



# Research Kernels

Our Latest Research Results – November 2014

## Impact of transient heat stress on polar lipid metabolism in seedlings of wheat near-isogenic lines contrasting in resistance to Hessian Fly (*Cecidomyiidae*) infestation

**Authors:** Y. Currie, M. Chen, N. Radoslav, G. Bai, L. Zhu

**Submitted to:** Arthropod-Plant Interactions

Heat stress causes the loss of plant resistance to many parasites, including the Hessian fly *Mayetiola destructor*, one of the most destructive pests of wheat. However, the mechanism for the loss of plant resistance under heat stress remains unknown. A better understanding of the mechanisms that lead to the loss of plant resistance under heat stress will help us to preserve plant resistance under high heat conditions. This is especially important under the scenario of global climate change. In this study, we found that heat stress can cause significant reduction in the abundance of total detectible polar lipids and double bond index (DBI) in wheat seedlings. We also found that the change in lipid abundance in the resistant wheat cultivar 'Molly' was significantly different from that in the susceptible cultivar 'Newton' following Hessian fly infestation. Our results suggest that changes in lipid metabolism caused by heat stress may be part of the mechanism that leads to the suppression of wheat resistance to Hessian fly infestation.

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## Stored grain pack factors for wheat: Comparison of methods

**Authors:** J. M. Boac, R. Bhadra, M. E. Casada, S. A. Thompson, A. P. Turner, M. D. Montross, S. G. McNeill, and R. G. Maghirang

**Submitted to:** Transactions of the ASABE

Grain stored in bins is subject to packing from overburden pressure, which increases grain bulk density and, thus, storage capacity. The increase in storage capacity necessitates accurate pack factor values for determining grain inventory by stored grain managers and government auditors. This study compared scale-measured mass of hard red winter (HRW) wheat in vertical storage bins to predicted mass based on three methods of determining pack factor: a science-based packing model (WPACKING), the USDA Risk Management Agency (RMA) method, and the USDA Farm Service Agency warehouse group (FSA-W) method. In most of the bins, the packing model under-

predicted the grain mass for steel bins, but slightly over-predicted for concrete bins. The RMA method predictions of mass were higher than the model and the FSA-W method for steel bins. However, the RMA predicted mass was slightly lower than the model and much lower than the FSA-W predictions for concrete bins. In most cases for concrete bins, the model and the two methods over-predicted the actual reported value. Overall, WPACKING predicted the mass of grain in the bins with less error compared to reported mass than the current RMA and FSA-W procedures. Some of the differences may be because the RMA and FSA-W methods do not include the effect of grain moisture content, grain depth, or bin wall type on pack factors. Contact Mark Casada, telephone 785-776-2758, email [Mark.Casada@ars.usda.gov](mailto:Mark.Casada@ars.usda.gov)

## Vaccines for prevention of bluetongue and epizootic hemorrhagic disease in livestock – a North American perspective

**Authors:** D.S. McVey, N.J. MacLachlan

**Submitted to:** Vector-Borne and Zoonotic Diseases  
Bluetongue (BT) and epizootic hemorrhagic disease (EHD) are non-contagious, insect transmitted diseases of domestic and wild ruminants caused by related but distinct viruses. Both BT (BTV) and EHD (EHDV) viruses cause hemorrhagic fevers in susceptible ruminants; however BT is principally a disease of domestic livestock whereas EHD is principally a disease of certain species of wild, non-African ungulates, notably White-tailed deer. The live-attenuated (modified live virus [MLV]) vaccines available in the United States (U.S.) for use in small ruminant livestock do provide good protection against clinical disease following infection with the homologous virus serotype. Although there is increasing justification that use of MLV vaccines should be avoided if possible, these are the only vaccines currently available in the U.S. Specifically, MLVs are used in California to protect sheep against infection with BTV serotypes 10, 11 and 17, and a MLV to BTV serotype 10 is licensed for use in sheep throughout the U.S. These MLV vaccines may need to continue to be used in the immediate future for protective immunization of sheep and goats against BT. There are no currently licensed vaccines available for EHD in the U.S. If there is a need to rapidly develop a vaccine to meet an emerging crisis associated with either BTV or EHDV infections, development of an inactivated virus vaccine in a conventional adjuvanted formulation will likely be required. With two doses of vaccine (and in some instances just one dose),

inactivated vaccines can provide substantial immunity to the epizootic serotype of either BTV or EHDV. This strategy is similar to that used in the 2006-2008 BTV serotype 8 outbreaks in northern Europe which provided vaccine to the field within 2 years of the initial incursion (by 2008). There are significant gaps in our scientific knowledge and available countermeasures to control an outbreak of orbivirus-induced disease, whether BT or EHD. It is concluded that a coordinated national research strategy to achieve a more optimal vaccine profile should be developed.

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### **Inducing RNA interference in the arbovirus vector, *Culicoides sonorensis***

**Authors:** M.K. Mills, D. Nayduch, K. Michel

**Submitted to:** Insect Molecular Biology

*Culicoides* midges transmit arboviruses that cause significant diseases in ruminant livestock and wildlife in the US and worldwide. Research on these important insect vectors has been hindered by lack of molecular tools and resources such as a sequenced genome and ways to manipulate gene expression. One tool widely used in studying gene function is RNA-interference or RNAi, which can be used to effectively silence gene expression in vivo so that the gene's function can be assessed. Here, we report the establishment of RNAi as a research tool for the adult female biting midge *Culicoides sonorensis*. A database from our previous study was mined to identify the genes involved in the RNAi machinery, and key components were found. A successful delivery mechanism for double-stranded RNA (used in the RNAi technique) was developed, and was subsequently used to "silence" the expression an inhibitor of apoptosis (IAP, involved in cell death) to demonstrate proof of concept. Successful silencing of the IAP gene was confirmed by both molecular methods (knockdown of mRNA confirmed by qRT-PCR) and by an observed phenotype (increased mortality in RNAi-treated midges). mRNA transcript level decreased significantly by 40% in RNAi-treated midges compared to normal levels. Median survival in RNAi-treated midges was shortened to less than 8 days compared to 30 days in appropriate controls. These results demonstrate RNAi as an exploitable method in the molecular toolset used to study midges. This tool can help in future studies aimed at understanding genetic components underlying the vector competence of *C. sonorensis*.

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### **Global epidemic invasion thresholds in directed cattle subpopulation networks having source, sink, and transit nodes**

**Authors:** P. Schumm, C. Scoglio, Q. Zhang, D. Balcan

**Submitted to:** Elsevier Journal of Theoretical Biology

This study considers disease spread in theoretical models of cattle movement systems. A cattle movement and demographic model simulates a large network of cattle premises and flows. When a theoretical disease is

introduced into the system, it has a possibility to initialize an epidemic. We derive analytic estimations of two thresholds to define the necessary criteria for an epidemic to break out across our model system. These thresholds quantify the minimal rates of cattle movement for a model disease to (a) become an epidemic in the system and (b) spread into "last-stop" locations, such as finishing feedlots. This second threshold helps model when potentially diseased animals might be arriving at slaughterhouses and would pose a threat to food safety. We conduct several numerical experiments to explore the analytic thresholds and find a primary result suggesting that the cattle premises that serve as transit nodes for cattle are the most significant type of premises in movement-based disease control.

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### **Using RNA-seq and in silico subtraction to identify resistance gene analog markers for *Lr16* in wheat**

**Authors:** Harrison, N., Fritz, A., Glasscock, J., Ahmed, S., Messina, D., Fellers, J.,

**Submitted to:** The Plant Genome

Leaf rust is a common wheat disease that is found all over the world. In the United States, the most cost-effective way to combat the disease is to use resistance genes. One of these resistance genes, *Lr16*, provides resistance to many races of leaf rust and is desirable in wheat breeding programs. Since it is difficult to accurately score resistance using visual methods, plant breeders need DNA markers that they can use to follow *Lr16* in their breeding programs. This paper describes a new technique to develop markers that takes advantage of the similarities among resistance genes and new high throughput DNA sequencing technology. A new DNA marker was developed for *Lr16* that is easy to use and expected to be efficient for identifying resistant plants.

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