



# Research Kernels

Our Latest Research Results – October 2014

## **Construction of dense linkage maps “on the fly” using early generation wheat breeding populations**

**Authors:** J.T. Eckard, J. L. Gonzalez-Hernandez, S. Chao, P. St. Amand, G. Bai

**Submitted to:** Molecular Breeding

Construction of genetic maps using DNA markers provide a blueprint for identification of useful genes that can be used in breeding. However, the map construction usually uses experimental populations that can not be directly used in breeding for new cultivars. In this study, we developed a dense and reliable genetic map using extant breeding populations derived from many crosses to eliminate an extra step for experimental population development. Using 565 segregating F1 progenies from 28 four-way cross breeding populations, 3,785 single nucleotide polymorphism (SNP) and 22 simple sequence repeat markers were located in a wheat genetic map. The map showed high rank-order concordance with a SNP consensus map developed from seven mapping populations. Therefore, direct use of breeding populations for mapping can be implemented in wheat breeding programs to speed up the molecular breeding process.

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## **Weather, disease, and wheat breeding effects on Kansas wheat varietal yields, 1985 to 2011**

**Authors:** A. Barkley, J. Tack, L. Nalley, J. Bergtold, R. Bowden, A. Fritz

**Submitted to:** Agronomy Journal

The objective of this research was to quantify the impacts of weather, disease, and genetic improvement on wheat yields of varieties grown in 11 locations in Kansas from 1985 to 2011. The results show that from 1985 through 2011, wheat breeding increased average wheat yields by 917 kg/ha, or 27% of total yield. Weather was found to have a large impact on wheat yields. Simulations demonstrated that a 1 degree Celsius increase in projected mean temperature was associated with a decrease in wheat yields of 715 kg/ha, or 21%. Diseases, insects, and shattering were other important factors that negatively influenced yields.

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## **Genetic mapping of race-specific stem rust resistance in the synthetic hexaploid W7984 x Opata M85 mapping population**

**Authors:** S. Dunckel, E. Olson, M. Rouse, R. Bowden, J. Poland

**Submitted to:** Theoretical and Applied Genetics

Stem rust is one of the most potentially destructive diseases of wheat and barley worldwide. Geneticists are constantly looking for new sources of resistance genes to control this disease. Mapping populations are an important genetic resource in wheat for locating genes on chromosomes. One of the well-studied mapping populations is the Synthetic x Opata reference population. Segregating lines from the reference population were screened at the seedling stage and four stem rust resistance genes were identified on chromosome arms 1AS, 2BS, 6AS, and 6AL. Some of the genes appear to be novel and need to be studied further to determine their usefulness for crop improvement.

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## **Consistency of wind erosion assessments across land use and land cover types: a critical analysis**

**Authors:** J. Li, G.S. Okin, J. Tatarko, N.P. Webb, J.E. Herrick

**Submitted to:** Aeolian Research

In recent decades, large areas of rangeland have been converted to cropland or vice versa in the western United States and elsewhere in the world, driven largely by increased crop prices, loss of access to irrigation water, and agricultural expansion or contraction. Wind erosion and dust emissions resulting from land use and land cover changes have not been well studied. Such an assessment is important because currently no prediction model is available that can provide field- to large area estimates of wind erosion on both rangeland and cropland that account for soil, vegetation, and management changes. In this paper, we compare dust transport estimates from available cropland models and a number of similar models developed for rangelands, for a bare soil surface with different levels of crust and surface roughness under different wind speeds. Our results show that the simulated dust movements are similar for cropland and rangeland models at large surface crust coverage and roughness. In situations of small to moderate crust cover and soil roughness, dust movement varied by over 1000 times among the tested

models. Analysis shows that dust movement simulated by cropland and rangeland models are correlated. Finally, we propose an approach to estimate changes in dust transport with changes in land use. Although this approach may be limited to situations of non-vegetated surfaces, it provides a preliminary method for land managers and policymakers to estimate potential wind erosion changes in response to land use change. Contact John Tatarko, telephone 970-492-7320, email [John.Tatarko@ars.usda.gov](mailto:John.Tatarko@ars.usda.gov)

### **Susceptibility of *Tribolium confusum* Jacqueline duVal to pyrethrin aerosol: effects of aerosol particle size, concentration, and exposure conditions**

**Authors:** F.H. Arthur, J.F. Campbell, G.R. Ducatte  
**Submitted to:** Journal of Economic Entomology  
Aerosol insecticides are being used as an alternative to the fumigant methyl bromide to control insects inside flour mills, but there is little information available on effectiveness of those aerosols when they are applied at different particle sizes. We conducted tests by exposing adult confused flour beetles for different time periods to pyrethrin aerosol applied at either 2 or 16 microns. After exposure, beetles were held in the arenas in which they were exposed or transferred to new arenas with and without flour. At 16 microns, all adults were knocked down by the aerosol and there was an effect of exposure time and transfer to untreated dishes with food on subsequent mortality. At 2 microns, there was no mortality due to the aerosol, even when concentration was increased by a factor of four. Results show that as the actual particle size applied decreases the effectiveness of aerosols may also decrease as well. Our results will enable industrial personnel who apply aerosols to adjust particle size of aerosols so that particles are dispensed at the size necessary to give maximum control of flour beetles inside mills. Contact Frank Arthur, telephone 785-776-2783, email [Frank.Arthur@ars.usda.gov](mailto:Frank.Arthur@ars.usda.gov)

### **Spiked GBS: a unified, open platform for single marker genotyping and whole-genome profiling**

**Authors:** T. Rife, S. Wu, R. Bowden, J. Poland  
**Submitted to:** BMC Spiked Genomics  
In plant breeding, there are two primary applications for DNA markers in selection: 1) selection of known genes using a single marker assay (known as marker-assisted selection); and 2) whole-genome profiling and prediction (known as genomic selection). Typically, marker platforms have addressed only one of these objectives. We have developed a new method called spiked genotyping-by-sequencing (sGBS), which combines targeted gene sequencing with whole-genome scanning. In breeding applications, the sGBS approach will allow breeders to obtain a whole-genome profile of important individuals while simultaneously targeting specific genes that are important. This should lead to greater speed and efficiency of selection strategies. Contact Robert Bowden, telephone 785-532-2368,

email [Robert.Bowden@ars.usda.gov](mailto:Robert.Bowden@ars.usda.gov)

### **Pyrosequencing Reveals the Predominance of *Pseudomonadaceae* in Gut Microbiome of a Gall Midge**

**Authors:** R. Bansal, S. Hulbert, J. Reese, R. Whitworth, J. Stuart, M. Chen  
**Submitted to:** Pathogens  
The gut of animals including insects hosts various microbes. Gut microbes perform a wide range of functions useful to the host, such as synthesizing vitamins and essential amino acids, preventing growth of harmful pathogens, and utilizing energy substrates that cannot be used directly by the host itself. Gut microbes in plant-feeding insects also play a role in insect-plant interactions. The Hessian fly is a very important insect pest of wheat. In this study, we analyzed the composition of microbes in the Hessian fly larval gut systematically for the first time. We found that the Hessian fly larval gut hosts diverse bacteria. The composition of microbes changes in different instar larvae of the insect. The research provides a foundation for future research on the roles of gut microbes in Hessian fly biology and its interaction with wheat. Contact Ming-Shun Chen, telephone 785-532-47198, email [Ming-Shun.Chen@ars.usda.gov](mailto:Ming-Shun.Chen@ars.usda.gov)

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