustainable agriculture. For my senior internship, I conducted an experiment comparing severities of soil-borne fungal disease given differing soil treatments on a nursery hardwood used in reforestation of agricultural riparian borders. This foray into conducting field research led me to a post-baccalaureate degree in environmental sciences with a focus on ecological restoration at Humboldt State University and an internship monitoring salmonid habitat with the Bureau of Land Management, as a precursor to attending Oregon State University for what has become my Ph.D. in botany and plant pathology. My work has been on the spread of wheat stripe rust, focusing on the local dispersal of its causal agent, *Puccinia striiformis* f.sp. *tritici* (PST), then on the relative susceptibility of wheat of differing ages and leaf positions to infection by PST, and now to using the parameters found in my field work to model wheat stripe rust spread spatiotemporally across a range of scales. I am now writing a post-doctoral fellowship proposal to apply my epidemiological skills to the spread of botrytis in raspberry.

Zachary Frederick – Washington State University

Zachary Frederick was born and raised in the small town of Trumansburg, New York, located in the winemaking region known as the Finger Lakes in central New York. Zack’s first laboratory experience was studying mycorrhizae in the lab of Dr. Maria Harrison at the Boyce Thompson Institute as a junior in high school. This experience inspired his choice to pursue his bachelor’s in Agricultural Biotechnology at the State University of New York at Cobleskill, which he received in 2011. Zack pursued his masters in Plant Pathology at Cornell University out of a desire to continue his scientific endeavors, but spend more time interfacing with growers to exchange information to improve disease management strategies. Zack completed his masters in 2013, after which he was accepted into the plant pathology program at Washington State University. He is here to present results from projects that ultimately aim to improve Verticillium wilt disease management strategies through input and cooperation with potato growers. Zack anticipates graduating in May 2017, and is now searching for a
place where his interests in an affable commerce of information between growers, universities, government, and industry aligns with the mission of a university or company.

Leslie Holland – University of California-Davis

I am a first-year PhD student at the University of California, Davis in the department of Plant Pathology. My research addresses the biology, population genetics and management of almond canker diseases. In 2013, I completed my BS degree with honors at New Mexico State University where I majored in Biology and served as a scholar in the Minority Access to Research Careers (MARC) program. I worked in several laboratories on campus and participated in a summer research internship at the University of Wisconsin, Madison. Projects I was involved in included optimizing a restriction site-associated DNA protocol, studying the interaction between noxious weed species and root-knot nematodes, and investigating the physiological impacts of reduced water treatments on cranberry production. I completed my MS degree in Plant Pathology at Washington State University (WSU) in 2015. My thesis research was centered on surveying Washington state vineyards for grapevine trunk diseases and characterizing the pathogens associated with these diseases. During my time at WSU I served as President of the graduate student association, attended regional and national research conferences, and was awarded scholarships from the University and wine grape industry in support of my research. During my first year at UC Davis, I have received the Eugene Cota-Robles Fellowship, Ogawa Research Endowment, and Miller Plant Science Scholarship. I am an active member of the UC Davis Plant Pathology student association where I have volunteered in annual events including the Plant Disease Clinic and Picnic Day. In addition to my research, I assist our lab group in plant disease diagnostic duties including field visits to collect samples, processing of these samples in the laboratory and providing recommendations to growers. These experiences are helping me become a more well-rounded plant pathologist.

Lauri Lutes – Oregon State University

Lauri Lutes completed her undergraduate degree in Biology in her home state at Indiana University South Bend, before working for the plant diagnostics company, Agdia, Inc. Through her positions at Agdia, Mrs. Lutes became involved with APS, and is currently serving as a member of the Diseases of Ornamental Plants committee. Ultimately, her interest in plant pathology - piqued by her involvement in APS and work at Agdia - led her to pursue a Master's degree with Dr. Jay Pscheidt at Oregon State University where she is currently surveying Oregon for the presence of sweet cherry viruses. Mrs. Lutes was awarded the Oregon Lottery Graduate Scholarship and named OSU's College of Agricultural Sciences Savery Outstanding Master's Student in the spring of 2016. Mrs. Lutes enjoys exploring the Oregon outdoors with her husband, five-year-old daughter, and puppy, Mimi.
Lindani Moyo – Washington State University

Lindani Moyo joined Dr. Pappu’s lab at the Plant Pathology Department at Washington State University in the Fall semester of 2015 as a Ph.D. student. The focus of his research is to investigate the plant-virus interactions at the molecular level using Potato virus Y- potato pathosystem. Specifically, he is investigating the host response to PYV infection by determining the virus-specific small interfering RNAs of various PVY strains and use the information to mine the potato transcriptome to better understand the effect of virus infection on host gene expression. Findings could potentially lead to novel virus control strategies. Lindani comes from Bulawayo, Zimbabwe and was born in Gwanda, Zimbabwe. He is married with a son and a daughter. Lindani has a diverse background in biological sciences. He received a B.Sc. (Hons) Degree in Applied Biology and Biochemistry at the National University of Science and Technology in Bulawayo in 2010. After graduating he did part-time jobs as a high school teacher and medical technician and then becoming a Research Fellow at the National University of Science and Technology in August 2011. As a Research Fellow he conducted research on microbes of concern to food safety and public health and concurrently pursued a M.S. in Applied Microbiology and Biotechnology within the same institution. He developed interest in molecular plant science upon taking a class on plant biotechnology and was fascinated by use of virus induced gene silencing techniques in functional genomics. In addition, Lindani has supervised undergraduate student projects on microbiology and taught undergraduate classes on Environmental Biotechnology pertaining to biosafety issues of GMO crops. After his Ph.D., Lindani will resume his Research Fellowship where he is expected to start projects from the skills gained; utilizing university research board funds. His long term goal is to research on the molecular characterization of plant virus isolates in Zimbabwe and to elucidate the molecular mechanism of viruses infecting indigenous crops in Zimbabwe and other African countries.

Cristian Olaya – Washington State University

Cristian Olaya joined Dr. Pappu’s lab in the Plant Pathology Department at Washington State University in the fall semester of 2014 as a Ph.D. student. The focus of his research is to investigate the genomics and proteomics of tospovirus infections of horticultural crops. Specifically, he is working on determining the 3D structures of selected tospoviral proteins using state of the art software to better understand the potential role of various motifs and study structure-function relationships. Another objective of his PhD research is to understand, at the molecular level, host plant’s response to infection by tospoviruses. Using next generation sequencing technologies, he is investigating host’s defense response to virus infection. Findings could potentially lead to novel virus control strategies. Cristian was born in Manizales, Colombia where he received his B.Sc. in Agricultural Engineering from the University of Caldas where he conducted research on the cytogenetics of Andean passion flower to determine the possibility of cross-compatibility with related species. Then, he moved to the city of Cali, Colombia to work in the virology research unit of the International Center for Tropical Agriculture (CIAT). At CIAT, he worked on the diagnosis and characterization of viruses affecting different crops (Cassava, Bean, Rice, Capsicum, Tomato, Tropical fruits and
Oil Palm) using a wide range of techniques including electron microscopy, biological and molecular tools. In 2014, he obtained his M.Sc. in Agricultural Sciences with an emphasis on Crop Protection from the National University of Colombia campus in Palmira. His M.Sc. dissertation research was on the biological and genomic characterization of a reovirus that infects cassava. Cristian’s long-term goal is to develop a research program focused on tropical plant virology at either a university or an international research center. He is interested in mentoring and training undergraduates and graduate students in the field of plant pathology engage stakeholders and address their plant protection needs.

**Sowmya Ramachandran – Washington State University**

I am currently a PhD student in the Department of Plant Pathology at Washington State University working under the mentorship of Dr. Scot Hulbert. Here, I work on host-pathogen interactions at the protein and RNA level, involving wheat rust pathogens and cereal crops. My research aims at identifying effector proteins secreted by the fungus for inciting disease on wheat. In addition, I am looking at the role of wheat miRNAs in the *Puccinia striiformis* – wheat patho-system, in an attempt to understand the small RNA-mediated defense responses to rust infections. Before joining WSU, I received my Master’s in Microbiology, from University of Delhi, India, where I studied fungal lipases and their various industrial applications. After receiving a National award for research and teaching, I gained experience in research at the Ambedkar Centre for Biomedical Research, India, as also in teaching microbiology as a guest faculty at University of Delhi. Besides research, I enjoy hiking and Indian classical dance. In the future, I hope to apply my skills in plant pathology to address problems related to global food security.

**Hannah Rivedal – Oregon State University**

Hannah Rivedal received her B.S. in Plant Pathology from the University of Wisconsin-Madison in 2013. During her undergraduate career, she explored research opportunities in plant pathology under the guidance of Drs. Amy Charkwoski and Ruth Genger. For her senior honors capstone project at UWM, Hannah studied potato tolerance to *Verticillium dahliae* in an organic system. Before pursuing a graduate degree, she worked as a field manager for Dr. Erin Silva in the agronomy department of UW-Madison. With Dr. Silva and the NOVIC research group, Hannah focused on organic cultivar selection for performance in northern climates as well as integrated pest management in organic systems. In June of 2014, Hannah moved to Oregon State University to begin pursuing a Ph.D. in the department of Botany and Plant Pathology under the guidance of Drs. Kenneth Johnson and Alexandra Stone. Her Ph.D. work is focused on diagnosing a soil borne fungal disease complex of winter squash. Her project has complementary aspects of classic applied pathology techniques with molecular identification to ascertain a valid diagnosis of the fungi involved in this disease complex. In addition to diagnosis, the ultimate goal is to provide control measures for growers in both conventional and organic squash production. Hannah has given three Extension talks about her work to the local squash grower community in the Willamette Valley. She attended the 2015 Fusarium Laboratory Workshop under the
instruction of Dr. John Leslie at Kansas State University and was the recipient of the Martin Stoner Memorial scholarship which allowed her to travel to the Conference on Soilborne Plant Pathogens and present the molecular aspect of her Ph.D. work. For the last two years she has been a teaching assistant for the Introductory Plant Pathology course at Oregon State University. She is the president of the Graduate Student Association of her department and volunteers regularly with department and community outreach events to help recruit young scientists to the field of Plant Pathology. In the future, she hopes to pursue a career doing participatory and Extension research with growers to manage yield limiting plant diseases.

Xuefei Wang – Washington State University

Xuefei Wang received her BS and MS degree from Huazhong Agricultural University, China. During her time as an undergraduate, she worked on a student innovation project as a group leader from 2008 to 2010. Her undergraduate research involved purification and chemical study of antibacterial agent, and metabolic flux analysis. She conducted her MS research under the guidance of Dr. Jibin Zhang on mechanism study of plant growth-stimulating and anti-fungi rhizobacteria in polluted soils. During her masters, she was co-advised by Dr. David Weller and worked in Dr. David Weller’s and Dr. Linda Thomashow’s lab (USDA-ARS) as a visiting scholar for six months. Xuefei Wang is currently a PhD student in department of plant pathology at Washington State University, Pullman, WA. In her PhD studies, she worked on the projects supported by Washington State Wine Commission and China Scholarship Council. Her research has focused on profiling naturally-occurring yeasts in regional vineyards and during fermentation, and their application to control Botrytis bunch rot. The goal of her PhD work will be to provide information about the diverse mycoflora, and to aid the grape growers and wine producers in their quest to produce exceptionally and consistently high quality wines. Upon completing her PhD, Xuefei aspires to seek a faculty position with a joint appointment in research and wine industry on fungal disease management and wine quality improvement.
Thank you for attending and have a safe journey home!!