Research Kernels

Our Latest Research Results - June 2013 part 1

Sorghum Grain and Flour Characterization and Evaluation in Gluten-Free Flour Tortilla

Authors: H. Khouryieh, F. Aramouni, M. Winger, T.J. Herald
Submitted to: Journal of the Science of Food and Agriculture

Sorghum is a drought resistant, heat tolerant crop that is safe for individuals with gluten sensitivity. There are limited studies that have addressed the use of sorghum flour as a gluten-free alternative. Tortilla sales represent $2.2 B business which is a significant segment of the food industry. Wheat tortillas are ubiquitously present from breakfast to dinner. However, limited research has been conducted to evaluate sorghum flour as a wheat-free flour alternative in tortillas. Four commercial sorghum hybrids were evaluated for process ability and tortilla quality. The research determined that there was a difference among the sorghum hybrids in the way the flour handled during processing and in the final tortilla quality. Selecting the appropriate sorghum hybrid prior to tortilla production is an important consideration.

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Conserved Loci of Leaf and Stem Rust Share Synteny Interrupted by Lineage-Specific Influx of Repeat Elements

Authors: J.P. Fellers, B.M. Soltani, M.A. Bruce, R. Linning, C.A. Cuomo, L.J. Szabo, G. Bakkeren
Submitted to: Genomics

Leaf rust of wheat, caused by the fungus Puccinia triticina, results in significant yield losses each year and is found wherever wheat is grown around the world. Wheat geneticists are constantly trying to find new leaf rust resistance genes to introduce into adapted varieties because the fungus usually overcomes genetic resistance in just a few years. To develop better resistance strategies, we need to know how the fungus manipulates the plant metabolism and how it can overcome host plant resistance. The objective of this research is to better understand the genes and gene organization in the leaf rust fungus by comparing to the stem rust fungus. Three large stretches of DNA from leaf rust were sequenced and the genes were identified. The leaf rust fungus DNA sequences were then compared to an existing database of the wheat stem rust fungus genomic sequence to determine similarities and differences. Gene order was similar, but sequence identity varied from 26-99%. Numerous repetitive elements called retrotransposons were also found in the leaf rust fungus DNA sequence. Identification of genes that are highly conserved between the two pathogens may reveal vulnerable targets of future control strategies. Comparisons may also reveal important differences in how leaf rust and stem rust have adapted to cause disease in wheat.

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Stable Resistance to Wheat Streak Mosaic Virus in Wheat Mediated by RNAi

Authors: L.F. Cruz, J.L. Shoup Rupp, H.N. Trick, J.P. Fellers
Submitted to: Crop Science

Wheat streak mosaic virus (WSMV) is a viral pathogen of wheat that causes significant yield losses each year in the Great Plains. Control measures include delayed planting and eliminating alternate sources of virus like volunteer wheat and other grasses. Plant breeding programs only have three resistance genes available for WSMV, however, each is sensitive to high temperatures and two of them have negative agronomic traits associated with the genes. This paper describes a new approach to obtaining virus resistance in wheat. The genetic sequence for a small fragment of the coat protein gene of WSMV was transformed into a spring wheat variety. This gene fragment triggers the virus defense responses of the plant and prevents the reproduction of the virus. Four resulting wheat lines were found to be resistant to WSMV infection and this resistance was stable over six generations. These new virus resistance genes are being transferred into adapted wheat varieties for further testing.

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Introgression of Stem Rust Resistance Genes SrTA10187 and SrTA10171 from Aegilops tauschii to Wheat

Authors: E.L. Olson, M.N. Rouse, R.L. Bowden, B. Gill, J.A. Poland, M.O. Pumphrey
Submitted to: Theoretical and Applied Genetics

Goat grass (*Aegilops tauschii*) is a progenitor species of modern bread wheat. This species has contributed many genes for resistance to disease and insect pest of wheat that are currently used in wheat breeding efforts. In a previous study, a collection of jointed goat grass was evaluated for resistance to a new and highly virulent race of wheat stem rust ("Ug99"). The Ug99 race of stem rust can infect most of the wheat varieties in the US and the world. Several accessions of goat grass were found

to be resistant to Ug99. In this study we crossed two of the resistant accessions with an elite hard winter wheat from Kansas. Resistant plants from this cross were selected and crossed again to the Kansas wheat. Following repeated selection for resistant plants and crossing to wheat, we developed two wheat germplasm lines with resistance to Ug99. Using a segregating population and molecular DNA markers, these two genes were mapped to wheat chromosomes 6D and 7D. These two new genes, designated Sr10187 (TA10187) and Sr10171 (TA10171) will be useful for breeding varieties with resistance to Ug99 stem rust.
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Defense Mechanisms in Resistant Wheat Seedlings in Response to Hessian Fly Attack

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Submitted to: Biomed Central (BMC) Genomics
Resistance is the main strategy to control Hessian fly, a destructive insect pest of wheat. However, resistance in wheat can be overcome by Hessian fly within a relatively short time, often in 6 to 8 years. A better understanding of the mechanisms of wheat resistance to Hessian fly is needed to improve durability of resistance. This study analyzed changes in gene expression in resistant and susceptible plants at different time points after Hessian fly infestation, and changes in accumulation of metabolites in those plants and time points as well. The combined analyses revealed that resources including membrane lipids, carbohydrates, and proteins/amino acids are rapidly released for active defense. The mobilized resources are likely rapidly converted into defense molecules with toxicity to the insect, or molecules that can be used to strengthen the cell wall. The combination of enhanced toxicity and strengthened cell walls are likely responsible for the death of Hessian fly larvae within plants that carry an effective resistance gene. The results provide a foundation for further research that may lead to improved durability of resistant wheat cultivars..
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Utilizing Local Surveillance Networks for Continental Scale Mosquito Sampling

Authors: E.C. Maki, L.W. Cohnstaedt
Submitted to: Journal of the American Mosquito Control Association
Researchers at the USDA in Manhattan, Kansas, used networking to bring mosquito control districts and public health departments together with individual collectors. These individuals were asked to help collect two species of disease transmitting mosquitoes throughout North America. Without networking to contact, communicate and coordinate with the collectors, sampling the entire

continental United States in a single year would not be possible. These collectors played an integral role because of their local knowledge of mosquito habitats, their ongoing surveillance of diseases, and introduced species, and their ability to limit mosquito populations; however this network of collectors is threatened due to budget cuts.
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Spatial Application of WEPS for estimating wind erosion in the Pacific Northwest

Authors: J. Gao, L.E. Wagner, F.A. Fox, S. Chung, J. Vaughn, and B.K. Lamb.
Submitted to: Transactions of the ASABE
Wind Erosion Prediction System (WEPS) is designed by the USDA-ARS to simulate soil erosion on cropland with uniform soil and a single crop. The strict condition is limited the WEPS in a large region with complex soils. We modified the WEPS source code to allow it not only to run on multiple grids, but also to "save the state" of the model so it can be re-initiated from that state in future runs to allow the model to be started and "stepped through time" incrementally under various future climate or forecast weather scenarios. We initially ran the WEPS on the whole state of Washington, with the entire Pacific Northwest region as our ultimate target area to provide PM_{10} and $PM_{2.5}$ emissions as input to the chemical transport model CMAQ that is used by the AIRPACT regional air-quality modeling system for the Pacific Northwest. With comparison of satellite image which covered a dust storm event, the WEPS simulation could reasonably show the distribution of dust emission. The study shows that WEPS can be successfully extended to run from one field grid to multiple grids and the model can identify the regions with high potential for soil erosion. The WEPS can be used for real-time monitoring of soil erosion and air quality in a large region if actual and forecast weather inputs are available.
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Application of the Wind Erosion Prediction System in the AIRPACT Regional Air Quality Modeling Framework

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Submitted to: Transactions of the ASABE

Wind erosion of soil is a major concern of the agricultural community as it removes the most fertile part of the soil, degrades soil productivity, and contributes to poor air quality, and reduced visibility. Because PM_{10} emitted from the soil surface can travel hundreds of kilometers down wind before being deposited back down to the surface, an important aspect of understanding the impact of agricultural activities and land-management practices on air quality in a changing climate is the ability to address various agricultural air pollutant sources within a comprehensive framework of a regional air quality modeling system. The Wind Erosion Prediction System (WEPS) is a new tool for treating erosion from agricultural fields. As a process-based model, WEPS represents a significant improvement in comparison to existing empirical windblown dust modeling algorithms. WEPS was originally intended for soil conservation applications and designed to simulate conditions of a single field over multiple years. In this work, we took advantage of the physical algorithms embedded in WEPS by first incorporating its EROSION submodel with the aid of several satellite products to develop a PM_{10} emissions module for regional windblown dust that can be employed within a comprehensive regional air quality framework. To demonstrate the capabilities of the new framework, we present here results from simulations of dust storms that occurred in central and eastern Washington during October 4 2009 and August 26 2010. Comparison of model results with observations indicate that the modeling framework performs well in predicting the onset and timing of dust storm and the spatial extent of the dust plume. The new modeling framework is able to predict elevated PM_{10} concentrations hundreds of kilometer downwind of erosion source regions associated with the windblown dust, although the magnitude of the PM_{10} concentrations are extremely sensitive to the assumption of surface soil moisture. Future work includes incorporating the full WEPS model into the regional modeling framework and targeted field measurements to evaluate the modeling framework more extensively.

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Single Kernel Near-Infrared Analysis Technique for Comprehensive Evaluation of Wheat Kernel Samples for Fusarium Head Blight Resistance

Authors: K.H.S. Peiris, Y. Dong, W.W. Buckus, F.E. Dowell

Submitted to: Cereal Chemistry

Fusarium head blight (FHB) of wheat is a destructive disease caused by several Fusarium species. Besides significant grain yield and quality losses, mycotoxins such as deoxynivalenol (DON) produced by the Fusarium fungi are a serious problem affecting grain marketability and food and feed safety. Wheat breeding programs need a method to rapidly evaluate numerous wheat lines for FHB resistance. We developed a method to estimate bulk DON content of wheat grain samples using single kernel DON levels estimated by a single kernel near infrared (SKNIR) system combined with single kernel weights. This method estimated bulk DON levels in 90% of 160 grain samples within 6.7 ppm DON. Distribution of single kernel DON levels among kernels in grain samples was used to compare FHB reaction of wheat varieties grown under FHB disease pressure with or without fungicide application. Study of the distribution of DON levels among all kernels as well as among DON containing kernels in a grain sample is helpful for an in-depth evaluation of the effect of varieties or fungicides on FHB reaction. The SKNIR single kernel DON analysis and study of single kernel DON distribution patterns demonstrated in this study may be helpful for wheat breeders for evaluation of the FHB resistance of varieties in relation to their resistance to spread of disease and resistance to DON accumulation.

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Economic Feasibility of Methoprene Applied As a Surface Treatment and As An Aerosol Alone and In Combination with Two Other Insecticides

Authors: E.A. Fontenot, F.H. Arthur, J.R. Nechols, M.R. Langemeier

Submitted to: Journal of Economic Entomology

Insect growth regulators (IGRs) used alone or combined with other insecticides are being evaluated for control of the Indianmeal moth, a common stored product pest, but there is little research regarding economic feasibility of treatments. We used mortality data from laboratory and field studies to conduct an economic risk analysis of different treatments. The optimal insecticide was a

combination of methoprene combined with the pyrethroid esfenvalerate, but more frequent treatment is needed to reduce risk when Indianmeal moth developed on an optimal diet compared to a sub-optimal diet. Results show how risk assessments can be developed to help minimize damage caused by the Indianmeal moth.

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The Case for a Generic Phytosanitary Irradiation Dose of 400 Gy for Lepidoptera That Infest Shipped Commodities as Pupae

Authors: G.J. Hallman, A.G. Parker, C.M. Blackburn

Generic treatments are very useful in facilitating trade in agricultural commodities that may be quarantined because of invasive species. Generic treatments using ionizing radiation are broadly applicable because they are effective across a broad range of pests and tolerated by a broad range of fresh fruits and vegetables at the doses required to control the pests. This paper proposes a generic dose of 400 Gy for all pupae of Lepidoptera in all commodities and fills an important gap in the present use of irradiation for fresh fruits and vegetables.

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Quantitative and Qualitative Assessment of Bacterial Pathogen Load in Calves with Acute Bovine Respiratory Disease

Authors: C.J. Roof, M.D. Apley, D.S. McVey, J.F. Coetzee, J.A. Kuszak, D.G. McClary

The objectives of the study were to evaluate (1) numbers of bacteria in different locations in the respiratory tract of clinically ill and clinically normal calves. One hundred ninety four steers, bulls, and heifers weighing 182-318kg were purchased at an Arkansas sale barn originating from multiple ranches and shipped 12 hours to a northern Kansas feedlot the following day. The cattle had been delivered to the sale barn within the 24 hour period prior to the sale. Fifteen calves were identified with signs of acute bovine respiratory disease (BRD) based on clinical signs and rectal temperature of 40° C or greater. An additional 5 calves with no clinical signs and rectal temperatures less than 40° C were selected as controls. Cattle were humanely euthanized following veterinary evaluation. At necropsy, samples for microbiologic analysis were collected from normal and/or affected tissue in each lung lobe. Samples were also collected from the tonsils and trachea. The pathogens were identified and density (per gram of lung tissue) was measured for each affected lung and then converted to total counts for each animal. Total colony forming units (CFU) of pathogens in lungs of cattle with both pure and mixed infections were over 10 million for *Pasturella multocida* and *Mannheimmia haemolytica*. Total affected consolidated lung tissue (pneumonia) ranged from 0.0%

to 45.0% of the lungs. Lungs from calves with no clinical signs of pneumonia often had bacteria present in the lungs. Bacteria isolated from the upper respiratory tract were similar to, but not identical to, the bacteria isolated from pneumonic lungs.

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Correlation of Histopathological Scores to Bacterial Presence and Status in Acute Bovine Respiratory Disease Cases

Authors: C.J. Roof, M.D. Apley, K. Janardhan, D.S. McVey, F. Coetzee, J.A. Kuszak, D.G. McClary

One hundred ninety-four steers, bulls, and heifers weighing 182-318 kg were purchased at an Arkansas sale barn and shipped 12 hours to a northern Kansas feedlot within 24 hours of purchase. There was no previous history of treatment and the cattle had been delivered to the sale barn within a 24 hour period prior to the sale. Objectives of the study were to evaluate the numbers of bacteria in the respiratory tract of clinically ill and clinically normal calves and compare the numbers to the extent of tissue damage and inflammation in the affected lung tissue. Fifteen calves were identified with signs of acute bovine respiratory disease (BRD) based on clinical signs and minimum rectal temperature of 40° C. An additional five calves with no clinical signs and rectal temperatures < 40° C were selected as controls. Cattle were humanely euthanized following recording of the clinical evaluations. At necropsy, samples for microscopic analysis were collected from normal and/or affected tissue of each lung lobe (pneumonia). The number of the bacterial pathogens per gram of lung tissue were performed for the affected tissue. Scores of 0-4 (normal to most severe, respectively) were assigned to the tissue samples and compared to the quantified bacterial pathogens to evaluate association between the pathologic process and the total agents in that tissue sample. The numbers of bacterial pathogens present in the entire lung for cattle with pneumonia were greater than 10 million for *Pasturella multocida* and *Mannheimmia haemolytica*, two major bovine respiratory disease pathogens. The lung tissue with the highest tissue damage scores (most severe pneumonia) had significantly greater numbers of bacteria.

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