



# Research Kernels

Our Latest Research Results – September 2014

## Quantitative trait loci for *Fusarium* head blight resistance in Huangcandou x 'Jagger' wheat population

**Authors:** J. Cai, G. Bai

**Submitted to:** Crop Science

*Fusarium* head blight (FHB), also called wheat scab, is a devastating disease in wheat, and growing resistant cultivars is the most effective strategy to control the disease. Huangcandou (HCD) is a Chinese wheat landrace that shows a high level of scab resistance. To determine genes conditioning scab resistance in HCD, we analyzed a population of recombinant inbred lines (RILs) for scab resistance and using DNA markers. The population was developed from the cross between HCD and 'Jagger', a susceptible hard winter wheat from Kansas. Marker analysis identified three chromosome regions from HCD and two from 'Jagger' that were associated with scab resistance. In HCD, scab resistance was associated with two regions on the short arms of chromosomes 3B, and one on the short arm of chromosome 3A. These regions explained 10% to 26.1% of phenotypic variation for scab resistance. 'Jagger' also has two chromosome regions (chromosomes 2D and 6D) contributing to scab resistance that explained less than 10% of phenotypic variations. A combination of scab resistance genes from both HCD and 'Jagger' can enhance scab resistance in wheat.

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## Genome-wide association analysis identified SNPs closely linked to a gene resistant to *Soil-borne wheat mosaic virus*

**Authors:** S. Liu, X. Yang, D. Zhang, G. Bai, S. Chao, W. Bockus

**Submitted to:** Theoretic Applied Genetics

*Soil-borne wheat mosaic virus* (SBWMV) disease can significantly reduce grain yield up to 80% in winter wheat in the Great Plains. Developing resistant wheat cultivars is the only feasible strategy to reduce the losses. In this study, we analyzed an association mapping population of 205 winter wheat accessions from the U.S.A. using wheat 9K SNP (single nucleotide polymorphism) chips and identified six new SNPs that were significantly associated with the SBWMV resistance gene on chromosome 5D. The SNP markers were further mapped close to the SBWMV resistance gene using recombinant inbred lines (RILs) from 'Heyne' / 'Trego'. The six SNPs are from two genes closely linked to the

SBWMV resistance gene. Two representative SNPs, *wsnp\_CAP11\_c209\_198467* and *wsnp\_JD\_c4438\_5568170*, from the two linked genes were converted into user-friendly KBioscience Kompetitive Allele-Specific PCR (KASP) assays. These markers can be easily used in marker-assisted improvement of wheat resistance to SBWMV. Contact Guihua Bai, telephone 785-532-1124, email [Guihua.Bai@ars.usda.gov](mailto:Guihua.Bai@ars.usda.gov)

## Gene discovery and differential expression analysis of humoral immune response elements in female *Culicoides sonorensis* (Diptera: Ceratopogonidae)

**Authors:** D. Nayduch, M.B. Lee, C.A. Sasaki

**Submitted to:** Parasites and Vectors

Female *Culicoides sonorensis* midges are important in the transmission of pathogenic viruses such as bluetongue virus and epizootic hemorrhagic disease virus, which have morbidity, mortality, fitness and economic impacts on US livestock and wildlife. We recently completed and published the transcriptome, which is a catalog of expressed genes, for this vector and also looked at how the expression of genes changes with diet (unfed vs. blood fed vs. sugar fed). Subsequently, those transcriptomes were analyzed in order to identify components of the insect innate immune system. Because the insect immune response is a key player in important processes including vector competence, or the ability for the midge to transmit pathogens, we also examined immune gene expression profiles in response to diet across time, on both a transcriptome-wide, whole-midge level and more specifically by examining antimicrobial peptide (AMP) gene expression in the digestive tract, which serves as a primary barrier to infection. We identified functional components of the three main insect humoral immune pathways including: immune deficiency (Imd), Toll and JAK/STAT. We found complete or nearly-complete sequences for all elements, including humoral factors, transmembrane receptors, signaling components, gene transcription factors/regulators and antimicrobial effectors (e.g. AMPs, thioester-containing proteins, and prophenoloxidase). Midges that were fed on either sugar or blood had altered expression of receptors, regulators, effectors (AMPs, PPO and TEPs). Further, blood had a greater effect than sucrose on the expression profiles of most innate immune components. All five AMPs were significantly upregulated in the alimentary canal after blood feeding, possibly in response to proliferating

populations of gut bacteria. Functional insight into *C. sonorensis* humoral/innate immune components updates our knowledge of the molecular functioning of this important vector. Future studies involving the manipulation of immune gene expression, such as gene silencing, will help in uncovering genetic components of vector competence. The results of such studies would serve as a platform for designing novel transmission-blocking strategies.

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### **Studying *Culicoides* vectors of BTV in the post-genomic era: resources, bottlenecks to progress and future directions.**

**Authors:** D. Nayduch, L.W. Cohnstaedt, C. Sasaki, D. Lawson, P. Kersey, M. Fife, S. Carpenter

**Submitted to:** Virus Research

*Culicoides* biting midges (Diptera: Ceratopogonidae) are a major vector group responsible for the biological transmission of a wide variety of globally significant arboviruses, including bluetongue virus (BTV). In this review we examine current biological resources for the study of this genus, with an emphasis on detailing the history of extant colonies and cell lines derived from *C. sonorensis*, the major vector of BTV in the USA. We then discuss the rapidly developing area of genomic and transcriptomic analyses of biological processes in vectors and introduce the newly formed *Culicoides* Genomics and Transcriptomics Alliance. Preliminary results from these fields are detailed and finally likely areas of future research are discussed from an entomological perspective describing limitations in our understanding of *Culicoides* biology that may impede progress in these areas.

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### **Registration of 'Cowboy' wheat**

**Authors:** S. Haley, J. Johnson, F. Peairs, J. Stromberger, E. Hudson-Arns, S. Seifort, R. Kottke, V. Valdez, J. Nachtman, J. Rudolph, G. Bai, X. Chen, R. Bowden, Y. Jin, J. Kolmer, M. Chen, B. Seabourn

**Submitted to:** Journal of Plant Registrations  
'Cowboy' (Reg. No. CV-1095, PI 668564) is a hard red winter wheat that was co-developed by the Colorado Agricultural Experiment Station and USDA-ARS researchers at Manhattan, KS, St. Paul, MN, and Pullman, WA, and released cooperatively by Colorado State University (CSU) and the University of Wyoming (UWYO) in August 2011. Cowboy was selected from the cross CO980829/'TAM 111' at Fort Collins, CO. and assigned experimental line number CO050322. TAM 111 is a hard red winter wheat cultivar released by Texas A&M University, and CO980829 is an experimental line from CSU. Cowboy has superior grain yield and adaptation under both non-irrigated and irrigated production systems in Wyoming and superior milling and baking quality characteristics.

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### **Soil erosion and organic carbon variations for central Great Plains cropping systems under residue removal**

**Authors:** R. Nelson, J. Tatarko, J.C. Ascough II

**Submitted to:** Soil and Tillage Research

The diversity of land uses and the potential of crop residues for biofuels within the United States Central Great Plains (CGP) requires sustainable production that provides optimal resource use while maintaining or enhancing local soil and environmental quality. This study examined average annual changes in soil erosion from rainfall and wind forces and trends in soil organic carbon (SOC) as a function of commodity and/or bioenergy-based crop rotations, yield variations, and different field management practices, including removal of residue, across all land capability class (LCC i.e., land productivity classes) soils in select areas of the CGP. Specifically, comparisons were made between crop rotations of corn, winter wheat, sorghum, cotton, fallow, and canola, subject to reduced tillage and no-till systems. The purpose was to assess cropping options, field management practices, and soil sustainability to provide an assessment across the region for use in soil conservation planning and possible bioenergy resource assessments in the CGP. Soil erosion and SOC were analyzed on all individual soils using water and wind erosion prediction models. Results were grouped by individual LCC and organized with respect to three different spatial resolutions: field-scale (individual soil type), field-scale summarized at a county level, and field-scale summarized at a regional level. Analyses indicate variation in soil erosion and SOC trends as a function of crop type, rotation, and field management practices across different soil types within a single county and at the regional level. Considerable variation in removable residue amounts also occurred across different rotations, especially with respect to crop type, rotation, soil type, and tillage. Results obtained in this study help advance the overall knowledge base of both commodity and bioenergy crop production agriculture and soil sustainability by providing high-resolution (i.e., individual soil type) informational data on soil erosion and soil carbon trends that could have a pronounced effect on producer economics and long-term land sustainability. Output from this project should be useful in guiding conservation and natural resource planning and assessing soil sustainability associated with supplying crop biomass for alternate energy development and production.

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