



Research Kernels

Our Latest Research Results – May 2014

Effect of diet and refugia on development of *Dermestes maculatus* DeGeer reared in laboratory

Authors: E.A. Fontenot, F.H. Arthur, K.L. Hartzler

Submitted to: Journal of Pest Science

The hide beetle can infest a wide variety of stored food products, particularly protein based food and feed. Mass-rearing of this insect can be difficult due to variation in development with different food products, and cannibalism of different life stages. We conducted studies to evaluate different food products for growth and development of the hide beetle. Commercial dog food and protein based shake powders were the best diets for the hide beetle and supported development to the adult stage. Utilizing cork and wood as refugial sites for larvae enabled them to escape cannibalism by other larvae and adults. Results show the hide beetle can be mass-reared under laboratory conditions using commercial dog food and by providing the larvae with refuge sites to avoid loss due to cannibalism. Contact Frank Arthur, telephone 785-776-2783, email Frank.Arthur@ars.usda.gov

Conserved and diversified roles of eIF5-mimic protein in eukaryotes

Authors: H. Hiralshi, J. Oatmin, L. Blunk, W. Gutierrez, J. Fellers

Submitted to: Proceedings of National Academy of Science

Each organism has specialized methods for controlling genes. Genes are transcribed into RNA, RNA is translated into proteins, and finally the proteins have an assigned function. At each point there are differing types of control. Some genes are controlled at transcription, others are controlled by how their RNA is processed and then proteins can be modified at their individual amino acids, which in turn, affect the protein function. The work reported here describes a protein that controls translation and how it is conserved in many multi-celled organisms. eIF5-mimic protein 1 (5MP1) competes with eIF2 for a binding site on RNA. The research isolated 5MP1 from several organisms, including wheat, wheat leaf rust, red flour beetle, and Giardia. 5MP1 has the same function in all of the organisms and can be used to replace a mutant 5MP1 in yeast. In red flour beetle, 5MP1 is important for development. This suggests that the 5MP1 is necessary for the specific organism. However, there are other organisms that have evolved without 5MP1.

Overall, the work shows that 5MP1 has been kept in the genome of many organisms, and its function is similar. Contact John Fellers, telephone 785-532-2367, email John.Fellers@ars.usda.gov

Effect of sorghum flour composition and particle size on quality properties of gluten-free bread

Authors: E.F. Trappey, H. Khouryieh, F. Aramouni, T. Herald

Submitted to: Food Science and Technology International

The numbers of gluten-free food products found on the grocery store shelves are on the rise as the market responds to individuals that are sensitive to gluten. Sorghum is the fifth most important cereal crop grown in the world. Sorghum does not contain gluten and maybe a viable grain alternative for the gluten-free food market. This research evaluated the effect milling extraction rate (60%, 80% and 100%) on bread quality using white food-grade sorghum. The sorghum flour was further processed to obtain different flour particle sizes. Starch damage and water absorption was determined to optimize the bread formulation. The effect of flour particle size on bread quality was determined by measuring loaf volume, crumb structure, and crumb firmness. The research concluded that smaller sorghum flour particle size resulted in better quality gluten-free bread compared to those made with larger flour particle size.

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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 Competitive Allele-Specific Polymerase (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

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 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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Effect of high molecular weight glutenin subunit composition in common wheat on dough properties and steamed bread quality

Authors: P. Zhang, T.O. Jondiko, M. Tilley, J.M. Awika

Submitted to: Journal of the Science of Food and Agriculture

Steamed bread is a popular food in Asian markets, especially China, where it represents more than 40% of national wheat consumption. Northern-style Chinese steamed bread is the most common type and is a daily staple in northern China and consistent product quality is becoming more important with rapid urbanization and mechanized/centralized processing. Wheat quality requirements for steamed bread are significantly different from those of pan bread, which is mainly due to the different processing methods, i.e. steaming versus baking. Medium protein content flour with moderate

gluten strength and good extensibility is desirable for both mechanized and handmade methods as excessive elasticity causes difficulty in steamed bread processing resulting in shrinkage and wrinkles of finished product. The high molecular weight glutenin subunit (HMW-GS) proteins are important in the formation of the gluten matrix, however, little is known about the relationship between glutenin characteristics and steamed bread quality. The objective of this study was to investigate and compare the function of HMW-GS in determining dough properties and steamed bread quality among a set of American hard white wheat cultivars with variable HMW-GS composition or deletions. Results demonstrated that specific deletions of HMW-GS viable strategy to develop new wheat genotypes for steamed bread processing. Contact Michael Tilley, telephone 785-776-2759, email Michael.Tilley@ars.usda.gov

The salivary secretome of the biting midge, *Culicoides sonorensis*

Authors: C.J. Lehiy, B.S. Drolet

Submitted to: PeerJ

Biting midges (noseeums, punkies) are common agricultural pests which transmit viruses such as bluetongue, epizootic hemorrhagic disease and Schmallenberg to livestock and wildlife. Proteins in the saliva of related flies have been shown to facilitate blood feeding by dilating vessels and preventing clotting. Additionally, some proteins may interact with the animal's immune system thereby affecting the ability of a virus delivered during feeding to establish infection. We identified 45 proteins in midge saliva and characterized their function based on their similarity with previously identified salivary proteins from other insects. Identifying the proteins in midge saliva is critical for understanding their role in blood feeding, virus transmission, and possibly the disease process in the animal. Contact Barbara Drolet, telephone 785-537-5569, email Barbara.Drolet@ars.usda.gov

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