



# Proceedings from the 2016 Sorghum Improvement Conference of North America (SICNA)

## “The New Faces of Sorghum”

September 19-21, 2016

*Manhattan Conference Center & Hilton Garden Inn  
Manhattan, Kansas*

Organized by:



# ACKNOWLEDGMENTS

A special thanks to the local organizing committee, SICNA steering committee and discipline chairs:

## **Feed the Future Innovation Lab for Collaborative Research on Sorghum and Millet**

Dr. Tim Dalton

Mr. Nat Bascom

Ms. Kira Everhart-Valentin

## **Department of Agronomy and the Center for Sorghum Improvement – Kansas State University**

Dr. Ignacio Ciampitti

Dr. Mithila Jugulam

Ms. Sandy Kemp

Dr. Geoffrey Morris

Dr. Ramasamy Perumal

Dr. Gary Pierzynski

Dr. Tesfaye Tesso

Dr. Curtis Thompson

## **Sorghum Checkoff and National Sorghum Producers**

Mr. Brent Bean

Ms. Sarah Sexton-Bowser

## **Cropping Systems Research Laboratory - USDA ARS**

Dr. Gloria Burow

## **Sorghum Improvement Conference of North America- Leadership**

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Dr. Gabriel Krishnamoorthy - Secretary

Dr. Robert Klein - Board representative, public sector

Dr. Larry Lambright - Board representative, private sector

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*Breeding & Genetics:* Chad Hayes

*Biotechnology:* Scott Sattler

*Entomology:* Scott Armstrong

*Plant Pathology:* Deanna Funnell-Harris

*Agronomy / Physiology:* Ignacio Ciampitti

*Technology Transfer:* Brian Arnall

*Chemistry & Utilization:* Joseph Awika

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Thank you to all of our 2016 sponsors – SICNA could not be possible without your support!

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# INTRODUCTION

The 2016 Sorghum Improvement Conference of North America (SICNA), held on September 19-21, 2016 with the theme “The New Faces of Sorghum,” was a resounding success. The 2016 conference saw new facets to the meeting and programs, including SICNA and National Sorghum Producers awards for outstanding achievement in sorghum improvement, an exciting graduate student poster competition and an outstanding graduate student award. The meeting was attended by nearly 200 participants that represented a diverse cross section of the sorghum industry from both public and private sectors, students, producer stakeholders and commodity group leaders.

The opening keynote address was delivered by Dr. Joe Cornelius, Program Director of Advanced Research Projects Agency - Energy (ARPA-E), and the TERRA project, an initiative that focuses on sorghum as the smart bioenergy crop of choice. TERRA is a transformative private-public sector initiative that integrates cutting edge technologies in genetics remote sensing, robotics, machine learning and computational analytics for sustainable production of food, feed, fuel and fiber. Dr. Cornelius presented a dynamic challenge to the sorghum research community and the industry to pursue research and innovations towards fulfillment of sorghum’s potential as the most sustainable and smart crop for biofuel production and mitigation of climate change.

The presentations on the first day of the meeting featured research under the following session themes:

- 1) New traits, phenotypes and mutants for sorghum breeding and biotechnology, and
- 2) Pushing sorghum: Agronomics and production

Also featured during the conference was a Sorghum Industry Expo, which saw the participation of researchers, producers and companies focused on sorghum improvement and utilization. In addition, attendees had the opportunity to attend one of three site visits:

- 1) Selecting for Performance at Pioneer-DuPont breeding nurseries
- 2) Unmanned aerial vehicles (UAVs) for sorghum production and research at the Kansas State University North Farm; or
- 3) Demonstration on ethanol production from crop-based feed stalks at BIVAP and Seaton Hall on the Kansas State University campus

The SICNA 2016 banquet was highlighted by numerous awards presentations, including the Center for Sorghum Improvement’s Outstanding Service Award presented to Dr. David Mengel, the first director of the Center for Sorghum Improvement at Kansas State University. The National Sorghum Producers’ Outstanding Achievement in Sorghum Improvement award was presented to Dr. John Burke, Director, Cropping Systems Research Laboratory, USDA-ARS, Lubbock, TX; Dr. Gary Pederson, Research Leader and curator of the active sorghum collection of the Germplasm Resources Information Network, USDA-ARS and Dr. Roger

Monk, Sorghum breeder and scientist from Pioneer Hi-Bred International–DuPont for their excellent body of work and career contributions towards sorghum improvement.

The newest generation of sorghum scientists was well-represented by the many graduate students in attendance. Several were recognized for their outstanding achievements at SICNA and in their research programs (see page 8 for the full list of winners).

The keynote address was presented by Mr. Doug Bice, Market Development Director for the U.S. Sorghum Checkoff on “Future Market Opportunities for Sorghum” and covered a wide range of specialized areas identified for their potential for driving increased sorghum presence in the commodity and consumer markets. The banquet was capped by a post-banquet social at the Flint Hills Discovery Center that facilitated networking and discussions on sorghum-related research topics and issues among the attendees.

The second day of the meeting involved sessions on:

- 1) New challenges in developing integrated approaches for insect and disease control in sorghum; and
- 2) Rising to the challenge: sorghum as superior food ingredient for today’s consumer

Panel discussions were conducted for all the sessions and provided excellent forum for exchange of information and interactions between researchers and industry that will drive future initiatives. An informative and lively industry panel entitled, “Biofuels - the industry of applied next-generation science,” was moderated by the new managing director of the Kansas State University Center for Sorghum Improvement, Ms. Sarah Sexton-Bowser. The panel provided interesting and valuable insights into the application of sorghum at the industry level for advancement of biofuels.

The 2016 business meeting was then convened by 2016 SICNA Chairman Dr. Bill Rooney and culminated with the voice election of new roster of leaders of SICNA:

**Board members:**

R. Klein – USDA  
G. Krishnamoorthy – Richardson Seeds  
P. Brown – U of Illinois  
C. Franks – Pioneer

**Discipline chairs:**

Agronomy/Physiology: N. Rajan – TAMU  
Biotechnology: G. Burow – USDA  
Breeding: R. Perumal – KSU  
Entomology/Pathology: D. Kerns, LSU, and C. Little, KSU  
Technology Transfer: J. Lofton – OSU  
Utilization: Y. Li – KSU

SICNA 2016 was organized by the Feed the Future Innovation Lab for Collaborative Research on Sorghum and Millet, the Kansas State University Department of Agronomy and the Kansas State University Center for Sorghum Improvement with support from the U.S. Sorghum Checkoff and the Plant Stress & Germplasm Development Unit - USDA-ARS in Lubbock, Texas. Special appreciation goes to everyone on the planning committee who provided dedicated leadership and countless hours in making the event a success. Acknowledgements and thanks are also accorded to 2016 industry sponsors and supporters who provided monetary and in-kind support for the conference.

The following proceedings from the 2016 SICNA conference include the abstracts of oral and poster presentations in addition to access to many of the Power Point slides presented by the speakers in each session at the meeting. You will also find the agenda and list of sponsors in additional sections of this proceedings.

Please refer to any of the content herein judiciously by appropriate citation of each of the work in your research documents, manuscripts, articles or presentations. An example of a citation from this proceeding as an example (this will vary based on journal format/requirements):

**Knoll, J.E., Anderson, W.F., Harris-Shultz, K.R., and Ni, X. (2016). Planting date effects on sweet sorghum production in Georgia. Proceedings of the 2016 SICNA Meeting, Manhattan, KS, Sept 19-21, 2016 (eds., K. E. Valentin, G. B. Burow, and M. Jugulam). p.\_\_\_\_.**

We hope you will find the 2016 SICNA proceedings as a valuable resource for your research, extension and worthy sorghum-related activities.

Sincerely,

*Editors of the 2016 Proceedings*

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# CONFERENCE PROGRAM

<b>Monday, September 19<sup>th</sup></b>	
3:00 - 6:30 p.m.	<b>Graduate student oral presentation competition</b> <i>(Sponsored by DuPont Pioneer)</i>
5:00 - 7:30 p.m.	<b>Registration open</b>
6:30 - 7:30 p.m.	<b>Welcome reception</b>
<b>Tuesday, September 20<sup>th</sup></b>	
7:00 - 8:15 a.m.	<b>Breakfast and registration</b> <b>Graduation student poster presentation judging</b>
8:15 - 9:15 a.m.	<b>Welcome and keynote by Joe Cornelius, TERRA Program Director</b>
9:30 - 11:15 a.m.	<p><b>Research session #1 - “New traits, phenotypes and mutants for sorghum breeding and biotechnology”</b> <i>(Session discipline co-chairs: Dr. Chad Hayes, USDA-ARS, and Dr. Scott Sattler, USDA-ARS)</i></p> <ul style="list-style-type: none"> <li>• Presentation: "Effective utilization of sorghum diversity for improved performance and specialty traits" <i>Dr. William Rooney, Texas A&amp;M University</i></li> <li>• Presentation: "A sorghum mutant resource as an efficient platform for gene discovery in grasses" <i>Dr. Yinping Jiao, Cold Spring Harbor Laboratory and USDA-ARS</i></li> <li>• Presentation: "Biotechnology solutions for better sorghum grain" <i>Dr. Clifford Weil, Purdue University</i></li> <li>• Discussion panel</li> </ul>
11:15 - 1:30 p.m.	<p><b>Lunch, featuring:</b></p> <ul style="list-style-type: none"> <li>• 2016 SICNA Industry Expo</li> <li>• Graduate student finalist presentations</li> <li>• General and graduate student poster presentations</li> </ul>
1:30 - 3:15 p.m.	<p><b>Research session #2 – “Pushing sorghum: Agronomics and production”</b> <i>Session discipline co-chairs: Dr. Ignacio Ciampitti, Kansas State University, and Dr. Brian Arnall, Oklahoma State University)</i></p>

	<ul style="list-style-type: none"> <li>• Presentation: "Challenges and opportunities to produce high yielding sorghum" <i>Dr. Brent Bean, Sorghum Checkoff</i></li> <li>• Presentation: "Crop Insurance as a limitation to realizing high yielding irrigated grain sorghum" <i>Dr. Jason Warren, Oklahoma State University</i></li> <li>• Presentation: "Germplasm with improved cold and drought tolerance" <i>Dr. John Burke, USDA-ARS</i></li> <li>• Discussion panel</li> </ul>
3:30 - 6:00 p.m.	<b>Site visits</b> <ul style="list-style-type: none"> <li>• Selecting for Performance - <i>Pioneer DuPont</i></li> <li>• Unmanned Aerial Vehicles (UAVs) for sorghum production and research - <i>North Farm</i></li> <li>• Ethanol production from crop-based feedstalks- <i>BIVAP/Seaton Hall</i></li> </ul>
6:30 - 8:00 p.m.	<b>Conference banquet</b> , featuring: <ul style="list-style-type: none"> <li>• Center for Sorghum Improvement Outstanding Service Award - awarded to Dr. David Mengel</li> <li>• Graduate student poster and oral presentation competition awards</li> <li>• NSP Association award for Outstanding Achievement in Improvement</li> <li>• Keynote: "Future sorghum market opportunities" <i>Doug Bice, Market Development Director, Sorghum Checkoff</i></li> </ul>
8:00 – 10:00 p.m.	<b>Post-banquet social</b> - Flint Hills Discovery Center
<b>Wednesday, September 21<sup>st</sup></b>	
7:00 - 8:15 a.m.	<b>Breakfast</b>
8:15 - 10:00 a.m.	<b>Research Session #3 – “New challenges in developing integrated approaches for insect and disease control in sorghum”</b> <i>(Session discipline co-chairs: Dr. Scott Armstrong, USDA-ARS, and Dr. Deanna Funnell-Harris, USDA-ARS)</i> <ul style="list-style-type: none"> <li>• Presentation: "New challenges in managing insect and disease problems in sorghum." <i>Dr. Scott Armstrong, USDA-ARS</i></li> <li>• Presentation: "Crop injury and management of sugarcane aphid in sorghum in the U.S.” <i>Dr. David Kerns, Louisiana State University</i></li> </ul>

	<ul style="list-style-type: none"> <li>• Presentation: "New challenges in determining resistance genes and pathways against sorghum diseases." <i>Dr. Deanna Funnell-Harris, USDA-ARS</i></li> <li>• Presentation: "The nature and impacts of sooty molds on sorghum." <i>Dr. Chris Little, Kansas State University</i></li> <li>• Discussion panel</li> </ul>
10:15 - 12:00 p.m.	<p><b>Research session #4 - "Rising to the challenge: Sorghum as a superior food ingredient for today's consumer"</b> <i>(Session discipline chair: Dr. Joseph Awika, Texas A&amp;M University)</i></p> <ul style="list-style-type: none"> <li>• Presentation: "Making lots of dough with sorghum: It's about performing proteins." <i>Dr. John Taylor, University of Pretoria</i></li> <li>• Presentation: "Sorghum bran as a natural antioxidant in meat systems." <i>Drs. Christopher Kerth and Rhonda Miller, Texas A&amp;M University</i></li> <li>• Discussion panel</li> </ul>
12:00 - 1:30 p.m.	<p><b>Lunch</b>, featuring:</p> <ul style="list-style-type: none"> <li>• Industry panel - "Biofuels - the industry of applied next-generation science" <i>(Sponsored by the Kansas Grain Sorghum Commission)</i></li> </ul>
1:30 - 3:00 p.m.	<b>Business meeting</b>
3:00 – 3:30 p.m.	<b>Closing</b>

# **2016 GRADUATE STUDENT AWARDS**

## **Graduate student oral presentation competition**

For an excellent performance in the 2016 SICNA, the graduate student oral presentation competition awards went to:

1st place - **Greg Wilson, Louisiana State University**

2nd place - **Ananda Bandara, Kansas State University**

3rd place - **Ryan Gilreath, Louisiana State University**

## **Graduate student poster competition**

For an excellent performance in the 2016 SICNA, the graduate student poster competition awards went to:

1st place - **Seth Menzer, Kansas State University**

2nd place - **Olatoye Marcus, Kansas State University**

3rd place - **Francisco Gomez, Texas A&M University**

## **2016 SICNA Outstanding graduate student**

In recognition of outstanding student contributions to sorghum research, the 2016 SICNA outstanding graduate student award went to:

**Ananda Bandara, Kansas State University**

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### Session 1: “New traits, phenotypes and mutants for sorghum breeding and biotechnology” (Biotechnology/Breeding/Genetics - BG)

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*(The Use of Genetic Diversity in Sorghum Breeding)*  
William L. Rooney

SICNA 2016 – BG2                    **A sorghum mutant resource as an efficient platform for gene discovery in grasses**  
Yinping Jiao, John Burke, Ratan Chopra, Gloria Burow, Junping Chen, Bo Wang, Chad Hayes, Yves Emendack, Doreen Ware, and Zhanguo Xin

SICNA 2016 – BG3                    **Biotechnology solutions for better sorghum grain**  
*(Precision high-throughput phenotyping and mutation breeding)*  
Clifford Weil

### Session 2: “Pushing sorghum: Agronomics and production” (Agronomy/Physiology/Technology Transfer - APT)

SICNA 2016 – APT1                    **Challenges and opportunities to produce high yielding sorghum**  
Brent W. Bean

SICNA 2016 – APT2                    **Crop insurance as a limitation to realizing high yielding irrigated grain sorghum**  
*(Economic Viability of Irrigation Grains Sorghum in the Southern High Plain)*  
Jason Warren, Art Stoecker, Rodney Jones, Karthik Ramaswamy, Brooke Lane, Andrew Paul, Jordan Gatlin, and Cameron Murley

SICNA 2016 – APT3                    **Germplasm with improved cold and drought tolerance**  
John Burke, Yves Emendack, Gloria Burow, Chad Hayes, and Zhanguo Xin

**Session 3: "New challenges in developing integrated approaches for insect and disease control in sorghum"** (Entomology/Plant Pathology - EP)

SICNA 2016 – EP1                    **Crop injury and management of sugarcane aphid in sorghum in the US**  
David Kerns, Michael Brewer

SICNA 2016 – EP2                    **The nature and impacts of sooty mold on sorghum**  
Chris Little

**Session 4: "Rising to the challenge: Sorghum as a superior food ingredient for today's consumer."** (Chemistry/Utilization/Market Trends - CUM)

SICNA 2016 – CUM1                    **Making lots of dough with sorghum: it's about performing proteins**  
John Taylor and Janet Taylor

SICNA 2016 – CUM2                    **Sorghum bran as a natural antioxidant in meat systems**  
Rhonda K. Miller and Chris R. Kerth

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R. Enniful, J. V.S. Sunoj, S.M. Impa, P.V.V Prasad, and S.V.K. Jagadish

SICNA 2016 - SOC2                    **Exploring germination and early vegetative stage cold tolerance in sorghum**  
A. Chilawal, R. Perumal, R. Bheemanahalli, V. S. J. Sunoj, A.R. Asebedo, and S.V.K Jagadish

SICNA 2016 - SOC3                    **Genome wide mapping of anti-fungal phytoalexins in sorghum (*Sorghum bicolor* (L.) Moench)**  
D. Elango, W. Xue, I.Gaffoor, G. W. Roth, and S. Chopra

SICNA 2016 - SOC4                    **Evaluating commercial sorghum hybrids for resistance to *Melanaphis sacchari***  
J. D. Gonzales

SICNA 2016 - SOC5                    **Evaluating residual control and field efficacy of insecticides on *Melanaphis sacchari***  
R. Gilreath

- SICNA 2016 - SOC6      **The feeding and reproductive behavior of two isolated lineages of sugarcane aphid [*Melanaphis sacchari* (Zehntner) (Aphididae)]**  
G.B. Wilson and D. Kerns
- SICNA 2016 - SOC7      ***Macrophomina phaseolina* induces charcoal rot susceptibility in grain sorghum: evidence from transcriptional and functional data**  
A.Y. Bandara, D.K. Weerasooriya, S. Liu, and C.R. Little.
- SICNA 2016 - SOC8      **Developing ACCase-inhibitor-resistant grain sorghum**  
M. Carlson, W. Rooney, G. Hodnett, J. Norsworthy, and M. Bagavathiannan

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D. Elango., S. Chopra., and G. W. Roth
- SICNA 2016 - P8      **Grain sorghum response to Huskie application following products containing mesotrione.**  
S. Menzer, C. Thompson, C., and M. Jugulam
- SICNA 2016 - P19      **Genetic structure and diversity of Nigerian sorghum breeding program accessions**  
F. Maina, A. Mamadou, M.i Abdou, F.Hamidou, A. Aziz Saïdou, S. Bouchet, and G. P. Morris.
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J.M. Faye, N. Cissé, B. Sine, D. Foncéka, J. F. Rami, and G. P. Morris
- SICNA 2016 – P23      **Model study on extraction of both fermentable sugars and no-structural carbohydrate from sweet sorghum using diffusion process.**  
N. B. Appiah-Nkansah, K. Zhang, W. Rooney, and D. Wang
- SICNA 2016 - P28      **Screening of sorghum lines for resistance against sugarcane aphid, *Melanaphis sacchari* (Zehntner).**  
S. Paudyal, J. S. Armstrong, K. Giles, and A. Limaje



SICNA 2016 - P29

**Sugarcane aphid resistant sorghums found within  
USDA-ARS Lubbock, TX genotypes**

A.J. Limaje, C. Hayes, J. S. Armstrong, A. Zarrabi, W. W. Hoback, S. Paudyal, and J. J. Burke

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SICNA 2016 – P17/SOC10

**Understanding sorghum stem lodging: a  
biomechanical analysis and advanced imaging  
techniques using x-ray computed tomography (CT) to  
improve stem lodging resistance**

F. E. Gomez, A. H. Muliana, K. J. Niklas, and W. L. Rooney

SICNA 2016 – P7/SOC11

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M. J.W. Maw, J. H. Houx III, F. B. Fritschi

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palatability of dry dog food manufactured with  
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B. Di Donfrancesco, K. Koppel, and G. Aldrich

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N. Rajan, S. Shafian, R. Schnell, D. Menefee, P. Pokhrel, J. Valasek, J. Olsenholler, and Y. Shi

SICNA 2016 - GPE2

**Planting date effects on sweet sorghum production in  
Georgia**

J. E. Knoll, W. F. Anderson, K. R. Harris-Shultz, and X. Ni

SICNA 2016 - GPE5

**A regional monitoring program for crop-to-weed gene  
flow of herbicide resistance following  
commercialization of ‘Inzen’ sorghum hybrids**

J. Ziggafos, R. Werle, B. Tenhumberg, J. Lindquist, A. Jhala, and M. Yerka

SICNA 2016 - GPE9

**A large-scale experiment to evaluate the impact of integrated tactics for managing johnsongrass in Inzen™ sorghum**

M. Bagavathiannan, B. Young, L. Schwartz, and J. Norsworthy

SICNA 2016 - GPE10

**U.S. sorghum genetic resources collection: 15 years of progress (2001-2016)**

G. Pederson, M. Spinks, L. Chalkley, P. Vankus, T. Fields, S. Jones, and D. Pinnow

SICNA 2016 - GPE11

**Should the choice of pollination control bag types in sorghum matter?**

D.S. Virk, R.E. Schaffert, A.A. Kumar, A. Gaddameedi and H. Senior

SICNA 2016 - GPE13

**Selection of *Melanaphis sacchari* tolerant dual purpose sorghum varieties for Haiti**

G. Pressoir, J. R. Charles, and M. D. Dorval

SICNA 2016 - GPE14

**GBS genotyping of eight new publicly-available sorghum RIL populations**

P. Hirannaiah, W. Rooney, S. Manjunatha, and P. J. Brown

SICNA 2016 – GPE15

**A comparison of PCR-based and GBS-based methodologies to fine-map anthracnose resistance loci in sorghum**

T. Felderhoff, L. McIntyre, A. Saballos, J. Olmstead, and W. Vermerris

SICNA 2016 - GPE16

**Mining sorghum diversity with Gramene**

J. Stein, M.K. Tello-Ruiz, A. Olson, Y. Jiao, S. Wei, J. Preece, S. Naithani, J. Mulvaney, P.Gupta, S. Kumari, K. Chougule, J. Elser, B. Wang, J. Thomason, D. Bolser, P. Kersey, P. Jaiswal, and D. Ware

SICNA 2016 - GPE21

**A sorghum-based nutraceutical as a potential therapeutic approach for the treatment of type-2 diabetes (T2D)**

J. Taylor, M. R. Links, and J. R. N.Taylor

SICNA 2016 - GPE22

**Development of a sweet sorghum biomass system to improve sugar yield for biofuel production**

E. Tobias, F. S. Ehrenhauser\*, C. Gaudet and D. Aragon

- SICNA 2016 - GPE25      **Functional properties of combined waxy/heterowaxy – high digestible protein traits in hard endosperm sorghum**  
T. F. Teferra, D. B. Amoako and J. M. Awika
- SICNA 2016 - GPE26      **Variable-pressure scanning electron microscopy images of sorghum predict resistance to storage insect pests**  
M. Pendleton, B. Pendleton, and G. Peterson
- SICNA 2016 - GPE27      **Genetic diversity of the sugarcane aphid (Homoptera: Aphididae) in the United States**  
K. Harris-Shultz, P. Wadl, H. Wang, Xi. Wang, and X.i Ni
- SICNA 2016 - GPE30      **Assessing the occurrence and diversity of storage insect pests of sorghum in Niger (West Africa)**  
H. Kadi Kadi and B. B. Pendleton
- SICNA 2016 - GPE31      **Marker-assisted backcross approach for important agronomic traits of Sorghum**  
R. Chopra, G. Burow, H. H. Hughes, J. Burke, Z. Xin, Y. Emendack, and C. Hayes

# FULL ABSTRACTS

## I. Research Session Abstracts

### Session I: “New traits, phenotypes and mutants for sorghum breeding and biotechnology”

(Biotechnology/Breeding/Genetics - BG)

SICNA 2016 – BG1

#### **Effective utilization of sorghum diversity for improved performance and specialty traits**

*(The Use of Genetic Diversity in Sorghum Breeding)*

William L. Rooney

Dept. of Soil and Crop Science, Texas A&M University

College Station, TX 77843

Genetic variation is essential for plant breeding programs to select improved germplasm and produce improved sorghum hybrids. However, the introduction of genetic variation into elite breeding germplasm is difficult because most genetic variation is present in germplasm with generally poor agronomic performance. Consequently, sorghum breeding programs rely exotic and unadapted sorghum germplasm as a source of elite alleles to enhance performance of new sorghum hybrids. The sorghum conversion program was a source of these alleles for many years but there is some evidence that these sources have been effectively utilized. This means that new sources of variation must be developed and utilized. In our sorghum improvement program, new sources of diversity from various sources are evaluated and developed in different ways. First, our program has assessed the genetic variation in both commercial and public sorghum breeding programs to assess the range of existing variation. Second, a new introgression program to develop new elite sources of diversity is now underway. Finally, mining existing variation in elite breeding programs must be continually assessed – as the variation may be present because it had not been screened. For example, tolerance and resistance to sugarcane aphid appears to be present in numerous elite genetic backgrounds.

SICNA 2016 – BG2

#### **A sorghum mutant resource as an efficient platform for gene discovery in grasses**

Yinping Jiao<sup>1,2</sup>, John Burke<sup>1</sup>, Ratan Chopra<sup>1</sup>, Gloria Burow<sup>1</sup>, Junping Chen<sup>1</sup>, Bo Wang<sup>2</sup>, Chad Hayes<sup>1</sup>, Yves Emendack<sup>1</sup>, Doreen Ware<sup>2,3\*</sup>, and Zhanguo Xin<sup>1\*</sup>

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<sup>3</sup>USDA-ARS NAA Plant, Soil and Nutrition Laboratory Research Unit, Cornell University, Ithaca, NY USA 14853

Sorghum (*Sorghum bicolor* L. Moench) is a versatile C4 crop and a model for research in family Poaceae. High-quality genome sequence is available for the elite inbred line BTx623, but functional validation of genes remains challenging due to the limited genomic and germplasm resources available for comprehensive analysis of induced mutations. In this study, we generated 6,400 pedigreed M<sub>4</sub> mutant pools from ethyl methane sulfonate (EMS)-mutagenized BTx623 seeds through single-seed descent.

Whole-genome sequencing of 256 phenotyped mutant lines revealed > 1.8 million canonical EMS-induced mutations, affecting >95% of genes in the sorghum genome. The vast majority (97.5%) of the induced mutations were distinct from natural variations. To demonstrate the utility of the sequenced sorghum mutant resource, we performed reverse genetics to identify eight genes potentially affecting drought tolerance, three of which had allelic mutations and two of which exhibited exact co-segregation with the phenotype of interest. Our results establish that a large-scale resource of sequenced pedigreed mutants provides an efficient platform for functional validation of genes in sorghum, thereby accelerating sorghum breeding. We also established high efficient pipeline of bulk sequencing of F2 individuals to identify the causal genes by forward genetics method in the mutant population. By so far, we have narrowed down to a single gene or small region for several important traits, including multi-seeded (*msd*), male sterile and et al. Moreover, findings made in sorghum could be readily translated to other members of the Poaceae via integrated genomics approaches.

SICNA 2016 – BG3

**Biotechnology solutions for better sorghum grain**

*(Precision high-throughput phenotyping and mutation breeding)*

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Despite its promise, “mutation breeding” has not produced the wealth of new varieties over the years that it should have, largely because we have been unable to phenotype, genotype and mutate with enough precision. Linkage drag and inability to test carefully each and every plant in very large, segregating populations have made the process too inefficient to be cost-effective. However, the technological landscape has changed and continues to advance rapidly. Many of the roadblocks to realizing success with mutation breeding are now falling away, so it is time to re-examine this approach with fresh eyes. Three examples involving seed traits, biomass traits and agronomic improvement suggest we can now take advantage of new and developing tools and technologies to make rapid gains using mutation breeding.

**Session 2: “Pushing sorghum: Agronomics and production”**

*(Agronomy/Physiology/Technology Transfer - APT)*

SICNA 2016 – APT I

**Challenges and opportunities to produce high yielding sorghum**

Brent W. Bean

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USA grain sorghum yields have not increased at the rate of other key crops over the last 30 years. Average sorghum yields must increase significantly in order to regain acres and to increase profitability for sorghum growers. Breeders, agronomists and growers should consider the following in order to increase yields: 1) change the perception of sorghum from being a drought tolerant crop that can be planted on marginal soils with limited inputs to one that is water efficient whose yield will increase in response to additional water, good soils and fertility, and timely management decisions. 2) Potential seed number is determined prior to flowering. Minimizing stress from the 5th to 8th leaf stage will maximize potential seed number per panicle. Adequate water and nutrients as well as weed and insect control are

all critical during this time. 3) Number of panicles can be directly impacted by seeding rate which can be adjusted to meet a given yield goal. The development of hybrids with little or no tillering would provide much needed control over the number of panicles produced. 4) Seed weight is directly related to stress post flowering. Sufficient water and nutrients plus disease and insect control will help maximize seed weight. Breeders should consider increasing the stay-green trait in hybrids to minimize post flowering stress. In addition, increasing the duration of grain fill could also result in higher seed weight. 5) Other factors that affect sorghum yield are timely irrigation and utilizing planting dates that minimize water and heat stress based on historical climatic data.

## SICNA 2016 – APT2

### **Crop insurance as a limitation to realizing high yielding irrigated grain sorghum**

*(Economic Viability of Irrigation Grains Sorghum in the Southern High Plain)*

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Declining water levels in the Ogallala Aquifer result in reduced well capacity as well as increased pumping costs. These two factors must be considered when conducting limited irrigation research in the region aimed at optimizing the economic use of the remaining water. In 2013 a field research project was initiated where irrigation capacities of 62, 47, 31, 16, and 7.8 L min<sup>-1</sup> ha<sup>-1</sup> were used to constrain irrigation applied to corn and grain sorghum. The 3 year average yield production functions for these crops will be discussed. Furthermore, an economic analysis based on simulations of an EPIC model that was validated with this field data shows that grain sorghum becomes economically advantageous at irrigation capacities below 47 L min<sup>-1</sup> ha<sup>-1</sup>. However, discussions with irrigated producers in the Oklahoma panhandle brought to light the poor insurance coverage available for grain sorghum in the area. As a result historical analysis of crop insurance as well as an analysis of the profitability of crop insurance for corn and grain sorghum was conducted using the EPIC results. This analysis suggests that at current premiums and county T yields it is more profitable to not utilize crop insurance for grain sorghum until farm proven yields can be increased. This fact occurs because the county T yields for irrigated grain sorghum are approximately 50% of the yields achieved in our experimental settings for both hybrid performance trials and our irrigation efficiency trials. This suggests that policies should be explored to overcome this limitation to the adoption of grain sorghum as a viable irrigated crop in the southern high plains.

## SICNA 2016 – APT3

### **Germplasm with improved cold and drought tolerance**

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Declining water availability from aquifers and more extreme weather events positions sorghum as the crop of choice in the future. Its' ability to grow and yield in marginal agricultural regions, combined with the many uses of the crop, is increasing sorghum's importance in global agriculture. Significant diversity exists within the National Genetic Resources Program exemplified by the 43077 accessions of Sorghum bicolor subsp. bicolor that can be found in the Germplasm Resource Information System (GRIN). The objective of this study was to screen ~2,000 accessions from the Sudan and Ethiopian collections for drought and/or cold tolerances. Techniques utilized to identify drought tolerances included a chlorophyll

fluorescence technique, maintenance of lower leaves under low light conditions, measurement of dhurrin levels, and field evaluation of leaf and plant death ratings under pre- and post-flowering drought tolerance. Laboratory germination studies and field low temperature nurseries identified cold tolerances. Photoperiod sensitive lines were converted into photoperiod insensitive lines and individual plant selections made over six generations. Lines exhibiting early season cold tolerance and lines exhibiting post-flowering drought tolerance have been identified. One line exhibits excellent early season cold tolerance, and both pre- and post-flowering drought tolerance. Additionally, new sources of sugarcane aphid resistance have been identified from these studies.

### **Session 3: “New challenges in developing integrated approaches for insect and disease control in sorghum”**

(Entomology/Plant Pathology - EP)

SICNA 2016 – EP1

#### **Crop injury and management of sugarcane aphid in sorghum in the US**

David Kerns<sup>1</sup> and Michael Brewer<sup>2</sup>

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Beginning in 2013, an outbreak of sugarcane aphid has been causing extensive injury to sorghum in the Southern U.S. Pre-boot and boot sorghum can be stunted or killed by heavy aphid infestations or rendered sterile. Later infestations may result in reduced seed number and seed weight. It is not unusual to note a 30-100% yield loss associated with high aphid populations. Additionally, leaves of infested sorghum, at heading, become extremely sticky from honeydew and coated with sooty mold fungus; which may hamper harvesting operations, causing as much as 50% of the grain to be expelled from the combine. Honeydew coated leaves are also often more difficult to desiccate with harvest aids and once the plants are desiccated, the aphid will often move into the head, further interfering with harvest. Since its detection, much research has focused developing best management practices for managing sugarcane aphid in sorghum. Among others, research has focused on developing economic thresholds, host-plant resistance, insecticide efficacy, biological control and pest biology. Best management practices include: early planting, selecting resistant hybrids, removing Johnson grass refuges, using insecticide seed treatments and timely application of efficacious insecticides.

SICNA 2016 - EP2

#### **The nature and impacts of sooty mold on sorghum**

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Sooty molds are ascomycete fungi that grow on plant leaf surfaces (i.e. "phyllosphere") as well as other plant tissues. Such growth is the result of infestation by honeydew-excreting insects, including the sugarcane aphid (*Melanaphis sacchari*) on grain sorghum (*Sorghum bicolor*). In general, sooty mold fungi colonize the honeydew layer on the phyllosphere and exhibit a cosmetic defect, but do not cause physiological damage discernable from aphid feeding itself. However, lessons learned from the citrus blackfly (*Aleurocanthus woglumi*) interaction with grapefruit (*Citrus paradisi*) indicated that these sooty mold deposits contained citrus fruit pathogens (i.e., *Fusarium*, *Aspergillus*, and *Penicillium* spp.). Sooty

mold-associated phyllosphere fungal communities are complex and may function as an undiscovered pathogen reservoir for sorghum. A working model for the sorghum phyllosphere and future research needs will be presented.

## **Session 4: "Rising to the challenge: Sorghum as a superior food ingredient for today's Consumer"**

(Chemistry/Utilization/Market Trends - CUM)

SICNA 2016 – CUM1

### **Making lots of dough with sorghum: it's about performing proteins**

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The sorghum prolamin protein, kafirin and its maize homologue zein, are remarkably inert. This is related to a combination of relative hydrophobicity, disulphide bond crosslinking and predominantly  $\alpha$ -helical conformation, leading to a high glass transition temperature ( $T_g$ ). Their inertness has been exploited in a vast body of research on bioplastic-type applications. This, however, is not matched by commercial application, due to their poor functionality and high cost compared to synthetic polymers. In dough-based foods, the inertness of kafirin and zein is a major drawback as essentially they merely act as fillers and impart a dry texture. The key to both types of applications is improving the performance of zein and kafirin. With zein, we have been focussing on simple chemical treatments. We found that organic acids and oxidising agents bring about a dramatic improvement in the extensibility and viscous flow properties of its dough and can reduce its  $T_g$  to ambient temperature. To improve kafirin performance, we have been studying high protein digestibility sorghum mutants that have suppressed synthesis of kafirin subclasses responsible for disulphide bonding. With isolated kafirins and using a simple protein coacervation process, we have for the first time demonstrated wheat gluten-like viscoelastic dough formation with kafirin. Kafirins isolated from the high protein digestibility mutants exhibit better fibril formation and consequently form better doughs than kafirin from normal sorghum. Clearly, the fact that viscoelastic dough can be made with kafirin opens up new research avenues, with the possibility that performing food doughs can be made directly using sorghum flour.

SICNA 2016 – CUM2

### **Sorghum bran as a natural antioxidant in meat systems**

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The sorghum bran from either Sumac, High Tannin or Onyx sorghum varieties have been used in a series of studies to understand the impact of sorghum bran addition on lipid oxidation in meat systems. Studies have measured raw and cooked color, cook loss, pH, TBARS as an indication of lipid oxidation, trained meat descriptive flavor and texture analysis, and volatile chemical compounds to understand compounds associated with trained panel flavor. Initial studies utilized fresh ground beef in a model system to induce high levels of lipid oxidation. Sumac sorghum bran at 0.25 and 2.0% addition retarded lipid oxidation. Lower levels of Sumac sorghum bran (0.25, 0.5 and 1.0%) was used in a second study where 10, 20 and 30% fat fresh ground beef was stored for up to 5 days. Lower levels of lipid oxidation were reported and all treatments had limited lipid oxidation compared to control patties. Ground beef



patties, 10 and 27% fat, were pre-cooked to initiate lipid oxidation in a third study using 0.25, 0.5 and 1.0% Sumac sorghum bran. Controls were defined as ground beef with no added sorghum bran or ground beef with rosemary extract or BHA/BHT added as common industry antioxidants. Lipid oxidation was retarded by the addition of sorghum bran at all levels. In a fourth study, sorghum brans with varying tannin contents were added to ground beef at 0.25 and 0.5%. Cooked ground beef patties containing sorghum brans with higher tannin content at 0.5% had lower levels of lipid oxidation after 5 days of retail storage. Use of Sumac and black tannin sorghum bran at 0.25, 0.5 and 0.75% addition were examined in pre cooked turkey patties, pre cooked chicken nugget, bratwursts, and pork sausage patties. In turkey patties, Sumac and black tannin sorghum bran retarded lipid oxidation, but lipid oxidation was not reported in pre cooked pork sausage patties, chicken nuggets and bratwursts; however, sorghum bran addition had no effect on flavor, texture, color or yield in these products. The last study was conducted in two phases. In the first phase, precooked pork and chicken crumbles were stored for 0 to 5 days in aerobic packages after 0.125, 0.25, 0.50 and 0.75% Sumac and Onyx sorghum bran addition. Products with 0.75% Onyx sorghum bran were darker, but sorghum bran addition of 0.5 and 0.75% limited lipid oxidation. In the second phase, 0.5% Sumac and Onyx sorghum bran were added to pre cooked ground chicken and pork products and frozen. After 0, 3, 6, 9 and 12 months, products were evaluated as previously defined. In conclusion, sorghum bran addition, especially sorghum brans with higher tannin content can be added as a natural antioxidant to various meat products to limit lipid oxidation.

## **2. Student oral competition abstracts (SOC)**

SICNA 2016 – SOC I

### **Characterizing parents of sorghum mapping populations exposed to water-deficit stress**

R. Enniful, J. V.S. Sunoj, S.M. Impa, P.V.V Prasad, and S.V.K. Jagadish  
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Drought is a key abiotic stress that limits crop productivity which highlights the need for drought tolerant crops such as sorghum. With global climate models projecting increased intensity and magnitude in water-deficit conditions, plant traits that augment resistance to water-deficit conditions are indispensable. Greenhouse experiments were conducted on a set of 11 sorghum mapping population parental lines. The research objective was to characterize these geographically diverse sorghum genotypes for shoot and root related physiological parameters, plus changes in the leaf lipidome under water-deficit stress. Using a 1m lysimeter columns, water-deficit stress (55% to 60% water-holding capacity) was imposed lasting for 15-days, starting from 35-days after emergence. Gravimetric pot weighing was followed daily to determine transpiration efficiency during this period. The LS-means for the cumulative water transpired was 1.77 liters for stressed plants and 7.87 liters for the well-watered plants. Almost all parameters varied significantly between stressed and well-watered plants regardless of genotypic variances. With respect to photosynthetic assimilation, stomatal conductance, stem height, leaf and tiller numbers, effects of the stress was genotype specific. The rooting depths recorded for stressed and well-watered plants ranged from 138 - 53 cm and 144 - 83 cm, respectively. Results from electrospray ionization-tandem mass spectrometry analysis showed significant effects of water-deficit stress on the regulation of leaf membrane lipid composition. In view of sorghum's adaptation to challenging environmental conditions, findings will provide a means to identify the appropriate mapping population to map genomic regions responsible for increased drought resilience in sorghum.

## SICNA 2016 – SOC2

### **Exploring germination and early vegetative stage cold tolerance in sorghum**

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Four promising cold stress tolerant sorghum lines (ARCH10747-1, ARCH10747-2, ARCH12012 and ARCH12045) selected over years of continuous screening, known source of early stage tolerance (SQR) and a US elite susceptible line (RTx430) were assessed for germination and early vegetative stage cold tolerance. Seeds with >90% *ex situ* germination were sown on four different planting dates (between April 01 to June 02, 2016) with 15-day intervals at KSU, Agricultural Research Center, Hays, Kansas. Significant increase in soil temperatures from 5.5 °C (planting 1) to 18 °C (planting 4) was recorded using data-loggers embedded in the soil, at high temporal resolution. Combined analyses across four-plantings revealed significant impact of soil temperature on seed germination percentage, root traits, leaf area and overall biomass. Lower soil temperature with planting 1 and 2 negatively affected all the traits measured compared to planting 3 and 4. Interestingly, ARCH-10747-2 outperformed the popular cold-tolerant line (SQR) by accumulating greater root biomass, leaf area and shoot dry weight in planting 1 and 2, while RTx430 performed better than other lines during regular June 02 planting. Additionally, temporal phenotyping at the plot level using UAV (Unmanned Aerial Vehicle) fitted with RGB and multispectral cameras recorded reflectance based PSII and PSI activity and other plant based parameters which will be discussed. Our current experiments indicate presence of novel cold tolerant allele/s in ARCH-10747-2 for minimizing early stage cold damage in sorghum and the potential to integrate this source into ongoing breeding programs.

## SICNA 2016 - SOC3

### **Genome wide mapping of anti-fungal phytoalexins in sorghum (*Sorghum bicolor* (L.) Moench)**

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Sorghum is an important cereal crop and anthracnose is a major fungal leaf and stalk disease of sorghum, that affects productivity up to 50% under favorable environmental conditions. Sorghum synthesizes site specific anti-fungal phytoalexins known as 3-deoxyanthocyanidins (3-DAs) in response to anthracnose pathogen invasion. 3-DAs are shown to have potential fungi-toxic effects. A genome wide association study (GWAS) was performed on a diverse Sorghum Association Panel (SAP) and an ICRISAT (International Crops Research Institute for the Semi-Arid Tropics) mini-core germplasm to map genes controlling the regulation of fungal induced 3-DAs in leaves. Three biological replicates of leaf samples were collected at V<sub>7</sub> stage after fungus infection with *Colletotrichum sublineola* pathogen by using approximately 10<sup>6</sup> spore's ml<sup>-1</sup>. The quantitative measurement of 3-DAs were carried out using spectrophotometer and confirmation of a sub-set by HPLC (High Performance Liquid Chromatography). Significant variability for anti-fungal compounds was observed among genotypes of these diversity panels. GWAS was performed using the GAPIT (Genome Association and Prediction Integrated Tool) software. Community resources of 79,132 SNP (Single Nucleotide Polymorphism) markers were used in this study. GWAS identifies several significant loci for 3-DAs including several putative wound induced and defense related genes were identified as candidate genes. This genome wide SNPs variation for 3-DAs in sorghum will be presented. Our results provides basis for anthracnose disease improvement through marker assisted selection and genomic selection for plant secondary metabolites that act as fungicides in sorghum.

## SICNA 2016 – SOC4

### **Evaluating commercial sorghum hybrids for resistance to melanaphis sacchari**

J. D. Gonzales

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During the 2015 season through field and growth chamber studies, grain sorghum, *Sorghum bicolor*, was evaluated for resistance to sugarcane aphid, *Melanaphis sacchari* (Zehntner), at three locations in Louisiana. Hybrids included a known resistant ATx2752/RTx2783, a known susceptible ATx2752/RTx430, and 14 hybrids with suspected resistance. The objective of this study was to determine the degree of resistance among the hybrids. The field study was a split-plot design with hybrids being the main plot. One sub-plot was protected from aphid infestation by means of insecticide Transform (sulfoxaflor), while the other was left untreated. In addition to the field study, a seedling susceptibility screening was conducted with the same hybrids in a growth chamber. Hybrids were planted in 8-inch pots, with five seedlings per pot. At the 2 to 3 leaf stage, seedlings were infested with ~50 aphids per plant. Each plot was rated on a 1-9 injury scale at 17 days after infestation. In field trials, under light to moderate aphid pressure, hybrids that appeared susceptible (demonstrated a yield benefit from sulfoxaflor applications) included: ATx2752/RTx430 and DG M756B39. Hybrids that exhibited possible tolerance (high aphid days but no yield benefit from spraying included: DG M77GB52, DG 765B, and R94153. Hybrids that exhibited possible antibiosis (low aphid days and no benefit from sulfoxaflor applications included: ATx2752/RTx2783, R84353, R9813, SP6929, SPX17514, SP7715, NKX760, P-83PI7, W-844-E, and DKS37-07. Additionally, ATx2752/RTx2783, DKS37-07, R9813, R84353, SP7715, SPX17414, SPX17514, NKX760 and W-844-E exhibited significantly less aphid feeding injury than ATx2752/RTx430 in the seedling susceptibility screening.

## SICNA 2016 – SOC5

### **Evaluating residual control and field efficacy of insecticides on *Melanaphis sacchari***

R. Gilreath

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In recent history, the sugarcane aphid (SCA), *Melanaphis sacchari* (Zehntner) has become an important economic pest of grain sorghum in the U.S. For more information about managing this pest, research was conducted evaluating the efficacy and residual control of three insecticides, Chlorpyrifos (Lorsban Advanced), Sulfoxaflor (Transform) and Flupyrifurone (Sivanto). During 2015 and 2016, studies were conducted at the Macon Ridge Research Station in Winnsboro, Louisiana. In a 2015 insecticide efficacy test, plots treated with Lorsban Advanced at 1 qt/ac, required re-treatment after 14 day based on a 50 SCA per leaf threshold. While Transform at 1 oz/ac required re-treatment after 21 days and Sivanto at 4 fl-oz/ac did not require re-treatment. To better understand residual activity, field-weathered bioassays were utilized during 2015 and 2016 using boot stage sorghum treated with Lorsban Advanced, Transform or Sivanto. At 0, 3, 7, 14 and 21 DAT, 8 leaves sampled from the 9<sup>th</sup> node were removed and bioassays were conducted using methods adapted from the Insecticide Resistance Action Committee (IRAC, Method No. 019). Bioassay arenas consisted of individual 29-ml Solo condiment cups with a 2-ml layer of 1% agar solution. A 3-cm hole was cut into each lid and sealed with single ply tissue paper to allow excess moisture to escape. Ten adult SCA were placed into each cup and placed in a growth chamber at 27° C ± 1 for 48h before assessing mortality. The LT50 for field-weathered Lorsban and Transform was approximately 6 days, while Sivanto was approximately 10 days.

## SICNA 2016 - SOC6

### **The feeding and reproductive behavior of two isolated lineages of sugarcane aphid [*Melanaphis sacchari* (Zehntner) (Aphididae)]**

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During the past four years, sugarcane aphid (SCA) [*Melanaphis sacchari* (Zehntner)] have significantly impacted grain sorghum (*Sorghum bicolor* L.) production in the United States and Mexico. Currently, the origin and biology of SCA (infesting sorghum) is not clearly understood but it's theorized that the host shift occurring in 2013 away from sugarcane was caused by either A) emergence of a new SCA biotype through mutation or recombination, B) U.S. introduction of an already previously evolved type, or C) a change in aphid gut symbionts. A series of experiments were initiated in 2016 investigating feeding and reproductive behaviors of this economically important pest. First: Potential host range was examined through 14 day no-choice studies of 54 graminaceae species and a 35 day field test of 12 hosts. Second: Electrical penetration graph (EPG) technique was then used to detect differences, if any, in feeding behavior of sugarcane and sorghum isolates on whole plant tissues for 9 grass hosts. Third: Aphid reproduction is currently being compared by cross bioassay of sugarcane and sorghum isolates on the same 9 grasses. Results from no-choice study significantly identified 15 hosts which supported either temporary or long-term parthenogenic reproduction. Of these, 6 species within the genus *Sorghum*, *Saccharum*, *Miscanthus*, and *Pennisetum* supported SCA colony development until death of host or longer than 21 days, with 9 other species lasting 7-21 days. Differences in 11 EPG waveforms and differences in adult longevity and fecundity will be tested for significance by analysis of variance using two-way and mixed-model respectively.

## SICNA 2016 - SOC7

### ***Macrophomina phaseolina* induces charcoal rot susceptibility in grain sorghum: evidence from transcriptional and functional data**

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Although *Macrophomina phaseolina* (MP) is a devastating plant pathogen causing charcoal rot disease in sorghum (*Sorghum bicolor* (L.) Moench), the molecular interaction between MP and sorghum is poorly understood. As a result of a recently conducted RNA-Seq experiment, three genes (*Sb08g011530*, *Sb05g000680*, and *Sb04g027860*) involved in nitric oxide (NO) biosynthesis, a gene that encodes *chlorophyllase-2* (*Sb02g012300*), and seven genes involved in the rhamnase biosynthetic pathway (*Sb01g038050*, *Sb01g039220*, *Sb01g043370*, *Sb02g029130*, *Sb08g022850*, *Sb09g018070*, and *Sb10g024490*) were among those found to be significantly up-regulated in the MP-inoculated susceptible genotype (Tx7000) at 7 days post-inoculation (DPI). Findings were functionally validated using two resistant (SC599, SC35) and susceptible (Tx7000, BTx3042) sorghum genotypes at 7 DPI. The in-situ NO production of MP- and mock-inoculated stem cross-sections was analyzed using a fluorescent dye (DAF-FM DA) and confocal microscopy. Strong green fluorescence observed in both MP-inoculated susceptible genotypes confirmed the presence of NO while no signal was detected in resistant genotypes. To confirm the effect of up-regulated *chlorophyllase-2*, stalk chlorophyll was extracted with acetone. Total chlorophyll content (mg/g stalk) was computed using spectrophotometer readings. Compared to control, MP significantly reduced total chlorophyll of Tx7000 (control, 1.56; MP-inoculated, 0.40) and BTx3042 (control, 1.45; MP-inoculated, 0.63) ( $P < 0.016$ ). No such effect was evident for the two resistant genotypes. HPLC analysis of stalk juice extracts showed significantly higher

( $P < 0.005$ ) rhamnose concentrations (mg/mL) in the susceptible genotypes (Tx7000, 7.2; BTx3042, 5.8) compared to control while no such effect was evident in the resistant genotypes (SC599, 1.6; SC35, 1.4). Data revealed MP's ability to promote charcoal rot susceptibility in a sorghum genotype-specific manner.

## SICNA 2016 - SOC8

### **Developing ACCase-inhibitor-resistant grain sorghum**

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Herbicide resistance is a trait of great importance to facilitate effective grass weed management in grain sorghum, including the management of johnsongrass. Grain sorghum with non-transgenic resistance (Inzen™ sorghum) to nicosulfuron, an acetolactate synthase-inhibitor, will be commercially available in the near future. Additional herbicide resistance traits will help protect the longevity of Inzen™ sorghum. The objective of this research is to transfer Fluazifop-P-butyl herbicide resistance from johnsongrass (WM2) into grain sorghum, using the *TX336 liap* line which facilitates wide-hybridization in sorghum. Initial crosses were made between WM2 (male) and *TX336 liap* (female) during fall 2014. The progenies that survived Fusilade™ herbicide at 105 g ai ha<sup>-1</sup> were selected. Flow cytometry analysis was conducted to identify ploidy of the progenies; a tetraploid individual was selected for further use. This tetraploid individual was backcrossed with WM2 (male) and a triploid (BC<sub>1</sub>F<sub>1</sub>) was isolated through embryo-rescue technique. This triploid progeny (male sterile) was then backcrossed with *TX336 liap* (male). One of the BC<sub>2</sub>F<sub>1</sub> progenies was identified as diploid having resistance to Fusilade™. Presence of 20 chromosomes was confirmed using chromosome staining technique. This individual was backcrossed with an elite sorghum line (male) and BC<sub>3</sub>F<sub>1</sub> plants are currently being characterized. Further research will involve additional backcrosses, breeding and field testing of the resistant line. This research also provided a better understanding of the risk of gene flow between sorghum and johnsongrass. Efforts are underway to integrate the herbicide resistance trait with a gene-flow mitigation trait to prevent unintended effects of gene flow.

## **3. Poster presentation abstracts (P)**

### SICNA 2016 - P4

#### **Seeding rate and N fertilization effects on BMR brachytic dwarf forage sorghum varieties**

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Brown mid-rib (BMR) forage sorghum is considered as reasonable alternative to maize silage. Traditional forage sorghum varieties are tall and prone to lodging with lower forage quality. Newer brachytic dwarf BMR lines are shorter, lodging resistant and have higher forage quality. A two year study was conducted during the 2014 and 2015 growing seasons to determine the effects of different seeding rates and N (nitrogen) fertilization rates on forage dry matter yield and forage quality. The experimental design was split-split-plot with four replications. In each replication, main plots were two varieties (AF 7202 and AF 7401), subplots were two seeding rates (80,000 and 120,000 seeds ac<sup>-1</sup>), and sub-subplots were two N rates (123 and 168 kg ac<sup>-1</sup>). The morphological, dry matter yield and forage quality parameters were recorded and analyzed. The earlier line, AF 7202, had higher yields, lower NDF (Neutral Detergent Fiber) and higher starch levels than AF 7401. Neither variety responded to an increase in seeding rate. AF 7202 was more responsive to the higher N rate than AF 7401. Crude protein was increased from

7.9% to 8.5% with increased N for both varieties. Other forage quality traits were unaffected by N rates. This study showed that the earlier line, AF 7202, managed with recommended seeding rates and higher N rates was the optimum treatment for high forage yield and quality.

## SICNA 2016 - P8

### **Grain sorghum response to Huskie application following products containing mesotrione**

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Options for rotating herbicide modes of action for post-emergence (POST) weed control are limited in grain sorghum. Huskie is a product that combines bromoxynil, a photosystem II inhibitor with pyrasulfotole, a 4-Hydroxyphenylpyruvate dioxygenase (HPPD) inhibitor for broad-spectrum weed control. However, growers are warned on the label that unacceptable injury may occur if Huskie is applied to acreage previously treated with any product containing mesotrione, another HPPD herbicide. The objective of this study was to determine whether Huskie treatments following application of products containing mesotrione did indeed result in unacceptable sorghum injury. Trials were conducted at the Ashland Bottoms research station in 2015 and 2016, and at the Tribune NE research station in 2016. Experimental treatments included pre-emergence (PRE) treatments with mesotrione followed by Huskie application, PRE treatments without mesotrione followed by Huskie application, and PRE treatments without mesotrione followed by POST treatments containing only bromoxynil. Crop response was rated 3, 7, 14 and 28 days after POST treatment (DAT), and sorghum was harvested at physiological maturity for yield. Results from the 2015 trial demonstrated greater sorghum injury in plots treated with Huskie than those treated with bromoxynil 3 DAT, but no difference was observed between Huskie treatments that followed mesotrione and those that did not. No injury was observed for any treatment 28 DAT, nor was any difference in yield observed as a result of HPPD herbicide injury. The potential to apply Huskie following PRE treatments containing mesotrione adds an important tool for season-long weed control in sorghum.

## SICNA 2016 - P19

### **Genetic structure and diversity of Nigerian sorghum breeding program accessions**

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The development of improved varieties in plant breeding can be enhanced by marker-assisted selection (MAS). However, utilization of MAS in crop improvement still remains challenging in developing countries where staple crops have been developed through conventional breeding. One such crop is sorghum (*Sorghum bicolor* L. Moench), an important crop with four racial groups distributed across agroclimatic zones in Niger. Developing new varieties for a better adaptation through genomic breeding is of ultimate importance, but little knowledge exists about Nigerien sorghum germplasm. Therefore, we analyzed 345 accessions (landraces and breeding lines) used by the Nigerien breeding program and the West African Sorghum Association Panel for their agronomic performances and adaptation to different environments. The objective of this study is to characterize the genetic structure and diversity of these breeding lines using Genotyping By Sequencing (GBS) method. In total, 106,887 Single Nucleotide Polymorphisms (SNPs) were identified using Tassel GBS Pipeline. To identify the accessions linked to the

genetic clusters, we performed two different approaches. The “Discriminant Analysis of Principal Components (DAPC)” that uses the Bayesian Information Criterion to identify the optimal number of clusters where as “Admixture” uses the maximum likelihood estimation to classify the accessions. Both methods reveal diverse subpopulations grouped by their racial group. The allele frequency shows a significant number of rare alleles that confer adaptation for a specific environment. Understanding the genetic structure of these breeding accessions assists in developing useful resources for marker-assisted selection that are important for sorghum improvement in Sub Saharan Africa.

SICNA 201 6 - P20

### **Genome-wide association studies of yield components under water limitation for a West African sorghum association panel**

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Sorghum, a major cereal food crop in many developing countries, is mainly affected by water limitation stress in the semi-arid regions. Improving sorghum’s adaptation to water-limited conditions is a fundamental factor for establishing food security in semi-arid areas of West Africa. With the recent advances in genomic approaches, it is feasible to dissect genomic regions controlling water limitation stress in sorghum. To identify genomic regions associated with water limiting conditions in West African sorghums, GWAS was conducted on 557 sorghum accessions (landraces and improved breeding lines) from the four West African countries of Senegal, Mali, Togo and Niger. Genotyping-by sequencing (GBS) was conducted using ApeKI restriction enzyme on these accessions. The GWAS analysis was Bre using a total of 106,887 SNP markers obtained after aligning the illumina read sequences data to the latest version of the sorghum reference genome v3.1 and SNP calling using the TASSEL GBS pipeline. The Bayesian model-based clustering method, neighbor joining tree, and principal components analysis revealed distinct groups with respect to the country of origin of these accessions. GWAS on the 2014 phenotypic data identified 9 SNP markers significantly associated with panicle weight, total grain weight per panicle, and canopy temperature. To confirm the current SNPs associated with yield components, further GWAS is being carried on the 2015 phenotypic data and can be very useful to improve local cultivars and improve food security in West Africa.

SICNA 2016 - P23

### **Model study on extraction of both fermentable sugars and no-structural carbohydrate from sweet sorghum using diffusion process**

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Sweet sorghum stores a high concentration of soluble sugars in its stalk and produces grain in the panicle. This grain represents a significant amount of starch. The ethanol industry currently uses sugarcane processing methods for sweet sorghum, however, sweet sorghum differs from sugarcane in that sweet sorghum produces significant quantities of grain which is predominantly starch. The objective of this research was to increase ethanol production from sweet sorghum by fully utilizing all fermentable sugars which include starch in the grain and nonstructural carbohydrates in the stalk. The diffusion process was utilized to extract fermentable sugars and nonstructural carbohydrates from chopped sweet sorghum biomass and grains. Response surface methodology (RSM) was applied in order to

optimize diffusion conditions and to explore effects of diffusion time, diffusion temperature, ratio of sweet sorghum grain to total biomass on starch-to-sugar efficiency, and total sugar recovery from sweet sorghum. RSM results showed that starch conversion efficiency and sugar recovery efficiency of 96% and 98.5%, respectively, were achieved at an optimized time of 114.9 min, temperature of 95 °C, and 22% grain loading.

SICNA 2016 - P28

### **Screening of sorghum lines for resistance against sugarcane aphid, *Melanaphis sacchari* (Zehnter)**

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Host-plant resistance is the one of the most sustainable methods of controlling sugarcane aphid, *Melanaphis sacchari* (Zehnter), a pest of sorghum (*Sorghum bicolor* (L.) Moench). Sugarcane aphid has been a consistent threat to sorghum growing regions of the United States since the summer of 2013. Twenty three different sorghum lines were screened for resistance in a free choice flat screen by infesting with sugarcane aphids at the 3-4 leaf. Chlorosis ratings were initiated when the susceptible control (580) was estimated to be 85% dead. All plants were evaluated using a chlorosis rating of 1–9 (little to high damage). Chlorophyll loss was also quantified in a no-choice test on the infested and uninfested leaves of each of the lines using SPAD-502 chlorophyll meter. From the free-choice study, sorghum lines HI30373, 95207, G1213, GW1489, 97157, TX 2783, W 7431, W844-E, and DKS-37-07 were highly resistant with rating  $\approx 3$ , indicating that good sources of host-plant resistance. Plant height, number of leaves, and chlorophyll values recorded suggests that the aforementioned lines are resistant to sugarcane aphid. Chlorophyll loss in susceptible check (580) was 60%, however, in the above resistant lines the loss figures were <20% indicating that good sources of resistance are inherent within these genotypes. Future studies will be conducted to determine the categories of resistance in these resistant lines which will be helpful in breeding programs and also field test for these sorghum lines.

SICNA 2016 - P29

### **Sugarcane aphid resistant sorghums found within USDA-ARS Lubbock, TX genotypes**

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The sugarcane aphid, *Melanaphis sacchari*, was discovered infesting grain sorghum in the southern United States in 2013 and has been a perennial pest through 2016. We evaluated 25 sorghum genotypes in a search for host plant resistance to this pest. Plants were started from seed (N = 16 replications per entry) and infested heavily at the 3 leaf stage, 8 d post emergence. After 3 weeks, plants were assessed for height, number of leaves, and chlorophyll content using a SPAD meter. Damage ratings were conducted using Webster's 1 to 9 scale, 1 being no damage, 9 being a dead plant. We used TX2783 and DKS-37-07 as resistant checks, and C-580 and JS222 as known susceptibles. Our results suggests that R.11143 was highly resistant, scoring a 3.1 damage rating compared to TX2783, and R.11259 which scored a 5.8 rating or moderate resistance to sugarcane aphid. The remaining 23 USDA-ARS lines ranged from moderately susceptible to highly susceptible. R.11143 and R.11259 are two pollinator lines developed by ARS Lubbock in 2011. R.11143 has a pedigree of TX2783/PI567946 and was originally selected based on good cold germination. TX2783 is a pollinator parent released by Texas A&M University with



documented resistance to the sugarcane aphid. PI 567946, also known as Hong Ke Zi, is a Chinese landrace with excellent cold germination and vigor. R.11259 has a pedigree of SC56//86EON361/BE2668 and was selected based on good stay-green ratings, high leaf dhurrin content and preliminary hybrid performance. SC56 is a good stay-green pollinator developed by the Texas A&M University and USDA Sorghum Conversion Program. 86EON361 and BE2668 are unreleased lines from Texas A&M University. These trials provide the first step in identifying host plant resistance to the sugarcane aphid in sorghum. Field trials conducted in Lubbock, TX confirm resistance of these lines.

#### **4. Dual submission (poster and oral) abstracts (P/SOC)**

SICNA 2016 – P12/SOC9

##### **The genetic architecture of panicle traits in sorghum using nested association mapping**

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Sorghum is an important crop in many agroclimatic regions worldwide, and has adapted to a wide range of conditions. This makes it an important crop for food security in the face of climate change for smallholder farmers in developing countries. Accordingly, global sorghum germplasm exhibits substantial variation in agroclimatic traits—traits that differ in germplasm from different agroclimatic zones—for example panicle architecture. Currently, our ability to improve sorghum adaptation and transfer useful alleles across different genetic backgrounds is constrained by our limited knowledge of the genomic regions that underlie agroclimatic traits. Nested Association Mapping (NAM), which uses multiple biparental families linked by a common parent, can improve dissection of agroclimatic traits by reducing the confounding effects of population structure and increasing the frequency of rare alleles. A sorghum NAM population comprised of 10 families and almost 2,500 recombinant inbred lines (RILs) has been developed and genotyped at approximately 100,000 SNPs with Genotyping-by-Sequencing (GBS). The population was phenotyped for rachis length and primary rachis branch length in two contrasting environments (locations) in Kansas, semi arid (Hays) and humid continental (Manhattan) for two years. Significant genotypic variation for these traits was observed. Association and joint linkage mapping confirmed several previously identified quantitative trait loci (QTL) and revealed many new QTL, which were of moderate and low effects for the panicle architecture traits. The QTL identified will be helpful in genomic enabled breeding for better adaptation and yield.

SICNA 2016 - P17/SOC10

##### **Understanding sorghum stem lodging: a biomechanical analysis and advanced imaging techniques using x-ray computed tomography (CT) to improve stem lodging resistance**

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Stem lodging in sorghum is a major agronomic problem that has far reaching economic consequences. More rapid and reliable advances in lodging resistance could be achieved through development of selective breeding tools that are not dependent on post hoc data or confounded by environmental factors. Biomechanics provides a superb tool to understand the functional design and mechanics of cereal crop stems, which ultimately determines the plants ability to maintain their mechanical stability. To develop a more complete understanding of the determinants of stem lodging, a series of experiments

were conducted from 2013-2015. In particular, a detailed mechanical analysis on the whole stalk of sorghum using a three-point bending protocol revealed that sorghum uses a variety of mechanical and morphological adaptations along its stem to provide better mechanical performance. Results demonstrate that nodes are stiffer, stronger, and more rigid than internodes. In general, internodes were weaker and more rigid between internodes 3 and 6, corresponding to the area where higher stem failure is observed. Significant genetic variation was found for all mechanical properties, and several of these mechanical properties were also found to be significantly associated with stem morphology and lodging. Finally, image analysis using a flatbed scanner and x-ray computed tomography show promise for rapid phenotyping of stem anatomy, morphology, and mechanical properties. These results indicate the potential of these methods as a selective breeding tool for indirect selection or as a selective breeding index of stem lodging resistance in sorghum and future improvement.

#### SICNA 2016 – P7/SOCI1

##### **Corn, sweet sorghum, and high biomass sorghum production on marginal lands in Missouri**

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Emerging biofuel feedstock systems are poised to have a lasting effect on midwestern USA marginal soils by converting from grasslands to cultivated systems. Three annual bioenergy crops, corn (*Zea mays* L.), sweet sorghum (*Sorghum bicolor* (L.) Moench), and high biomass sorghum were grown in rotation with soybean (*Glycine max* L.) for five years at two Missouri locations, following the conversion of the land from perennial grass to row crop systems. Intermittent drought occurred in both sites during three of the five years notably reducing yield; a terminal drought in 2011 reduced sorghum yields and inhibited maize grain development at both sites. Overall theoretical ethanol yields from sweet sorghum were greater than from maize. The central Missouri site maintained greater dry matter yield (DM), and theoretical ethanol yield than the southwestern Missouri site. Due to the occurrence of drought during the study, the findings have relevance for evaluating marginal land management impacts in a changing climate.

#### SICNA 2016 – P24/SOCI2

##### **Sensory profiles, consumer acceptance, and palatability of dry dog food manufactured with sorghum**

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Sorghum is a key world grain and Kansas is the top producer in the US. To increase the use of sorghum, industries such as pet food have been targeted. However, for success it is important to understand sorghum's characteristics such as the sensory properties, pet owners' acceptance, and pets' acceptance of the final products. The objectives of this study were to 1) develop a sensory profile for dry dog food containing sorghum, 2) assess consumer acceptance of the dog food products, and 3) investigate dogs' acceptance of products fed in their household environment. Three samples containing different sorghum fractions (bran, flour, and whole sorghum) and a control sample containing mixed grains were manufactured. A trained human descriptive sensory panel described the sensory characteristics of the samples. A total of 105 pet owners evaluated the samples for appearance, color, aroma, and overall liking. A total of 30 dogs of different size, age, and breed were selected for a one-bowl in-home palatability study to test pet acceptance of samples.

Differences among samples from the descriptive analysis were small and related to a few appearance and texture characteristics. The consumer panel found the whole sorghum and the control samples to be most liked overall, in appearance, and color. No difference was found in aroma liking, in accord with the similar aroma profile. The slight difference in liking scores seems to be caused by the different appearance of the samples. The whole sorghum diet was accepted at the same level as the control diet and the results suggest that improvement in appearance of other samples will improve consumer acceptance to that of the control. Further, the dogs seemed to like the foods manufactured with sorghum and other grains equally. This study indicates the potential for an increased use of sorghum in dry dog food.

## **6. General poster exhibition abstracts (GPE)**

SICNA 2016 - GPE1

### **Unmanned aerial vehicle- based remote sensing for monitoring sorghum growth and development**

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Remote sensing is an effective method for estimating crop biophysical properties. High resolution multispectral unmanned aerial vehicle (UAV) remote sensing imagery was collected from a sorghum variety testing location at the Texas A&M Brazos Farm (30°32'26.02"N and 96°25'33.34"W) using the Sentek GEMS multispectral camera on the Anaconda fixed-wing UAV platform. Each plot was 15 m long and 3.5 m wide. Red and NIR images were collected at an altitude of 40 m above the ground at approximately 11:30 AM CST on 24 May, 10 June and 18 June in 2016. For radiometric calibration of the aerial imagery, calibration tarps were laid out in the field. Digital count (DC) values corresponding to the calibration tarps were extracted from the UAV imagery and correlated with the known average tarp reflectances. Linear calibration equations relating DC values to reflectance in the red, green and NIR wavebands were developed. These calibration equations were used to convert the UAV image DC to reflectance. Reflectance values for the pixels representing each plot were averaged to calculate NDVI. We collected overhead photographs of selected plots using a digital camera on both image acquisition dates to determine actual canopy cover. LAI was measured for selected plots using a LAI-2200C plant canopy analyzer (LI-COR, Lincoln, NE). Results of this study indicate a highly significant relationship between NDVI estimated from high-resolution UAV remote sensing data and crop biophysical variables. The coefficient of determination ( $R^2$ ) between NDVI and LAI was 0.88, while the  $R^2$  between NDVI and percent canopy cover was 0.89. Preliminary results from this study show that UAV-based remote sensing data could be used effectively for estimating plant biophysical parameters.

SICNA 2016 - GPE2

### **Planting date effects on sweet sorghum production in Georgia**

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Sweet sorghum accumulates sugary juice in its stalk which, along with the other plant components, can be used as feedstocks for biofuels and other bio-based products. The juice has a short shelf-life, and a bio-refinery would require a steady supply of sweet sorghum juice or syrup in order to operate, so a long harvest season is necessary. Two strategies to lengthen the harvest season are to plant multiple

varieties of different maturities and to plant the crop at multiple times. This experiment was conducted to determine how different varieties respond to varying planting dates in Georgia. The experiment consisted of eight inbred lines and 15 hybrids. In 2013 and 2015 all 23 entries were planted in three replications at three planting dates (late April, mid-May, and mid-June) in a split-plot design, with planting dates as the main plots and entries as subplots. The April planting took longer to flower and also had greater biomass yields than later plantings; however, in 2015 the June planting had the greatest sugar yield. The June planting had the highest juice soluble solids concentration in both years. Biomass yields were lowest and lodging percentage was highest for the June planting in 2013, possibly due to excessive rainfall. In 2015, however, lodging was greatest in the April planting, and least in the June planting. The harvest season lasted 49 days in 2013 and 63 days in 2015. Sugarcane aphid (*Melanaphis sacchari*) infestations occurred in 2015, and damage and aphid population dynamics varied by planting dates.

#### SICNA 2016 - GPE5

##### **A regional monitoring program for crop-to-weed gene flow of herbicide resistance following commercialization of 'Inzen' sorghum hybrids**

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'Inzen' grain sorghum hybrids resistant to ALS-inhibiting herbicides are in the final stages of commercialization by DuPont-Pioneer. High on-farm adoption of this technology is expected, but gene flow of ALS-resistance (ALS-R) to the weeds shattercane and johnsongrass is inevitable. Here we present the current status and future directions for a riskassessment framework of ALS-R evolution in shattercane and johnsongrass to be used in a regional monitoring program in Nebraska and Kansas. Current (shattercane) and emerging (johnsongrass) models will be used to predict the evolution of ALS-R weeds under various cropping systems including Inzen hybrids. Molecular markers unique to Inzen hybrids will provide data on the relative frequencies of ALS-R weed evolution due to gene flow from Inzen or de novo mutations selected for by repeated ALS-inhibitor applications. Grower surveys conducted at the time of Inzen commercialization will establish a baseline estimate of where ALS-R weeds are a problem, and at five and ten years thereafter. Grower education through extension programs will provide information on the risks associated with crop-to-weed gene flow, and will encourage no-cost self-reporting of ALS-R weeds on farms. PCR-based assays will be made available to participating universities to preliminarily screen sorghum, shattercane, and johnsongrass for Inzen alleles. Additional molecular markers based on Inzen DNA sequence at the ALS locus will be used to confirm gene flow events. These data are needed by federal agencies to make science-based decisions regarding the ecological risk of introducing crop nuclear technologies (GMO and non-GMO) where sympatric wild relatives grow.

#### SICNA 2016 - GPE9

##### **A large-scale experiment to evaluate the impact of integrated tactics for managing johnsongrass in Inzen™ sorghum**

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Sorghum with non-transgenic herbicide resistance (Inzen™ sorghum) to nicosulfuron, an acetolactate-synthase (ALS)-inhibitor, will soon be available for commercial cultivation. This trait will provide a valuable grass weed management tool for sorghum producers, including the management of johnsongrass for which no selective control option exists in sorghum till today. However, potential risk

of pollen-mediated gene flow and transfer of the herbicide resistance trait into johnsongrass may jeopardize the longevity of the tool. Development of best management practices and stewardship protocols have been shown to be beneficial in similar situations. The objective of this experiment is to understand the value of integrated tactics for managing johnsongrass in Inzen™ sorghum production systems. Large-scale experiments were initiated in summer 2016 in College Station, TX and Keiser, AR in areas with high densities of johnsongrass infestation. The treatments include 1) Dual II Magnum® PRE (1 pt/A) fb Atrazine (1 qt/A+1% COC) at 12" sorghum (standard practice in conventional sorghum), 2) Dual II Magnum® PRE (1 pt/A) fb Atrazine (1 qt/A+1% COC)+Zest® (12 oz/A) at 12" sorghum (standard Inzen™ program), 3) Program #2 fb Roundup Weathermax® (32 oz/A) desiccant prior to harvest, 4) Program #3 fb Chaff removal at harvest, 5) Program #4 fb shred/disk the field after harvest and treat the regrowth with Select (8 oz/A) at 30 cm height. To simulate a worst-case scenario, known ALS-inhibitor-resistant johnsongrass seedlings were transplanted into each plot. Soil seedbank proportion of ALS-inhibitor-resistant as well as susceptible johnsongrass will be monitored, along with above-ground johnsongrass population densities over a 4-yr period. It is anticipated that results will provide a greater understanding of the impact of integrated tactics on the management of johnsongrass within Inzen™ sorghum production systems.

## SICNA 2016 - GPE10

### **U.S. sorghum genetic resources collection: 15 years of progress (2001-2016)**

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The U.S. sorghum genetic resources collection at Griffin, GA, is one of the largest collections in the National Plant Germplasm System. In 2001, improved maintenance was greatly needed as accessions weren't regenerated routinely, viability tests weren't conducted, and most seed was stored in 4C instead of -18C. Utilization was reduced. In 15 years, the sorghum collection has been greatly improved. Collection size at Griffin has increased from 30,705 to 39,934 accessions with availability improving from 92.6% to 95.1%. Regenerations of over 21,000 accessions have been conducted by ARS scientists in St. Croix and Puerto Rico since 2001. Viability tests have been conducted on 96.4% of the collection. Viability results showed that 89.6% of the accessions have >50% viability and 53.8% have >80% viability. Backups at Ft. Collins, CO, have increased from 90.4% to 96% with 21.6% also backed up in Svalbard, Norway. Observation data loaded in GRIN has increased from 536,472 records in 2001 to 1,020,705 records in 2016. Accession longevity has been improved through -18C storage of 34,686 accessions (86.9%) in 2016 compared with 8,300 accessions in 2001. All of these improvements in the sorghum collection have resulted in much greater utilization by researchers. Distributions increased from 8,057 samples shipped in 2001 to 17,720 samples already shipped in the first half of 2016. An average of 14,700 accessions have been distributed each year for the past 10 years. The U.S. sorghum collection will continue to provide valuable genetic resources for future decades of sorghum research.

## SICNA 2016 - GPE11

### **Should the choice of pollination control bag types in sorghum matter?**

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We report results of two studies, one conducted in Brazil in the winter season and another in India during the rainy season, which highlight the importance of selecting appropriate pollination bag type in sorghum. The Brazilian study used three varieties with different grain colours and five pollination bag treatments; no bagging, traditional paper bag, paper bag plus protective plastic screen bag, nonwoven duraweb® SG1 polypropylene bag and nonwoven duraweb® SG2 polyester bag. The paper bags performed worse for bird control; duraweb® SG1 bag was the best performer followed by duraweb® SG2 bag for panicle weight, seed weight and average seed weight per panicle, and control of bird damage. The ICRISAT study was conducted with four genotypes and five bag types (no bagging, standard paper bag, and three nonwoven fabric bags— duraweb® SG1, duraweb® SG2 and duraweb® SG3). The grain mould attack was the highest under the butter-paper and the lowest under the duraweb® SG1 bags, which showed even lower mould than the no-bag treatment. The duraweb® SG1 bags also showed significantly higher 100-seed weight than the paper bags or no bagging. After the no-bagging treatment, the paper bags were most vulnerable to bird damage. None of the new bag types made of nonwoven fabrics showed any bird damage. The evidence from both studies shows that newly developed nonwoven fabric bags provide a better alternative to paper bags in terms of greater protection against birds and in providing healthy and ambient micro-environment for the developing seed.

### SICNA 2016 - GPE13

#### **Selection of *Melanaphis sacchari* tolerant dual purpose sorghum varieties for Haiti**

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First infestations of *Melanaphis sacchari* on sorghum in Haiti were recorded in autumn 2015. By August 2016 all growing regions were affected by this new pest. Varieties grown by farmers have shown to be highly susceptible resulting in high yield losses all across the country. We initiated screening for aphid tolerance late 2015 at our research stations. Inbred families from cycle 1 and 2 of our sorghum recurrent selection population (a genetically diverse population under selection for high grain and stem sugar yields) were evaluated in winter 2015-2016 for aphid tolerance. 8 S3 families out of 174 from cycle 1 and 12 S1 families out of 60 from cycle 2 showed high yield and tolerance to aphids. Dekabès (IS23572, our check for alcohol-rum quality) also showed a high level of tolerance to *Melanaphis sacchari*. In May 2016, 46 S2 and 80 S4 families were planted along with the susceptible (Papèsèk) and tolerant (Dekabès) checks. While many S2 families from cycle 2 still segregate for aphid tolerance, all selected families from cycle 1 and 2 showed, or segregated for, high levels of tolerance. Some advanced lines even show a complete absence of aphids. S3 and S5 families will now be tested in multilocation trials across Haiti in autumn 2016. Families with high level of purity and homogeneity will be simultaneously increased to initiate seed production. Generation of cycle 3 is also under way.

### SICNA 2016 - GPE14

#### **GBS genotyping of eight new publicly-available sorghum RIL populations**

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Sorghum is the world's fifth most important cereal crop, and is critical to food security in semi-arid regions. RIL populations enable QTL discovery and genetic improvement as well as characterization of the recombination landscape within a crop. In this study, we report the generation of marker-dense genetic linkage maps for eight new publicly-available sorghum RIL populations. 1,626 lines from eight

biparental RIL populations were genotyped using genotyping by sequencing (GBS) with a modified ApeKI protocol that includes Y-adapters. SNPs were called against v3 of the sorghum genome using the TASSEL5 GBS v2 pipeline. Imputation was performed using FSFHap in TASSEL, and genetic maps were constructed using MSTMAP. These data augment the existing sorghum NAM population with additional families containing BTx623 as a common parent.

## SICNA 2016 - GPE15

### **A comparison of PCR-based and GBS-based methodologies to fine-map anthracnose resistance loci in sorghum**

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*Colletotrichum sublineola* is an aggressive fungal pathogen that causes the disease anthracnose sorghum. The resulting leaf blight and stem rot can cause yield reductions of up to 70%. The sorghum acreage in the southeastern U.S. is increasing steadily. Successful cultivation of sorghum in this region, where *Colletotrichum sublineola* is endemic, is contingent upon anthracnose resistance. We generated a biparental mapping population of 135 F<sub>4</sub> and F<sub>5</sub> sorghum lines to identify anthracnose resistance genes in the highly resistant line 'Bk7'. The population was phenotyped in three Florida environments and genotyped by sequencing (GBS). Two resistance loci were identified - on chromosomes 7 and 9 - using association analysis between the GBS-derived markers and phenotype. Both loci contained multiple candidate resistance genes. Fine mapping of the locus on chromosome 9 was performed on a BC<sub>1</sub>S<sub>1</sub> population generated from four sweet sorghum cultivars derived from the sorghum lines 'Bk7' and 'Mer 81-4'. The efficacy of fine-mapping with PCR-based SNP markers was compared to that using GBS. In both instances the size of the resistance locus could be reduced substantially, but the GBS procedure provided much greater resolution, at a substantially higher cost. This case formed the basis for a comparison of the merits of both genotyping methods under a number of different scenarios (population size, marker density, labor cost) to assist in deciding on the most effective genotyping procedure. Supported by the Southeastern Sun Grant Center/USDA-NIFA Award No. 2010-38502-21854, USDA-BRDI Award No. 2011-10006-30358, and US DOE award No. DE-SC0014439.

## SICNA 2016 - GPE16

### **Mining sorghum diversity with Gramene**

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Rapid gains in sorghum research places new demands on information systems to provide meaningful visualization, mining and interpretation of available data. Gramene ([www.gramene.org](http://www.gramene.org)) empowers researchers by integrating genotypic and functional genomics data within comparative genomic and pathway frameworks. Incorporating several published large-scale population studies, our sorghum browser displays millions of variant genotypes in several hundred accessions, including the US sorghum association panel (SAP), and the re-sequenced wild relative *S. propinquum*. Moreover, we incorporate ~1.8 million EMS-induced mutations catalogued within the USDA BTx623 mutant collection. All told, this diversity predicts stop-gained alleles in over 4500 genes and missense alleles in over 25,700 genes,

presenting a formidable resource for gene function discovery. This presentation will demonstrate a reverse genetics use-case, using Gramene's BioMart tool to mine variation using either specific genes of interest, or other criteria such as homology, InterPro domain, or Gene Ontology (GO). We will also highlight Gramene's other resources that inform gene function in sorghum, including published transcriptome and methylome data, comparative genomics analyses, and annotated pathways. Phylogenetic gene trees and whole genome alignments enable users to glean functional information from orthologs in 39 plant species. The Plant Reactome provides visualization of ~200 annotated pathways in sorghum and over 60 other plants. Gramene promises to help researchers improve sorghum as a crop, but also sets up sorghum as a model system to understand traits such as yield, abiotic stress and C4 photosynthesis in other plants. Gramene is supported by an NSF grant IOS-1127112, and partially by the USDA-ARS (1907-21000-030-00D).

#### SICNA 2016- GPE21

##### **A sorghum-based nutraceutical as a potential therapeutic approach for the treatment of type-2 diabetes (T2D)**

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Kafirin, the sorghum prolamin protein is uniquely hydrophobic, resistant to pepsin digestion and can be fabricated into films, scaffolds and microparticles. Active compounds can be encapsulated within kafirin microparticles with potential for nutraceutical and biomedical applications. Obesity and its associated diseases, especially T2D, are assuming pandemic proportions in developing countries. Affordable, nutraceutical-type therapies based on local plant foods are desperately needed. Kafirin microparticles (KEMS) were investigated as an oral delivery system for sorghum condensed tannins (SCT) to inhibit intestinal carbohydrate digesting enzymes. Isolated SCT was 20,000 times more effective at inhibiting  $\alpha$ -glucosidase compared to acarbose (an anti-diabetic drug treatment for T2D), while acarbose was a better  $\alpha$ -amylase inhibitor. Using coacervation, SCT was encapsulated in KEMS at high efficiency. Quantitative data and electron microscopy revealed that KEMS encapsulating SCT were slightly digested and retained their inhibitory activity against both amylases during simulated gastrointestinal digestion with pepsin and trypsin-chymotrypsin. Un-encapsulated SCT, however, lost most of its inhibitory activity. Further work investigated SCT-KEMS as a potential anti-hyperglycaemic nutraceutical agent in vivo. Oral starch tolerance tests were performed on healthy rats. SCT-KEMS prevented a blood glucose spike and decreased the maximum blood glucose level when compared to the water control, to that of the acarbose standard. Neither SCT-KEMS nor acarbose elevated serum insulin levels. The unpleasant taste of SCT was also masked by kafirin encapsulation. Using kafirin microparticles to encapsulate SCT enables control of glycaemic response similar to that obtained with acarbose. Hence, SCT-KEMS has potential as a simple nutraceutical therapy for T2D.

#### SICNA 2016 - GPE22

##### **Development of a sweet sorghum biomass system to improve sugar yield for biofuel production**

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High biomass sweet sorghum (up to 25 to/acre) is an energy crop that can be used for production of syrup, biofuels and other value-added products. Sweet sorghum is under consideration in Louisiana due to its similarity to sugar cane and as a potential ratoon crop. However, processing in a sugar cane mill is



challenged by the high content of leafy matter and the excessive starch levels (>1%) due to the grain holding panicles. Both challenges can be addressed by adjusted mill settings and application of amylase. Nonetheless, it seems sensible to separate the high-value starch as byproduct and reduce the trash level prior to milling. The separation of seed heads and leaves from stalks could therefore increase sugar yield and facilitate utilization of sweet sorghum. A separator prototype was designed and built at the Audubon Sugar Institute to separate seed heads and leaves from billets, for sorghum harvested with a sugar cane combine. Preliminary results have shown that leaves can be separated from stalks and panicles with efficiencies up to 83% while panicles were separated from stalks with selectivity up to 53%. The presence of panicles and leaves reduced the fermentable sugar yield per ton of sweet sorghum by 44%.

## SICNA 2016 - GPE25

### **Functional properties of combined waxy/heterowaxy – high digestible protein traits in hard endosperm sorghum**

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Sorghum is a high value food crop, but has reduced endosperm functionality compared to other grains. The influence of combining waxy/heterowaxy with high protein digestibility (HD) traits in a hard endosperm on starch functionality and protein digestibility of sorghum was investigated. The protein digestibility was assessed using in vitro pepsin assay. The starch pasting properties were analyzed using rapid visco-analyzer. The water absorption and solubility indices of the samples were also measured. The improved lines had protein digestibility (68.5% for raw and 62.5% cooked) higher ( $p < 0.05$ ) than that of the low digestible (LD) control (67.2% for raw and 48.5% for cooked) and similar to that of the HD control (79.8% for raw and 62.9% for cooked). The improved lines had higher water absorption and solubility indices; which indicates better suitability as ingredients in dough and batter systems. Similarly, lower final viscosity and pasting temperature were recorded for the new lines indicating reduced tendency of starch to retrograde. Greatly improved kernel hardness index (ranging from 50.3 to 79.5) was also observed for the improved HD lines compared to control HD (29.7). The combination of the waxy/heterowaxy with HD traits in sorghum is promising as a means to improve sorghum functionality as a food ingredient.

## SICNA 2016 - GPE26

### **Variable-pressure scanning electron microscopy images of sorghum predict resistance to storage insect pests**

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Insect pests destroy 30-40% of stored grain especially in developing countries in the tropics. The maize weevil, *Sitophilus zeamais* Motschulsky, is the most important insect pest of stored sorghum, *Sorghum bicolor* (L.) Moench, and other grains worldwide. Maize weevil larvae and adults feed on grain in the field and in storage. The female chews into a kernel, deposits an egg, and seals the hole. As many as 400 eggs can be produced per female. Six generations may be produced each year. To evaluate resistance of sorghum grain, three female and two male newly emerged maize weevils were placed with 5 g of grain of each sorghum genotype into a vial and replicated 10 times. Damage (scored 1 to 5, with 5 being

most) and weight loss (in percentage) of sorghum genotypes were assessed once every 3 weeks for 105 days. Seguifa was most resistant of eight sorghum genotypes evaluated. A Tescan Vega 3 XMU Variable-Pressure Scanning Electron Microscope was used to compare the sorghum genotypes to determine if morphological differences in the grain were related to resistance. To prepare sorghum for VPSEM, each kernel was cut in half and mounted with the cut side up. Following gold coating with a Hummer sputter coater, the grains were observed with the VPSEM. The degree of resistance to maize weevil was positively correlated to the distance from the pericarp to aleurone layer of kernels of the eight sorghum genotypes.

## SICNA 2016 - GPE27

### **Genetic diversity of the sugarcane aphid (Homoptera: Aphididae) in the United States**

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The sugarcane aphid, *Melanaphis sacchari*, has become a serious pest causing severe economic losses to sorghum grown in the southern United States (U.S.). Since its original detection in four states in 2013, *M. sacchari* on sorghum has now spread to 17 states. The presence of one or multiple biotypes in the U.S. has not yet been established. In this study, high throughput sequencing of *M. sacchari* DNA was used to develop microsatellite markers. A total of 8,665,267 reads and 1.44 Gb of nucleotides were generated. *M. sacchari* DNA from 48 samples from 17 locations across 7 states and one U.S. territory was amplified using 38 microsatellite markers as well as 14 previously published microsatellite markers. Genotyping with the 52 microsatellite markers indicated that the samples of *M. sacchari* were all one biotype with the exception of a single sample collected from Sinton, TX, which had the predominant biotype as well as another biotype. The invasive *M. sacchari* on sorghum appears to be spreading in the U.S. as primarily one asexual clone.

## SICNA 2016 - GPE30

### **Assessing the occurrence and diversity of storage insect pests of sorghum in Niger (West Africa)**

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In developing countries like Niger (West Africa), the most important constraints of having sufficient food is the post-harvest preservation of its quality and quantity. Worldwide, beetles and moths are the most destructive insect pests of stored sorghum grain. They destroy 5-35% of stored grain, but destroy 40% or more in tropical and subtropical countries. A survey found that farmers identified eight storage insect pests that cause damages to stored products in two regions in Niger. To control these stored insect pests, toxic pesticides are mainly used by farmers. Alternatives are needed to reduce pesticide residue in food. This study was to monitor the presence and assess the diversity of storage insect pests of sorghum in different storage systems. Sorghum grain samples with infested insect pests were sieved to recover and count the number of insect pests in each variety. Diversity of insect was monitored by using 3 trapping systems set up in 5 sites in Niamey.

Preliminary results indicate that the diversity was higher in improved varieties, up to 7 species of stored insect pests were recorded on SSD-35. For the 2 local varieties sieved, only 4 species of stored insect pests were recovered. Monitoring results showed that the “The Dome Trap” (pheromone based) was more efficient in capturing 11 species of storage insect pests as compared to “Pherocom-Glue” Trap and Water bottle trap. Knowledge about the diversity and application of simple detection system for storage insect pests are keys to recommend control strategies to guarantee grain quality in Niger.

SICNA 2016 - GPE3 I

**Marker-assisted backcross approach for important agronomic traits of Sorghum**

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Sequencing technologies are useful for identification of thousands of single nucleotide polymorphisms (SNPs) in a cost effective manner. QTL mapping, association mapping and Mutmap approaches provide opportunities for use of such SNPs to associate and identify genes that control important agronomic traits. We are integrating genomics methods and translating DNA polymorphisms into easy access SNP-DNA markers for efficient breeding of important traits in sorghum. Our laboratory is utilizing Marker-assisted backcrossing (MABC) of valuable SNPs from genes which control or contribute towards enhanced abiotic stress tolerance and yield. We are currently employing MABC approach for yield related traits such as multi-seed (*msd*), seed size (*ss*) and stress related traits such as bloomless (*blm*) and cold tolerance (*ct*). We are applying marker technology for selection of heterozygotes ( $F_1$ ), parental genotypes and stacking of traits using allele-specific chemistry (KASP). Marker assisted backcross in sorghum breeding is a cost effective approach towards developing lines with valuable traits in an efficient and timely manner.