



**Joint Meeting:
20th Biennial
International Plant Resistance
To Insects Workshop
&
Annual Session of
Western Extension/Education Research
Activity-066 (WERA-066): Integrated
Management of Russian Wheat Aphid
and other Cereal Arthropod Pests
April 1 - 4, 2012
Minneapolis, Minnesota USA**

Overview, IPRI 2012 & WERA-066, University Hotel, Minneapolis
Workshop Registration, Hotel Foyer (2nd floor)

Sunday, April 1, University Ballroom

4:00-7:00 p.m. Registration

5:00-6:00 p.m. IPRI Steering Committee Meeting

7:00-10:00 p.m. Welcome Mixer

Monday, April 2, University Ballroom

7:00-8:00 a.m. Poster set-up, University Ballroom foyer

7:30 -9:30 a.m. Registration, Hotel Foyer (2nd floor)

8:00 a.m.-5:00 p.m. Poster viewing, University Ballroom foyer

8:00-8:15 a.m. Welcome

8:15 a.m.–12:00 p.m. Symposium: New Tools for Understanding Plant Resistance and Pest Biology

12:00-1:30 p.m. Lunch break

1:30–4:17 p.m. Student Oral Presentation Competition

4:17-5:15 p.m. Ad hoc breakout sessions

6:00-6:30 p.m. IPRI Steering Committee Meeting

6:30-9:00 p.m. IPRI Banquet, Awards and Business Meeting

Tuesday, April 3, University Ballroom

7:00 a.m.-5:00 p.m. Poster viewing

7:30 -9:30 a.m. Registration, Hotel Foyer (2nd floor)

8:00 a.m.-12:15 p.m. Symposium: Creating a Dialog about Plant Resistance: Academia, Government and Industry

12:15-1:45 p.m. Lunch break

1:45-4:10 p.m. Submitted oral presentations

4:10-5:15 p.m. Ad hoc breakout sessions

Wednesday, April 4, University Ballroom

7:00 a.m.-12:00 p.m. Poster viewing

8:15-11:15 a.m. Symposium: International Perspectives on Plant Resistance to Cereal-Insect Pests

11:15 a.m.-12:00 p.m. IPRI business meeting/concluding remarks/adjourn 2012 IPRI Workshop

12:00–1:30 p.m. Lunch break; Poster removal

1:30–3:00 p.m. WERA-066 meeting

IPRI Lifetime Achievement Award

Dr. **James A. Webster** is receiving the IPRI Lifetime Achievement Award based on his extensive research contributions to and leadership in insect plant resistance for over 30 years. Jim began his productive career after obtaining an M.S. degree from the University of Kentucky and a Ph.D. degree at Kansas State University. His master's thesis involved research on resistance to green peach aphid in tobacco, and his doctoral dissertation research focused on resistance to potato leafhopper in alfalfa. Jim conducted his dissertation research under the tutelage of R.H. Painter and E.L. Sorensen.



Jim's 32-year professional career was spent with the USDA Agricultural Research Service, first at East Lansing, MI, where he worked on resistance to cereal leaf beetle from 1968-1981, and then at Stillwater, Oklahoma, until the year 2000. His research at Stillwater involved studying resistance first to the greenbug and later to the Russian wheat aphid. Jim also served as Research Leader and Laboratory Director at the ARS-Stillwater facility from 1993-1999. He also

served on graduate faculties at Michigan State University and Oklahoma State University. After his retirement in 2000, Jim continued as an adjunct professor of entomology at OSU for a few more years until his students and committee assignments were finished.

There are several notable milestones in Dr. Webster's career in plant resistance to insects. He identified, characterized and collaboratively advanced germplasm with resistance to various insect pests. In cooperation with plant breeders, Dr. Webster co-released several insect-resistant germplasm lines for further development by state and private plant breeders. He authored the first U.S. publication on original, Russian wheat aphid plant-resistance research, and Jim was the first to report detection of Russian wheat aphid resistance in triticale and barley, and yellow sugar cane resistance in sorghum.

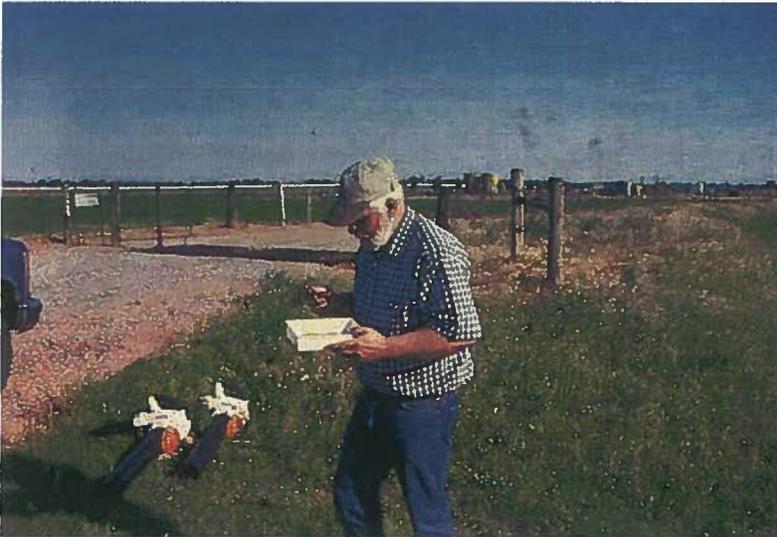
Dr. Webster played an international role in the development of plant resistance to insects, having professional collaborations in various countries including Poland, Mexico, and South Africa, and mentoring students and scientists from several nations. Upon invitation from the Small-Grain Centre in Bethlehem, South Africa, Jim traveled to South Africa in 1990 and exchanged ideas about plant resistance to the Russian wheat aphid during a month long stay. That visit helped to foster a long-term relationship between South African scientists and scientists at the ARS Stillwater lab. Also in 1990, Jim served as an Organizing Committee Member and Co-Editor of the Proceedings, "Aphid-Plant Interactions: Populations to Molecules," an international aphid symposium, and an Oklahoma State University Centennial Event. The symposium drew over 200 participants from 23 nations and 29 U.S. states.

Dr. Webster has been active in IPRI, including participation in 16 workshops, including the 1974 Organizational Workshop in Indianapolis, and since retirement, in the 2004 workshop in Baton Rouge, and 2008 workshop in Ft. Collins. He served on the IPRI Steering Committee from 1988-1994, and was on the Program Committee with John Burd and David Porter for the 1994 meeting in Stillwater.

IPRI Lifetime Achievement Award

The IPRI Lifetime Achievement Award is given to Dr. **John D. Burd** based on his substantial and novel contributions to understanding aphid-host plant interactions and his leadership in plant resistance to insects for over 20 years. John received an M.S. degree in 1984 from Texas Tech University in Range and Wildlife Science, and a Ph.D. degree in entomology from Oklahoma State University in 1991. He was then hired as Research Entomologist at the USDA-ARS Laboratory in Stillwater, Oklahoma, and eventually became Lead Scientist for the Biologically-Based Cereal Aphid Management project there.

Dr. Burd had several outstanding research accomplishments involving plant resistance to insects during his research career. He characterized feeding-induced changes by the Russian wheat aphid in the capacity and efficiency of the primary photochemistry of photosystem II for



resistant and susceptible plants, and identified candidate sites of action involved in the plant-damage response. John determined the effect of feeding by the Russian wheat aphid and by the greenbug on constituent, nonstructural carbohydrate content in wheat and characterized the resultant whole-plant stresses, thereby providing new insight into how aphids exploit their hosts by altering sink-to-source transition and regulating phloem translocation.

Along with collaborators, John redefined the central tenet of the biotype concept for greenbugs, showing that virulence on crop plants does not coincide with greenbug fitness, and the use of plant resistance did not selected for virulent biotypes of greenbug. He characterized the evolutionary status of greenbug host races, demonstrated the importance of non-cultivated hosts for maintaining biotypic diversity, and discovered 16 new biotypes of the greenbug. John mentored and helped train graduate students in plant resistance to insects while serving as an advisor and on graduate committees at the University of Nebraska, Oklahoma State University, University of Wyoming, and Texas A&M University.

Dr. Burd's contributions to the science of plant resistance to insects were truly international in scope. Among his research accomplishments, John co-pioneered the first studies on biotypic variation among a worldwide collection of the Russian wheat aphid, and he also discovered three new Russian wheat aphid biotypes from Texas and Wyoming. He also served in various capacities that promoted interactions internationally among plant resistance scientists and practitioners. John was active in the IPRI Working Group. He served on the IPRI Steering Committee from 2002-2008, and co-organized the 1994 workshop in Stillwater and the 2008 workshop in Fort Collins, Colorado. Dr. Burd served as Vice-Chair of the Program Committee for the International Plant Protection Congress, and on the Organizing Committee of the International Aphid Congress as the North American representative.

Monday, April 2, University Ballroom

7:00-8:00 a.m. Poster set-up, University Ballroom foyer

7:30 a.m.-4:30 p.m. Registration, Hotel Foyer (2nd floor)

8:00 a.m.-5:00 p.m. POSTER VIEWING, University Ballroom foyer

8:00-8:15 a.m. Welcome

8:15 a.m.-12:00 p.m. SYMPOSIUM: NEW TOOLS FOR UNDERSTANDING PLANT RESISTANCE AND PEST BIOLOGY, Moderator: Marion Harris, Department of Entomology, North Dakota State University, Fargo ND, USA.

8:15 a.m. Introduction

8:20 a.m. Protein interaction reporter: "News" on protein topologies in an insect-transmitted plant virus. **Michele Cilia**, USDA-ARS, Cornell University, Ithaca, NY.

8:45 a.m. Using Targeted Mass Spectrometry to Study Virus Transmission by Aphids. **Michael Bereman**, University of Washington.

9:10 a.m. Establishing the root-knot nematode *Meloidogyne hapla* as a tractable genetic/genomic platform to study plant – parasite interactions. **Valerie M Williamson**¹, VP Thomas¹, DM Bird², SL Fudali¹, J Gimeno¹, J Schaff³, EH Scholl², C Opperman², D Nielsen⁴. ¹Dept. of Nematology, University of California, Davis; ²Dept. of Plant Pathology, North Carolina State University; ³Genome Sciences Lab, North Carolina State University; ⁴Bioinformatics Res. Center, NC State Univ.

9:35 a.m. Identification of Hessian fly *Avirulence* genes. **Jeff Stuart**¹, R. Aggarwal¹, T. Benatti¹, C. Zhao¹, L. Navarro¹, M-S. Chen², K. Anderson³, M. O. Harris³, R. Shukle⁴. ¹Department of Entomology, Purdue University, West Lafayette, IN 47907; ²USDA-ARS and Department of Entomology, Kansas State University, Manhattan, KS 66502; ³Department of Entomology, North Dakota State University, Fargo, ND 58105; ⁴USDA-ARS and Department of Entomology, Purdue University, West Lafayette, IN 47907.

10:00-10:20 a.m. Break

10:20 a.m. Genetic mapping of aphid resistance in maize. L Meihls, H Kaur, **Georg Jander**, Boyce Thompson Institute for Plant Research, Ithaca, NY 14853.

10:45 a.m. Virus induced gene silencing reveals putative wheat defense mechanisms against *Diuraphis noxia*. **Nora L Lapitan**, V Valdez, L van Eck, Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO 80523.

11:10 a.m. Integration of DNA Markers with Chromosome Engineering for Efficient Introgression of Resistance Genes from Wild Grasses into Wheat. **Steven Xu**¹, Z Niu¹, DL Kindworth¹, S Chao¹, T Friesen¹, JD Faris¹, Y Jin², X. Cai³, MO Harris³. ¹USDA-ARS, Fargo ND 58108; ²USDA-ARS, Minneapolis MN 55108; ³North Dakota State University, Fargo, ND 58108.

11:35 a.m.-12:00 p.m. Discussion

12:00-1:30 p.m. LUNCH BREAK

1:30–4:12 p.m. STUDENT ORAL PRESENTATION COMPETITION, Moderator: Michael Stout, Louisiana St. Univ., Baton Rouge LA, USA.

1:30 p.m. Introduction

M.S. students

1:35 p.m. Transcriptomic changes in *Diuraphis noxia* when transferred from preference to non-preference hosts. **N Francois V Burger**, A-M Botha, Department of Genetics, Stellenbosch University, Private BagX1, Matieland, 7601, South Africa.

1:47 p.m. Gene expression profile of *Helicoverpa zea* in response to *HzSNPV*. **Jeffrey E Noland**, HC Noland, SM Hum-Musser, RO Musser, Department of Biological Sciences, Western Illinois University, Macomb, IL 61455.

1:59 p.m. The genomic response of *Helicoverpa zea* after feeding on phytohormone treated Tomato Plants. **Holly C Noland**, SM Hum-Musser, RO Musser, Department of Biological Sciences, Western Illinois University, Macomb, IL 61455.

2:11 p.m. Identification and Genetic Characterization of Soybean Aphid Resistance in Early Maturing Soybean Genotypes. **Siddhi J Bhusal**¹, G-L Jiang¹, KJ Tilmon¹, LS Hesler².

2:23 p.m. Isolated wheat ncRNA after Russian wheat aphid infestation. **Vic Nicolis**, S-M Greyling, E Venter, Department of Botany and Plant Biotechnology, University of Johannesburg, South Africa.

2:35 p.m. Gene regulation of *Helicoverpa zea* salivary glands following herbivory on *Glycine max* leaf tissue. **Ben Ade**, SM Hum-Musser, RO Musser, Department of Biological Sciences, Western Illinois University, Macomb, IL 61455.

BREAK 2:47 – 3:05 p.m.

Ph.D. students

3:05 p.m. Identification of a Putative E3 RING-H2 Ubiquitin Ligase from Poplar Trees that Negatively Impacts the Feeding and Development of the Defoliating Pest, *Orgyia leucostigma*. **Justin Burum**¹, B Gross¹, A Wilke¹, A Grant², S Regan². ¹University of North Dakota, Grand Forks, ND 58202, ²Queens University Kingston, Ontario.

3:17 p.m. Interactions of host plant resistance, seed treatment, and biological control in soybean aphid management. **Thelma Heidel**¹, DW Ragsdale². ¹Department of Entomology, University of Minnesota, ²Department of Entomology, Texas A&M.

3:29 p.m. Silencing of Russian wheat aphid resistance response related genes using viral induced gene silencing. **Thia Schultz**, A-M Botha, Cereal Genomics, Stellenbosch University.

3:41 p.m. Are two genes better than one for soybean aphid management? **Michael McCarville**¹, M O'Neal¹, K Tilmon², B Potter³, B McCornack⁴, E Cullen⁵, J Tooker⁶. ¹Dept. of Entomology, Iowa State University, ²Dept. of Plant Sciences, South Dakota State University, ³Southwest Research & Outreach Center, University of Minnesota, ⁴Dept. of Entomology, Kansas State University, ⁵Dept. of Entomology, University of Wisconsin, ⁶Dept. of Entomology, Penn State University.

3:53 p.m. Mapping and characterization of selected *Diuraphis noxia* resistance genes in *Triticum aestivum*. **Anandi Bierman**¹, NLV Lapitan², A-M Botha¹, ¹Department of Genetics,

Stellenbosch University, Private BagX1, Matieland, 7601, South Africa; ²Department of Soil & Crop Sciences, Colorado St. Univ., Ft. Collins CO, USA.

4:05 p.m. Inbreeding alters volatile signalling phenotypes and affects indirect defense against herbivores in horsenettle (*Solanum carolinense* L). **Rupesh R Kariyat**¹, KE Mauck², CM De Moraes², AG Stephenson¹. ¹208 Mueller Lab, Department of Biology, The Pennsylvania State University, PA, 16802, ²555 ASI Building, Department of Entomology, The Pennsylvania State University, PA.

4:20 – 5:15 p.m. AD HOC BREAKOUT SESSIONS

6:00-6:30 p.m. IPRI STEERING COMMITTEE MEETING

6:30-9:00 p.m. IPRI BANQUET AND BUSINESS MEETING

Banquet speaker: **John Reese**, Department of Entomology, Kansas State University, Manhattan, KS USA. “Host Plant Resistance: One Old Guy’s Perspective.”

Awards: IPRI Lifetime Achievement; Student Competitions.

Tuesday, April 3, University Ballroom

7:00a.m.-5:00 p.m. POSTER VIEWING

8:00 a.m.-12:00 p.m. SYMPOSIUM: CREATING A DIALOG ABOUT PLANT RESISTANCE: ACADEMIA, GOVERNMENT AND INDUSTRY, Moderator: Lee French, French Agricultural Research, Lamberton MN, USA.

8:00 a.m. Introduction

8:05 a.m. Insect host plant resistance: A perspective from the western Minnesota countryside. **Bruce Potter**, University of Minnesota, Lamberton, MN USA.

8:27 a.m. Molecular Inferences of *Aphis glycines*-Resistant Soybean and Virulence Evolution. **Andy P Michel**¹, R Bansal¹, MA Rouf Mian². ¹Dept. of Entomology, Ohio Agricultural Research and Development Center; ²USDA-ARS Corn and Soybean Unit, Dept. of Horticulture and Crop Sciences, The Ohio State University.

8:49 a.m. Western Corn Rootworm and Bt Corn in Iowa. **Aaron J Gassmann**, JL Petzold-Maxwell, RS Keweshan, MW Dunbar, Department of Entomology, Iowa State University, Ames, IA.

9:11 a.m. Lessons from the Field; Bt-Rootworm Performance Problems and Corn Rootworm Resistance in Minnesota. **Ken Ostlie**, B. Potter, L. French, Department of Entomology, University of Minnesota, St. Paul, MN 55108-6125.

9:33 a.m. Native resistance in maize to the western corn rootworm. **Bruce Hibbard**¹, M Bohn². ¹USDA-ARS, ²University of Illinois.

9:55 – 10:15 a.m. Break

10:15 a.m. Insect Resistance Management for corn rootworm. **Rachel Binning**, Pioneer Hi-Bred.

10:37 a.m. Insect Management Traits in Corn: Current Landscape and Future Directions. **Timothy Hey**, T Meade, D Rule, GD Thompson, Dow AgroSciences, Indianapolis, Indiana USA.

10:59 a.m. RNAi as an Approach for Next Generation Corn Rootworm Management. **Thomas L Clark**, Entomology Programs Lead, Monsanto Company, 700 Chesterfield PKWY West GG3M, Chesterfield, MO 63017.

11:21 a.m. Corn Rootworm Management – Syngenta's Multi-faceted Approach. **Miloud Araba**, Ryan Kurtz, Jon Sagers, Craig Nichols, Syngenta Corp.

11:43 a.m. Panel Discussion

12:15-1:45 p.m. LUNCH BREAK

1:45 – 3:55 p.m. SUBMITTED ORAL PRESENTATIONS, Moderator: Louis Hesler, USDA North Central Agricultural Research Laboratory, Brookings SD, USA.

1:45 p.m. Introductory remarks.

1:50 p.m. A Calcium-binding and other functional proteins in the saliva of the green rice leafhopper, *Nephotettix cincticeps*. **M Hattori**¹, S Komatsu², M Nakamura¹, Y Tamura¹,
¹National Institute of Agrobiological Sciences, ²National Institute of Crop Sciences.

2:05 p.m. Strategies to identify genes mediating the virulence of brown plant hopper to resistant rice. **Tetsuya Kobayashi**, M Hattori. National Institute of Agrobiological Sciences, 1-2 Ohwashi, Tsukuba, Ibaraki 305-8634, Japan.

2:20 p.m. Phloem-specific resistance in Brassica oleracea against the whitefly *Aleyrodes proletella*. **Colette Broekgaarden**, G. Steenhuis, J. Bucher, B. Vosman.

2:35 p.m. Effects of aphid feeding on the anatomy and physiology of barley and wheat leaves under ambient CO₂ conditions. **Saheed S Adekilekun**, Department of Botany, Obafemi Awolowo University, Ile-Ife, Nigeria; Department of Botany, Rhodes University, Grahamstown South Africa.

2:50 – 3:10 p.m. BREAK

3:10 p.m. Development of a resistance gene pyramid wheat containing H25 and H26 resistance to Hessian fly (*Mayetiola destructor*). **Brandon Schemerhorn**^{1,2}, R. Shukle^{1,2}, R. Smith¹, Y. Crane¹. ¹USDA-ARS / ²Purdue University.

3:25 p.m. Effects of antinutrient proteins on Hessian fly (Diptera: Cecidomyiidae) larvae. **Richard H Shukle**¹, S Subramanyam², CE Williams¹. ¹USDA-ARS/Dept. of Entomology, Purdue University, West Lafayette, IN 47907, ²Department of Agronomy, Purdue University, West Lafayette, IN 47907.

3:40 p.m. Comparison of localized versus regional resistance and susceptibility in wheat cells responding to first-instar Hessian fly larval attack. **Christie Williams**¹, Jill Nemacheck¹, S Subramanyam², K Saltzmann³. ¹USDA-ARS Crop Production and Pest Control Research Unit, Purdue University, Dept. of Entomology, West Lafayette, IN, ²Purdue University Dept. of Agronomy, West Lafayette, IN., Purdue University Dept. of Entomology, West Lafayette, IN, ³Purdue University, Dept. of Entomology, West Lafayette, IN.

3:55 Prey foraging by *Hippodamia convergens* for cereal aphids on wheat. **Norman Elliott**, USDA-ARS, 1301 N. Western Rd., Stillwater, Oklahoma, USA.

4:10 – 5:15 p.m. AD HOC BREAKOUT SESSIONS

Wednesday, April 4, University Ballroom

7:00 a.m.-12:00 p.m. POSTER VIEWING

8:15 a.m. SYMPOSIUM: INTERNATIONAL PERSPECTIVES ON PLANT RESISTANCE TO CEREAL INSECT PESTS, Moderator: Anna-Maria Botha, Department of Genetics, Stellenbosch University, Matieland, South Africa.

8:15 a.m. Introductory remarks.

8:20 a.m. Mining genebank holdings using the Focused Identification of Germplasm Strategy (FIGS): sources of resistance in wheat to Russian wheat aphid, Sunn pest and Hessian fly. **M El Bouhssini**, K. Street, A. Bari, A. Amri, International Center for Agricultural Research in the Dry Areas (ICARDA), P.O. Box 5466, Aleppo, Syria.

8:45 a.m. The association mapping for *Sitobion avenae* resistance and tolerance in bread wheat germplasm. **F Li**^{1,2,3}, **Liang Chen**^{1,2}, **J Peng**^{1,2,4*}. ¹Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan, Hubei 430074, China, ²Key Laboratory of Plant Germplasm Enhancement and Specialty Agriculture, Chinese Academy of Sciences, Wuhan, Hubei 430074, China, ³Graduate University of Chinese Academy of Sciences, 19 Yuquan Road, Beijing 100049, China, ⁴Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO 80526-1170, USA.

9:10 a.m. Host cell modulation by aphid effector proteins. **P Rodriguez**¹, **T Warbroek**¹, **M Armstrong**², **P Birch**², **Jorunn Bos**¹. ¹James Hutton Institute; ²University of Dundee.

9:35-9:55 a.m. Break

9:55 a.m. Evoking the induced systemic resistance of wheat to impart resistance against the Russian wheat aphid. **Eddie Venter**¹, **C Mansoor**¹, **A-M Botha**²; ¹Department of Botany and Plant Biotechnology, University of Johannesburg, South Africa; ²Department of Genetics, University of Stellenbosch, South Africa.

10:20 a.m. Proteomic Analysis of Secreted Saliva from Russian Wheat Aphid (*Diuraphis noxia* Kurd.) Biotypes that Differ in Virulence to Wheat. **Scott J Nicholson**, **G Puterka**, USDA-ARS.

10:45 – 11:15 a.m. Panel Discussion

11:15 a.m. - 12:00 p.m. IPRI business meeting/concluding remarks

12:00 – 1:30 p.m. LUNCH BREAK, POSTER REMOVAL

1:30 – 3:00 p.m. PRESENTATIONS, STATE REPORTS: WESTERN EXTENSION/EDUCATION RESEARCH ACTIVITY-066 (WERA-066): INTEGRATED MANAGEMENT OF RUSSIAN WHEAT APHID AND OTHER CEREAL ARTHROPOD PESTS, Moderator: Gary Puterka, USDA-ARS, Stillwater OK, USA.

POSTERS

Poster viewing: Monday, 8 a.m. – 5 p.m.; Tuesday, 7a.m. – 5 p.m.; Wednesday, 7 a.m. – noon.
University Ballroom foyer

1. The influence of rice plant age on resistance to the rice water weevil. **Michael Stout**, J Hamm, LSU Ag Center, Baton Rouge LA,, USA.
2. Effect of silicon on resistance of two rice cultivars against sugarcane borer, *Diatraea saccharalis*. JKSidhu, **Michael J Stout**, LE Datnoff, LSU Ag Center, Baton Rouge LA USA.
3. Next Generation sequencing of the genomes of 11 International RWA biotypes. **Anna-Maria Botha**¹, NFV Burger¹, A-M Castro², M El-Bouhssini³, J Havelka⁴, A Jankielsohn⁵, NLV Lapitan⁶, F Peairs⁷, G Puterka⁸, CM Smith⁹, P Stary⁴, M Zurovcova⁴. ¹ Department of Genetics, Faculty of AgriSciences, Stellenbosch University, Private BagX1, Matieland, 7601, South Africa; ²Genetics Faculty of Agricultural Sci, UNLP, CINICET, CC31, 1900-La Plata, Argentina; ³International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria; ⁴Biology Centre of the Academy of Sciences of the Czech Republic, Institute of Entomology, Czech Academy of Sciences; ⁵ARC-Small Grain Institute, Crop Protection, Private Bag X29, Bethlehem, 9700; ⁶Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO 80523, USA; ⁷Department of BioAgricultural Sciences and Pest Management, Colorado State University, Fort Collins, CO 80523, USA; ⁸ARS-USDA, 1301 N. Western Rd, Stillwater, OK 74075, USA; ⁹Department of Entomology, Kansas State University, Manhattan, KS 66506-4004, USA.
4. Russian Wheat Aphid Biotypic Diversity and Distribution in the Western United States. **Gary Puterka**¹, S Nicholson¹, Mike Brown¹, F Peairs², B Hammon², E Bynum³, J Michels³. ¹USDA-ARS, Stillwater, ²Colorado State University, Ft. Collins, ³Texas A&M Exp. Stn. Bushland, TX.
5. A miRNA Genechip® analysis of the wheat – Russian wheat aphid interaction. **Sonia-Mari Greyling**, V Nicolis, E Venter, Department of Botany and Plant Biotechnology, University of Johannesburg, South Africa.
6. Gene-for-Gene Interactions Between Hessian Fly and Wheat: Phenotypes and Fitness Costs. **Marion O Harris**¹, T Freeman¹, K Anderson¹, J Moore¹, S Payne¹, A Zhang¹ and J Stuart², ¹North Dakota State University, Fargo, ND, ²Purdue University, West Lafayette, IN.
7. Marker-assisted breeding for Hessian fly and disease resistance in spring wheat. **NA Bosque-Pérez**¹, J Chen², LM Unger¹, DR See³, S Odubiyi, J Wheeler². ¹Department of Plant, Soil and Entomological Sciences, P.O. Box 442339, University of Idaho, Moscow, ID 83844-2339; ²Department of Plant, Soil and Entomological Sciences, University of Idaho Aberdeen R & E Center, 1691 S 2700 W, Aberdeen, ID 83210; ³Western Regional Small Grains Genotyping Center, USDA-ARS, 209 Johnson Hall, Washington State University, Pullman, WA 99164.
8. Ultrastructure of the antennal sensillae of the peach fruit flies *Bactrocera zonata* (Saunders) (Diptera: Tephritidae). **Azza A Awad**¹, NA Ali², HO Mohamed². ¹Zoology Department, Faculty of Science, Assiut University; ²Plant Protection Res. Institute, Agricultural Research Center, Giza, Egypt.
9. Novel germplasm sources of soybean for resistance against different biotypes of soybean aphid. **Raman Bansal**¹, MA Rouf Mian², AP Michel¹. ¹The Ohio State University, Wooster OH-44691, ²USDA-ARS, Wooster, OH-44691.

10. Inheritance and Mapping of Soybean Aphid Resistance in Soybean Accession PI603432B. **Mukhtar Agoub**¹, G-L Jiang¹, J Orf². ¹Plant Science Dept., South Dakota State University; ²Department of Agronomy and Plant Genetics, University of Minnesota.
11. Chemical Analysis of Spinach Resistance to Aphids and Leaf miners. **Nasir Masood**¹, M Ashfaq². ¹University college of Agriculture and Environmental Sciences, The Islamia University of Bahawalpur 63100, Punjab, Pakistan; ²University of Agriculture Faisalabad 38040, Punjab, Pakistan.
12. Utilizing Varietal Resistance to Manage Tarnished Plant Bug in Cotton. **Glenn Studebaker**, F Bourland, University of Arkansas, Division of Agriculture.
13. Pheromone Traps and Molecular Markers Genotype Hessian flies for Virulence to Resistance Gene *H13* in wheat. AJ Johnson¹, **Richard H Shukle**¹, GD Buntin², KL Flanders³, FPF Reay-Jones⁴, DD Reising⁵, BJ Schemerhorn¹, JJ Stuart⁶. ¹USDA-ARS/Dept. of Entomology, Purdue University, West Lafayette, IN 47907; ²Dept. of Entomology, University of Georgia, Griffin, GA 30223; ³Dept. of Entomology, Auburn University, Auburn, AL 36849; ⁴Dept. of Entomology, Clemson University, Clemson, SC 29631; ⁵Dept. of Entomology, North Carolina State University, Raleigh, NC 27607, ⁶Dept. of Entomology, Purdue University, West Lafayette, IN 47907.
14. The Host-Plant Resistance Puzzle for Soybean Aphid Management. **Louis S. Hesler**¹, G-L Jiang², KE Dashiell¹, S Bhusal², EA Beckendorf¹, D Schneider¹. ¹North Central Agricultural Research Laboratory, USDA-ARS, Brookings SD; ²Plant Science Department, South Dakota St. Univ., Brookings SD.
15. Identification and Characterization of Resistance to the Soybean Aphid in Wild Soybean. **Louis S. Hesler**, EA Beckendorf, USDA-ARS, North Central Agricultural Research Laboratory, Brookings SD USA.

STUDENT POSTERS

*Poster viewing: Monday, 8 a.m. – 5 p.m.; Tuesday, 7a.m. – 5 p.m.; Wednesday, 7 a.m. – noon.
University Ballroom foyer*

- S1. Identification of Resistance to Codling Moth and Leafroller in Malus. **Joseph Schwarz**, J Brunner, C Peace, K Evans, WSU apple-breeding program.
- S2. Impact of Rhizobial Seed Inoculants on Soybean Aphid Densities, **Samantha M Brunner**¹, DA Prischmann-Voldseth¹, RJ Goos². ¹NDSU Entomology, ²NDSU Soil Science.
- S3. Inheritance of Resistance to Soybean Stem Borer (*Dectes texanus* Leconte) in Soybean PI165673. **Lina Aguirre-Rojas**, CM Smith, W Schapaugh, B McCornack, L Buschman, Kansas State University.
- S4. Multiple Categories of Resistance to Wheat Curl Mite (Acari: Eriophyidae) expressed in *Aegilops* spp. accessions. **Sandra Garcés Carrera**¹, H Davis¹, L Aguirre-Rojas¹, M Murugan², CM Smith¹. ¹Kansas State University, ²Tamil Nadu Agricultural University, Coimbatore India.
- S5. How virulent are North Dakota Hessian fly to wheat resistance genes? **Kirk Anderson**, M Harris, North Dakota State University.

Presenters of oral presentations and posters are denoted in **bold lettering**.

ABSTRACTS

Monday, April 2

SYMPOSIUM: NEW TOOLS FOR UNDERSTANDING PLANT RESISTANCE AND PEST BIOLOGY

8:20 a.m. Protein interaction reporter: "News" on protein topologies in an insect-transmitted plant virus. **Michele Cilia**, USDA-ARS, Cornell University, Ithaca, NY, and 8:45 a.m. Using Targeted Mass Spectrometry to Study Virus Transmission by Aphids. **Michael Bereman**, University of Washington. **Abstract:** A majority of plant viruses and a large number of important animal viruses are transmitted by insect vectors. Nearly all insect-transmitted animal viruses are internalized and circulate in their insect vectors, while plant viruses are divided between those that are carried on the cuticle linings of mouthparts and foreguts and those that circulate in their vectors. Members of the *Luteoviridae* are economically important circulative viruses in staple food crops and are retained in the vascular tissues (phloem) of host plants. Phloem-retention facilitates circulative transmission by aphid vectors. This presentation will highlight new and exciting proteomic insights into the regulation of circulative transmission by aphids and plants as well as excellent agreement of our data with previously published studies on the biology of circulative transmission. Finally, examples from our data will also be presented to show how proteomics technologies can enable us to develop novel strategies that disrupt virus movement within and between hosts.

9:10 a.m. Establishing the root-knot nematode *Meloidogyne hapla* as a tractable genetic/genomic platform to study plant – parasite interactions. **Valerie M Williamson**¹, VP Thomas¹, DM Bird², SL Fudali¹, J Gimeno¹, J Schaff³, EH Scholl², C Opperman², D Nielsen⁴. ¹Dept. of Nematology, University of California, Davis; ²Dept. of Plant Pathology, North Carolina State University; ³Genome Sciences Lab, North Carolina State University; ⁴Bioinformatics Res. Center, NC State Univ. **Abstract:** Root-knot nematodes (*Meloidogyne* spp.) cause major yield losses to many crops, but efforts to understand how these pests recognize and interact with their hosts have been hampered by their obligate parasitic life cycle. We have been developing *Meloidogyne hapla* as a model system to facilitate in depth investigation of genes important for parasitism. This species was selected because of its agricultural importance, variable host range, tractable genetics, and small genome. The genome of *M. hapla* is 54 Mb, and a well-annotated sequence that spans 99% of the genome is available. *M. hapla* is a simple diploid (n=16) and reproduces by facultative meiotic parthenogenesis, a reproductive mode that permits out-crossing and inbreeding. We have established F2 lines from parental strains that differ in behavior and pathogenicity and, using co-dominant SNP-based markers, produced an integrated map showing excellent correspondence between the genetic map and genome assembly. Co-dominant markers segregate predominantly 1:1 in F2 progeny, and heterozygous loci are underrepresented; thus, these F2 lines resemble recombinant inbred lines. Analysis of local crossover intervals revealed that the recombination rate is the highest found to date for a metazoan. The same progeny lines have been used for analyses of the inheritance of phenotypic traits modulating parasitism, behavior and survival. We have shown that a trait required for clumping behavior maps to a single locus. Scorable differences in traits for attraction to and parasitism of particular hosts also segregate in these populations and quantitative trait loci responsible for these phenotypes have been identified. We have also initiated a project using *M. hapla* F2 lines and the plant host, *Medicago truncatula*, to address the broad question: "How does the genetic makeup of the pathogen influence host gene

expression?” More specifically, we consider the influence of allelic variation at each nematode locus on the expression of each plant gene. Our approach is to perform a cross-species expression quantitative trait locus (eQTL) mapping experiment, followed by regulatory network inference to characterize the cross-talk between organisms. We are in the process of assessing replicate pools of host plants individually infected with each of over 100 nematode RILs and determining the combined transcriptomes of each individual by Illumina-based RNA-Seq. Analysis of an initial 30 RILs has yielded an unprecedented insight into *M. hapla* genome organization, and both nematode and host expression profiles.

9:35 a.m. Identification of Hessian fly *Avirulence* gene. **Jeff Stuart**¹, R. Aggarwal¹, T. Benatti¹, C. Zhao¹, L. Navarro¹, M-S. Chen², K. Anderson³, M. O. Harris³, R. Shukle⁴. ¹Department of Entomology, Purdue University, West Lafayette, IN 47907; ²USDA-ARS and Department of Entomology, Kansas State University, Manhattan, KS 66502; ³Department of Entomology, North Dakota State University, Fargo, ND 58105; ⁴USDA-ARS and Department of Entomology, Purdue University, West Lafayette, IN 47907. **Abstract:** Our work is focused on exploiting the genetic tractability and small genome of the Hessian fly (*Mayetiola destructor*) in an effort to reveal the genes and gene products that are involved in host plant specification and gall formation. Here we demonstrate the utility of the sequenced Hessian fly genome in mapping Hessian fly mutations that are associated with the ability of Hessian fly larvae to successfully infest and damage wheat (*Triticum* spp.) seedlings carrying Hessian fly resistance (*R*) genes. Results are consistent with the gene-for-gene hypothesis, in which *R* gene products elicit an effector-triggered immunity in wheat upon detection of Hessian fly avirulence (*Avr*) gene encoded effectors. *Avr* genes corresponding to Hessian fly *R* genes *H5*, *H6*, *H9*, *H13*, *H24*, and *Hdic* have been positioned on the Hessian fly chromosomes. The position of each of these genes has been resolved to less than 800 kb. The *Avr* gene corresponding to virulence to *H5* (*vH5*) is autosomal. The remaining *Avr* genes are X-linked. The positions of the virulence causing mutations indicates that each *Avr* gene encodes a secreted protein expressed in the salivary glands of avirulent first instar Hessian fly larvae. These proteins have no sequence similarity to other proteins in GenBank. However, some are members of gene families that appear to be experiencing highly diversifying selection. We conclude that the Hessian fly has adapted a suite of effector proteins it uses to attack its host like a plant pathogen.

10:20 a.m. Genetic mapping of aphid resistance in maize. L Meihls, H Kaur, **Georg Jander**, Boyce Thompson Institute for Plant Research, Ithaca, NY 14853. **Abstract:** Plants vary greatly in their resistance to the estimated one million or more species of herbivorous insects. Even among isolates of a single plant species there are often large differences in the susceptibility to insect attack. In one such example, there is a greater than 100-fold range in the number of progeny produced by *Rhopalosiphum maidis* (corn leaf aphid) on a well-characterized population of maize inbred lines. Recent advances in maize genome sequencing and genetic mapping make it feasible to identify the genetic basis of such natural variation in herbivore resistance. Crosses between maize inbred lines show that there are both dominant and recessive *R. maidis* resistance mechanisms in maize. Genetic mapping using recombinant inbred lines narrowed the position of a recessive aphid resistance quantitative trait locus (QTL) to a genomic interval containing only 31 genes. A QTL for the modification of benzoxazinoids, maize secondary metabolites that are known to influence aphid feeding, is positioned in the same area of the maize genome. Therefore, a benzoxazinoid biosynthetic enzyme encoded in the area of the QTL likely mediates natural variation in maize aphid resistance by converting a defensive benzoxazinoid into one that is less deleterious for aphid feeding.

10:45 a.m. Virus induced gene silencing reveals putative wheat defense mechanisms against *Diuraphis noxia*. **Nora L Lapitan**, V Valdez, L van Eck, Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO 80523. **Abstract:** The phloem feeder, *Diuraphis noxia* (commonly known as Russian wheat aphid, RWA), causes significant economic losses in wheat in many parts of the world. In the U.S., at least seven biotypes exist that cause virulence against specific *Dn*---resistance genes in wheat. The underlying mechanism of wheat resistance against the RWA is poorly understood. Global transcript profiling studies have identified genes that are differentially expressed between resistant and susceptible cultivars during aphid feeding. However, the role of candidate genes involved in wheat defense against the RWA has not been tested. Virus---induced gene silencing (VIGS) offers many advantages as a reverse genetics approach in wheat, given the lack of a facile transformation system and its polyploidy genome. We optimized the VIGS technique to test candidate genes involved in wheat's interaction with the RWA. Two types of candidate genes were tested: 1) genes that were significantly up---regulated in susceptible vs. resistant near---isogenic lines (NILs); and 2) genes that were significantly up---regulated the resistant vs. susceptible NILs during aphid feeding. Under the first category, silencing of *1-3,1-4* β -glucanase resulted in enhanced resistance of the susceptible NIL compared to the susceptible control. Under the second category, silencing of *WRKY53* resulted in reduced resistance in the resistant NIL compared to the resistant control. Yeast two hybrid experiments were conducted to identify proteins that bind to the *WRKY53* transcription factor. This talk will discuss the results and their implications for the wheat---aphid interaction and the plant's defense mechanisms.

11:10 a.m. Integration of DNA Markers with Chromosome Engineering for Efficient Introgression of Resistance Genes from Wild Grasses into Wheat. **Steven Xu**¹, Z Niu¹, DL Kindworth¹, S Chao¹, T Friesen¹, JD Faris¹, Y Jin², X. Cai³, MO Harris³. ¹USDA-ARS, Fargo ND 58108; ²USDA-ARS, Minneapolis MN 55108; ³North Dakota State University, Fargo, ND 58108. **Abstract:** Wheat is one of the major food crops and its production is constantly threatened by numerous diseases and insects. Many wild grasses related to wheat possess potent resistance genes and represent a valuable genetic resource for wheat improvement, especially for disease and insect resistance. However, introgression of resistance genes from wild grasses into wheat has been a challenging task due to inherent difficulty and low efficiency in inducing and recovering homoologous recombinants through classical chromosome engineering. An efficient procedure for alien gene introgression is essential for utilization of resistance genes from the wheat-grasses. In an effort to utilize wild species-derived resistance genes effective against Ug99 stem rust races, a serious threat to global wheat production, we developed a highly efficient scheme of chromosome engineering for introgression of resistance genes derived from wild grasses. In this procedure, we first developed a large backcross population of *ph1b*-induced homoologous recombinants and then identified the recombinants carrying the gene of interest on small interstitial segments using robust DNA markers and high-throughput phenotyping and genotyping. By using this procedure, we developed wheat germplasm carrying four Ug99-resistant genes on minimal alien chromatin in a short period of time. We are currently applying this procedure to transfer more genes for resistance to stem rust, leaf rust and Hessian fly, from wild grasses into the wheat genome. This study demonstrated that integration of modern genomic and marker technology by classical chromosome engineering and breeding greatly improved the efficiency for transferring resistance genes from wild relatives into modern crops.

STUDENT ORAL PRESENTATION COMPETITION

1:35 p.m. Transcriptomic changes in *Diuraphis noxia* when transferred from preference to non-preference hosts. **N Francois V Burger**, A-M Botha, Department of Genetics, Stellenbosch University, Private BagX1, Matieland, 7601, South Africa. **Abstract:** Russian wheat aphid (RWA) (*Diuraphis noxia*, Kurdjimov) sets itself apart from other cereal aphids because of a unique ability to manipulate its host's defensive mechanisms to avoid detection. This allows the aphid to feed on phloem of wheat without the launching of an effective response from its infested host. The actual direct damage caused by RWA feeding results in a minor loss of nutrient rich phloem which could usually be balanced by a higher output in photosynthesis. However, RWA possesses the ability of lowering, or disrupting, photosynthetic capability by initiating the hypersensitive response (HR) in the host. Previous studies have suggested that a proteinaceous compound in the saliva of RWA, predicted to follow a gene-for-gene model, is responsible for the aberrant HR onset. Observing the changes in salivary transcription could uncover other targets responsible for the activation of this ineffective defence response. In this study we transferred two aphid biotypes (SA1 and SAM) between preference and non-preference hosts while sampling RWA heads (containing their salivary glands) at two time intervals coinciding with both the HR (± 4 hours) and systemic acquired resistance (± 48 hours) defence responses. cDNA, obtained from total RNA, was used to obtain transcripts produced under the pressure of host shifts. cDNA-Amplified Fragment Length Polymorphisms (cDNA-AFLPs) were performed to identify novel transcripts and changes in transcription rates after which these were excised and sequenced to obtain their identity. Preliminary results suggest gene regulatory changes in RWA associated with Carbohydrate metabolism and transport, transmembrane proteins along with heat shock factors.

1:47 p.m. Gene expression profile of *Helicoverpa zea* in response to *HzSNPV*. **Jeffrey E Noland**, HC Noland, SM Hum-Musser, RO Musser, Department of Biological Sciences, Western Illinois University, Macomb, IL 61455. **Abstract:** *Helicoverpa zea* is a widely known agricultural pest that is linked to 1 billion dollars in damage and management annually. Potential biological controls for *H. zea* are baculoviruses such as the *Helicoverpa zea Single Nucleocapsid Nucleopolyhedrovirus (HzSNPV)*. We tested the transcriptomic response of *H. zea* as whole larvae, as well as the midgut after a 24 hour period. Examining the midgut allowed for a view into the main site of infection, whereas the whole body showed responses surrounding the infection in addition to the gut. Results for both microarrays were log transformed and analyzed for statistical significance with a t-test. There were 831 significant putative genes in the midgut tissue and 77% of genes were down-regulated and 23% were up-regulated compared to the non-infected control. While in the whole larvae only 179 significantly putative genes altered, 70% of these genes were up-regulated and 30% down-regulated compared to the non-infected control. The low number of genes found in the whole body compared to the gut alone suggested that the virus had not spread much beyond the midgut in the first 24 hours. Several digestive related genes were down-regulated such as aminopeptidases and serine proteases. Immune response and apoptosis related genes were a bit more complicated with genes like antimicrobial peptides being both up and down-regulated. In general, detoxification genes in the midgut were down-regulated as a result of infection. This first transcriptomic study of *H. zea* to *HzSNPV* that we are aware of provides further ground work to understanding the global physiological changes the virus induces.

1:59 p.m. The genomic response of *Helicoverpa zea* after feeding on phytohormone treated Tomato Plants. **Holly C Noland**, SM Hum-Musser, RO Musser, Department of Biological

Sciences, Western Illinois University, Macomb, IL 61455. **Abstract:** *Helicoverpa zea* is a prevalent insect pest that has a wide geographical distribution and feeds on a wide range of prominent agricultural crops. We investigated caterpillar's transcriptomic response to tomato plant defense activated by salicylic acid and jasmonic acid. Plants were grown in the lab for eight weeks and then sprayed with salicylic acid or jasmonic acid and allowed to generate defenses over 24 hours. Plants treated with jasmonate stimulated significantly higher levels of anti-nutritive defenses such as protease inhibitors in comparison to salicylate treated plants. Recently molted 6th instar caterpillars were allowed to feed on these phytohormone treated plants for 24 hours. Whole body caterpillars were analyzed through microarray analysis to determine the transcriptomic response and tested for statistical significance with a t-test. 1,331 significantly putative genes were altered from feeding on the plants compared to the control fed caterpillars. Caterpillars that fed on jasmonic acid treated plants showed an up-regulation in genes responsible for digestive enzymes such as proteases and lipases correlating to anti-nutritive defenses. In addition detoxification, amino acid metabolism, dehydrogenases, and transferases were stimulated. While salicylate treated plants showed an up-regulation in genes responsible for chitinases and immune responses. This is one of the first transcriptomic studies to correlate caterpillar gene alteration to inducible plant defenses. Understanding how *H. zea* responds to induced plant defenses will provide information for developing biological control.

2:11 p.m. Identification and Genetic Characterization of Soybean Aphid Resistance in Early Maturing Soybean Genotypes. **Siddhi J Bhusal**¹, G-L Jiang¹, KJ Tilmon¹, LS Hesler².

Abstract: Soybean aphid (SA, *Aphis glycines* Matsumura) has been an important pest of soybean crop in the United States since 2000. Identification and genetic characterization of SA resistance in early maturing soybean genotypes (maturity group '0' and '00') will facilitate development of aphid-resistant cultivars in the northern regions. To evaluate the SA resistance in early maturing soybeans, a total of 334 soybean genotypes including resistant and susceptible checks were tested in a no-choice screening by artificial inoculation of soybean aphids in the greenhouse, and evaluated under natural infestation of aphids in the field. Three genotypes PI603712, PI464911 and PI430491 exhibited resistance with less than 50 aphids per plant in two weeks after inoculation in the greenhouse, and four genotypes PI603432B, PI612759B, PI200595 and PI603426D showed moderate resistance with less than 100 aphids per plant. In the field, however, only PI603712 was resistant and PI430491 was moderately resistant, with less than 100 aphids and 100-200 aphids per plant at peak infestation, respectively. PI603712 exhibited higher resistance than known sources of SA resistance in the field. It indicates that PI603712 may be a new source of gene(s) for SA resistance. Further study on its inheritance and molecular marker analysis are in progress.

2:23 p.m. Isolated wheat ncRNA after Russian wheat aphid infestation. **Vic Nicolis**, S-M Greyling, E Venter, Department of Botany and Plant Biotechnology, University of Johannesburg, South Africa. **Abstract:** The Russian wheat aphid (*Diuraphis noxia* Kurdjumov) is an economically important pest of small grains in South Africa. Resistant wheat cultivars have been successfully used against the Russian wheat aphid, however, new resistance breaking biotypes have emerged in recent years. In order to understand the interaction between *D. noxia* and wheat it is imperative to study all levels of the interaction. The aim of this project was to isolate and characterise non-coding RNA from wheat that is involved in the RWA-wheat interaction. This was achieved by creating a library enriched for small ncRNA molecules (18 – 350 bases) from selected time points from 30 min to 72 hpi. The library was created by performing subtractive hybridisation of ncRNA transcripts (SHORT) on ncRNA isolated from resistant (Tugela Dn) and

susceptible (Tugela) wheat infested by the SA 1 biotype. The resultant cDNA clones from the normalised library were sequence characterised and are currently being studied as to their function during the defence response at key time points of the interaction.

2:35 p.m. Gene regulation of *Helicoverpa zea* salivary glands following herbivory on *Glycine max* leaf tissue. **Ben Ade**, SM Hum-Musser, RO Musser, Department of Biological Sciences, Western Illinois University, Macomb, IL 61455. **Abstract:** Gene expression of *Helicoverpa zea* (corn earworm) caterpillar salivary gland tissue was measured in response to being fed on *Glycine max* (soybean) leaf tissue. Two groups of *H. zea* caterpillars were used in the experiment, a control group which was fed an artificial diet, and the experimental group that was fed on mature *G. max* leaves *in vitro*. Total RNA was extracted from surgically removed labial salivary gland tissue of actively feeding caterpillars. Total RNA was then amplified using T7 primers and labeled with fluorescent dyes to produce amplified and labeled cRNA which was then hybridized on a custom oligo-nucleotide microarray. Microarray analysis showed that a total of 1143 genes were significantly different ($P < 0.05$ t-test) from the soy fed experimental group compared to the diet-fed control group. Of the 1143 genes, 293 did not have annotations. Among the significantly altered caterpillar salivary gland genes altered were genes which encode for proteases, metabolic pathways, cytochrome P450 system, and other detoxification and immune system genes. These data provide an insight into the gene expression of *H. zea* caterpillars in response to the plant defenses of *G. max*.

3:05 p.m. Identification of a Putative E3 RING-H2 Ubiquitin Ligase from Poplar Trees that Negatively Impacts the Feeding and Development of the Defoliating Pest, *Orgyia leucostigma*. **Justin Burum**¹, B Gross¹, A Wilke¹, A Grant², S Regan². ¹University of North Dakota, Grand Forks, ND 58202, ²Queens University Kingston, Ontario. **Abstract:** Insect herbivory results in significant economic losses to planted and natural forests. In response, forest trees deploy diverse constitutive and inducible defenses. To explore the genetic architecture of tree defenses, we conducted a forward genetics screen of 600 activation tagged *P. tremula* x *P. alba* (Pt x Pa) trees and tentatively identified the mutant E8-16 as resistant to *Orgyia leucostigma* (white marked tussock moth, WTM) larvae feeding. Follow-up choice bioassays with extensive replication Choice demonstrated larvae consumed 43.4% less area and 68.8% less leaf weight on E8-16 compared to Pt x Pa wildtype leaf disks (N=6 pairs, both $p < 0.001$, nested ANOVA). In no-choice bioassays, larvae reared on E8-16 trees gained 43.5% less dry weight than larvae on wildtype trees (N=10, $p = 0.003$, two-sample t-test). To determine which poplar gene(s) is activated by proximity to the T-DNA, we used SiteFinder PCR and TAIL PCR to demonstrate E8-16 contains a single T-DNA on chromosome 10. Realtime PCR analysis of the three genes located within 20 kb of the T-DNA revealed only 10s12800 had elevated expression in E8-16 versus wildtype leaves (4.1-fold, $p < 0.0001$, nested ANOVA). Based on sequence conservation, 10s12800 is a putative E3 RING-H2 ubiquitin ligase involved in the terminal step of the ubiquitin-proteasome pathway that marks target proteins with ubiquitin for degradation by the 26S proteasome. Experiments are ongoing to: 1) over-express 10s12800 in multiple genetic backgrounds to recapitulate the E8-16 phenotype; and 2) generate global transcript profiles of E8-16 and wildtype leaves using oligo microarrays.

3:17 p.m. Interactions of host plant resistance, seed treatment, and biological control in soybean aphid management. **Thelma Heidel**¹, DW Ragsdale². ¹Department of Entomology, University of Minnesota, ²Department of Entomology, Texas A&M. **Abstract:** The soybean aphid, *Aphis glycines*, is a major economic pest of Midwest soybeans, and several control options are currently available for soybean aphid management. Understanding how these control options interact with

one another is a critical component in developing a successful soybean aphid integrated pest management (IPM) plan. In this study, we investigated the interactions of three aphid management options – host plant resistance, insecticide seed treatment, and biological control. We conducted a two-year field trial with replicated plots to study how Rag1 host plant resistance and thiamethoxam seed treatment affect aphid and natural enemy abundance. Whole-plant aphid counts were utilized to estimate aphid abundance, and sweep nets and visual plant observations were used to estimate natural enemy abundance. Results show that patterns in natural enemy abundance did not always follow aphid abundance, indicating an interaction between these management options. Aphid abundance was consistently lowest in plots combining both Rag1 resistance and seed treatment. Coccinellidae were the most abundant natural enemies in all treatments, and abundance of these beetles was consistently lowest in the combined Rag1 resistance and seed treatment plots.

3:29 p.m. Silencing of Russian wheat aphid resistance response related genes using viral induced gene silencing. **Thia Schultz**, A-M Botha, Cereal Genomics, Stellenbosch University. **Abstract:** Wheat is one of the most cultivated crops in the world, and in South Africa (SA), the demand exceeds the supply. In 2010/11, the SA Grain Organization imported 1.3 million metric tons of wheat for domestic consumption. In SA, wheat production is hampered by many factors which include biotic and abiotic stressors. One of the biotic stressors that cause large scale damage to wheat crops, resulting in a yield losses of up to 80% if not sprayed, is the Russian wheat aphid (RWA) (*Diuraphis noxia*: Kurdjomov). In previous studies, genes were identified that may confer resistance to RWA using cDNA-Amplified Fragment Length Polymorphisms (CDNA-AFLPs) and AFFYMETRIX arrays. In order to test their association to RWA resistance and wounding, a gene-splicing method called viral induced gene silencing (VIGS) was employed. Genes partaking in the hypersensitive response were chosen for silencing in near isogenic wheat lines (NILs) (i.e., RWA resistant TugelaDN (Dn1) and susceptible Tugela). Aphid fecundity measurements were taken to measure the susceptibility of NILs after RWA feeding using mean aphid produced per day (a/d) as measurement. Tugela susceptible plants had the highest mean number of aphid produced per day (2.6 a/d), while the aphids feeding on the TugelaDN plants showed a lower mean (1.9 a/d). Under wounding conditions; silencing of ascorbate peroxidase resulted in the expression of susceptibility in TugelaDN plants with a 2.2 a/d measurement. Under infestation conditions; TugelaDN plants with glutathione-S-transferase (GST) silenced showed a statistically significant increase in susceptibility with a nymph production of (2.21 a/d).

3:41 p.m. Are two genes better than one for soybean aphid management? **Michael McCarville**¹, M O'Neal¹, K Tilmon², B Potter³, B McCornack⁴, E Cullen⁵, J Tooker⁶. ¹Dept. of Entomology, Iowa State University, ²Dept. of Plant Sciences, South Dakota State University, ³Southwest Research & Outreach Center, University of Minnesota, ⁴Dept. of Entomology, Kansas State University, ⁵Dept. of Entomology, University of Wisconsin, ⁶Dept. of Entomology, Penn State University. **Abstract:** The soybean aphid is currently the leading insect threat to soybean production in the Midwestern United States. Host plant resistant varieties have recently been released for soybean aphid control. These varieties all contain the Rag1 gene conferring antibiosis resistance to the soybean aphid. In other systems aphid pests have rapidly developed virulence to single gene resistance traits. We conducted a small plot field experiment with seven locations across six states, Minnesota, South Dakota, Iowa (2 locations), Kansas, Wisconsin, and Pennsylvania. We evaluated near-isolines of soybean for the ability of single gene resistant lines containing the Rag1 and Rag2 genes and a pyramid line containing both genes to limit plant exposure to aphids (CAD) and protect yield as compared with a susceptible line. For all

locations, we used a split-plot design with soybean line as the whole plot effect and aphid exposure, “aphid-free” or “untreated”, as the sub-plot effect. Aphid-free sub-plots were kept at densities of >50 aphids plant⁻¹ with foliar applications of insecticide. All three soybean aphid-resistant lines significantly decreased CAD at all locations but the Wisconsin site. The pyramid line accumulated significantly fewer CAD than both single gene lines at four of the seven locations. Yield data was pooled from the three locations with the highest aphid pressure, Minnesota, South Dakota, and northern Iowa. Yield was significantly reduced in the untreated sub-plot for the susceptible line and numerically reduced for both single gene lines. We were unable to measure a yield decrease, significant or numerical, for the pyramid line.

3:53 p.m. Mapping and characterization of selected *Diuraphis noxia* resistance genes in *Triticum aestivum*. **Anandi Bierman**¹, NLV Lapitan², A-M Botha¹. ¹Department of Genetics, Stellenbosch University, Private BagX1, Matieland, 7601, South Africa; ²Department of Soil & Crop Sciences, Colorado St. Univ., Ft. Collins CO USA. **Abstract:** Eleven sources of resistance (*Dn* resistance genes) against Russian wheat aphid (*Diuraphis noxia* Kurdjomov) have been identified to date. Incorporating these *Dn* genes into agronomically well adapted cultivars is still the most effective means to confer resistance against this economically important pest of wheat and barley. However, little molecular information about the *Dn* genes is known since none of them have been cloned and sequenced through their chromosomal locations are known. Through this study we aim to fine map the resistance gene *Dn1* AFLP, EST and SSR markers, where after we propose to clone and sequence the gene following map-based cloning strategies. Presently, our mapping populations consists of 571 individuals that derived from an F₃/₄ population segregating for *Dn1* and originating from a cross between Tugela and TugelaDN. To date thirteen primer pairs have been screened of which four proved informative. One of these, M-CTT E-ACC, has already produced 83 bins scored and a maximum of 41 polymorphic bands. Once a genetic map has been saturated, the physical map will be constructed using map based cloning and chromosome walking. Because of the large and repetitive nature of the wheat genome, the mapping project will supported Fluorescent IN Situ Hybridization (FISH) of chromosome 7D and its subsequent isolation through micro-dissection in order to sequence the chromosome and aid physical mapping.

4:05 p.m. Inbreeding alters volatile signalling phenotypes and affects indirect defense against herbivores in horsenettle (*Solanum carolinense* L.). **Rupesh R Kariyat**¹, KE Mauck², CM De Moraes², AG Stephenson¹. ¹208 Mueller Lab, Department of Biology, The Pennsylvania State University, PA, 16802, ²555 ASI Building, Department of Entomology, The Pennsylvania State University, PA. **Abstract:** The ecological consequences of inter-individual variation in plant volatile emissions remain largely unexplored. We examined the effects of inbreeding on constitutive and herbivore-induced volatile emissions in horsenettle (*Solanum carolinense* L.) and on the composition of the insect community attracted to herbivore-damaged and undamaged plants in the field. Inbred plants exhibited higher constitutive emissions, but weaker induction of volatiles following herbivory. Moreover, many individual compounds previously implicated in the recruitment of predators and parasitoids (e.g. terpenes) were induced relatively weakly (or not at all) in inbred plants. In trapping experiments, undamaged inbred plants attracted greater numbers of generalist insect herbivores than undamaged outcrossed plants. But inbred plants recruited fewer herbivore natural enemies (predators and parasitoids) when damaged. Taken together, these findings suggest that inbreeding depression negatively impacts the overall pattern of volatile emissions – increasing the apparency of undamaged plants to herbivores, while reducing the recruitment of predatory insects to herbivore-damaged plants.

Tuesday, April 3

SYMPOSIUM: CREATING A DIALOG ABOUT PLANT RESISTANCE: ACADEMIA, GOVERNMENT AND INDUSTRY

8:05 a.m. Insect host plant resistance: A perspective from the western Minnesota countryside. **Bruce Potter**, University of Minnesota, Lamberton, MN USA. **Abstract:** The transgenic inclusion of Bt into corn is an example of host plant resistance that has provided long-term economic advantages to Minnesota producers. On the other hand, performance issues of the Bt events for corn rootworm have been observed and populations of soybean aphid adapted to resistant varieties have been documented even before the resistance genes have been widely deployed. Successful host plant resistance strategies depend, in part, on the interaction of the insect and trait with the cropping system. The grower/seed company interface and its impact on the adoption of host plant resistance and the loss of resistance traits effectiveness will be discussed.

8:27 a.m. Molecular Inferences of *Aphis glycines*-Resistant Soybean and Virulence Evolution. **Andy P Michel**¹, R Bansal¹, MA Rouf Mian². ¹Dept. of Entomology, Ohio Agricultural Research and Development Center; ²USDA-ARS Corn and Soybean Unit, Dept. of Horticulture and Crop Sciences, The Ohio State University. **Abstract:** The soybean aphid, *Aphis glycines*, has become the most important soybean insect pest in the North Central US region since its first discovery in 2000. By screening thousands of soybean PIs, several soybean varieties have been discovered with host-plant resistance to the soybean aphid. Currently there are 4 formally described resistance genes (termed *Rag* for **R**esistance to *A*phis *g*lycines), with *Rag1* being commercially released in 2010. However, soybean aphids have been found that can overcome this resistance, despite the lack of intense selection pressure. Referred to as biotypes, these aphids expressing virulence to *Rag* traits threatens the efficacy and sustainability of host-plant resistance as an aphid management tactic. Therefore, research is needed to describe both the genetic mechanisms for soybean aphid virulence and the potential for virulence spread across the soybean growing region. Data will be presented on the transcriptomic level changes upon exposure to *Rag1*, as well as how the reliance and colonization of two host plants influences the distribution of genetic variation and biotype movement.

8:49 a.m. Western Corn Rootworm and Bt Corn in Iowa. **Aaron J Gassmann**, JL Petzold-Maxwell, RS Keweshan, MW Dunbar, Department of Entomology, Iowa State University, Ames, IA. **Abstract:** The western corn rootworm, *Diabrotica virgifera virgifera*, is a major pest of corn in the United States and is currently managed by planting corn that produces insecticidal toxins derived from the bacterium *Bacillus thuringiensis* (Bt). During the summers of 2009 through 2011, we sampled western corn rootworm populations from fields throughout Iowa in response to complaints by growers of injury to Bt corn. Eggs collected from these populations were used to conduct laboratory bioassays. Neonate larvae from each population were assayed against two Bt hybrids, one producing Cry3Bb1 and another producing Cry34/Cry35Ab1. Larvae also were evaluated on the non-Bt near isogenic hybrid of each Bt hybrid. Larval survival was measured after 17 days. Populations from fields with a history of cultivation of Cry3Bb1 corn had significantly higher survival on Cry3Bb1 corn in laboratory bioassays than did western corn rootworm from fields not associated with severe injury to Cry3Bb1 corn. No differences were detected for survival on Cry34/35Ab1 corn. We conducted a field experiment in 2011 in two fields identified in 2009 as harboring Cry3Bb1-resistant western corn rootworm and found that injury to Cry3Bb1 corn was higher than any of the other treatments tested, except for non-Bt corn

without insecticide. Survival of western corn rootworm did not differ between non-Bt corn and Cry3Bb1 corn. These data highlight the challenges surrounding management of western corn rootworm with Bt corn in continuous corn fields, and underscore the need for sound integrated pest management when applying Bt corn to manage western corn rootworm.

9:11 a.m. Lessons from the Field; Bt-Rootworm Performance Problems and Corn Rootworm Resistance in Minnesota. **Ken Ostlie**, B. Potter, L. French, Department of Entomology, University of Minnesota, St. Paul, MN 55108-6125. **Abstract:** Performance problems with transgenic corn rootworm resistance traits first appeared in MN in 2009. Diet overlay bioassays from two 2009 problem fields near Luverne MN revealed resistance ratios for western corn rootworms of 2.5X to over 4X. Given problems inherent with this assessment of resistance, we shifted focus to performance of Bt-RW traits under field conditions. Performance of Bt-RW traits was evaluated in a Cry3Bb1 performance problem field near Dennison, MN in 2011. Field efficacy of YieldGard VT Triple declined markedly in this problem field compared to its effectiveness in non-problem fields. More intriguingly, delays in 50% beetle emergence normally reflecting survivor exposure to the Cry3Bb1 protein also disappeared. Effects on beetle survival and development were greater than differences apparent in root injury, lodging and yield. Performance of management alternatives in this problem field were also compared. Potential IRM and IPM implications will be discussed.

9:33 a.m. Native resistance in maize to the western corn rootworm. **Bruce Hibbard**¹, M Bohn². ¹USDA-ARS, ²University of Illinois. **Abstract:** The western corn rootworm, *Diabrotica virgifera virgifera* LeConte, has been named most expensive pest to control by CABI International. Additional management options would be extremely useful. Previously, we identified a number of sources of maize with natural resistance to western corn rootworm larval feeding. More recently, several mapping populations were formed to work toward an understanding of genetic mechanisms and assist in moving resistance into elite, modern lines. Several quantitative trait loci have now been identified for traits that include reduced feeding damage, root regrowth, and root size. These data will be discussed along with implications for the possibility having native resistance options for rootworm management in the future.

10:15 a.m. Insect Resistance Management for corn rootworm. **Rachel Binning**, Pioneer Hi-Bred. **Abstract:** Corn rootworm continues to be the most economically damaging pest to corn in the United States. Our history tells us that CRW has been highly adaptable to many of the insect control tactics that have been utilized to date. Recent data suggest that Bt corn as a transgenic approach for CRW control is also vulnerable to CRW adaptation. This talk will discuss some of our key considerations for CRW management and our message to our customers.

10:37 a.m. Insect Management Traits in Corn: Current Landscape and Future Directions. **Timothy Hey**, T Meade, D Rule, GD Thompson, Dow AgroSciences, Indianapolis, Indiana USA. **Abstract:** It was 1995 when Event 176, the first transgenic insect trait, was registered for corn in the United States. The first and subsequent insect traits have provided great value resulting in rapid adoption in multiple geographies. There has since been steady improvement in the diversity and value of insect traits available. This presentation will cover the history of corn insect resistance traits, the traits available today and what might be expected in the future.

10:59 a.m. RNAi as an Approach for Next Generation Corn Rootworm Management. **Thomas L Clark**, Entomology Programs Lead, Monsanto Company, 700 Chesterfield PKWY West GG3M, Chesterfield, MO 63017. **Abstract:** Currently, all commercialized transgenic

approaches for managing western corn rootworm (WCR), *Diabrotica virgifera virgifera* LeConte, and northern corn rootworm, *Diabrotica barberi* Smith and Lawrence, in the USA utilize a Bt as the insecticidal mode of action. While this approach has proven to be an excellent tactic for maize producers in the USA, additional modes of action will likely be required to ensure the long term success of transgenic approaches for rootworm management. We recently reported that ingestion of dsRNAs from selected target gene templates can induce larval stunting and mortality in artificial feeding assays. Furthermore, we demonstrated that maize plants expressing selected dsRNAs protect roots from rootworm feeding damage. Here, we demonstrate that *in-planta* dsRNAs alone and in combination with Bt significantly impacts multiple aspects of WCR life history while challenging these pests to a novel mode of action. Beyond root feeding protection, our results indicate that this approach may serve as an effective resistance management option as we move forward with additional options for managing rootworms of maize.

11:21 a.m. Corn Rootworm Management – Syngenta’s Multi-faceted Approach. **Miloud Araba**, Ryan Kurtz, Jon Sagers, Craig Nichols, Syngenta Corp. **Abstract:** Syngenta offers an industry leading insect control portfolio which includes crop protection chemistry and trait products. Syngenta is committed to this global need and continues its research and development programs to preserve the yield potential of agricultural crops. In this presentation, Syngenta will describe its views on management options for key pest insects such as corn rootworm. Syngenta recognizes the importance of using a multi-faceted approach to preserving these technologies, providing durable pest insect control, supporting IRM practices and resistance monitoring activities to this end.

SUBMITTED ORAL PRESENTATIONS

1:50 p.m. A Calcium-binding and other functional proteins in the saliva of the green rice leafhopper, *Nephotettix cincticeps*. **M Hattori**¹, S Komatsu², M Nakamura¹, Y Tamura¹.

¹National Institute of Agrobiological Sciences, ²National Institute of Crop Sciences. **Abstract:** The green rice leafhopper *Nephotettix cincticeps* is a major insect pest of rice in temperate East Asia. It uses stylets to intracellularly penetrate plant tissues and ingests from mainly phloem and xylem. The leafhopper discharges watery and gelling saliva in the feeding process. Insect saliva is considered to have the ability to suppress plant basal defense. Saliva of phloem-feeding insects may cause a series of biochemical or physiological alteration of their host plant to suppress sieve-element sealing and avoid toxic substances. So far only a few studies have been made on the molecular identification of salivary components in the phloem-feeding insects. To understand the feeding mechanism of the leafhopper, we identified and cloned various proteins including enzymes from watery saliva and stylet sheaths. A calcium-binding protein with EF-hand motifs was the most predominant salivary protein in this insect. The protein was detected in the phloem sap of rice plant exposed to leafhoppers, verifying that it is injected into the sieve tubes prior to feeding. It would bind Ca²⁺ ions that flow into sieve tubes in response to stylet puncturing. The activity of two salivary enzymes, laccase (laccase-1 group) and β -glucosidase (glycosyl hydrolase family 1) activities was detected in stylet sheaths, suggesting that they are involved in gelling of sheath saliva. Pectinase, protease, and dehydrogenase known as aphid salivary components were not found.

2:05 p.m. Strategies to identify genes mediating the virulence of brown plant hopper to resistant rice. **Tetsuya Kobayashi**, M Hattori. National Institute of Agrobiological Sciences, 1-2 Ohwashi, Tsukuba, Ibaraki 305-8634, Japan. **Abstract:** The brown plant hopper (BPH;

Nilaparvata lugens) is a major threat to rice production in Asia. Rice varieties resistant to BPH have been bred and released since the 1970s, while development of virulent biotypes that can attack these varieties hindered the use of host-plant resistance in the fields. Currently, more than 30 resistant genes to BPH were identified and some were cloned. Cloning of BPH resistant genes in rice will enable us to reveal molecular mechanisms of host varietal resistance. On the other hand, study on attacking mechanism of virulent BPH biotypes to resistant rice varieties has not been fully studied. So far, proteome or enzymatic analyses of BPH biotypes have not succeeded in identifying the major factors mediating the virulence. Unlike other insect pests, virulence of BPH biotypes is under polygenic control, thus, identification of virulent genes is considered to be difficult. Recent development of high-throughput sequencing and genotyping technologies enabled us to search responsible genes for virulence of BPH biotypes because global transcriptome analysis and map-based cloning using high density genetic map are now available in non-model insects such as BPH. We have begun to develop inbred lines of different BPH biotypes, and inheritance of virulence was analyzed in the laboratory.

2:20 p.m. Phloem-specific resistance in *Brassica oleracea* against the whitefly *Aleyrodes proletella*. **Colette Broekgaarden**, G. Steenhuis, J. Bucher, B. Vosman. **Abstract:** Plants have developed defense traits to overcome attacks by herbivorous insects. For many resistance traits heritable variation exists in nature, leading to differences in herbivore performance on plants from the same species. In our research we exploit natural variation in plant species from the Brassicaceae family for resistance to phloem-feeding insects to identify and elucidate plant resistance mechanisms. In general, we use no-choice experiments on field- and/or greenhouse-grown plants to monitor herbivore performance. So far, we have identified very effective sources of resistance towards the cabbage whitefly [*Aleyrodes proletella* L. (Hemiptera: Aleyrodidae)] in *Brassica oleracea* and *Arabidopsis thaliana*. For *B. oleracea*, we have shown that the resistance is mainly based on antibiosis (traits that reduce herbivore performance) and not on antixenosis (traits that deter herbivory). This was further supported by laboratory choice experiments that indicated little or no discrimination between the resistant and a susceptible *B. oleracea* cultivar based on plant volatiles. We showed that resistance is dependent on plant age, that is, resistance increased during plant development, and is mainly independent of environmental factors. Analysis of probing behavior revealed that the resistance trait affects *A. proletella* at the phloem level and that morphological differences between the two cultivars are most likely not involved. We suggest that compounds present in the phloem reduce sap ingestion by the whitefly and that this explains the observed resistance.

2:35 p.m. Effects of aphid feeding on the anatomy and physiology of barley and wheat leaves under ambient CO₂ conditions. **Saheed S Adekilekun**, Department of Botany, Obafemi Awolowo University, Ile-Ife, Nigeria; Department of Botany, Rhodes University, Grahamstown South Africa. **Abstract:** The effects of feeding by the Russian wheat aphid (RWA) and the Bird cherry-oat aphid (BCA) on the leaf structure and physiology of barley and wheat cultivars has been studied using Transmission Electron Microscopy (TEM) at ambient CO₂. This study revealed that aphid feeding caused severe damage to the phloem tissue as a whole, the tissues includes the sieve element-companion cell complexes and associated parenchyma, as well as to the thick-walled sieve tubes. BCA caused less severe damage to the vasculature and to the associated sieve elements of the vascular bundle; damage was equally less severe in aphid-infested resistant plant cultivars when compared to the susceptible counterparts and those infested by RWA. Feeding related damage was assessed using fluorescence microscope-based investigations using the phloem mobile fluorophore, 5,6 carboxyfluorescein and aniline blue

fluorochrome – a specific stain for callose which is formed in the phloem as a result of feeding and probing (plant response to cell wounding). These experiments showed that BCA inflicted less severe damage to the vascular tissue than those infested with RWA, where extensive wound callose deposition occurred. This in turn, was shown to impact on the transport capacity of the phloem within damaged leaves. Studies are ongoing on these effects at the elevated CO₂ levels.

3:10 p.m. Development of a resistance gene pyramid wheat containing H25 and H26 resistance to Hessian fly (*Mayetiola destructor*). **Brandon Schemerhorn**^{1,2}, R. Shukle^{1,2}, R. Smith¹, Y. Crane¹. ¹USDA-ARS / ²Purdue University. **Abstract:** Even with the advances of genomics in the understanding of Hessian fly biology, the primary means of controlling the fly infestations on wheat is through the use of cultural practices and resistance genes in wheat. Here we report the first known resistance pyramid created for Hessian fly containing two genes not previously commercially released in the United States. We discuss the reasoning for choosing these two lines, as well as our experimental data showing this germplasm to be effective against Hessian fly in laboratory setting.

3:25 p.m. Effects of antinutrient proteins on Hessian fly (Diptera: Cecidomyiidae) larvae. **Richard H Shukle**¹, S Subramanyam², CE Williams¹. ¹USDA-ARS/Dept. of Entomology, Purdue University, West Lafayette, IN 47907, ²Department of Agronomy, Purdue University, West Lafayette, IN 47907. **Abstract:** One strategy to enhance the durability of Hessian fly resistance (R) genes in wheat is to combine them with transgenes for resistance. To identify potential transgenes for resistance a protocol for rapidly screening the proteins they encode for efficacy toward resistance is required. However, the Hessian fly is an obligate parasite of wheat and related grasses. Consequently, no protocol for in vitro delivery of antinutrient or toxic proteins to feeding larvae is available. We report here the development of a Hessian fly in planta translocation feeding assay and the evaluation of eight lectins and the Bowman-Birk serine proteinase inhibitor for potential in transgenic resistance. Of the antinutrient proteins evaluated, *Galanthus nivalis* L. agglutinin (GNA), commonly termed snowdrop lectin, was the most efficacious. Ingestion of GNA caused a significant reduction in growth of Hessian fly larvae, disruption of midgut microvilli, and changes in transcript level of genes involved in carbohydrate metabolism, digestion, detoxification, and stress response.

3:40 p.m. Comparison of localized versus regional resistance and susceptibility in wheat cells responding to first-instar Hessian fly larval attack. **Christie Williams**¹, Jill Nemacheck¹, S Subramanyam², K Saltzmann³. ¹USDA-ARS Crop Production and Pest Control Research Unit, Purdue University, Dept. of Entomology, West Lafayette, IN, ²Purdue University Dept. of Agronomy, West Lafayette, IN., ³Purdue University Dept. of Entomology, West Lafayette, IN. **Abstract:** Previous reports have characterized Hessian fly-responsive gene expression in wheat during both compatible and incompatible interactions, using whole leaf sheath samples. However, the larvae are very small and as they attempt to establish feeding sites directly interact with only a few plant cells. During the first few days of attack, major responses of the plant may be spatially localized and thus undetectable in samples from whole leaf sheath. Laser-capture micro-dissection (LCM) was used to sample small groups of wheat cells directly below larval mandibles to assess the responses at larval feeding sites. Comparisons of whole leaf sheath versus LCM microarray data identified genes that were highly responsive locally but not detected regionally in whole tissue samples. Several categories of genes involved in resistance and susceptibility will be discussed.

3:55 Prey foraging by *Hippodamia Convergens* for cereal aphids on wheat. **Norman Elliott**, USDA-ARS, 1301 N. Western Rd., Stillwater, Oklahoma, USA. **Abstract:** We investigated predation by adult convergent lady beetle, *Hippodamia convergens* Guerin-Meneville, on English grain aphid, *Sitobion avenae* L., on wheat, *Triticum aestivum* L., plants in a laboratory arena and developed a functional response model for the number of aphids eaten by an adult female convergent lady beetle. Beetle hunger and the number of aphids per plant were significantly correlated with the time spent searching a wheat plant and the number of aphids eaten during the plant visit. Partial correlation coefficients for hunger after adjusting for the effect of the number of aphids per plant were not significant for the time spent searching a plant or for the number of aphids eaten during a plant visit. Knowledge of the number of aphids per plant was sufficient for predicting searching time and predation. A Holling Type II functional response model was developed and tested. Comparison of the expected proportion of English grain aphids eaten versus the observed proportion eaten showed that there was no statistically significant bias in model predictions. However, wide variation in observed versus predicted predation rates was evident.

Wednesday, April 4

SYMPOSIUM: INTERNATIONAL PERSPECTIVES ON PLANT RESISTANCE TO CEREAL INSECT PESTS.

8: 20 a.m. Mining genebank holdings using the Focused Identification of Germplasm Strategy (FIGS): sources of resistance in wheat to Russian wheat aphid, Sunn pest and Hessian fly. **M El Bouhssini**, K. Street, A. Bari, A. Amri, International Center for Agricultural Research in the Dry Areas (ICARDA), P.O. Box 5466, Aleppo, Syria. **Abstract:** Russian wheat aphid (RWA), *Diuraphis noxia* (Kurdjumov), Sunn pest, *Eurygaster integriceps* Puton, and Hessian fly, *Mayetiola destructor* (Say) are important insect pests of wheat in North Africa, West and Central Asia. The Focused Identification of Germplasm Strategy (FIGS) enables large genebank collections to be “mined” for specific traits such as insect pest resistance. FIGS is based on the paradigm of co-evolution of, and interaction between, host and pest. It analyzes the agro-climatic characteristics of sites from which plant germplasm was originally collected, to make predictions of best-bet accessions that are most likely to contain the trait of interest. FIGS was used to identify three trait-specific best-bet subsets, totaling 1544 accessions of bread and durum wheat, from a total of 16,000 geo-referenced accessions conserved in the genebanks of the International Center for Agricultural Research in the Dry Areas (ICARDA), the Vavilov Institute and the Australian Winter Cereals Collection. The selected material was subjected to field and greenhouse screening in Syria for resistance to RWA and Sunn pest. Screening for Hessian fly resistance was carried out in the greenhouse in Syria, Morocco and the USA. Forty-four resistant accessions were identified: 12 bread wheat lines to RWA, one durum wheat and eight bread wheat accessions to Sunn pest, and 23 durum wheat lines to the Great Plains Hessian fly biotype in the USA. The results also showed the effectiveness of the FIGS approach in identifying genotypes with valuable traits. FIGS has the potential to reduce the resources required to exploit genetic resource collections.

8:45 a.m. The association mapping for *Sitobion avenae* resistance and tolerance in bread wheat germplasm. **F Li**^{1,2,3}, **Liang Chen**^{1,2}, **J Peng**^{1,2,4*}. ¹Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan, Hubei 430074, China, ²Key Laboratory of Plant Germplasm Enhancement and Specialty Agriculture, Chinese Academy of Sciences, Wuhan, Hubei 430074, China, ³Graduate University of Chinese Academy of Sciences, 19 Yuquan Road, Beijing 100049, China, ⁴Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO 80526-1170,

USA. **Abstract:** *Sitobion avenae* is one of the most important wheat pests. To identify loci for *S. avenae* resistance and tolerance, association mapping was conducted using two bread wheat populations mainly from China and central Asia. The bread wheat germplasm was evaluated the resistance and tolerance to *S. avenae* at two different locations. The peak aphid density and 10000 kernel weight loss rate were used to calculate the resistance index and tolerance index, respectively. Totally, forty-six accessions exhibited high or moderate levels resistance, and forty-eight genotypes showed highly tolerate or moderately tolerate to *S. avenae*. SSR based phylogenetic relationship were assessed for the *S. avenae* resistance accessions and tolerance accessions. After association analyzes, seven SSR loci were identified significantly associated with *S. avenae* resistance index, and eleven loci showed a significant association with *S. avenae* tolerance index, the loci for *S. avenae* resistance/tolerance and RWA resistance were compared also. In addition, the phenotypic allelic effects the average allele effect of these loci were estimated. This information generated in this study should be helpful for utilization of the *S. avenae* resistance/tolerance germplasm and selection of parental lines in *S. avenae* resistance breeding programs.

9:10 a.m. Host cell modulation by aphid effector proteins. P Rodriguez¹, T Warbroek¹, M Armstrong², P Birch², **Jorunn Bos**¹. ¹James Hutton Institute; ²University of Dundee. **Abstract:** Like most plant parasites, aphids require intimate associations with their hosts to gain access to nutrients. Aphids predominantly feed from the phloem, and have stylets that navigate through different layers of leaf tissue to form an interface with the host where signals are exchanged. Indeed, aphid feeding induces clogging of phloem sieve elements, which is suppressed by the aphid in successful host interactions. In addition, aphids can alter host plant phenotypes by, for example, inducing the formation of galls or causing leaf curling. Suppression of host defences and alternating plant physiology is common among phytopathogens and involves secretion of molecules (effectors) that manipulate host cell processes. Recent evidence suggests that aphids, like other plant parasites, secrete effectors that may share functional features with plant pathogen effectors. The identification and characterization of such effectors is crucial to gain insight into the molecular mechanisms underlying plant resistance and susceptibility to aphids. Our research aims to further characterize the activities of aphid effectors that function inside plant cells to investigate their involvement in host (cell) manipulation. We have screened a set of candidate effectors from the broad host range of *M. persicae* using yeast-two-hybrid assays against a potato library to identify potential host targets. Hence we will report our progress on identifying and characterizing effector-target interactions. In the long term, our research will provide new knowledge on plant-aphid interactions that is crucial to develop effective and sustainable control strategies.

9:55 a.m. Evoking the induced systemic resistance of wheat to impart resistance against the Russian wheat aphid. **Eddie Venter**¹, C Mansoor¹, A-M Botha², ¹Department of Botany and Plant Biotechnology, University of Johannesburg, South Africa; ²Department of Genetics, University of Stellenbosch, South Africa. **Abstract:** *Diuraphis noxia* Kurdjumov is an aphid pest that hampers the global production of wheat. Infestation of wheat by *D. noxia* reduces crop yield and leads to the death of susceptible cultivars. To date resistant cultivars were used in conjunction with pesticide application to control infestations. However, the development of resistance breaking biotypes is complicating this management strategy. This study aimed to ascertain the effect that potassium phosphate treatment has on the induced systemic resistance (ISR) in wheat. The effects of potassium phosphate on induced systemic resistance against *D. noxia* were accomplished through studying the regulation of lipoxygenase and phenyl ammonia lyase at gene

regulation and enzyme activity levels. The results indicated that the treatment of wheat with potassium phosphate induces genes differentially in treated resistant and susceptible cultivars. A phenotypic study showed later development and less severity of symptoms, as well as decreased numbers of aphids on plants treated with potassium phosphate in comparison with untreated plants for both resistant and susceptible cultivars. The result of the gene expression and enzyme activities indicated that several of the ISR-linked genes were similarly regulated after potassium phosphate treatment. The gene expression data strongly supports treatment of wheat with potassium phosphate to induce the ISR for increased resistance to *D. noxia* infestation. This will assist farmers to combat infestations by *D. noxia* in future.

10:20 a.m. Proteomic Analysis of Secreted Saliva from Russian Wheat Aphid (*Diuraphis noxia* Kurd.) Biotypes that Differ in Virulence to Wheat. **Scott J Nicholson**, G Puterka, USDA-ARS. **Abstract:** *Diuraphis noxia*, Russian Wheat Aphid (RWA), biotypes are classified by their differential virulence to wheat varieties containing resistance genes. RWA salivary proteins, unlike those of most aphid species, cause foliar damage and physiological alterations in plants. A comparative proteomic analysis of secreted saliva from four differentially virulent RWA biotypes identified thirty-four individual proteins. The five major proteins were glucose dehydrogenase, lipophorin, chitinase, CiV16.8g1-like, and lava lamp. Fourteen proteins quantitatively varied among biotypes; trehalase, β -N-acetylglucosaminidase (chitinase), two separate glucose dehydrogenases, calreticulin, aminopeptidase, acetylglucosaminyltransferase, hydroxymethylglutaryl-CoA lyase, acyltransferase, ficolin-3, lava lamp, retinaldehyde-binding protein, and two proteins of unknown function. Fifty-four percent of spectral counts were associated with glucose dehydrogenase, which is thought to detoxify plant defensive compounds. One-dimensional electrophoresis detected nine protein bands from 9–60 kDa that quantitatively differed. Two-dimensional electrophoresis identified six major gel zones with quantitative and qualitative variance in proteins. Our findings reveal that the salivary proteome of RWA, a phytotoxic aphid, differs considerably from those reported for nonphytotoxic aphids.

GENERAL POSTERS

1. The influence of rice plant age on resistance to the rice water weevil. **Michael Stout**, J Hamm, LSU Ag Center, Baton Rouge LA USA. **Abstract:** The resistance and tolerance of plants to their herbivorous consumers changes as plants age and pass through various ontogenetic stages. These age- or stage-related changes in plant resistance occur for various reasons, including age-related changes in plant primary or secondary metabolism, age-related changes in plant physical or morphological features, and changes in the availability of feeding sites. The experiments described here were undertaken to characterize the relationship between rice (*Oryza sativa*) plant age and susceptibility to infestation by the rice water weevil (*Lissorhoptrus oryzophilus*), the most important insect pest of rice in the U.S. In a series of field and greenhouse choice and no-choice experiments, rice plants were found to be susceptible to infestation by rice water weevils from the two-leaf stage to the panicle differentiation stage. However, rice plants were clearly most susceptible to infestation by rice water weevils during the tillering stage of plant development. The implications of these findings for management of this important pest are discussed.

2. Effect of silicon on resistance of two rice cultivars against sugarcane borer, *Diatraea saccharalis*. JKSidhu, **Michael J Stout**, LE Datnoff, LSU Ag Center, Baton Rouge LA USA. **Abstract:** Two rice cultivars, Cocodrie and XL723, were used to investigate the effect of silicon

soil amendments on resistance to sugarcane borer, *D. saccharalis*. Relative growth rates of sugarcane borer larvae and boring success were lower on plants treated with silicon than on untreated plants. Mean silicon content was higher in the silicon treated plants as compared to the control plants.

3. Next Generation sequencing of the genomes of 11 International RWA biotypes. **Anna-Maria Botha**¹, NFV Burger¹, A-M Castro², M El-Bouhssini³, J Havelka⁴, A Jankielsohn⁵, NLV Lapitan⁶, F Peairs⁷, G Puterka⁸, CM Smith⁹, P Stary⁴, M Zurovcova⁴. ¹Department of Genetics, Faculty of AgriSciences, Stellenbosch University, Private BagX1, Matieland, 7601, South Africa; ²Genetics Faculty of Agricultural Sci, UNLP, CINICET, CC31, 1900-La Plata, Argentina; ³International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria; ⁴Biology Centre of the Academy of Sciences of the Czech Republic, Institute of Entomology, Czech Academy of Sciences; ⁵ARC-Small Grain Institute, Crop Protection, Private Bag X29, Bethlehem, 9700; ⁶Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO 80523, USA; ⁷Department of BioAgricultural Sciences and Pest Management, Colorado State University, Fort Collins, CO 80523, USA; ⁸ARS-USDA, 1301 N. Western Rd, Stillwater, OK 74075, USA; ⁹Department of Entomology, Kansas State University, Manhattan, KS 66506-4004, USA.

Abstract: Scientists researching poorly characterized species struggle to gain understanding of the species they study on a sub-cellular level due to the time and investment required to build up an informative knowledge base. This becomes problematic when a poorly characterized species is a pest of a major economically important food crop, such as in the case of Russian Wheat Aphid (RWA) (*Diuraphis noxia*, Kurdjmov). This phloem sucking insect occurring in all major wheat producing centres of the world (except Australia) has been well studied, yet little molecular data has been acquired due to a lack of a solid foundation of available data to build on. Thus, we decided to sequence the genomes of 11 RWA biotypes sampled from South Africa, the USA, Argentina, Syria and the Czech Republic. Genomic DNA was extracted, pooled and sequenced using both Roche's 454 sequencing and the ABI's SOLiD system with individual samples verified through using Sanger sequencing. Identifying individual biotypes would be possible, given that RWAs propagate in a clonal form in most, if not all, non-native countries. Our aims with this collaborative effort therefore are (1) to produce a representative sequence backbone of the RWA genome; (2) unlock the genomic complexities of this economically important cereal pest; (3) compare the genome of RWA to that of other arthropod genomes; and (4) to draw up a geographic distribution of RWA genealogy and so compare how biotype formation is driven in different areas if more specimens from areas other than those sampled can be obtained.

4. Russian Wheat Aphid Biotypic Diversity and Distribution in the Western United States. **Gary Puterka**¹, S Nicholson¹, Mike Brown¹, F Peairs², B Hammon², E Bynum³, J Michels³, ¹USDA-ARS, Stillwater, ²Colorado State University, Ft. Collins, ³Texas A&M Exp. Stn. Bushland, TX.

Abstract: A multi-state survey of Russian wheat aphid biotype composition in wheat was conducted in the spring of 2010 and 2011. Aphid collections from Texas, Colorado, Kansas, Oklahoma and Utah were evaluated on 9 plant differentials in replicated screening flat experiments under greenhouse conditions. In 2010, RWA could only be located in Texas due to harsh summer and winter conditions. Greater than 90% of the collections were RWA1. In 2011, RWA1 again dominated the RWA biotype complex in Texas and Colorado. Results indicate there has been a major shift of the biotype complex to RWA1. Prior to this study, RWA2 dominated the biotype complex from 2005-2007.

5. A miRNA Genechip® analysis of the wheat – Russian wheat aphid interaction. **Sonia-Mari Greyling**, V Nicolis, E Venter, Department of Botany and Plant Biotechnology, University of Johannesburg, South Africa. **Abstract:** Wheat is the second largest summer and largest winter cereal crop produced in South Africa. Historically the Russian wheat aphid (*Diuraphis noxia* Kurdjumov) threatened wheat production in the Free State province, but it has now also been detected in the wheat production areas of the Western Cape. The problem is further exacerbated by the development of at least two new resistance breaking biotypes that have overcome the most prevalently used resistance alleles. Understanding how the plants respond at several levels after infestation is essential if a more effective method for control is to be established. This study aimed to identify the role that microRNA (miRNA) plays during the Russian wheat aphid interaction with wheat. The first generation Affymetrix Genechip® miRNA array was used to analyse the regulation of wheat miRNA molecules at early (5 hpi) and later (24 hpi) time points of the interaction. This analysis has resulted in the identification of differentially regulated miRNA molecules between resistant (Tugela Dn) and susceptible (Tugela) wheat cultivars at both time intervals. The array data is currently being further analysed to establish the role that miRNA plays at the regulatory level during the RWA – wheat interaction.

6. Gene-for-Gene Interactions Between Hessian Fly and Wheat: Phenotypes and Fitness Costs. **Marion O Harris**¹, T Freeman¹, K Anderson¹, J Moore¹, S Payne¹, A Zhang¹ and J Stuart², ¹North Dakota State University, Fargo, ND, ²Purdue University, West Lafayette, IN. **Abstract:** The Hessian fly is unusual among insects in showing gene-for-gene interactions, a phenomenon first reported by the plant pathologist Harold Flor in the 1940s. Hessian fly gene-for-gene interactions (Hatchett and Gallun, 1970) became apparent after two discoveries: 1) grasses have *resistance* genes (*H* genes) that confer a highly effective resistance to the Hessian fly and 2) the Hessian fly defeats this resistance through mutations in matching *Avirulence* (*Avr*) genes. For example, on the *H13* gene-protected plant, attacking larvae that express the matching *vH13* gene are detected, with detection triggering downstream resistance responses. As a result, the insect dies and the plant lives. On the other hand, mutations in the Hessian fly *vH13* gene prevent the requisite *H13/vH13* interaction from occurring and the *H13* gene-mediated surveillance system fails. As a result, the plant dies and the insect lives. Another interesting feature of Hessian fly-grass interactions is induced susceptibility, which comes from the Hessian fly's status as a gall-maker. Attack triggers the creation of a gall nutritive tissue, which subsequently breaks down to provide a liquid diet to the larva. We used imaging techniques (light, SEM, TEM) and measured plant and insect survival, growth and reproductive success to further explore the four interactions that are possible between the grass *H13* resistance gene and the Hessian fly *vH13* gene. The negative impact of the gall nutritive tissue on plant growth creates strong selection pressure for the evolution of plant *resistance* genes that prevent the Hessian fly from inducing susceptibility. Because neither the constitutive or induced components of *H* gene resistance have fitness costs for the plant, we expect that a large numbers of *H* genes will be found in grass genomes.

7. Marker-assisted breeding for Hessian fly and disease resistance in spring wheat. **NA Bosque-Pérez**¹, J Chen², LM Unger¹, DR See³, S Odubiyi, J Wheeler². ¹Department of Plant, Soil and Entomological Sciences, P.O. Box 442339, University of Idaho, Moscow, ID 83844-2339; ²Department of Plant, Soil and Entomological Sciences, University of Idaho Aberdeen R & E Center, 1691 S 2700 W, Aberdeen, ID 83210; ³Western Regional Small Grains Genotyping Center, USDA-ARS, 209 Johnson Hall, Washington State University, Pullman, WA 99164. **Abstract:** Hessian fly, *Mayetiola destructor* Say, is one of the most destructive pests of wheat worldwide. Resistant varieties offer the most reliable mean for control of this pest. Compared to

expensive phenotypic screening, molecular marker assisted selection (MAS) can accelerate development of resistant cultivars. Additionally, MAS can facilitate pyramiding of genes that confer fly and disease resistance. The H25 gene, derived from rye, confers resistance to most fly biotypes in the US. H25 was mapped on chromosome 4A and microsatellite marker Xgwm610 identified and tightly linked to H25 in previous studies. The objectives of this study were to: 1) evaluate the effectiveness of using Xgwm610 to select for fly resistance in early generations (F1 and F3) in two spring wheat populations, and 2) pyramid fly resistance with resistance to stripe rust and Fusarium head blight via MAS. Eleven and eight F1 individuals were derived from crosses IDO586/Jerome // Lassik and JFSN*4/IDO584 // Lassik, respectively. IDO586 and IDO584 carry H25. Lassik is a fly-susceptible, disease resistant genotype that carries the genes Yr36 and FHB1 based on markers Uhw89 and Umn10, respectively. Comparisons of marker data and fly resistance responses of four F3 families showed that Xgwm610 predicted 63 to 71% of fly resistance in two populations, suggesting that Xgwm610 can be used to select for fly resistance in early generations. F3 individuals that possess marker alleles for resistance to Hessian fly, stripe rust and Fusarium head blight have been identified, indicating that it is possible to pyramid multiple resistant genes using MAS.

8. Ultrastructural descriptions for the antennal sensillae of males and females peach fruit flies *Bactrocera zonata* (Saunders) (Diptera: Tephritidae) infested mango fruits. **Azza A Awad¹**, NA Ali², HO Mohamed². ¹Zoology Department, Faculty of Science, Assiut University; ²Plant Protection Research Institute, ARC. **Abstract:** Antennal morphology and funicular sensillae of males and females peach fruit flies, *Bactrocera zonata* (Saunders), were studied with scanning electron microscopy (SEM). This study focused on the sensillae found on the three segments of the fruit flies antennae. Those are a scape, a pedicel, and flagellum or funiculus that bears the arista. Antennal segments of females tended to be larger than those of the males. The first two antennal segments, scape and pedicel are heavily covered with microtrichia and bear bristles. Numerous microtrichia as well as trichoid (I, II), basiconic, clavate, and coeloconic sensillae were observed on the funiculus, and the sensillar characteristics were similar to those reported for other tephritid species. Scanning electron microscope studies showed some differences in size and also in position of some sensillae on the antennae of the females of *Bactrocera zonata* (Saunders). Those are sensillae found on the funiculus like trichoid and clavate sensillae. This study indicated that those sensillae were significantly larger in females. This difference may be related to the function of the female's chemo-receptors. On the other hand, that phenomenon could be related to the emitted sex pheromone received by the antennae of males. Also, one could explain the preferences behavior of the perception of host plant volatiles and their relation with the presence of all those type of sensillae on the antennae of the fruit flies.

9. Novel germplasm sources of soybean for resistance against different biotypes of soybean aphid. **Raman Bansal¹**, MA Rouf Mian², AP Michel¹. ¹The Ohio State University, Wooster OH-44691, ²USDA-ARS, Wooster, OH-44691. **Abstract:** The soybean aphid, *Aphis glycines* Matsumura is a major pest of soybean throughout soybean-growing regions of the U.S. We screened 1086 soybean accessions for resistance against *A. glycines*. Based on growth chamber screening and subsequent field trials, we identified 12 accessions showing resistance against biotype 1 of *A. glycines*. All soybean accessions in the resistant category belonged to maturity group III or IV. Presently, we are investigating the response of these resistant accessions to biotype 2 and biotype 3 of *A. glycines*. We also identified 11 soybean accessions that appeared tolerant to biotype 1 infestation. The current study provides the basis to develop resistant soybean cultivars to manage *A. glycines* in the field.

10. Inheritance and Mapping of Soybean Aphid Resistance in Soybean Accession PI603432B. **Mukhtar Agoub**¹, G-L Jiang¹, J Ori². ¹Plant Science Dept., South Dakota State University; ²Department of Agronomy and Plant Genetics, University of Minnesota. **Abstract:** The soybean aphid (*Aphis glycine* Matsumura) has been found colonizing soybean plants (*Glycine max* (L.)) in the upper Midwestern United States since 2000. The objective of this study is to determine the inheritance of soybean aphid resistance in the soybean accession PI603432B and susceptible varieties (MN0602CN and MN060281), and F2 plants and F2:4 lines from each cross were screened for aphid resistance in the field and greenhouse, respectively. DNA samples were collected from individual plants. To determine if PI603432B has the same gene(s) as those in previously identified PIs, 12 SSR markers that were reported to be associated with soybean aphid resistance were screened using bulk segregate analysis (BSA). The segregation for aphid resistance in the F2 and F2:4 populations derived from both crosses appeared to fit a single dominant gene model. The data of simple sequence repeat (SSR) marker screening indicated that PI 603432B might be a new source of aphid resistance carrying *Rag2* in maturity group 0.

11. Chemical Analysis of Spinach Resistance to Aphids and Leaf miners. **Nasir Masood**¹, M Ashfaq². ¹University college of Agriculture and Environmental Sciences, The Islamia University of Bahawalpur 63100, Punjab, Pakistan; ²University of Agriculture Faisalabad 38040, Punjab, Pakistan. **Abstract:** Host plant resistance is an essential factor of integrated pest management (IPM) while understanding the biochemical mechanisms could speed up the resistance breeding. To study the biochemical mechanisms of spinach plant resistance to its major insect pests, leafminer (*Liriomyza langei*) and aphids, sixteen Spinach genotypes with various degree of resistance were planted in growth chambers and a field with four replications. Sugars, protein, chlorophylls, carotenoids, and phenolics were extracted from plant leaves, and damage by leafminers and numbers of aphids in different species were recorded. Leafminer stings per cm² leaf area of young plants were highly correlated with sting/cm² of mature plants. This suggests that leafminer-resistant varieties for mature spinach plants may also be deployed for baby leaf production. Sucrose concentration of young plants was correlated with leafminer stings per cm² leaf ($r = 0.729$, $p = 0.01$) and mines per plant ($r = 0.789$, $p = 0.01$), suggesting that low sucrose content could be used as a marker for early screening or selection for leafminer resistance. Leafminer stings/cm² were negatively associated with contents of flavonoids ($r = -0.558$, $p = 0.05$) and chlorogenic acid ($r = -0.5978$, $p = 0.05$), while mines per plant were negatively associated with concentrations of flavonoid ($r = -0.701$, $p = 0.01$), chlorogenic acid ($r = -0.592$, $p = 0.05$) and rutin ($r = -0.601$, $p = 0.05$), implying a role of phenolics in the leafminer resistance. Total number of apterous aphids including *Myzus persicae*, *Macrosiphum euphorbiae* and *Aulacorthum solani* per 100 g plant weight was correlated with contents of protein ($r = 0.889$, $p = 0.01$), β -carotene ($r = 0.826$, $p = 0.01$), lutein ($r = 0.815$, $p = 0.01$), chlorophyll ($r = 0.734$, $p = 0.01$), and glucose ($r = -0.768$, $p = 0.01$) of young spinach plants, which could serve as early indicators of aphid resistance. Aphids per 100 g plant weight were also associated with chicoric acid concentration of mature spinach plant ($r = 0.749$, $p = 0.01$). This study provides insights into the mechanism of resistance to leafminers and aphids as well as screening and selection tools for breeding insect-resistant spinach.

12. Utilizing Varietal Resistance to Manage Tarnished Plant Bug in Cotton. **Glenn Stuebaker**, F Bourland, University of Arkansas, Division of Agriculture. **Abstract:** The tarnished plant bug is considered the most damaging pest of cotton in the mid-southern United States. Cotton growers average 3 to 5 insecticide applications a year to manage this pest. Insecticide efficacy has steadily begun to decrease causing some concern over possible insecticide resistance

developing in the tarnished plant bug. Certain cotton varieties show less damage from tarnished plant bug in ultra-small plot (2 rows x 20-ft). These varieties were evaluated in large plots (16-20 rows x 100-ft) and in commercial fields (40 to 80 acres in size). In large block replicated trials, resistant varieties did not reach treatment threshold (3 plant bugs per 5 row-ft) until later in the season and at about half the rate of more susceptible varieties. The same also held for commercially grown cotton in large fields. Utilizing resistant varieties does appear to be a more viable tool in managing tarnished plant bugs and should reduce costs as well as the pesticide load on the environment.

13. Pheromone Traps and Molecular Markers Genotype Hessian flies for Virulence to Resistance Gene *H13* in wheat. AJ Johnson¹, **Richard H Shukle**¹, GD Buntin², KL Flanders³, FPF Reay-Jones⁴, DD Reisig⁵, BJ Schemerhorn¹, JJ Stuart⁶; ¹USDA-ARS/Dept. of Entomology, Purdue University, West Lafayette, IN 47907; ²Dept. of Entomology, University of Georgia, Griffin, GA 30223; ³Dept. of Entomology, Auburn University, Auburn, AL 36849; ⁴Dept. of Entomology, Clemson University, Clemson, SC 29631; ⁵Dept. of Entomology, North Carolina State University, Raleigh, NC 27607, ⁶Dept. of Entomology, Purdue University, West Lafayette, IN 47907. **Abstract:** Hessian flies (HF, *Mayetiola destructor*) differ in their ability to survive on and permanently stunt wheat seedlings carrying the HF resistance gene *H13*. This ability is determined by mutations in a single HF gene (*vH13*), which was recently discovered using genomic methodologies. Six different *vH13* alleles have been discovered, 3 avirulent alleles (Avr1, Avr2, and Avr3) that differ with respect to the number of imperfect direct repeats and 3 virulent alleles (vir1, vir2, and vir3) that each have a different insertion. To determine the frequency of each allele in field populations, we are using sex-pheromone-baited traps to collect males from fields in the southeastern U.S. and PCR to amplify and characterize each male's genotype. Results will inform wheat breeders and wheat growers with respect to the frequency of *H13*-virulence in local HF populations and monitor changes in the frequency of *H13*-virulence in populations that are exposed to *H13*.

14. The Host-Plant Resistance Puzzle for Soybean Aphid Management. **Louis S Hesler**¹, G-L Jiang², KE Dashiell¹, S Bhusal², EA Beckendorf¹, D Schneider¹. ¹North Central Agricultural Research Laboratory, USDA-ARS, Brookings SD; ²Plant Science Department, South Dakota St. Univ., Brookings SD. **Abstract:** Soybean aphid is a major pest in northern soybean-producing regions of North America, causing yield loss and leading to increased aphicide application. Plant resistance is a potential, alternative management strategy. Several aphid-resistant lines and some resistance genes have been identified. We conducted field and laboratory tests to screen for and evaluate soybean lines for resistance. An overview of tests is presented here of field evaluations in 2006, 2008, 2009 and 2011, and selected laboratory tests from 2008. Field tests in 2006 showed that aphid levels on lines predicted to be aphid-resistant based on genetic markers for the *Rag1* resistance gene ranged from 800 to ~6400 aphids per plant (APP), and non-resistant lines reached 12,390 APP. In 2008, *Rag-* and *Rag1* plants averaged <400 APP, whereas *Rag2*-plants averaged 890 APP. Lab tests using aphids field-collected in 2008 showed only a low level of resistance on *Rag2* plants. *Rag1-* and *Rag2*-plants field-tested in 2011 each had heavy infestation ratings that did not differ from susceptible check lines. The results suggest that plants with a single aphid-resistance gene may not adequately reduce aphid populations below injurious levels in any given year.

15. Identification and Characterization of Resistance to the Soybean Aphid in Wild Soybean. **Louis S Hesler**, EA Beckendorf, USDA-ARS, North Central Agricultural Research Laboratory,

Brookings SD USA. **Abstract:** A wide range of sources of resistance to soybean aphid, *Aphis glycines*, may be needed in light of the discovery of biotypes of this soybean pest that overcome previously discovered plant resistance genes. A total of 136 lines of wild soybean, *Glycines soja*, were screened for resistance in terms of population growth of soybean aphid in environmental-chamber tests. Seventeen lines showed resistance. Follow-up tests characterized these lines as having antibiosis, antixenosis, or both forms of resistance expressed. These results indicate that wild soybean is a potentially promising source of resistance to soybean aphid and that additional research is warranted.

16. Barley germplasm resistant to both Russian wheat aphid and greenbug. **DW Mornhinweg**¹, **DE Obert**^{1,2}, **BF Carver**³, ¹USDA-ARS, ²Limagrain, ³Oklahoma State University. **Abstract:** Both Russian wheat aphid, *Diuraphis noxia* (Kurdjumov), and greenbug, *Schizaphis graminum* (Rondani) are potential pests on winter cereals grown in the southern plains. In outbreak years, both aphids can drastically reduce grain yield of susceptible cultivars. In barley, two single dominant genes, *Rsg1* and *Rsg2*, confer resistance to the most prevalent biotypes of greenbug. Greenbug-resistant winter barley cultivars are available to growers in the southern plains. There are no RWA-resistant winter barley cultivars for the US. RWA resistance from 8 different sources was transferred by backcross breeding into Post 90, a high yielding, greenbug resistant cultivar with *Rsg1* resistance. Promising lines breeding true for resistance to both aphids were evaluated for agronomics in Idaho and Oklahoma. Eight germplasm lines, STARS 1006B – STARS 1013B, with grain yield equal to or greater than the recurrent parent, Post 90, have been released. Each line carries RWA resistance from one of 8 different sources as well as *Rsg1* greenbug resistance.

STUDENT POSTERS

S1. Identification of Resistance to Codling Moth and Leafroller in *Malus*. **Joseph Schwarz**, **J Brunner**, **C Peace**, **K Evans**, WSU apple-breeding program. **Abstract:** A whole-leaf bioassay method was developed that provided apple-leaf quality over time. Data on the development and mortality of OBLR larvae reared on an artificial (pinto bean) diet provided a timeline on which to evaluate larval performance on leaves. Delicious and Granny Smith represented standard control apple varieties. Larvae feeding on Viking, Yellow Transparent, Liberty, Virginiagold, Antonovka and Poeltsamaa had the longest development time, while those on Florina (males) and Cox Orange Pippin (females) had the shortest and were similar to those on Granny Smith, Delicious, and pinto bean. Larvae reared on pinto bean weighed more than those on any apple variety. Males had lower pupal weight and developed faster than females. Female pupae varied more in weight than males. Pupal weight was inversely correlated with development time. No female larvae survived on Lady or Northern Spy, and males survived least on Lady and Northern Spy. Male larvae survived best on Cox Orange Pippin and pinto bean. Overall, there was about 10% or less survivorship of male and female larvae feeding on Lady, Northern Spy, Viking, Yellow Transparent, and Antonovka. Some varieties showed gender-specific effects. Moreover, larvae that fed on Antonovka had developmental abnormalities suggestive of juvenile hormone effects. Other varieties showed abnormalities suggesting plant protease activity. Adult emergence was positively correlated with pupation day. The reproductive assessment of adults showed that when reared on some varieties fecundity was significantly reduced. Apple varieties that negatively impacted larval survival and development showed both negative and positive impacts on fecundity.

S2. Impact of Rhizobial Seed Inoculants on Soybean Aphid Densities, **Samantha M Brunner**¹, DA Prischmann-Voldseth¹, RJ Goos². ¹NDSU Entomology, ²NDSU Soil Science. **Abstract:** Commercial soybean production often involves the use of seed inoculants to decrease the need for nitrogen (N) fertilizer and increase plant health and yield. These commercial inoculants typically contain a mixture of *Bradyrhizobium japonicum* and other molecules or organisms, such as lipochitooligosaccharides, *Azospirillum brasilense*, and/or *Delfita acidovorans*. *Bradyrhizobium japonicum* is an N-fixing bacterium symbiotically associated with soybean roots that fixes atmospheric N gas, converting it into a form that is biologically available to the plant. The other chemical and biotic components in the inoculants affect plant physiology in various ways, including altering nodulation, N-fixation, and/or plant growth. Thus, specific inoculants may differentially affect host plant quality for herbivorous insects, including invasive soybean aphids (Hemiptera: Aphididae: *Aphis glycines* Matsumura). To investigate the impact of commercially-available rhizobial seed inoculants on soybean aphid densities we conducted a two year field study using four inoculants, a non-inoculated control, and a high soil N control intended to suppress nodulation and N-fixation while still providing adequate N for plant growth. Two cages were erected in each field plot (one with aphids and one without aphids) to assess how treatments impacted parameters associated with plant quality independent of aphid presence (e.g. height, number of pods, above-ground biomass, N content of foliage, root nodule weight). In order to determine how treatments affected aphid establishment on plants and subsequent reproduction, half of the cages were infested with five adult soybean aphids and their densities quantified after 24 hrs and then weekly for nine weeks.

S3. Inheritance of Resistance to Soybean Stem Borer (*Dectes texanus* Leconte) in Soybean PI165673. **Lina Aguirre-Rojas**, CM Smith, W Schapaugh, B McCornack, L Buschman, Kansas State University. **Abstract:** Soybean stem borer, *Dectes texanus* LeConte, is a pest of soybeans *Glycine max* (L.) in North America and causes significant yield losses because of lodging of the infested plants. Soybean stem borer infestations are increasing across Kansas and other states, necessitating the development of effective tactics to control this pest. The use of resistant cultivars is a desirable strategy to control soybean stem borer, since cultural and chemical options are limited. In previous studies, soybean PI165673 was shown to exhibit resistance to soybean stem borer. The objective of this research is to determine the inheritance of resistance to soybean stem borer in PI165673. Two F2 plant populations from crosses between PI165673 with the susceptible soybean accessions KS5004N (101 plants) and K07_1544 (113 plants) were tested in the field for resistance to soybean stem borer. Twenty days after infestation, the numbers of oviposition punctures (OvP) and larvae (Lv) were counted on each plant from the top five fully developed petioles to estimate the OvP/Lv resistance ratio. Segregation for resistance in the KS5004N/PI165673 F2 population indicated that resistance is controlled by one or two epistatic genes inherited as recessive traits. Segregation for resistance in the K07_1544/PI165673 F2 population indicated that resistance is controlled by two epistatic genes inherited as recessive traits. F2 - derived F3 families from crosses between PI165673 and each susceptible parent will be further evaluated for soybean stem borer resistance. QTL mapping of resistance is in progress using parental polymorphic SSR markers.

S4. Multiple Categories of Resistance to Wheat Curl Mite (Acari: Eriophyidae) expressed in *Aegilops* spp. accessions. **Sandra Garcés Carrera**¹, H Davis¹, L Aguirre-Rojas¹, M Murugan², CM Smith¹. ¹Kansas State University, ²Tamil Nadu Agricultural University, Coimbatore India. **Abstract:** The wheat curl mite (WCM), *Aceria tosichella* Keifer, is an important pest in the western plains of the United States as well as in most major wheat growing regions of the world.

WCM feeding damage and indirect damage by transmission of wheat streak mosaic virus (WSMV), Triticum mosaic virus (TriMV) and High Plains virus (HPV) can result in up to almost 100% yield loss. Mite resistant wheat cultivars have been shown to reduce the spread of WSMV by inhibiting the reproductive capacity of the mite. However, this resistance may be quickly overcome by WCM virulence, so additional sources of WCM resistance must be identified to provide long-term management of this pest. Seven *Aegilops* spp. accessions (TA) were evaluated in choice and non-choice tests to determine their category of resistance to the WCM. TA 1578, 1695, 2394, and 2556 exhibited antibiosis and antixenosis resistance to WCM, demonstrated by the low numbers of WCM adults and nymphs infesting plants, compared to the resistant and susceptible control plants. TA 1582, 1583, 1597 and the susceptible control 'Jagger' exhibited some level of tolerance to WCM infestations, as demonstrated by low tolerance index values (< 1.0). All seven *Aegilops* spp. accessions demonstrated at least one type of plant resistance that could be transferred into commercial wheat varieties for improved control of the WCM.

S5. How virulent are North Dakota Hessian fly to wheat resistance genes? **Kirk Anderson**, M Harris, North Dakota State University. **Abstract:** The Hessian fly, *Mayetiola destructor* (Say), is a well-documented pest of wheat in the eastern United States and the Great Plains. Because Hessian flies are not considered a problem in North Dakota, little information is available on this insect in the Northern Plains. By applying traditional and expanded biotyping methods to a North Dakota Hessian fly population we were able to establish the biotype composition and determine the frequency of virulence to the available resistance genes (*H* genes). From the traditional biotyping, using 4 resistance genes, we determined that 13 of the 16 biotypes were present in the North Dakota population. Great Plains (GP) was the most common biotype. Biotype L, the most virulent of the 16 biotypes, was not present. Expanded biotyping, using *H1-H32*, identified six *H* genes that gave complete protection from the North Dakota population. These six would be good candidates for incorporating into a resistance breeding program. Resistance to the remaining *H* genes was variable. Some *H* genes had a good degree of resistance while others were completely ineffective. The unexpectedly high level of virulence found in the North Dakota Hessian fly population is difficult to explain. Few (if any) of the *H* genes have been knowingly deployed in North Dakota. Perhaps virulence has developed in wild hosts or through the un-intentional deployment of *H* genes in wheat cultivars. Consequently, future introductions of Hessian fly *H*-genes into North Dakota wheat need to be done with virulence in mind.

Presenters of oral presentations and posters are in **bold lettering**.

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Department of Genetics
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Stellenbosch University
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Matieland, 7601, South Africa
anna.oberholster@up.ac.za

Dolores Mornhinweg (2016)
Wheat, Peanut and Other Field
Crops Research Unit
USDA-ARS
1301 N. Western Rd.
Stillwater OK 74075-2714
Dolores.Mornhinweg@ars.usda.gov

James A. Reinert (2014)
(Turfgrass & Ornamental Plants)
TAES Faculty Fellow &
TAMU Regents Fellow
Texas A&M University
Res & Ext Center
17360 Coit Road
Dallas, TX 75252-6599
J-Reinert@tamu.edu

Richard O. Musser (2016)
Department of Biological
Sciences
Western Illinois University
Macomb IL 61455
RO-Musser@wiu.edu

Nora Lapitan (2014)
Department of Soil and
Crop Sciences
Colorado State University
Fort Collins CO 80523
nlapitan@nsf.gov

Marion Harris (2012)
Department of Entomology
North Dakota State University
Fargo ND 58105
Marion.Harris@ndsu.edu

Lee French (2012)
French Agricultural Research, Inc.
41295 County Road 54
Lamberton MN 56152
Lfrench@rrcnet.org

Louis Hesler (2012)
North Central Agricultural
Research Laboratory
USDA-ARS
2923 Medary Ave.
Brookings SD 57006
Louis.Hesler@ars.usda.gov

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