



Research Kernels

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Domain organization and phylogenetic analysis of proteins from the chitin deacetylase gene family of *Tribolium castaneum* and three other species of insects

Chitin is the main component of insect exoskeleton, conferring both rigidity and flexibility, and protecting the insect from injury, predation, infection, and desiccation. Chitin is also the major component of a membrane that coats the lining of the midgut, protecting it from abrasion and self-digestion. Until recently, very little has been known about the enzymes that are needed for modifying the the properties of the freshly-synthesized, raw chitin to form the finished product with all its variations according to the requirements in the various body regions for cuticle that is either hard or soft, stiff or flexible, thick or thin. We used bioinformatics to identify nine different chitin deacetylase genes in the red flour beetle. Each of these enzymes appears to have a different function, and to modify the properties of cuticle in different regions of the insect exoskeleton. Each of these newly-discovered genes can become a target in screening assays for new biopesticides that disrupt molting and related physiological processes.

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A rapid small-scale method to evaluate dough viscoelastic properties

The processing of dough (wheat flour + water) into a useful product requires that it undergo mechanical (work) input virtually every step of the way, from initial mixing and fermentation, to sheeting and proofing, and final baking. Thus, its rheological properties also influence every step of the bread baking process and are important quality factors to consider for bakers and cereal chemists. The current standard methods for measuring dough viscoelastic properties, such as extensibility and resistance-to-extension, require a large amount of sample and are time-consuming. The objective of this study was to develop a rapid, small-scale method to evaluate dough extensibility and resistance-to-extension properties. A total of 20 hard red winter wheat flour samples, varying in protein content and rheological properties, were studied. The standard Extensigraph method, as well as a small-scale Texture Analyzer (TA) method utilizing a Kieffer rig, were compared to a newly developed method using near infrared spectroscopy (NIRS). Coefficient of determination (R^2) between resistance-to-extension measured by the NIRS and by Extensigraph was 0.90, while that of extensibility was 0.86. Spearman rank correlation coefficient (r) between extensibility measured by Extensigraph and by TA was 0.85, while that of resistance to extension was 0.71. The results showed that the NIRS measurements had high correlation with the standard measurements. These results indicate that NIRS has excellent potential as a rapid small-scale method to predict both dough extensibility and resistance-to-extension.

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Adaptation of polyphenol oxidase measuring methods (AACCI Method 22-85) for wheat meal and flour and their relationship to alkaline noodle color

Noodle color is a critical sensory attribute in raw noodles. Darkening of noodles is due to the polyphenol oxidase (PPO) activity, which is a concern for the noodle industry and breeders. A method for measuring PPO activity of wheat kernels has been approved by the AACCI, but no detailed procedures were elucidated for measuring PPO activity of wheat meal and flour. Here we modified that PPO method (AACCI Method 22-85) for whole wheat meal and refined flour, and measured PPO on 76 samples of wheat kernels, meals, and flours. The modified method was less time consuming (10 min vs. 60 min for reaction time) and less laborious. The modified PPO test for wheat meal provided the most reliable data, followed by flour, and kernel. The values of wheat meal PPO obtained from the modified method showed the similar trend to the ones from the wheat kernel method. The wheat meal PPO was the best indicator of discoloration of alkaline noodle.

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Effects of fine grain habitat complexity on egg parasitism by three species of *Trichogramma*

The Indianmeal moth is a serious pest of raw and finished stored products and attacks both packaged and bulk commodities as well as spillage. We determined how different substrates affected the ability of three different species of *Trichogramma* to parasitize Indianmeal moth eggs. The study was conducted in 10-cm Petri dishes that were either empty, contained flour, or contained millet. *Trichogramma deion* parasitized more eggs than the other two species in the empty dishes and in the dish containing flour. Parasitism was consistently low for all three species in the millet-filled dishes. *Trichogramma deion* may be the best-suited for use as a biological control agent for Indianmeal moth. *Trichogramma* could provide a new tool for the retail organic food industry to manage insect pests.

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Alignment between genetic and physical maps of *Gibberella zeae*

Gibberella zeae (*Fusarium graminearum*) is the primary cause of Fusarium Head Blight of wheat and barley. This disease has been one of the most important biological constraints on small grain production and marketing in the U.S. Previously, we described a genetic map of the genome of this fungus. Using sequenced DNA markers, we aligned the genetic map with the genomic DNA sequence of the fungus that was published by the Broad Institute. The alignments grouped the linkage groups and supercontigs into four sets, confirming that there are four chromosomes in this fungus. Approximately 99% of the sequence was anchored to the genetic map, indicating the high quality of the sequence assembly and the relative completeness and validity of the genetic map.

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Intragenic recombination in pseudogenes is a source of novel disease resistance in native agricultural ecosystems

Little is known about the evolution of new specificities in plant disease resistance genes. In this study, we reconstructed a possible evolutionary history of the wheat leaf rust resistance gene, Lr21. In wild populations of a wheat ancestor, *Aegilops tauschii*, both functional and nonfunctional versions of Lr21 were found. The functional version of the gene appeared to be a chimera resulting from recombination between the two nonfunctional versions. The two nonfunctional versions also occur in bread wheat varieties Wichita and Fielder, respectively. These two susceptible varieties were crossed and one out of 5876 progeny was resistant to leaf rust. When the resistant plant was tested, it had a chimeric recombination of the versions from the parents. This was the first demonstration of the evolution of a new resistance gene specificity by rearrangement of two nonfunctional resistance genes. This might be exploited in the design of new resistance genes by recombining existing genes.

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Triticum mosaic virus: a new virus isolated from wheat in Kansas

In 2006, wheat plants were discovered in Kansas that had mosaic symptoms similar to those caused by Wheat streak mosaic virus (WSMV). However, diagnostic tests determined that the diseased plants did not have WSMV. Other diagnostic tests also determined the disease was not caused by any other known wheat viruses. So, using classic virology techniques, purifications were made from infected plants and using an electron microscope, virus-like particles were found in the purifications. Other tests showed that the virus was similar in physical properties to WSMV, but very different in genetic sequence. It was determined that this was a newly discovered virus, and the name Triticum mosaic virus has been proposed. It is not known where the virus originated, how it is transmitted from plant to plant, or what the optimum environmental conditions are needed for the virus to flourish. Currently, experiments are being undertaken to further characterize the virus and to begin to find genetic resistance in wheat lines.

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