IPRI PROGRAM 2008

TABLE OF CONTENTS

PROGRAM SUMMARY

SUNDAY, February 10, 2008

4:00 p.m. – 7:00 p.m.	IPRI Registration Location: Foyer
4:00 p.m. – 5:00 p.m.	Steering Committee Meeting Location: TBA
5:00 p.m. – 10:00 p.m.	Poster Set-up Location: Colorado Room
7:00 p.m. – 10:00 p.m.	Joint IPRI/WERA-66 Mixer Location: Colorado Room

Workshop Speaker Ready Room: Executive Board Room

MONDAY, February 11, 2008

8:00 a.m. – 12:00 p.m.	IPRI Registration Location: Foyer
7:00 a.m. – 5:00 p.m.	Posters Available for Viewing Location: Colorado Room
8:00 a.m. – 8:30 a.m.	Welcome Location: Arizona Room
8:30 a.m. – 9:00 a.m.	Keynote Address
9:30 a.m. – 12:00 p.m.	Session I. Contributed Papers
12:00 p.m. – 1:00 p.m.	Lunch
1:00 p.m. – 2:53 p.m.	Session II. Student Competition
3:30 p.m. – 4:45 p.m.	Session III. Contributed Papers
7:00 p.m. – 10:00 p.m.	IPRI Banquet Location: Arizona Room

Workshop Speaker Ready Room: Executive Board Room

TUESDAY, February 12, 2008

7:00 a.m. – 5:00 p.m.	Posters Available for Viewing
8:00 a.m. – 12:00 p.m.	Session IV. Symposium: Workshop on Funding Strategies for the Future of Plant-Insect Interactions
12:00 p.m. – 1:30 p.m.	Lunch
1:30 p.m. – 5:00 p.m.	Session V. Symposium: Hessian Fly

Workshop Speaker Ready Room: Executive Board Room

WEDNESDAY, February 13, 2008

7:00 a.m. – 1:00 p.m.	Poster Removal
8:00 a.m. – 12:00 p.m.	Session VI Insect Biotype Workshop
8:05 a.m. – 8:50 a.m.	Invitational Paper
8:50 a.m. – 10:05 a.m.	Contributed Papers
10:30 a.m. – 12:00 p.m.	Panel – Audience Discussion
12:00 p.m. – 1:00 p.m.	Lunch
1:00 p.m. – 5:00 p.m.	Session VII WERA-66 Meeting Call to Order and State Reports Final Business Meeting

Sunday, February 10th

4:00 p.m. – 7:00 p.m.	IPRI Registration Location: Foyer
4:00 p.m. – 5:00 p.m.	Steering Committee Meeting Location: TBA
5:00 p.m. – 10:00 p.m.	Poster Set-up Location: Colorado Room
7:00 p.m. – 10:00 p.m.	Joint IPRI/WERA-66 Mixer Location: Colorado Room

Workshop Speaker Ready Room: Executive Board Room

Monday, February 11th

8:00 a.m. – 12:00 p.m.	IPRI Registration Location: Foyer
7:00 a.m. – 6:00 p.m.	Posters Available for Viewing Location: Colorado Room

8:00 a.m. – 8:10 a.m.	Call To Order and Announcements Location: Arizona Room
8:10 a.m. – 8:20 a.m.	Welcoming Address Thomas O. Holtzer Head, Department of Bioagricultural Sciences and Pest Management, Colorado State University, Ft. Collins, CO 80523. tholtzer@shep.agsci.colostate.edu
8:20 a.m. – 8:30 a.m.	Welcome from WERA-66 Chair Phillip E. Sloderbeck Professor, Department of Entomology, Kansas State University, Southwest Area Extension Office, Garden City, KS 67846. psloderb@oznet.ksu.edu

8:30 a.m. – 9:00 a.m.	Keynote Address "WHAT GOES AROUND COMES AROUND" Johnie N. Jenkins Director, Crop Science Research Laboratory, USDA, Agricultural Research Service, Mississippi State, MS 39762. Johnie.Jenkins@ars.usda.gov

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9:00 a.m. – 9:30 a.m.	Break

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9:30 a.m. – 12:00 p.m.	Session I. Contributed Papers
Moderator:	Michael Jackson Research Entomologist, USDA, Agricultural Research Service, Charleston, SC 29414. Mike.Jackson@ars.usda.gov

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9:30 a.m. – 9:45 a.m.	HISTORY OF WESTERN CORN ROOTWORM (WCR) RESISTANCE BREEDING BY FAR AND SWS, Karl Nau[1], Lee French[2], Peter Goertz[1], John Mihm[2], and Frank Rober[1], Sudwestsaat[1] and French Agricultural Research, Inc[2]. lfrench@rrcnet.org
9:45 a.m. – 10:00 a.m.	NATIVE RESISTANCE OF MAIZE TO WESTERN CORN ROOTWORM LARVAL FEEDING, Bruce E. Hibbard[1], Sherry A. Flint-Garcia[1], Martin O. Bohn[2], and Kenton E. Dashiell[3], USDA-ARS, 205 Curtis Hall, University of Missouri, Columbia, MO 65211[1], S-110 Turner Hall, Crop Science Department, University of Illinois, 1102 South Goodwin Avenue, Urbana, IL 61801[2], Integrated Cropping System Research Unit, North Central Agricultural Research Laboratory, 2923 Medary Avenue, Brookings, SD 57006[3]. bruce.hibbard@ars.usda.gov
10:00 a.m. – 10:15 a.m.	FEEDING STIMULANTS FOR WESTERN CORN ROOTWORM LARVAE AND IMPLICATIONS FOR RESISTANCE, Elisa J. Bernklau[1], Louis B. Bjostad[2], and Bruce E.

	Hibbard[1], USDA-ARS, 205 Curtis Hall, University of Missouri, Columbia, MO 65211[1], Colorado State University, Department of Bioagricultural Sciences and Pest Management, Fort Collins, CO 80523[2]. bernklau@lamar.colostate.edu
10:15 a.m. – 10:30 a.m.	INDUCED RESISTANCE IN RICE TO FALL ARMYWORM, Michael Stout, L.D. Newsom Professor of Integrated Pest Management, Department of Entomology, 402 Life Sciences Building, Louisiana State University Baton Rouge, LA 70803. mstout@agcenter.lsu.edu
10:30 a.m. – 10:45 a.m.	INSECT HOST RESISTANCE IN WARM-SEASON TURFGRASSES, James A. Reinert, Texas A&M AgriLIFE Research, Texas A&M University System, 17360 Coit Rd, Dallas, TX 75252. j-reinert@tamu.edu
10:45 a.m. – 11:00 a.m.	IMPACT OF CHINCH BUG FEEDING ON PHOTOSYNTHESIS OF FORAGE PEARL MILLET, Xinzhi Ni[1], Jeffrey P. Wilson[1], and David Buntin[2], Crop Genetics and Breeding Research Unit, USDA-ARS, Tifton, GA 31793[1], Department of Entomology, University of Georgia, Griffin, GA 30223[2]. xinzhi.ni@ars.usda.gov
11:00 a.m. – 11:15 a.m.	MICROBIAL TECHNOLOGY OF BACILLUS THURINGIENSIS VAR. KURSTAKI (BERLINER) FORMULATION AGAINST DEFOLIATOR SPODOPTERA LITURA (FABRICIUS) IN GROUNDNUT (ARACHIS HYPOGEA), S. Palaniappan, and J. Satheesh, School of Biotechnology, SRM University Chennai, Tamil nadu – 603203, India. Jm_satheesh2005@yahoo.com
11:15 a.m. – 11:30 a.m.	SWEETPOTATO WHITEFLY – FINDING RESISTANCE IN CUCURBITACEAE, Alvin M. Simmons, and Amnon Levi, USDA-ARS, U.S. Vegetable Laboratory, 2700 Savannah Highway, Charleston, SC 29414. Alvin.simmons@ars.usda.gov

11:30 a.m. – 11:45 a.m.	CHALLENGES IN DEVELOPING PEST RESISTANT SWEETPOTATOES, Michael Jackson, USDA-ARS, U.S. Vegetable Laboratory, 2700 Savannah Highway, Charleston, SC 29414. mike.Jackson@ars.usda.gov
11:45 a.m. – 12:00 p.m.	TO FLY OR NOT TO FLY? REVISITING THE FLIGHT COORDINATION CONCEPT IN APHID, Yvan Pelletier, Potato Research Center AAFC, 850 Lincoln Rd., Fredericton, NB E3B 4Z7, Canada pelletiery@agr.gc.ca

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12:00 a.m. – 1:00 p.m. Lunch

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1:00 p.m. – 2:53 p.m. Session II.
Student Competition Symposium

Moderator & Head Judge: Lee French
Owner, French Agricultural Research, Inc., Lamberton, MN 56152. lfrench@rrcnet.org

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1:00 p.m. – 1:05 p.m.	Introduction Lee French
1:05 p.m. – 1:17 p.m.	ENDOSYMBIONT INVOLVEMENT IN THE DEVELOPMENT OF NEW DIURAPHIS NOXIA BIOTYPES, Dirk H. Swanevelder[1], Eduard Venter[2], and Anna-Maria Botha[1], Department of Genetics & FABI, University of Pretoria, Hillcrest, Pretoria[1], Department of Plant Biotechnology, University of Johannesburg, Auckland Park, South Africa[2]. Anna.oberholster@up.ac.za
1:17 p.m. – 1:29 p.m.	COSTS AND BENEFITS OF GENE-FOR-GENE RESISTANCE AGAINST AN INSECT PARASITE OF WHEAT, K.M. Anderson, and M.O. Harris, Department of Entomology, 202 Hultz Hall, North Dakota State University, Fargo, ND 58105. kirk.Anderson@ndsu.edu
1:29 p.m. – 1:41 p.m.	SCREENING FOR RESISTANCE AND

	IMPACT OF ONION THRIPS (THRIPS TABACI LINDEMAN) AND IRIS YELLOW SPOT VIRUS ON ONION GROWTH, John Diaz-Montano[1], Anthony M. Shelton[1], Brian A. Nault[1], and Marc Fuchs[2], Cornell University-New York State Agricultural Experiment Station, Department of Entomology, 630 W. North St., Geneva, NY[1], NYSAES, Cornell University, Department of Plant Pathology, 630 W. North St., Geneva, NY[2]. Jd325@cornell.edu
1:41 p.m. – 1:53 p.m.	ARABIDOPSIS – GREEN PEACH APHID INTERACTION: INVOLVEMENT OF HOST LIPID, Joe Louis[1], Vijay Singh[1], Jessica Morton[2], John C. Reese[3], and Jyoti Shah[1], Department of Biological Sciences, University of North Texas, Denton, TX 76203[1], Division of Biology, Kansas State University, Manhattan, KS 66506[2], Department of Entomology, Kansas State University, Manhattan, KS 66506[3]. joelouis@unt.edu
1:53 p.m. – 2:05 p.m.	INTERACTIONS AMONG BIOLOGICAL CONTROL, CULTURAL CONTROL AND BARLEY RESISTANCE TO THE RUSSIAN WHEAT APHID, DIURAPHIS NOXIA (KURDJUMOV), IN COLORADO, KANSAS AND NEBRASKA, Paola Sotelo[1], C. Michael Smith[1], Frank B. Peairs[2], Terri Randolph[2], and Gary L. Hein[3], Department of Entomology, Kansas State University, Manhattan, KS 66506[1], Department of Bioagricultural Sciences and Pest Management, Colorado State University, Fort Collins, CO 80523[2], University of Nebraska, Panhandle Research & Extension Center, Scottsbluff, NE 69361[3]. pasotelo@ksu.edu
2:05 p.m. – 2:17 p.m.	DRINK AND FLY: XYLEM SAP CONSUMPTION AND THE TRADE-OFF BETWEEN DISPERSAL AND REPRODUCTION IN WINGED MACROSIPHUM EUPHORBIAE, J. Pompon[1,2], M.A. giguere[1], D. Quiring[2], and Y. Pelletier[1], Potato Research Centre, AAC, Fredericton, NB,

	Canada[1], Department of Biology, University of New Brunswick, Fredericton, NB, Canada[2]. pomponj@agr.gc.ca
2:17 p.m. – 2:29 p.m.	VIRUS-INDUCED GENE SILENCING IN WHEAT TO IDENTIFY GENES FOR RESISTANCE TO DIURAPHIS NOXIA (KURDJUMOV), Laura Starkus[1], Kun Yan Zhu[1], Ming-Shun Chen[1], Xiang Liu[1], Li Huang[2], and Mike Smith[1], Department of Entomology, Kansas State University, Manhattan, KS 66506, Department of Crop Sciences and Plant Pathology, Montana State University, Bozeman, MT 59715. lstarkus@ksu.edu
2:29 p.m. – 2:41 p.m.	TRANSCRIPTIONAL REGULATION IN WHEAT RESULTS IN DISTINCT MODES OF RESISTANCE TO DIURAPHIS NOXIA, Leon van Eck[1,2], Nora L.V. Lapitan[2], Anna-Maria Botha[1], Department of Genetics, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Hillcrest, Pretoria 0002, South Africa[1], Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO 80523[2]. Lvaneck@simla.colostate.edu
2: 41 p.m. – 2:53 p.m.	USE OF ELECTRICAL PENETRATION GRAPH (EPG) TECHNIQUE TO STUDY THE MECHANISMS OF RESISTANCE TO SOUTHERN CHINCH BUG (BLISSUS INSULARIS BARBER, HEMIPTERA: BLISSIDAE) IN ST. AUGUSTINEGRASS, Murugesan Rangasamy[1], Heather J. McAuslane[1], Elaine A. Backus[2], Ron H. Cherry[3], and Russell T. Nagatta[3], Department of Entomology and Nematology, University of Florida, Gainesville, FL[1], USDA-ARS, Crop Diseases, Pests and Genetics, 9611 S. Riverbend Ave, Parlier, CA 93648[2], Everglades Research and Education Center, IFAS, Belle Glade, FL[3]. muruent@ufl.edu

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2:53 p.m. – 3:30 p.m. Break

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3:30 p.m. – 5:00 p.m.	Session III. Contributed Papers
Moderator:	Louis Hesler Research Entomologist, USDA, Agricultural Research Service, Brookings, SD 57006. louis.hesler@ars.usda.gov

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3:30 p.m. – 3:15 p.m.	TOMATO PLANT GENE EXPRESSION ALTERED BY CATERPILLAR LABIAL SALIVA REVEALED BY MICROARRAY ANALYSIS, Richard O. Musser[1], Heiko Vogel[2], Sue M. Hum-Musser[1], and Brad Bennett[1], Department of Biological Sciences, Western Illinois University, Macomb, IL 61455[1], Max Planck Institute for Chemical Ecology, Department of Entomology, Beutenberg Campus, Jena, D-07745, Germany[2]. RO-Musser@wiu.edu
3:15 p.m. – 3:30 p.m.	MOLECULAR CHARACTERIZATION OF SALIVA-SPECIFIC LACCASE FOUND IN THE GREEN RICE LEAFHOPPER, NEPHOTETTIX CINCTICEPS (UHLER) (HOMOPTERA: CICADELLIDAE), Makoto Hattori[1], Kazuko Tsuchihara[2], Hirosato Konishi[1], Yasumori Tamura[1], Masatoshi Nakamura[1], and Tsuyoshi Hasegawa[1], National Institute of Agrobiological Sciences, 1-2 Ohwashi, Tsukuba, Ibaraki 305-8634, Japan[1], Iwaki Meisei University, 5-5-1 Iino, Chou-dai, Iwaki, Fukushima 970-8551, Japan[2]. hatto@affrc.go.jp
3:30 p.m. – 3:45 p.m.	IDENTIFICATION OF PHLOEM SIEVE ELEMENTS AS THE SITE OF RESISTANCE TO SILVERLEAF WHITEFLY IN RESISTANT ALFLAFA GENOTYPES, G. P. Walker[1], and Y. X. Jiang[2], Department of Entomology, University of California, Riverside, CA 92521[1], Bureau of Entomology and Pest Control, Department of Agriculture and Consumer Service, State of Florida, 1203 Governors Square Blvd., Suite 300 Tallahassee, FL 32301[2]. Gregory.walker@ucr.edu
3:45 p.m. – 4:00 p.m.	SEVERAL SPECIFIC DEFENCE

STRATEGIES ARE ELUCIDATED IN WHEAT CONTAINING DIFFERENT DN GENES, Anna-Maria Botha[1], Dirk Swanevelder[1], Thia Schultz[1], Leon van Eck[2], and Nora L.V. Lapitan[2], Department of Genetics, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, Gauteng 0002, South Africa[1], Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO 80523[2]. anna.oberholster@up.ac.za

4:00 p.m. – 4:15 p.m.

MAPPING OF A NEW RESISTANCE GENE TO THE GREEN RICE LEAFHOPPER, NEPHOTETTIX CINCTICEPS UHLER, IN THE RICE CULTIVAR NONA BOKRA, Yasumori Tamura[1], Hattori Makoto[1], Utako Yamanouchi[1], Yasunori Nonoue[2], Tsuyu Ando[2], Sachie Ito[2], Masahiro Yano[1], National Institute of Agrobiological Sciences, 1-2 Ohwashi, Tsukuba, Ibaraki 305-8634, Japan[1], Institute of the Society for Techno-Innovation of Agriculture, Forestry, and Fisheries, 446-1 Ippaizuka, Kamiyokoba, Tsukuba, Ibaraki 305-0854, Japan[2]. yaumori@affrc.go.jp

4:15 p.m. – 4:30 p.m.

PLANT DEFENSE RESPONSES TO APHID GOSSYPII (COTTON-MELON APHID) FEEDING IN RESISTANT AND SUSCEPTIBLE MELON (CUCUMIS MELO), James A. Anstead[1], Preethi Samuel[2], and Gary Thompson[1], Department of Biochemistry and Molecular Biology, Oklahoma State University, Stillwater, OK 74078[1], Department of Applied Science, University of Arkansas, Little Rock, AR[2]. James.anstead@okstate.edu

4:30 p.m. – 4:45 p.m.

RESISTANCE GENE-MEDIATED HOST DEFENSE IN WHEAT AGAINST GREENBUG FEEDING THROUGH GENE EXPRESSION PROFILING WITH AFFYMETRIX GENECHIPS, Yiqun Weng[1], Jackie C. Rudd[1], Jianfa Bai[2], and Nanyan Lu[2], Texas AgriLife Research, 6500 Amarillo Blvd., Amarillo, TX 79106[1], Gene Expression Facility, Kansas State University, Manhattan, KS 66506[2]. y-weng@tamu.edu

Workshop Speaker Ready Room: Executive Board Room

7:00 p.m. – 10:00 p.m.	IPRI Banquet Location: Arizona Room
Organizers:	Steering Committee
	IPRI Business Election of New Steering Committee Members Site Selection for 2010
	Presentation of Student Awards Lee French
Banquet Speaker:	Jan E. Leach Professor, Department of Bioagricultural Sciences and Pest Management, Colorado State University, Ft. Collins, CO 80523. jan.leach@colostate.edu

Tuesday, February 12th

7:00 a.m. – 5:00 p.m.	Posters Available for Viewing
8:00 a.m. – 12:00 p.m.	Session IV. Symposium: Workshop on Funding Strategies for the Future of Plant-Insect Interactions
Organizers:	Gary A. Thompson Head, Department of Biochemistry and Molecular Biology, Oklahoma State University, Stillwater, OK 74078. gary.Thompson@okstate.edu
	Christie E. Williams Research Molecular Biologist, USDA,

	Agricultural Research Service, West Lafayette, IN 47907. Christie.Williams@ars.usda.gov
8:00 a.m. – 8:15 a.m.	INTRODUCTORY REMARKS, Christie E. Williams, Research Molecular Biologist, USDA, Agricultural Research Service, West Lafayette, IN 47907. Christie.Williams@ars.usda.gov
8:15 a.m. – 8:45 a.m.	NEED FOR NEW MODELS OF PLANT-INSECT INTERACTIONS, Linda L. Walling, Professor, Department of Botany and Plant Sciences, and Associate Dean of Biological Sciences, College of Natural and Agricultural Sciences, University of California, Riverside, CA 92521. linda.walling@ucr.edu
8:45 a.m. – 9:15 a.m.	INFRASTRUCTURE NEEDS FOR STUDIES OF PLANT-INSECT INTERACTIONS, Jeff J. Stuart, Professor, Department of Entomology, Purdue University, West Lafayette, IN 47907. stuartjj@purdue.edu
9:15 a.m. – 9:45 a.m.	INTEGRATING THE VARIOUS LEVELS OF PLANT-INSECT INTERACTIONS, Gary W. Felton, Professor and Head, Department of Entomology, The Pennsylvania State University, University Park, PA 16802. gwf10@psu.edu
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9:45 a.m. – 10:00 a.m.	Break
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10:00 a.m. – 11:00 a.m.	PANEL-AUDIENCE DISCUSSION OF THE TOPICS
11:00 a.m. – 11:30 a.m.	USDA FUNDING OPPORTUNITIES FOR PLANT-INSECT INTERACTIONS, Gary W. Felton, Professor and Head, Department of Entomology, The Pennsylvania State University, University Park, PA 16802. gwf10@psu.edu
11:30 a.m. – 12:00 p.m.	NSF RESEARCH COORDINATION

	NETWORK FOR PLANT-INSECT INTERACTIONS, Gary A. Thompson, Head, Department of Biochemistry and Molecular Biology, Oklahoma State University, Stillwater, OK 74078. gary.Thompson@okstate.edu

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12:00 p.m. – 1:30 p.m.	Lunch

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1:30 p.m. – 5:00 p.m.	Session V. Symposium: Hessian Fly
Organizers:	Jeff J. Stuart, Professor, Department of Entomology, Purdue University, West Lafayette, IN 47907. stuartjj@purdue.edu Marion O. Harris, Professor, Department of Entomology, North Dakota State University, Fargo, ND 58105. marion.harris@ndsu.edu

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1:30 p.m. – 2:00 p.m.	LIFE SUCKS: BIOGRAPHY OF A HESSIAN FLY, Christie E. Williams, Research Molecular Biologist, USDA, Agricultural Research Service, West Lafayette, IN 47907. Christie.Williams@ars.usda.gov
2:00 p.m. – 2:30 p.m.	HESSIAN FLY/WHEAT INTERACTIONS, Richard H. Shukle, Research Entomologist, USDA, Agricultural Research Service, West Lafayette, IN 47907. shukle@purdue.edu
2:30 p.m. – 3:00 p.m.	SUBCELLULAR RESPONSES OF WHEAT EPIDERMAL CELLS ATTACKED BY AVIRULENT HESSIAN FLY LARVAE, Marion O. Harris, Karin Anderson, Kirk Anderson, Department of Entomology, North Dakota State University, Fargo, ND 58105, Tom Freeman, Jayma Moore, and Scott Payne, Electron Microscopy Center, North Dakota State University, Fargo, ND 58105

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3:00 p.m. – 3:30 p.m.	Break

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3:30 p.m. – 4:00 p.m.	TRANSCRIPTIONAL AND METABOLIC REPROGRAMMING OF HOST PLANTS FOLLOWING HESSIAN FLY ATTACK DURING COMPATIBLE AND INCOMPATIBLE INTERACTIONS, Ming-shun Chen, Research Plant/Insect Geneticist, USDA, Agricultural Research Service, Manhattan, KS 66506. ming-shun.chen@ars.usda.gov
4:00 p.m. – 4:30 p.m.	POPULATION VARIATION IN THE HESSIAN FLY, Brandon J. Schemerhorn, Research Entomologist, USDA, Agricultural Research Service, West Lafayette, IN 47907. brandi.schemerhorn@ars.usda.gov
4:30 p.m. – 5:00 p.m.	PANEL-AUDIENCE DISCUSSION OF THE TOPICS

Workshop Speaker Ready Room: Executive Board Room

Wednesday, February 13th

7:00 a.m. – 1:00 p.m.	Poster Removal
8:00 a.m. – 12:00 p.m.	Session VI. Insect Biotype Workshop
Moderators:	C. Michael Smith, Professor, Department of Entomology, Kansas State University, Manhattan, KS 66506. cmsmith@ksu.edu Michael J. Stout, Professor, Department of Entomology, Louisiana State University, Baton Rouge, LA 70803. mstout@agctr.lsu.edu
8:00 a.m. – 8:05 a.m.	INTRODUCTION C. Michael Smith
8:05 a.m. – 8:50 a.m.	INVITATIONAL ADDRESS: PHYLOGENY

	(COI) OF HAPLOTYPES AND BIOTYPES, AND CYTOPLASMIC INCOMPATIBILITY-INDUCED REPRODUCTIVE BARRIERS IN THE BEMISIA TABACI COMPLEX, Judith K. Brown, Professor, Department of Plant Sciences, University of Arizona, Tucson, AZ 85721. jbrown@ag.arizona.edu
8:50 a.m. – 9:05 a.m.	RUSSIAN WHEAT APHID RESISTANCE BREEDING IN WINTER WHEAT – CURRENT STATUS, Scott Haley[1], Frank Peairs[2], and Nora Lapitan[1], Department of Soil and Crop Sciences[1], and Department of Bioagricultural Sciences and Pest Management[2], Colorado State University, Fort Collins, CO 80523. scott.haley@colostate.edu
9:05 a.m. – 9: 20 a.m.	SCHIZAPHIS GRAMINUM BIOLOGY ON PASPALUM VAGINATUM: A NEW BIOTYPE ON A NEW HOST, Gregg Nuessly[1], Russell Nagata[1], and John Burd[2], Everglades Research and Education Center, University of Florida, IFAS, 3200 E. Palm Beach Rd., Belle Glade, FL 33430[1], USDA-ARS, Wheat, Peanut and Other Field Crops Research, 1301 N. Western Rd., Stillwater, OK 74075[2]. gnuessly@ufl.edu
9:20 a.m. – 9:35 a.m.	ELICITING PROTEINS FROM DIURAPHIS NOXIA BIOTYPES DIFFER IN SIZE AND COMPOSITION, Rosetta Andrews van Zyl, and Anna-Maria Botha, Department of Genetics, Forestry and Agricultural Biotechnology Institute, University of Pretoria, South Africa. Anna.oberholster@up.ac.za
9:35 a.m. – 9:50 a.m.	DIFFERENTIALLY EXPRESSED GENES IN WHEAT DURING FEEDING BY TWO RUSSIAN WHEAT APHID BIOTYPES AND FUNCTIONAL ANALYSIS OF DEFENSE RESPONSE GENES, Nora Lapitan[1], Ann Hess[2], Junhua Peng[1,3], Hong Wang[1], and Anna-Maria Botha[4], Department of Soil and Crop Sciences[1], and Department of Statistics[2], Colorado State University, Fort Collins, CO 80523, Wuhan Botanical Garden/Institute, The Chinese Academy of Sciences, Hubei 430074,

	China[3], Department of Genetics, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, Gauteng 0002, South Africa[4]. Nora.Lapitan@colostate.edu
9:50 a.m. – 10:05 a.m.	AFLP-LINKED RELATIONSHIPS BETWEEN DIURAPHIS NOXIA POPULATIONS IN THE EASTERN AND WESTERN HEMISPHERES, C. Michael Smith, Xiang Liu, and Jeremy Marshall, Department of Entomology, Kansas State University, Manhattan, KS 66506. cmsmith@ksu.edu

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10:05 a.m. – 10:30 a.m.	Break

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10:30 a.m. – 12:00 p.m.	PANEL-AUDIENCE DISCUSSION OF THE TOPICS

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12:00 p.m. – 1:00 p.m.	Lunch

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1:00 p.m. – 5:00 p.m.	Session VII WERA-66 Meeting
Chairman:	Phillip E. Sloderbeck Professor, Department of Entomology, Kansas State University, Southwest Area Extension Office, Garden City, KS 67846. psloderb@oznet.ksu.edu

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1:00 p.m. – 3:00 p.m.	Call to Order and State Reports

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3:00 p.m. – 3:30 p.m.	Break

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3:00 p.m. – 5:00 p.m.	Final Business Meeting

Poster Presentations

#1

Zoysiagrass (*Zoysia3* spp.) Resistance to Fall Armyworm (Lepidoptera: Noctuidae): II. Polyphenols and Flavonoids – Components of Resistance

Trent C. Hale, Richard H. White, James A. Reinert & M. E. Snook

Texas A&M AgriLIFE Research, Texas A&M University System,
17360 Coit Rd Dallas, TX 75252-6599

Presented by James A. Reinert
*Corresponding author: 972/231-5362 j-reinert@tamu.edu.

Leaf tissue collected from six zoysiagrass (*Zoysia* spp.) cultivars was analyzed for polyphenols and flavonoids by high performance liquid chromatography (HPLC). The experiment investigated the effects of sampling date and N fertilization rate on green leaf chemistry of zoysiagrass and their relationship to fall armyworm (FAW) [*Spodoptera frugiperda* (J. E. Smith)] resistance. Six zoysiagrasses cultivars {>Crowne= (*Z. japonica* Steud.), >Palisades= (*Z. japonica* Steud.), >El Toro= (*Z. japonica* Steud.), >Meyer= (*Z. japonica* Steud.), >Cavalier= [*Z. matrella* (L.) Merr.], and 'Emerald' (*Z. japonica* Stued. x *Z. tenuifolia* Willd. ex Trin.} were planted in a randomized split-plot design with 4 replicates using cultivars as the main plot and 12.2 and 48.9 kg of N ha^{-1} $month^{-1}$ [$(NH_4)_2SO_4$] as the split plots. Flavonoid concentration decreased as the amount of applied N increased. Flavonoid concentration was greatest in June and steadily declined throughout July and August. Two unidentified flavonoids (luteolin-glycosides) were consistently associated with FAW mortality when analyzed by stepwise regression techniques. Unidentified luteolin 3 had an inverse relationship with mortality, while unidentified luteolin 9 was positively correlated with mortality. Additional research is needed to determine if the concentration of luteolins found in resistant zoysiagrasses are sufficient to cause biocidal activity in FAW.

#2

Screening Maize Germplasm for Resistance to Western and Northern Corn Rootworms (Chrysomelidae: *Diabrotica* spp.)

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Corn rootworms (Coleoptera: Chrysomelidae) are devastating pests of maize (*Zea mays* L.), with a subterranean larval stage that consumes root tissue. To lessen reliance on soil insecticides and provide alternatives for genetically modified maize hybrids, researchers have developed novel maize germplasm and evaluated its resistance and/or tolerance to corn rootworm larvae. Historically, evaluations of corn germplasm have focused solely on western corn rootworms, even though different rootworm species frequently co-exist in soil. Here we report the results of an ongoing research project assessing the resistance and tolerance of four maize genotypes to both western (WCR, *Diabrotica virgifera virgifera* LeConte) and northern (NCR, *Diabrotica barberi* Smith & Lawrence) corn rootworm larvae. Corn lines were planted in field plots previously managed under a four-year rotation of corn, soybeans, oats, and winter wheat to ensure that experimental corn plots were not contaminated by feral rootworm populations. We mechanically infested plots with WCR eggs, NCR eggs, or an agar only control. Resistance and tolerance to immature rootworms were evaluated using previously established methods, including the Iowa 1-6 root damage rating scale, root dry weight, and compensatory root growth ratings. Differences in maize germplasm and rootworm species will be discussed.

#3

Determination of the relative date palm host plant cultivar oviposition preference of Red date palm weevil *Rhynchophorus ferrugineus* Oliv.

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Red date palm weevil (RDW) *Rhynchophorus ferrugineus* Oliv. (Coleoptera: Curculionidae) is the most devastating economic pest of data palm *Phoenix dactylifera* L. with wide geographical distribution. In Arabian peninsula, it was detected attacking date palm in mid 1980s. In Saudi Arabia, it was recorded for the 1st time in 1986 in Al-Katif Region. This polyphagous insect is also widely distributed in southern Asia and Melanesia where it feeds on a variety of palms including coconut, sago, date, and oil palm. Comparison of relative date palm host plant cultivars preference studies on Red date palm weevil oviposition has been investigated at Natural Resources and Environmental Research Institute, King Abdulaziz City for Science and Technology, Riyadh, Saudi Arabia. The experiment has been carried out in a 1m ×1m × 20cm pixy glass arena provided with steel mesh with zipper on the top to carry out different operations . Sixteen females with one week old mated females of RDW were taken form lab colony. Eight different local date palm cultivars Khalas, Khasab, Sillage, Sukkary, Khuddary, Barhee, Nabute and Minifi were selected for this experiment. Females were offered 2-cm soft tissues from the apical region. Slices of 1-cm thickness from soft tissue are being provided to females for eggs laying and are replaced after every 2-days. These slices are examined for number of eggs laid to compare eggs laying preference of RDW on various date palm cultivars.

#4

Effects of Minute Pirate Bugs (*Orius insidiosus*) Populations on the Reproductive Stage of Different Transgenic and Isoline Corn Hybrids Using Both a Nondestructive Sampling Technique and Yellow Sticky Cards

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Field studies were conducted at the three locations during corn season of 2007 at Mead, Clay Center and Concord, Nebraska to evaluate the effects of minute pirate bugs, *Orius insidiosus* (Say) populations on the reproductive stage of different transgenic and isoline corn hybrids using both a nondestructive sampling technique and yellow sticky cards. The treatments were: a) a Cry1Ab corn (RX715AF2/YGCB AF2), b) a Cry1Ab corn isoline hybrid (RX715RR2 AR2), c) a Cry1Ab corn isoline hybrid (RX715RR2 AR2) plus an insecticide application, d) a Cry3Bb1 and CP4 EPSPS corn (RX715VT3), and e) conventional hybrid corn (RX715 AF2). A nondestructive sampling technique and yellow sticky cards revealed the lowest average counts of adults in the Cry1Ab corn isoline hybrid plus an insecticide application with 0.3417 adults/plant and 0.4583 adults/card/day, respectively. No significant differences were shown among Cry1Ab corn, Cry1Ab corn isoline hybrid, Cry3Bb1 and Cp4 EPSPS, and conventional hybrid corn. In the nondestructive sampling, the three sites were significantly different to each other with 0.7375, 0.5625 and 0.2400 average adults/plant for Concord, Mead and Clay Center, respectively. Among the sites, Mead obtained numerically and statistically significant highest counts (1.0357 adults card per day) in the sticky cards than the other two project sites. Results suggested that the nondestructive sampling technique and the yellow sticky card were effective for monitoring *Orius insidiosus* (Say) population at the reproductive stage of different transgenic and isoline corn hybrids. Both techniques were comparable yielding similar results. In both sampling techniques, Cry1Ab corn isoline hybrid plus insecticide recorded significantly lowest counts compared to Cry1Ab corn, Cry1Ab corn isoline hybrid, Cry3Bb1 and Cp4 EPSPS corn, and conventional hybrid corn in Nebraska. It revealed that transgenic corn does not have significant effect on the population of *Orius insidiosus* (Say). However, counts were significantly varies in each site in both sampling techniques.

#5

Molecular, Biochemical, and Biological Analyses of Tomato Plants Simultaneously Attacked by Herbivores from Two Different Feeding Guilds

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#6

Inheritance of Chinch bug Resistance in Pearl Millet.

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Pearl millet [*Pennisetum glaucum* (L.)] is a promising alternative feed grain for southeastern crop productions systems, because of its ability to reliably produce grain, under drought conditions on sandy, acidic, and low fertility soils. Chinch bug [*Blissus leucopterus leucopterus* (Say) (Heteroptera:Blissidae)] infestation was very high in 2006 and 2007 confirming early predictions that chinch bug would be the most important insect pest on pearl millet. The objective of this research was to determine if chinch bug resistance exists in current elite inbred parental materials, and if so what level of inheritance was demonstrated for this trait. In September 2006, 38 inbred lines replicated six times were assessed for resistance under heavy natural chinch bug infestation. In 2007 149 F_1 Hybrid progenies, replicated three times were assessed twice (July 16 & 30) under heavy natural chinch bug infestation. Plots were scored 0 (no damage) to 4 (dead) for insect damage. Inbred lines ranged 0.9 to 2.8, and hybrids ranged 1.0 to 3.3. Observed inheritance (h_n^2) for this population was 0.69 with a $P<0.001$.

#7

Expression of Genes Encoding Peroxidases in Non-Host Rice Induced by Hessian Fly (*Mayetiola destructor*) Attacks

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The preferred host of the Hessian fly is wheat. Although it can also live on barley, rye, and wheat-related wild grasses, the Hessian fly can not survive on rice plants. To investigate non-host resistance mechanisms, we systematically analyzed the expression levels of rice genes following Hessian fly attacks using Affymetrix microarrays. Among the genes affected by Hessian fly attacks there was a diverse group of peroxidase genes. Totally there are193 peroxidase gene probes in the rice microarray representing 161 unique genes, including 4 glutathione peroxidase, 9 thioredoxin peroxidase, 12 ascorbate peroxidase, and 136 class III peroxidase genes. The glutathione peroxidase, thioredoxin peroxidase, and ascorbate peroxidase genes were not significantly affected by Hessian fly attacks. Exclusively, 17 of the class III peroxidase genes were up-regulated to at least two fold, and half of the affected genes were up-regulated more than 10 times. These peroxidase genes responded very quickly. Most of the up-regulated genes reached maximum RNA level within 12 hours after the initial Hessian fly attack. Nearly all up-regulated peroxidase genes encode secretory proteins, which were predicted to locate extracellularly. Considering class III peroxidases are mainly involved in cell elongation, cell wall construction and differentiation, the specific, prompt, and dramatic upregulation of class III peroxidase genes suggested that the strengthening of cell walls in rice seedlings is likely part of the induced non-host defense mechanisms in rice against the Hessian fly attack. (Key words: Rice, Non-host Resistance, Hessian fly, Peroxidase, Induced)

#8

Resistance to silverleaf whitefly, *Bemisia argentifolii* (Hemiptera: Aleyrodidae) in *Gossypium thurberi*, a wild cotton species

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Gossypium thurberi Todaro is a wild cotton species native to Mexico and parts of the southwestern United States. Four years of field studies in California's Imperial Valley revealed consistent very high levels of resistance in *G. thurberi* against silverleaf whitefly, *Bemisia argentifolii* Bellows and Perring, an important pest of cotton in many regions of the world. Naturally developing field infestations in plots of *G. thurberi* were significantly lower than in plots of the commercial cotton cultivars DP 5415, Siokra L23, and Stoneville 474. *G. thurberi* has two morphological traits that, in past research, have been associated with lower levels of whitefly susceptibility: smooth-leaf and okra-leaf; however, the levels of resistance observed in *G. thurberi* were significantly greater than in the cotton cultivar DP 5415, which is a smooth-leaf cotton, and Siokra L23 which, like *G. thurberi*, has both smooth-leaf and okra-leaf traits. Therefore, the high level of resistance in *G. thurberi* seems to be due to factors above and beyond smooth-leaf and okra-leaf. Siokra L23, which is among the least whitefly-susceptible cotton cultivars, developed whitefly populations over 30 times those on *G. thurberi* in all three years that Siokra L23 was tested. The difference in whitefly population development between *G. thurberi* and the other two cotton cultivars was even more striking, up to a 475-fold difference. In contrast to the clear results on naturally developing field infestations, experiments comparing nymphal survival among *G. thurberi* and commercial cotton cultivars did not detect antibiosis, and both choice and no-choice oviposition experiments did not detect antixenosis. Thus, the mechanisms of resistance in *G. thurberi* remain unknown.

#9

Hessian fly, *Mayetiola destructor*, larval midgut and salivary gland morphology: light and electron microscopy studies

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The morphology of Hessian fly larval (first instar) midgut and salivary gland tissue is described by light and transmission electron microscopy. These data serve as the basis for future research aimed at understanding the mechanisms of wheat resistance to Hessian fly. Future studies include (1) a comparison of the midgut morphology of larvae that have fed on resistant vs. susceptible wheat cultivars and (2) the use of *in situ* hybridization in salivary gland tissue to determine the cytological location of gene transcripts putatively involved in conferring susceptibility of wheat plants to Hessian fly attack.

#10

Comparison of Gene Expression in the Salivary Glands of Three Major Insect Pests of Cereals

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The Hessian fly, the orange wheat blossom midge, and the Asian rice gall midge are among the most important insect pests of cereals worldwide. Plant resistance is the most effective method of control; however, the use of resistant cultivars leads to the development of biotypes that can survive on formerly resistant cultivars. How these insects hijack their host plant's development to feed and protect the larvae is unknown. However, it is believed salivary secretions from the larvae are the signals that cause abnormal plant growth in susceptible plants or elicit a defense response in resistant plants. We have created a database of genes expressed in the salivary glands of these insects. From this database we have been able to identify genes that are similar between the species and genes that are unique to each species. These results are allowing us to understand how these pests hijack a susceptible plant's development as well as the signals a resistant plant recognizes to defend itself.

#11

Marker-assisted selection for resistance to Hessian fly in spring wheat

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The Hessian fly, *Mayetiola destructor*, is an important pest of spring wheat in the Pacific Northwest. The most effective control method is the use of resistant cultivars. Wheat cultivars resistant to the fly are available and are increasingly being used to control this pest in northern Idaho. However, there is potential for emergence of biotypes capable of attacking resistant cultivars. Utilization of multiple genes for resistance is important in an overall pest management strategy. Numerous lines derived from crosses of sources carrying the *H3* and *H25* genes for fly resistance were evaluated in 2006 and 2007. This included hard red spring wheat lines derived from the cross Jefferson/IDO584, and hard white spring lines derived from the crosses IDO584/Jerome and IDO586/Jerome. Susceptible (Alturas) and resistant checks [Jefferson (*H3*) and IDO584, IDO586, and Cataldo (*H25*)] were also evaluated. Field assessments were done under natural fly infestation and laboratory ones using artificial infestation. Mean number of insects per plant and percent-infested plants were determined. Several breeding lines showed no infested plants in laboratory tests and also exhibited the best performance in the field. Molecular marker tests are being used to confirm if both the *H3* and *H25* resistance genes are present in some of the resistant breeding lines. Results from these tests will assist us in determining which lines with multiple resistance genes to advance in the breeding program.

#12

Genetic Variation of Field Populations of Wheat Curl Mite, *Aceria tosichella* Keifer

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The wheat curl mite (WCM), *Aceria tosichella* Keifer, is a vector of two viruses, wheat streak mosaic virus (WSMV) and high plain virus (HPV), in winter wheat. WSMV is the most serious disease of winter wheat in the western Great Plains of the US, but both diseases are often found together in mixed population within wheat fields. An important management strategy targeted at managing the vector population has included growing a mite-resistant wheat variety (e.g. TAM 107); however, this resistance was not stable in the field and resistance was overcome by the mites.

Because of the important management implications of WCM biotypes, Polymerase Chain Reaction-Restriction Fragment Length Polymorphisms (PCR-RFLP) of mitochondrial DNA (mtDNA) at cytochrome oxidase I and II gene (COI and COII) and ribosomal DNA (rDNA) between internal transcribed spacer 1 and 2 (ITS1 and ITS2) including the 5.8S gene were used to examine genetic variation of WCM at various spacial scales in Nebraska, Kansas, and Montana wheat fields. In 2003, WCM collected from fields in two Nebraska counties (Cheyenne and Banner). The mtDNA data from both counties show that these haplotypes make up a mixed population, even within a wheat head. As a result, single mite transfer techniques were used to avoid mixed populations in 2004 and 2005. In 2004, both mtDNA and rDNA were used to determine genetic variation and the occurrence of interbreeding. In 2005, only rDNA was used to determine genetic variation of WCM.

The PCR-RFLP results showed that WCM can be easily separated into two types, type 1 (NE biotype) and type 2 (all other biotypes). The analysis of molecular variance (AMOVA) showed that the majority of the WCM genetic variability occurred within wheat heads (~50%) compared to sites within fields, fields or states. Even though extensive mixing of populations occurred within wheat heads, a low amount of interbreeding was found in western NE in 2004 (8.4%). These results indicate that WCM biotypes are regionally mixed and the development and deployment of mite-resistant wheat varieties must account for the widespread presence of these biotypes.

#13

Introgression of Russian Wheat Aphid Resistance from Tetraploid Wheat Germplasm

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#14

Categories of Russian Wheat Aphid, Diuraphis noxia (Mordvilko), Biotype 2 Resistance in Wheat Genotypes

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Diuraphis noxia is a serious global pest of world cereal crops in all continents except Australia, and is the most significant pest of cereal grain production in the U. S. western High Plains. Although 11 cereal genes control D. noxia resistance, resistance-breaking D. noxia biotypes exist in all cereal producing regions of the world except Australia. D. noxia biotype '2' is virulent to the D. noxia resistance genes Dn1 - Dn6. Thus, a need exists for an improved understanding of the categories of resistance in all sources of D. noxia biotype 2 resistance. In this study, wheat genotypes containing the resistance genes Dn4, Dn6, Dn7, Dnx, & a susceptible control (Dn0) were infested with D. noxia biotype 2 to determine the extent of the antibiosis and tolerance categories of resistance operating in each genotype. All infested resistant genotypes expressed some chlorosis & leaf rolling, and tolerance indices (TI) for shoots, roots & plant height of Dn6 were significantly lower (more tolerant) than those of Dn0. Plant height TI of Dnx plants was also significantly less than that of Dn0. Thus, both Dn6 & Dnx plants are tolerant to D. noxia biotype 2 infestation. Both Dn7 & Dnx plants exert antibiosis effects,significantly reducing D. noxia populations compared to Dn0. Despite the strong resistance of the Dn7 genotype from rye, Dn7 has deleterious effects on bread wheat baking quality. Dnx, from bread wheat, carries no negative quality traits & offers a suitable genotype for ready adaptation into Kansas wheat cultivars.

#15

EVIDENCE OF GENETIC DIVERSITY WITHIN RUSSIAN WHEAT APHID POPULATIONS COLLECTED IN WESTERN COLORADO

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Russian wheat aphids were collected from grasses and wheat at a site in western Colorado. Isofemale lines were established from each host, and colonies from each isofemale line were placed on 24 differential wheat and barley lines previously used for other biotype experiments. Cholorsis responses indicated differences in resistance responses among the Russian wheat aphid. Differences occured between isolines collected on different hosts as well as within the hosts.

#16

Comparative Gut Transcriptome Analysis of Biotype 1 and 2 Russian Wheat Aphid, *Diuraphis noxia* (Kurdjumov).

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#17

Limited nuclear and mitochondrial DNA variation among Russian wheat aphid (*Duraphis noxia*) biotypes from the United States and South Africa

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Since the introduction of *Diuraphis noxia* (Russian wheat aphid) in the United States in 1986, only one population existed. In 2003, a new population of the biotype appeared in Colorado, which overcame existing resistant cultivars. In subsequent years, at least six new populations were discovered in the Great Plains states. These newly emerged populations are referred to as biotypes, and are characterized by differential reactions to a set of wheat and barley genotypes containing different Russian wheat aphid resistance genes (*Dn* genes). The objective of this study was to analyze the genetic divergence among eight US biotypes and two South African biotypes using DNA markers. DNA markers used included simple sequence repeats (SSRs), randomly amplified polymorphic DNA (RAPD) markers, and amplified fragment length polymorphism (AFLP) markers. The mitochondrial cytochrome oxidase subunit I gene (*mtCOI*) was also completely sequenced and compared for nucleotide divergence among the US biotypes and South African biotypes. Over 12000 DNA fragments and *mtCOI* DNA sequences revealed limited polymorphism and nucleotide sequence divergence among the eight US biotypes. Phylogenetic trees established based on AFLP data and *mtCOI* sequence data show that the South African biotypes significantly differed from the US biotypes. The low level of genetic differentiation in both nuclear and mitochondrial genomes may be explained by founder effect, since the RWA species was just established in the US 20 years ago.

#18

Greenhouse Screening for Bird Cherry-Oat Aphid Resistance in Barley

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Bird cherry-oat aphid (BCOA), *Rhopalosiphum padi* (L.), has been reported to cause yield loss in small grains through its role as a vector of the PAV strain of Barley yellow dwarf virus (BYDV) and by feeding damage to winter and spring small grains. Barley accessions have been reported to have BCOA resistance based on antibiotic effect of seedlings on BCOA. Whether this antibiosis translates to resistance in terms of grain yield has yet to be shown. Screening for BCOA resistance at the seedling stage has been difficult due to lack of visual symptoms on seedlings using traditional greenhouse screening methods. In an attempt to develop a seedling screening technique for BCOA we varied flat type, soil type, infestation date, infestation rate, temperature, and day length. Seventy-eight barleys, reported to be antibiotic to BCOA, were screened with aviruliferous BCOA using traditional seedling screening methods under high temperature and long days. Seedlings were rated visually on a scale of 1 to 7 (1= resistant and 7= dead). Potential resistant and susceptible checks were identified. In this study, a replicated (2X) screening of the Barley Core Collection was conducted using this technique and rating scale. Surviving seedlings were rescued and transplanted to pots in the greenhouse. The second screening was more severe than the first. The first screening had 5 and 54 percent survival of the susceptible and resistant checks respectively while the second screening had 0.4 and 11 percent survival of susceptible and resistant checks. Accession seedling survival was 95, 81, 79, 65, 45, and 27 percent for ratings of 1, 2, 3, 4, 5, and 6 respectively for the first screen and 93, 40, 77, 61, 59, and 47 respectively for the second screening. Resistance was found in 266 and 279 accessions for the first and second screening respectively. If seedling survival translates to field resistance in terms of grain yield, this seedling screening technique will be useful for identification of BCOA resistance.

Susceptible checks died while 1,189 seedlings from 284 accessions survived and were transplanted to pots in the greenhouse. Plant height, percent fertile tillers, grain yield and yield components were measured to verify the rating scale and identify resistance.

Traits measured included, leaf number, tiller number, root mass, crown root number, leaf length and width, plant height, fresh weight, dry weight and internode length.

#19

Understanding Mechanisms of Host Resistance against Greenbug in Cereal Crops – an Interdisciplinary, Collaborative Approach

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At Texas AgriLife Research - Amarillo, we have an ongoing research program focusing on elucidating the mechanisms of interactions between the phloem-feeding aphid pests and cereal crop hosts using the wheat-greenbug as a model system. During this workshop, recent results from our research on the following projects will be presented:

(1) Map-based cloning of greenbug resistance gene in wheat. This NRI-supported project aims to clone the *Aegilops tauschii*-derived greenbug resistance gene *Gb3* from wheat. So far, over 30 SSR, AFLP-, EST- or RFLP-converted STS markers were placed on a high-resolution map in the *Gb3*, two of which are being used to screen an *Ae. tauschii* BAC library to initiate chromosome walking. The *Gb3*-linked markers have been successfully applied in marker-assisted selection for greenbug resistance in the Texas Wheat Improvement Program.

(2) Molecular mapping of greenbug resistance genes *gb1*, *Gb2*, *Gb6* in wheat, and *Rsg1*, *Rsg2* in barley. We plan to identify molecular markers for these genes that can be used in marker-assisted selection and development of wheat/barley germplasm with multiple resistance.

(3) Exploring *Brachypodium distachyon* as a new model species to study molecular mechanisms of plant-aphid interactions in the grass genome. Diploid accessions with distinct greenbug-feeding responses were identified. SSR markers were developed and phylogenetic relationships of *B. distachyon* with rice, wheat and ryegrass were evaluated.

(4) Expression profiling of host defense responses against greenbug feeding. Molecular defense responses of near isogenic wheat lines of *Gb3* were investigated with Affymetrix GeneChips providing new insights in host defense mechanisms.

(5) Physiological basis of *Gb3*-mediated host resistance against the greenbug in wheat. Free amino acid dynamics were examined in the greenbug and two near isogenic wheat lines of *Gb3* in a 12-day time frame after infestation using an optimized SPME-GC-FID (solid phase micro-extraction/gas chromatography-flame ionization detection).

(6) Development of cross-species transferable microsatellite markers for evaluation of biotypic diversity in the greenbug. Over 120 SSR markers were developed through database mining of the pea aphid and green peach aphid EST and genomic resources. Cross species transferability of these markers was evaluated. Thirty seven SSRs were used to evaluate genetic diversities among forty greenbug biotypes. Host-associated genotypic variation and geographical differentiation among these clones were revealed.

#20

Resistance to soybean aphid among soybean lines

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Growth-chamber experiments were used to identify and characterize host-plant resistance among several soybean lines to the soybean aphid, *Aphis glycines* Matsumura (Hemiptera: Aphididae). Reproduction by aphids was diminished on lines Cobb, Tie-feng 8, Braxton, PI 230977, Perrin, Tracy-M, D75-10169, Dowling and Jackson, and fewer aphids reached reproductive maturity on Cobb, Tie-feng 8, PI 230977, Dowling and Jackson. Nymphiposition was reduced in no-choice tests on Cobb, PI 230977, PI 71506, Dowling and Jackson. Tracy-M and D75-10169 were antixenotic to *A. glycines* in a host-selection test. A greater proportion of aphids remained after 48 h on unifoliolate leaves of susceptible lines such as 91B91, Cook and Davis, whereas aphids tended to be found on stems and trifoliolate leaves of resistant lines such as PI 230977, Perrin, Tracy-M, D75-10169, Jackson and Dowling. However, aphids were equally distributed among shoot structures of PI 71506. Irrespective of shoot structure, relatively low numbers of *A. glycines* were found on PI 230977, PI 71506, Dowling and Jackson. Based on these results, several of the lines tested may be valuable to soybean breeding programs as sources of resistance to *A. glycines*.

#21

SURVIVORSHIP OF FALL ARMYWORM (LEPIDOPTERA: NOCTUIDAE) ON JASMONATE-TREATED LEAVES OF CONVENTIONAL AND TRANSGENIC BT COTTON

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Paper Abstracts

Graduate Student Papers

#1

Endosymbiont involvement in the development of new *Diuraphis noxia* biotypes

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Aphids are totally dependent on their endosymbionts for survival. Feeding on a nitrogen poor diet, the aphids' endosymbiont enables survival by increasing and recycling essential amino acids. In *Buchnera aphidicola*, the endosymbiont of *Diuraphis noxia* (RWA), the rate limiting anthranilate synthase (E.C. 4.1.3.27) and the whole leucine gene pathway are located on plasmids. But RWA seems less dependent on *B. aphidicola* for essential amino acids than other wheat feeding aphids: the plasmids are present in lower copy numbers and pseudogenes occur. This study investigated the role of the endosymbiont in the development of new RWA biotypes. Plasmid copy numbers and gene expression levels of pleuABCD were resolved by qPCRs. Sequences of this plasmid were obtained from ten RWA biotypes to determine the level of variation. We found that differences in copy numbers amongst biotypes are not a true reflection of gene expression levels. In some of the biotypes, a single, triple cytosine insertion occurred upstream of the leucine gene cluster. The position of this insertion implies a role in gene expression regulation; also supported by gene expression levels. These results suggest that *Buchnera aphidicola* is still actively involved in RWA adaption.

Keywords:
Buchnera aphidicola, gene expression levels, Russian wheat aphid biotypes, leucine plasmid

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#2

Costs and benefits of gene-for-gene resistance against an insect parasite of wheat

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Using near-isogenic winter wheat genotypes with the *H6*, *H9* or *H13* resistance (*R*) genes and a control genotype without an *R* gene, we examined the fitness costs of Hessian fly larval attack and successful plant defense. Our experimental design and ability to use avirulent Hessian fly larvae to induce, but not damage, *R* gene plants allowed us to quantify the benefits of gene-for-gene resistance and two types of costs, the cost of the induced defense triggered by the *R-Avr* interaction, realized in the presence of Hessian fly attack, and the cost of the constitutive expression of the *R* product, realized in the absence of Hessian fly attack. Plant measurements included time of reproduction, the number of heads and seeds produced, offspring (seed) viability and growth. When attacked and un-attacked plants were compared within a single genotype, no costs from induction of plant defense were observed. In some situations the opposite was true. For example, in the case of *H9* and *H13*, plants attacked by larvae produced significantly more heads than un-attacked plants. *H13* plants attacked by Hessian fly larvae also produced significantly more seed than un-attacked *H13* plants. When genotypes were compared in the absence of Hessian fly larvae, *H6* and *H9* reached the reproductive stage earlier than the susceptible control and *H13*. *H13* produced more heads and seeds when compared to the other genotypes. When seed viability and seedling growth were examined, no differences were found between the four genotypes. Our data support the hypothesis that, resistance genes and the induced resistance that they mediate have significant benefits for the plant without incurring fitness costs.

#3

Screening for Resistance and Impact of Onion Thrips (*Thrips tabaci* Lindeman) and *Iris yellow spot virus* on Onion Growth

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Onions, *Allium cepa* L., are an important crop in New York state and onion thrips (OT), *Thrips tabaci* Lindeman, are a devastating onion pest. OT feeding alone can cause substantial yield losses but can be even more problematic when it occurs with *Iris yellow spot virus* (IYSV) transmitted by OT. IYSV was confirmed in the summer of 2006 in New York state. OT are difficult to control with conventional insecticides. For these reasons and the importance of onion production in New York, field studies on onion resistance to OT and/or to IYSV were performed. In the first experiment, 22 onion varieties were screened for resistance to OT and/or IYSV. The number of thrips larvae was counted weekly and visual leaf damage ratings of feeding were made. In the second experiment, the impact of OT/IYSV interaction on plant growth was studied. There were two treatments, protected with an insecticide and the other not protected. Eight varieties showed the lowest leaf damage compared to susceptible varieties. Five of these varieties (Colorado 6, OLYSO5N5, Cometa, Tioga and BGS-230) may possess antibiosis and/or antixenosis because of the lower number of thrips found on them. The other three varieties (Peso, Delgado and Calibra) had higher number of thrips indicating possible tolerance. There was a significant reduction in plant height and weight in the varieties evaluated. At the end of the season all the plants (1,256) were tested to detect the presence of IYSV using ELISA tests. About 10% of the plants resulted infected with IYSV.

#4

Arabidopsis - Green peach aphid interaction: involvement of host lipid

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Aphids have a distinct feeding behavior as compared to other herbivorous insects. The phloem-specific feeding behavior of Green peach aphids (GPA), using their incredibly slender stylets, help them to feed continuously from a single sieve element for an extended period of time. In addition to extensive plant damage, GPA also acts as a vector for economically important plant viruses. The *Arabidopsis thaliana* - *Myzus persicae* (Sülzer) (GPA) (HEMIPTERA: APHIDIDAE) model helped us to characterize the response of GPA on *Arabidopsis thaliana*. We had previously demonstrated that a recessive mutation in the *SSI2* gene results in heightened resistance to GPA in the *ssi2* mutant plant. Microarray studies identified a gene At5g14180, which in comparison to the wild type (WT) plant is expressed at elevated levels in leaves of the *ssi2* mutant and in GPA infested wild type plants. At5g14180 encodes a protein with homology to lipases. Mutations in At5g14180 resulting from the insertion of T-DNA within the gene impacted host plant resistance to GPA. No-choice test (antibiosis) indicated that there is an increased number of GPA on the At5g14180 mutant as compared to WT plants. However, choice test (antixenosis) showed comparable numbers of GPAs on the mutant and WT plants. Comparison of GPA feeding behavior on WT versus the lipase mutant indicated that there was no significant difference in the total duration of the sieve element phase (SEP) spent by GPA on lipid mutant and WT plant, suggesting that the mutation does not deter aphid feeding. Since, both *SSI2* and At5g14180 encode proteins involved in lipid metabolism, and mutations in At5g14180 attenuate the *ssi2*-conferred heightened resistance to GPA, we suggest that a lipid or lipid-derived product is involved in antibiosis against GPA.

#5

Interactions Among Biological Control, Cultural Control and Barley Resistance to the Russian Wheat Aphid, *Diuraphis noxia* (Kurdjumov), in Colorado, Kansas and Nebraska

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The Russian wheat aphid, *Diuraphis noxia* (Kurdjumov) (RWA) is considered an important pest in barley in the Western Plains since its introduction to the USA in the mid 1980s. This study was conducted to determine the interaction among biological, cultural control and host plant resistance in three barley fields located in Colorado, Kansas, and Nebraska. The experimental design used was a split-plot design with two main plot treatments (early, and delayed planting dates). Within each main treatment plot, four split-plot treatments (varieties) were randomized. These treatments included two new RWA biotype 1 and 2 resistant barley cultivars, Stoneham and Sydney, and the susceptible cultivar Otis under triamethoxam-protected and unprotected regimes. Aphid, natural enemy and incidence sampling was conducted at four dates from late May through early July in 2007. Differences in the mean number of RWA were detected by location and variety during the second sampling, when unprotected Otis plants contained the highest numbers of aphids in Colorado and Kansas. On the third sampling date, unprotected Otis plants in Nebraska contained the highest number of RWA. There were complex interactions between the natural enemies observed in the three fields and these are being subjected to further analyses.

#6

Drink and Fly: Xylem sap consumption and the trade-off between dispersal and reproduction in winged *Macrosiphum euphorbiae*.

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Host plant acceptance can be recognized as the occurrence of sustained feeding or oviposition. After plant acceptance winged aphids allocate more resources to reproduction and loose their ability to fly because wing loading increases and/or wing muscle histolysis. Winged aphids often consume xylem sap instead of the nutrient-richer phloem sap. This feeding behaviour, unique to winged forms, could be related to a trade-off between dispersal and reproduction.

The feeding behaviour of both alate and apterous *M. euphorbiae* of different age and starvation status was monitored using Electrical Penetration Graph (EPG). Reproductive rate and flight ability were also measured.

Contrary to what is generally accepted in the literature, aphids were able to fly after 8 days of feeding on potato (var. Shepody). Furthermore, both alate and apterous aphids consumed xylem sap, but the time alates spent consuming xylem sap decreased with their age. Other results and the role of xylem sap consumption in the dispersal-reproduction trade-off will be discussed.

#7

Virus-Induced Gene Silencing in Wheat to Identify Genes for Resistance to *Diuraphis noxia* (Kurdjumov)

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The Russian wheat aphid *Diuraphis noxia* (Kurdjumov) is pest on cereal grains. Aphid characteristics, such as leaf rolling and the development of new biotypes, can make it difficult to treat infested crops with pesticides or biological control agents. Therefore it is desirable to identify new sources of wheat resistance. Virus-induced gene silencing (VIGS) utilizes the plant defense system to silence viruses in inoculated plants. Accumulation of virus RNA in the plant triggers the defense system to silence sequences homologous to the introduced virus. Sequences from the plant can be inserted into the virus and silenced along with the virus. The VIGS method can be used to screen EST sequences from resistant wheat for their role in resistance. EST sequences will be used to design primers to amplify DNA from deletion line wheat to determine to location of the EST sequences. Once location has been confirmed the candidate EST sequences from resistant wheat will be silenced and evaluated for their role in resistance to *D. noxia*. Resistant plants will be inoculated with Barley streak mosaic virus (BSMV) containing a candidate gene; the gene will be silenced along the virus in asymptomatic leaves. Controls will include resistant plants inoculated with BSMV without EST sequences and non-inoculated plants. Aphids will then be allowed to feed on the plants to assess changes in resistance. The resistance category antibiosis will be measured as aphid population at the end of the experiment.

#8

Transcriptional regulation in wheat results in distinct modes of resistance to *Diuraphis noxia*

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Russian wheat aphid (*Diuraphis noxia*, Mordv.) feeding on susceptible cultivars of hexaploid wheat (*Triticum aestivum* L.) leads to leaf rolling, chlorosis and death. Although several *D. noxia* (*Dn*) resistance genes have been identified, none have been cloned or characterized. Plants expressing *Dn* genes exhibit distinct modes of *D. noxia* resistance, such as antibiosis (*Dn1*); tolerance (*Dn2*); and antixenosis (*Dn5*). Little is known about the components involved in establishing a successful defense response against *D. noxia* attack and how these differ between the different resistance categories. Here we report on downstream events involved in *D. noxia* attack by comparing responses of near-isogenic lines containing different *Dn* genes. Differentially regulated transcripts obtained using cDNA-AFLP analysis were cloned, sequenced and classified into functional categories based on inferred similarity to database sequences. Transcripts involved in such diverse processes as stress, signal transduction, photosynthesis, metabolism and gene regulation were differentially regulated during *D. noxia* feeding. Detailed expression analysis using qRT-PCR and RNA hybridization provided evidence that the time and intensity of induction of specific pathways is critical for the development of a particular mode of resistance. These include: generation of kinase signaling cascades and induction of ancillary processes such as ubiquitination, leading to a sustained oxidative burst and a hypersensitive response during antibiosis; tolerance as a passive resistance mechanism to counter aphid-induced symptoms through repair or *de novo* synthesis of photosystem proteins; and the possible involvement of ethylene-mediated pathways in generating volatile compounds during antixenosis. This is the first report on the involvement of KCO1, a vacuolar K^+ channel, in assisting cytosolic Ca^{2+}-influx and prevention of leaf rolling, as well as the role of iron homeostasis as a gene regulatory mechanism for sustaining the oxidative burst during the antibiotic defense response.

#9

Use of Electrical Penetration Graph (EPG) Technique to Study the Mechanisms of Resistance to Southern Chinch Bug (*Blissus insularis* Barber, Hemiptera: Blissidae) in St. Augustinegrass

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St. Augustinegrass, *Stenotaphrum secundatum* (Walt.) Kuntze, is the most commonly grown lawn grass in Florida and southern chinch bug, *Blissus insularis* Barber (Hemiptera: Blissidae), is its most serious insect pest. Host plant resistance has long been one of the most successful management tools to control the southern chinch bug. Resistance to southern chinch bug has been identified in the St. Augustinegrass lines 'Floratam', 'FX-10' and 'NUF-76'. However, Floratam's resistance was overcome in the mid 1980s by most populations of chinch bug in Florida. Previous choice and no-choice tests and ovipositional and developmental studies revealed strong antixenosis in FX-10 and NUF-76 and antibiosis in NUF- 76. The purpose of our current research was to investigate potential mechanisms of southern chinch bug resistance in FX-10 and NUF-76 using the electrical penetration graph (EPG) technique. St. Augustinegrass lines selected for study of chinch bug feeding behavior included a resistant (FX-10) and a susceptible (Floratam) polyploid line and a resistant (NUF-76) and a susceptible ('Palmetto') line. Polyploid St. Augustinegrass lines are much courser in growth form than are diploids lines which is likely to affect stylet behavior during feeding. The feeding behavior of adult chinch bugs was monitored using a four-channel AC-DC monitor and the waveforms were recorded for 24 h using the WinDaq Pro software. Restricted maximum likelihood estimation ANOVA was used to find out whether the frequencies or durations of each waveform type or overall probing were significantly different on the four St. Augustinegrass lines. Southern chinch bugs made more frequent probes, produced longer-duration waveform events for pathway-related behaviors and spent less time in ingestion-related waveforms on FX-10 and NUF-76, compared to the susceptible Floratam and Palmetto. Relatively more stylet probes per insect on FX-10 and NUF-76 than on Floratam and Palmetto suggest the presence of stylet penetration impediments around the vascular bundle in resistant varieties. In addition, the short duration of presumed phloem sap ingestion on FX-10 and NUF-76 suggests the possible presence of resistance factors in phloem sap or blockage of sieve elements. We conclude, based on this research and previous studies that the strong antixenosis found in FX-10 and NUF-76 and antibiosis in NUF-76 may be due to factors around the vascular bundle impeding stylet penetration and possible presence of feeding deterrents or toxins in phloem sap or sieve tube blocking mechanisms.

Program Papers

Native Resistance of Maize to Western Corn Rootworm Larval Feeding

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The western corn rootworm (WCR) is a major insect pest in continuous corn production. By feeding on corn roots, WCR causes economic losses due to plant lodging and decreased nutrient uptake. Currently, insecticides and transgenic corn are only available options for its control under continuous corn production. Maize germplasm CRW3(S1)C6 is a synthetic population developed with resistance to WCR. This recently released germplasm is significantly less damaged than susceptible corn lines when under moderate to heavy rootworm pressure and offers a source of native resistance to WCR for transfer of desired resistance genes into high yielding commercial varieties. A mapping population was derived from this germplasm and phenotypic data has been collected for damage, regrowth, and root size. Upon completion of molecular work and correlation of phenotypic and genotypic data, QTL may be available to facilitate transfer of resistance genes to elite germplasm with minimal transfer of undesired genetic code.

Feeding Stimulants for Western Corn Rootworm Larvae and Implications for Resistance

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We have isolated and identified a blend of compounds from the roots of germinating corn that serve as feeding stimulants for neonate western corn rootworm larvae, *Diabrotica virgifera virgifera* LeConte. The active blend is a combination of simple sugars (30:4:4 mg/ml glucose:fructose:sucrose in the corn root) plus at least one of the free fatty acids in germinating corn roots (2:5 mg/ml oleic acid:linoleic acid in the corn root). GC-MS analysis of root extracts from germinating corn seedlings revealed a blend of compounds from a variety of chemical classes. When the major components were tested in feeding bioassays, the sugars and lipids were shown to be essential for feeding by larvae, but the two classes of compounds were only effective when combined. The sugars alone elicited feeding by only 40% of larvae, but the percent of larvae feeding was increased significantly with the addition of the free fatty acid. The amino acids alone did not elicit any feeding by western corn rootworm larvae, nor did they improve feeding on the sugar blend. The presence or absence of these feeding stimulants may be responsible for preferential feeding by WCR larvae on one variety of corn over another. It may be possible to use plant breeding to produce corn plants that are less palatable to the larvae, and therefore, more resistant to rootworm damage.

INDUCED RESISTANCE IN RICE TO FALL ARMYWORM

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Rice, *Oryza sativa*, is the most important staple food for a significant portion of the world's population. Despite the importance of rice, however, induced resistance in rice is not well-studied; in fact, to our knowledge, direct induced resistance following attack by chewing insects has not been demonstrated in rice. We conducted a series of experiments designed to detect induced resistance in rice following feeding by larvae of the fall armyworm (*Spodoptera frugiperda*) and following application of jasmonic acid. Relative growth rates of fall armyworm larvae were lower when fed leaves from plants previously damaged by armyworms than when fed leaves from undamaged plants. This response was systemic. Growth rates were also reduced on foliage from plants treated with jasmonic acid. We also provide preliminary evidence that the high endogenous levels of salicylic acid found in rice leaves may interfere with responses to chewing insects.

"Insect Host Resistance in Warm-Season Turfgrasses."

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The Southern Chinch Bug, *Blissus insularis* Barber, was brought under excellent control when 'Floratam' St. Augustinegrass was released in 1973 and deployed throughout the southern United States. This resistance was lost as early as 1985 in Florida and now in Texas as early as 2005 with the discovery of the new virulent strain of Texas VTSCB-2005 biotype. 'NUF-76', a diploid breeding line of St. Augustinegrass, has been identified and is being developed in Florida with good resistance to the 'Floratam' resistant biotype. Studies in Texas have shown that several populations of Southern Chinch Bugs from the Bay City–Wharton, TX area (the heart of the St. Augustinegrass production in Texas) are not affected by the resistance in either 'Floratam', 'FX-10' or 'NUF-76' and adult mortality on these cultivars is at a level of less than 20% within 7 days of confined feeding. Evaluations of hybrids from the Texas breeding program have not provided promising results.

The Tropical Sod Webworm, *Herpetogramma phaeopteralis* Guenee, is another serious pest of St. Augustinegrass and when this grass is defoliated it can take up to three weeks for a lawn to recover. Commercial cultivars of St. Augustinegrass were evaluated for resistance. Thirteen commercial cultivars and two other genotypes were evaluated in the lab for resistance to this pest. 'Amerishade', 'BitterBlue', 'Floratine', 'FX-10', 'NUF-76' and 'Winchester' each provided excellent sources of host resistance with near 100% mortality of confined larvae, while 'Delmar', 'Floralawn', 'Floratam', 'Mercedes', 'Palmetto', 'Raleigh', 'Seville' and 'Texas Common' were each vary susceptible hosts and produced little mortality of the confined larvae in a no-choice experiment. Additional elite hybrids from the Dallas breeding program were evaluated but provided little resistance to this pest.

Impact of Chinch Bug Feeding on Photosynthesis of Forage Pearl Millet

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Chinch bug [*Blissus leucopterus leucopterus* (Say)] (Heteroptera: Blissidae) is one of the most important insect pests on pearl millet (*Pennisetum glaucum* L. R. Br.) production in the Coastal Plain region. Twenty-nine forage pearl millet germplasm entries were assessed for chinch bug resistance using modified chlorosis and stunting ratings. The chlorosis rating scale (1-4) was: 1 = all plants were normal and green; 2 = less than 25% of the plants showing leaf discoloration; 3 = 26 - 50% of the plants showing leaf discoloration; and 4 = over 50% of the plants showing leaf discoloration. The stunting rating scale (1-4) was: 1 = all plants had normal height; 2 = less than 50% of the plants were stunted; 3 = more than 50% of the plants but not all plants were stunted; and 4 = all plants were stunted. Leaf chlorosis ratings differed among the 29 entries ($F = 4.75$, df = 28, 85; $P = 0.0001$), but the stunting ratings did not ($F = 1.42$, df = 28, 85; $P = 0.1125$). While chlorophyll content (SPAD meter measurements) on flag leaves was not significantly different among the entries ($F = 1.27$, df = 28, 85; $P = 0.2039$), photosynthetic rate differed ($F = 1.9$, df = 28, 85; $P = 0.0129$) among the 29 entries. To differentiate the impact of chinch bug feeding on light and dark reactions of plant photosynthesis, light and CO_2 (or A/Ci) response curves of the symptomatic and asymptomatic plants within the most resistant (entry 1245) and susceptible (entry 1223) germplasm entries were compared. In the most resistant germplasm (entry 1245), chinch bug-injured (symptomatic) plants showed a suppressed light response curve, but CO_2 response curve was not affected when compared with the asymptomatic plants. In contrast, in the most susceptible entry (entry 1223), both light and CO_2 response curves were suppressed in the symptomatic plants when compared with the asymptomatic plants. The experiment results indicated that the least amount of chinch bug injury in the resistant pearl millet germplasm might be related to the minimal impact of chinch bug feeding on CO_2 assimilation capacity (or CO_2 response curves).

MICROBIAL TECHNOLOGY OF *Bacillus thuringiensis* VAR. KURSTAKI (BERLINER) FORMULATION AGAINST DEFOLIATOR *Spodoptera litura* (FABRICIUS) IN GROUNDNUT (ARACHIS HYPOGEA).

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Crop losses world wide due to insect pests is estimated about 15%. Among pests, the tobacco caterpillar *Spodoptera litura* is to be one of the deadliest pest in all crops. .The residual affects of the postcodes and induced resistance in insects has promoted the use of microorganism as an alternative. The natural pathogenic microorganisms which control the pests is *Bacillus thuringiensis.* Among the several crops in south India, the most commercial crop species like groundnut (Arachis Hypogea) and castor plants was mostly infected with *Spodoptera litura* larvae. The bacterial formulation fits very well to the groundnut ecosystem as the required micro climatic factors such as humidity to cause epizootics on the larvae are very much available and there is, therefore, much scope for use of *Bacillus thuringiensis* formulation in groundnut. In the light of the above, the present investigation was undertaken to develop a bentonite *Bacillus thuringiensis* formulation to be used against the groundnut defoliator *Spodoptera litura*. This paper aims to study about the efficacy of *Bacillus thuringiensis* against *Spodoptera litura* in groundnut species under laboratory and pot culture conditions. This paper also contains formulation of bentonite based bacterial pesticide, mode of action of *Bacillus thuringiensis* in insect pest and the bionomics of *Spodoptera litura* in both natural and artificial diet.

Key words: *Bacillus thuringiensis*, *Spodoptera litura,* Arachis Hypogea, Bentonite.

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To fly or not to fly? Revisiting the flight coordination concept in aphid.

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The winged form of an aphid species is the first to colonize new host plants. For that reason, they are often used to evaluate crop resistance to aphids. Short contact and probing time by an alate on a plant is interpreted as indication of resistance (antixenosis). However, the proportion of aphids entering flight activity during host selection behavior evaluation tests can vary greatly between replications. One can then ask how much of the "decision" to fly is guided by the host quality of the plant.

We revisited the concepts developed mainly by Moerike and Johnson stating that winged aphids go through physiological phases where they fly, search for an acceptable host and settle. Our results demonstrated that either host colonization or flight activity can occur at an early stage of development and are mainly dictated by physiological and environmental conditions. Those results contradict the accepted concepts and the coordination of aphid flight requires a redefinition.

Molecular characterization of saliva-specific laccase found in the green rice leafhopper, *Nephotettix cincticeps* (Uhler) (Homoptera: Cicadellidae)

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The green rice leafhopper (GRH), *Nephotettix cincticeps*, is an important insect pest of rice in Japan. This species causes damage directly by feeding and indirectly by transmitting viral and phytoplasma diseases (Ōya and Sato, 1981; Kawabe, 1985; Nakashima and Hayashi, 1995). GRH discharges coagulable and watery saliva during probing and feeding (Sogawa, 1968). It is considered that the saliva of vascular feeders plays important physiological roles in detoxifying toxic substances and/or ingesting sap from the plant. Recently, we have found that in *N. cincticeps*, a laccase type of phenoloxidase (EC 1.10.3.2, p-diphenol: oxygen oxidoreductase) is contained in the V-cells of the posterior lobe of the salivary glands and is secreted in the watery saliva (Hattori et al., 2005). In insects, the existence of laccase in the cuticles of many species has been well known; however, no reports have described the presence of laccase in the salivary glands of hemipteran insects.

To characterize the saliva-specific laccase, we cloned and sequenced genes encoding laccase from *N. cincticeps*: 2 laccase-1 type cDNAs (NcLac1S and NcLac1G) from the salivary glands and 1 laccase-2 type cDNA (NcLac2) from the epidermis were obtained. The NcLac1S, NcLac1G, and NcLac2 transcripts encode proteins with 701 amino acids (aa), 792 aa, and 729 aa, respectively. All the 3 cDNAs contain putative secretion signal sequences, 10 histidines and 1 cysteine that form copper-binding centers, and 1 methionine in the T1 copper center. Only the putative protein of NcLac1S is predicted to be soluble, whereas those of NcLac1G and NcLac2 are hydrophobic and have 2 transmembrane helices. Real-time RT-PCR revealed that the NcLac1S transcript was expressed exclusively in the salivary glands. NcLac1G expression, on the other hand, was detected not only in the salivary glands but also in the epidermis, midgut, and Malpighian tubules, in a descending order. The expression level of NcLac2 was the most abundant in the epidermis. The overall results indicate that the NcLac1S transcript is responsible for the laccase detected in the salivary glands and the saliva of this insect.

Hattori M, Konishi H, Tamura Y, Konno K, Sogawa K. 2005. Laccase-type phenoloxidase in salivary glands and watery saliva of the green rice leafhopper, *Nephotettix cincticeps*. Journal of Insect Physiology 51(12):1359-1365.

Identification of Phloem Sieve Elements as the Site of Resistance to Silverleaf Whitefly in Resistant Alfalfa Genotypes

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Experiments were conducted to locate the plant tissue where resistance is expressed against silverleaf whitefly, *Bemisia argentifolii* Bellows & Perring (Hemiptera: Aleyrodidae), in alfalfa, *Medicago sativa* L., genotypes previously shown to have high levels of resistance against this pest. Previous work demonstrated that resistance in the resistant alfalfa genotypes was expressed primarily as high first instar mortality; consequently this study focused on first instar nymphs. Examination of stylets in cleared leaf tissue indicated that first instar nymphs located vascular bundles with equal success on resistant and susceptible alfalfa genotypes. Furthermore, electrical penetration graphs (DC-EPGs) indicated that sieve elements were penetrated and phloem ingestion behavior was initiated with equal success on resistant and susceptible genotypes. Thus, the mechanism of resistance does not reside in tissues encountered by the stylets prior to penetrating a phloem sieve element. Honeydew production (as a proxy for ingestion) was greatly reduced on two resistant genotypes compared to the two susceptible genotypes. The frequency distribution of honeydew production was bimodal indicating that most individuals on the resistant genotypes produced little or no honeydew while some produced as much honeydew as whiteflies on the susceptible genotypes. This indicates that expression of resistance is an all-or-nothing phenomenon; an individual nymph either encounters resistance and cannot sustain ingestion or it does not encounter resistance and ingests just as well as on a susceptible plant. Intermediates are rare. DC-EPGs indicate that phloem ingestion behavior is significantly reduced on two of the resistant genotypes compared to the susceptible genotypes. The primary reason for this appears to be more frequent termination of phloem ingestion behavior on the resistant genotypes. On one of the resistant genotypes, the productivity of EPG-measured phloem ingestion behavior (honeydew produced per minute of phloem ingestion behavior) was reduced compared to a susceptible control.

Several specific defence strategies are elucidated in Wheat Containing different *Dn* genes

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The Russian wheat aphid (*Diuraphis noxia*, RWA, Homoptera: Aphididae) serves as a model organism for the study of molecular interactions between cereals and phloem-feeding insects, with the recognition and signalling events during the hypersensitive response (HR) and systemic acquired resistance (SAR) being of particular interest to plant breeders. Wheat lines containing different resistance genes to the Russian wheat aphid exhibit different resistance or tolerance responses. We investigated these responses at transcriptome level in near-isogenic wheat lines (NILs) containing the *Dn1*, *Dn2* and *Dn5* resistance genes, respectively. Affymetrix gene technology (i.e. Affymetrix GeneChip® Wheat Genome Array) and cDNA-amplified fragment length polymorphisms (cDNA-AFLP) transcript profiling were utilized. Quantitative PCR and Northern blot analyses were applied to confirm expression differences. Following these approaches, we have identified genes associated with the different resistance phenotypes afforded by some of the *Dn* genes.

Mapping of a new resistance gene to the green rice leafhopper, *Nephotettix cincticeps* Uhler, in the rice cultivar Nona Bokra

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The green rice leafhopper (GRH), *Nephotettix cincticeps* Uhler (Homoptera: Cicadellidae), is an insect pest of rice and is distributed in temperate Asia. GRH causes direct damage by sucking sap from the xylem and phloem of susceptible rice varieties and indirect damage by transmitting viral and phytoplasmal diseases. The control of this insect depends exclusively on the use of insecticides; this practice often brings about problems such as the development of insecticide resistance, environment pollution, and disruption of natural balance. To avoid these problems, effective biological control measures are required. The cultivation of GRH-resistant varieties would be an effective method to control this pest. Several indica rice cultivars are known to be GRH resistant, and their GRH resistance genes have been mapped on rice chromosomes (Yasui 2007).

We discovered a new resistance gene in the indica rice cultivar “Nona Bokra”. In order to determine the chromosomal location of this GRH resistance gene, we first used 12 chromosome substitution lines (CSLs). In each line, a different chromosome of the indica cultivar “Nona Bokra” was substituted in the genetic background of a GRH-susceptible japonica cultivar “Koshihikari.” The substituted chromosomes cover all chromosomes derived from Nona Bokra in the entire set of CSLs. Bioassays revealed that 1 CSL with the chromosome 5 region derived from Nona Bokra in the genetic background of Koshihikari was GRH resistant, while the other 11 CSLs did not show resistance to GRH. These results suggested that the GRH resistance gene in Nona Bokra was located on chromosome 5. Approximately 5,000 F2 plants derived from the heterozygotes of chromosome 5 substitution line were used for the high-resolution mapping of this GRH resistant gene. In addition to the SSR markers reported by International Rice Genome Sequencing Project (2005), newly developed SSR and CAPS markers on chromosome 5 were used for linkage analyses. Finally, we succeeded in mapping the candidate region of the GRH resistant gene in the 31 kb region between the flanking makers YT-2 and YT-8. In this region, some reading frames were predicted by the Rice GAAS (Rice Genome Automated Annotation System: http://RiceGASS.dna.affrc.go.jp/). Presently, we are promoting the identification of the GRH resistance gene.

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Plant defense responses to *Aphid gossypii* (cotton-melon aphid) feeding in resistant and susceptible melon (*Cucumis Melo*).

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Resistance to *A. gossypii* in melon is controlled at the Vat (Virus aphid transmission) locus by a major dominant gene, *Vat.* The genetic and physical characterization of the *Vat* gene and its product supports a model of a resistance (R)-gene mediated resistance against *A. gossypii* that is similar to plant resistance against a wide range of pathogenic organisms. However, the specific recognition, signaling pathways, and proximate causes of resistance against this aphid are unknown. Differences in response to *A. gossypii* infestations between the nearly-isogenic melon lines, PMR 5 (Vat^-) and AR 5 (Vat^+), were investigated using microarray analysis and quantitative real-time PCR. The results showed differential upregulation of a number of genes under aphid infestation, including genes involved in the ethylene plant defense pathway. Analysis of the expression patterns of ethylene signaling and synthesis genes (by QRT-PCR) showed feeding aphids evoked an earlier and stronger response in resistant melons than susceptible.

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Resistance Gene-mediated Host Defense in Wheat against Greenbug Feeding through Gene Expression Profiling with Affymetrix GeneChips

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In a 2-genotype, 3-time-point (0, 24 and 48 hours after infestation with biotype E greenbugs, hai), 3-replicate expression profiling experiment with Affymetrix GeneChips, the wheat greenbug resistance gene *Gb3*-mediated host molecular defense against greenbug feeding was investigated. The R and S genotypes/super pools were respectively composed of 8 homozygous resistant or 8 susceptible F_7 recombinant inbred lines (RILs) (3 plants per RILs) derived from a cross between two near isogenic lines (NILs) of *Gb3*. Of the 55K transcripts surveyed, only 47 showed significant differences in constitutive expression between the R and S pools (P = 0.05). Of the ~61,000 probe sets, on average 40% were flagged as 'present' in each gene chip. Of the ~24,000 'present' probe sets, appropriately 9,000 showed significant expression level changes at 24 and/or 48 hai, of which ~6,000 have predicated functions (with threshold = 1E-10). Among the 6,000 or so transcripts with significant changes in expression level in both genotypes at 24hai, 165 were significantly up-regulated in the R pool as compared with those in the S pool at either 24hai or 48hai or both. Preliminary analysis of the data indicated that host defense to greenbug feeding in wheat are similar to both that against plant pathogen attacks and plant wounding responses.

Eliciting proteins from *Diuraphis noxia* biotypes differ in size and composition.

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The molecular basis for the aphid-plant interaction is mostly unknown, and is predicted to follow a gene-for-gene model. The present study is aimed to detect salivary protein fractions in different *Diuraphis noxia* (Russian wheat aphid, RWA) biotypes which are recognized by the plant's resistance genes and trigger defence responses. For the present study, we used two SA RWA biotypes (SA1 or *wt* and SAM or *mutant*). The *mutant* RWA biotype evolved from the SA RWA biotype through selection pressure induced by force-feeding on a resistant host plant. We extracted total protein from the two SA RWA biotypes, purified them by size exclusion using high pressure liquid chromatography (HPLC), and investigated their phenotypic and biochemical responses after injection into near isogenic wheat lines. The purified proteins from the two biotypes induced significantly higher activities of selected pathogenesis-related (i.e., peroxidase and chitinase) enzymes in resistant plants in comparison to susceptible ones. We also characterized the size and composition of the respective proteins on SDS-PAGE and using isoelectrical focusing (IEF). The eliciting proteins from the two biotypes differ in size and character implicating possible gene duplication and/or protein modification events during the adaptation to the resistant hosts.

Schizaphis graminum biology on *Paspalum vaginatum*; a new biotype on a new host.

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Greenbug, *Schizaphis graminum* (Rondani) (Hemiptera: Aphididae) damaging seashore paspalum (*Paspalum vaginatum* Swartz) turfgrass was first discovered in November 2003 at Belle Glade, Florida. Problems caused by greenbug feeding were initially misdiagnosed as fertilizer, disease, other insects, or water management problems because aphids were not previously found on warm season turfgrasses. By April 2004, it had spread to golf courses across southern Florida. Damage symptoms on *P. vaginatum* progress from water soaked lesions surrounding feeding sites within 24 h to chlorotic and necrotic leaf tips within 96 h. In feeding trials on indicator plants, the Florida isolate of greenbug exhibited a unique biotypic profile most commonly found on non-cultivated grass hosts. It was virulent on the wheat variety GRS1201 that is resistant to the principal agricultural biotypes attacking small grains and to all currently available resistant sorghum varieties. Tests for resistance on seashore paspalum were conducted on six available varieties: 'Aloha', 'SeaDwarf', 'SeaGreen', 'SeaIsle', 'SeaWay', and 'SeaWolf'. Greenbug did not produce offspring or survive on SeaWolf. Development rates (mean ± SEM) ranged from 7.6 ± 0.2 to 8.2 ± 0.2 d on the remaining varieties. These rates were faster than those reported for greenbug on cool season range grasses, but slower than those reported for virulent biotypes on cool season cultivated grasses. Greenbug longevity and fecundity on Aloha were significantly less than on the other varieties. The estimated intrinsic rate of natural increase (r_m) for greenbug ranged from 0.24 to 0.26 across these varieties. Values for net reproductive rate (R_o) ranged from 12.3 on Aloha to 40.4 on SeaWay. Aloha was released for commercial production and sale in 2005.

AFLP - Linked Relationships Between Diuraphis noxia Populations in the Eastern and Western Hemispheres

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Diuraphis noxia is a serious global pest of world cereal crops in all continents except Australia, and is the most significant pest of cereal grain production in the U. S. western High Plains. Over 30,000 cereal crop accessions have been evaluated for D. noxia resistance worldwide, and resistance genes have been bred into improved varieties in South Africa and the U.S. to significantly reduce losses. However, D. noxia virulence has been documented in Africa, Asia, the Americas and Europe since 2003. In the present study, AFLP (amplified fragment length polymorphism) PCR primers were used to evaluate genomic DNA differences and similarities between D. noxia North American biotypes and D. noxia populations from Africa, Asia, Europe and South America. Data were subjected to principle component analyses and relationships between populations were established. Implications for differences between different populations will be discussed.

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