

Our Latest Research Results - November 2012

Assessing Effects of Esfenvalerate Aerosol Applications on Resident Populations of *Tribolium castaneum* (Herbst), the Red Flour Beetle, Through Direct and Indirect Sampling

Authors: F.H. Arthur, J.F. Campbell, E.A. Fontenot
Submitted to: Journal of Stored Products Research
Aerosol insecticides are used to control red flour beetles in flour mills, but there is little information on how these aerosols affect resident beetle populations. We conducted studies by placing food (flour) containing different life stages of beetles underneath metal shelves inside small sheds. The sheds were either untreated or sprayed every 2 or 4 weeks with the labeled rate of the pesticide esfenvalerate, trade name Conquer. The aerosol treatments did not affect the population development in the flour. However, there were more dead beetles in the treatments compared to the controls, and more live beetles in pheromone traps in the controls compared to the treatments. Results show that although the aerosol applications reduced overall insect numbers, the presence of available food material allowed for continued population development.
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Transcript Analysis and Expression Profiling of Three Heat Shock Protein 70 Genes in the Ectoparasitoid *Habrobracon hebetor* (Hymenoptera: Braconidae)

Authors: H. Chen, H. Zhang, J.E. Throne, K.Y. Zhu
Submitted to: Journal of Insect Physiology
The Indianmeal moth is a major pest of stored grain and processed commodities. There is a small wasp that does not sting humans but parasitizes the Indianmeal moth, and releasing these parasitic wasps would be an environmentally friendly way to control the Indianmeal moth. But, there is currently no way to store these wasps for when they are needed for controlling the Indianmeal moth. We previously showed that the wasp can enter reproductive diapause (a resting stage where they don't produce offspring) when reared at low temperature and short photoperiod, and diapausing females have a higher rate of survival during cold storage and lay more eggs after cold storage than nondiapausing females. Heat shock proteins (HSPs) are known as chaperones that help with folding of other proteins when cells are under environmental stresses, and HSPs are essential for cold survival during insect diapause. We identified

three HSP genes in the wasp, and characterized their expression levels during exposure to cold. Knowing how heat shock protein genes respond to cold stress may allow enhancement of diapause and prolonging the duration of low-temperature storage of insects by finding ways to artificially control the expression of these genes. Contact James Throne, telephone 785-776-2796, email James.Throne@ars.usda.gov

Validation of Quantitative Trait Loci for Aluminum Tolerance in Chinese Wheat Landrace FSW

Authors: J. Dai, G. Bai, D. Zhang, D. Hong
Submitted to: Euphytica
Aluminum (Al) toxicity limits wheat production in acidic soils. Al-tolerant cultivars can reduce Al damage. A Chinese landrace, FSW, shows a high level of Al tolerance. The quantitative trait loci (QTL) conditioning resistance to Al toxicity were validated in a new mapping population. Two previously reported QTLs for Al tolerance from FSW were confirmed. The major QTL on chromosome 4DL co-segregated with the Al-activated malate transporter gene (ALMT1). However, sequence analysis of ALMT1 gene indicated that FSW contained a marker allele that is different from the one reported in the resistance sources from Brazil. Another QTL on chromosome 3BL showed a minor effect on Al tolerance in the population. The two QTLs showed an epistatic effect for Al tolerance. SSR markers closely linked to the QTLs have potential to be used for marker-assisted selection marker-assisted breeding for Al tolerant cultivars.
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Functional Genomic Approaches in Cereal Rusts

Authors: G. Bakeren, X. Song, V. Panwar, R. Linning, X. Wang, C. Rampitsch, B. McCallum, B. Saville, J. P. Fellers
Submitted to: Canadian Journal of Plant Pathology
Cereal rusts cause significant economic losses each year. Plant breeders typically select for disease resistance genes to combat infection. Unfortunately, disease resistance genes frequently succumb to new races of the cereal rust fungi. Although study of rust fungi is difficult because they cannot be cultured on laboratory media, great advances are now occurring in understanding the genomes of rust pathogens and their arsenal of effector proteins that they use to attack plants.

Understanding the mechanisms of pathogen attack may help us design better, more durable defenses in the plant.

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Genetic Structure of a Diverse Sorghum Collection and Association Mapping for Grain Quality

Authors: S. Sukumaran, W. Xiang, S. Bean, J.F. Pedersen, M.R. Tuinstra, T.T. Tesso, M.T. Hambelin, J. Yu

Submitted to: The Plant Genome

Grain sorghum is a genetically diverse crop, however little is known how this diversity relates to grain quality traits. To gain an understanding of the relationships between grain quality and genetic diversity in sorghum, candidate gene association mapping was used on a diverse collection of 300 sorghum accessions. Data analysis resulted in the identification of eight significant marker-trait associations including markers for grain hardness and starch synthesis genes. Knowledge on the genetic basis of grain quality traits will complement breeding efforts to improve sorghum grain quality.

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Staphylococcus aureus in the House Fly (Musca domestica L.): Temporospatial Fate of Bacteria and Expression of the Antimicrobial Peptide Defensin

Authors: D. Nayduch, H. Cho, C. Joyner

Submitted to: Journal of Medical Entomology

House flies feed and breed in feces, garbage and other microbe-rich habitats. Because of these activities, flies often harbor and disseminate bacteria, some pathogenic to humans and livestock. Previous surveys of house flies have detected the pathogen *Staphylococcus aureus*, a bacteria species that causes skin and wound infections, toxic shock syndrome and food poisoning. The potential of flies to disseminate, transport or vector this bacterium is not known. In this paper, we used a transformed strain of *S. aureus* that expressed a green-flourescent protein (GFP) tag so that we could track its association with house flies. Flies were fed known amounts of bacteria (ranging from about 150,000 to 350,000 colonies) and then processed as follows. In the first experiment, flies were dissected to remove the alimentary canal and view bacteria within regions of the gut by microscopy at 2, 4 and 6 h post ingestion. In the second experiment, flies were fed bacteria and then homogenized for culture analysis (at 2, 4, and 6 h), or flies were housed individually so we could collect and culture their excrement (at 2, 3, and 4 h). Finally, we fed flies bacteria and looked at the expression of an antimicrobial gene defensin, part of the house fly immune system involved in destroying bacteria, in respect to location in the gut or systemically in the body at 2, 4, and 6 h. At 2 h post-

ingestion (PI), live bacteria were present in the crop, an anterior storage sack in the fly gut from which vomitus is expelled, and the midgut, which is analogous to the intestine. As soon as 4 h PI, GFP-*S. aureus* were visualized in feces in the hindgut and rectum of flies, but many were destroyed and non-viable. Bacteria persisted up to 6 h PI but significantly decreased over time. Excretion of viable GFP-*S. aureus* peaked at 2 h PI and, although significantly less, continued up to 4 h PI. defensin was detected at high levels locally in the digestive tract (proximal to bacteria) and systemically in fat body (which sits in the fly body cavity) at 2, 4 and 6 h PI. To our knowledge, this is the first study to report a local and systemic response to a bacterium with lysine-type peptidoglycan, such as *S. aureus*, in flies exposed to bacteria by feeding. While flies harbored *S. aureus* for up to 6 h PI, our data indicate that the highest probability of vectoring biologically-relevant amounts of bacteria occurred between 0-2 h PI. The combined effects of excretion, digestion and antimicrobial responses likely contribute to loss of ingested bacteria. Nonetheless, we demonstrated that house flies are relevant vectors for *S. aureus* up to 2 h PI and environmental reservoirs up to 6 h PI. These findings indicate that in both human and livestock environments where flies have opportunities to ingest this pathogen, they would be able to disseminate bacteria effectively, and therefore serve as source of cross contamination between otherwise clean and filthy areas.

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