

Title: Identification of Four Bacterial Isolates from Residues of Native Wheat that Antagonize Wheat Pathogenic Fungi

Author: Nichole Baye

Abstract:

Four bacterial strains isolated from native wheat residues that antagonize wheat pathogenic fungi have been maintained in the Soil Microbiology Laboratory at South Dakota State University. These organisms have been studied for potential use as biocontrol agents. Several different methods were employed to ascertain the identity of these four organisms. The methods used incorporated membrane fatty acid methyl ester analysis (FAME), partial 16S ribosomal DNA (rDNA) sequencing, cellular and colonial morphological study, and physiological tests. FAME analysis concluded that strains 1BA and 1D3 were *Bacillus lentimorbus*, and that strains 1BC and 1BE were *Bacillus subtilis*. All four strains had identical partial 16S rRNA sequences with the best match for *Bacillus amyloliquefaciens*. Colonial and cellular morphology along with biochemical tests indicated that all four organisms most closely matched *Bacillus firmus*. The conflicting result, among these tests, implies that these organisms may belong to a new but related taxon to *Bacillus subtilis*, *Bacillus lentimorbus*, *Bacillus amyloliquefaciens*, and *Bacillus firmus*. Further studies with these organisms will involve assaying for their mode of action against fungi.

Title: Migratory Dendritic Cells as a Regulator of Immunity

Gamal Elmubark

Abstract:

Dendritic cells are a heterogeneous group of cells found in the blood, lymph, lymph nodes and in small amount in non-lymphoid tissue through out the body. Dendritic cells are the major antigen presenting cells of the immune system, presenting processed antigen to the effector T cells in the lymph nodes. In addition to the initiation of the immune response, dendritic cells have shown to promote lasting immunity and thus may play a role in the proliferation and resolution of inflammation. It seems clear that manipulation of dendritic cells may represent a strong candidate for regulation of the immune response.

The overall objective of this study is to functionally and phenotypically define the lymph-borne antigen presenting cells (APC) and to define the migratory mechanism of afferent and efferent (APC) *in vivo*, and hence to obtain a full picture of the migratory potentials, differentiation and eventual destination of blood born afferent lymph dendritic cell precursors. To fulfill these objectives this project will be divided into several phases. The first phase will be directed towards determining the origin of the afferent lymph dendritic cell (ALDC), which is expected to be derived from blood precursors.

In the second phase, we will determine the fate of ALDC after they present their antigen to the effector cells in the lymph nodes. Current dogma suggests that Dc end their life in the lymph node and die by apoptosis. *In vivo* analysis of the migration of DC will be followed by direct fluorescence labeling of the ALDC and analysis of their appearance in different tissues, in order to examine their ability to pass through lymph nodes via the efferent lymph, or die within the node.

Protective effects of Nicotinamide in Human Cortical Neurons.

Surajkumar Bhansali

Abstract:

Introduction: In previous studies it was observed that tertiary butylhydroperoxide (t-BuOOH) causes significant cell death in human cortical neurons (HCN2 cells) in culture. In addition, previous studies have shown that nicotinamide is able to prevent cell death induced by t-BuOOH in HCN2 cells. However, the molecular mechanism(s) by which nicotinamide protect human brain cells at the cellular level is unclear. This study involves examining the protective effects of nicotinamide in regulating the levels of various pro- and anti-apoptotic proteins with the help of techniques of genomics.

Methods: HCN2 cells in one flask were treated with 1mM nicotinamide for 15 min before being treated with 100 μ M t-BuOOH; the other two flasks were left untreated or treated with 100 μ M t-BuOOH respectively for 24hrs. In other studies the same treatments were done for 6 hrs. Total RNA was extracted using Tri reagent and quantified by UV spectrophotometer. Integrity of RNA was determined by gel electrophoresis. DNA microarray was done using ResGen Microarray Gene Filters from Research Genetics.

Results: The control cells showed higher amounts of RNA than both t-BuOOH treated and nicotinamide treated cells after 6 hrs. No measurable total RNA was observed in treated cells following 24 hrs of treatment, although there was measurable total RNA in control cells. RNA gel was used to confirm the integrity of RNA in with both 6 and 24 hr treatment.

Conclusions: The result does indicate that the cells may be shutting off its transcription machinery in response to t-BuOOH treatment. Therefore it will be intriguing to determine identify the genes and the sequence at which they are turned on and turned off before the RNA is destroyed in treated cells and compare that with control cells. So far there has been no difference in the total quantity of RNA that has been measured in cells that were treated with t-BuOOH alone versus cells that were treated with both nicotinamide and t-BuOOH.

Title: Isolation and Characterization of the agrp Gene in Domestic and Wild Pigs.

Juanita Perera

Abstract:

The agrp gene plays an important role in energy homeostasis. Its gene product, agouti-related protein (AGRP), antagonizes the action of the melanocortin-4 receptors (MC4Rs) in the hypothalamus and exhibits potent appetite stimulant activity. Alleles of agrp are likely to produce proteins with different structural and functional properties. Studies on genes regulating energy balance will provide the information necessary for improving the production efficiency in livestock. Kent Donelan, a former graduate student in our lab, sequenced the agrp gene in 16 breed panels of domestic pigs. Unexpectedly he did not find polymorphisms in the agrp gene. It may be that agrp is highly conserved over evolutionary time due to the critical and essential role it plays in energy homeostasis. Alternatively, intensive selective breeding of pigs for thousands of years may have resulted in the disappearance of low frequency polymorphisms in agrp. We predict that polymorphisms may still exist in pigs that have not undergone intensive selective breeding, such as pigs that live in the wild. Therefore, we intend to isolate and sequence the agrp genes in the wild relatives of domestic pigs. Desirable agrp alleles (those that promote positive production traits) present in wild pigs may also exist within untested domestic stocks. It may also be possible to introduce favorable agrp alleles into domestic pigs via conventional breeding and/or transgenesis. We believe that this study has the potential to significantly improve the pig production efficiency.