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11. Genetics

University of Central Oklahoma

Abstracts from the 2014 Oklahoma Research Day

Held at the University of Central Oklahoma

05. Mathematics and Science

11. Genetics

05.11.01 Construction of Peanut Premature Stage Whole Plant cDNA library

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Langston University

Peanut is a legume of economic importance and has been improved in past decades. However, the genomic mechanism behind peanut breeding is still unknown because of the lack of peanut genomic information. The objective of this study is to construct a peanut premature stage whole plant cDNA library, which will lay the foundation for premature peanut expressed gene discovery. Peanut premature tissues were collected by quick frozen in liquid nitrogen. The tissues were then processed for total RNA isolation and mRNA purification. A standard cDNA library was constructed. The result showed that pre-amplified peanut premature plant cDNA library contained 106 colony forming units with the average insert size about 1 Kb. The quality control test showed that the restriction analyzed library displayed significant smear bands across the electrophoresis image regions. The library was amplified at 37°C over night and the plasmid DNAs were then purified for future sequencing procedures. The constructed cDNA library can be used for following high-throughput DNA sequencing to study the gene expression profile in this peanut premature growing stage. Through the bioinformatics comparative study of peanut premature gene expression profile to other mature peanut plant gene expression profile, the major expressed genes that specifically related to this particular growing stage will be identified. It will provide valuable information for peanut genetic breeding and future peanut genomic studies.

05.11.02 Characterization of Developmental Gene Expression in a Dictyostelium Mutant Lacking ERK1 and RegA

Troy, King Jr. , David Schwebs, Jeffrey Hadwiger

Oklahoma State University

In this project, we wanted to observe if a mutant lacking the ERK1 and RegA gene has any changes in developmental gene expression because ERK1 and RegA play a central role in development signaling. Our goal is to compare mutant gene expression with wild-type gene expression at different stages of development. We hypothesize that developmental gene expression might be accelerated since this mutant develops faster than wild-type cells. We used reporter genes containing the lacZ gene to examine the timing and distribution of developmental gene expression. We examined the expression of these genes by staining for the expression of β-galactosidase. The expression of the prestalk specific reporter gene ecmA:lacZ (vector p91) in erk1-regA- cells was detected in the anterior region of developing aggregates and that distribution is similar to that observed for wild-type cells. The level of this gene expression was enhanced when erk1-regA- cells were developed in chimeric aggregates that contained an excess of wild-type cells suggesting that erk1-regA- cells are deficient in producing an extracellular signal that induces ecmA gene expression.

05.11.03 Genetic Analysis of Tetracycline Resistant Fecal Coliforms Isolated From Refuge Bison and Longhorn Cattle versus Agricultural Cattle

Joseph, Kheir , Dennis Frisby, Tahzeeba Frisby

Cameron University

Antibiotics are commonly used for a variety of therapeutic and non-therapeutic purposes. Although numerous studies have been conducted to address concerns about the spread of antibiotic resistance among bacteria associated with agriculture animals and human populations, little to no data is available regarding the spread of antibiotic resistance in bacteria associated with wild animal populations with presumably little selective pressure. The present study focuses on the prevalence of tetracycline resistant bacteria isolated from wild populations of American bison and Texas Longhorn cattle in the Wichita Mountains Wildlife Refuge in comparison to agricultural cattle. Samples were collected as swabs from freshly voided feces from each of the test animals and isolates were isolated on MacConkey or Eosin Methylene Blue agar as Gram-negative, lactose-fermenters. Each isolate was then tested for resistance to the tetracycline on LB supplemented with the antibiotic. Standard PCR was used to test each isolate for tetracycline resistant markers. The markers tested are tetA, tetB and tetM, while using 16S rRNA primer as a control. TetB was most abundant. The appearance of similar genetic markers within animals of differing environments with differing selective pressures suggests that it is possible that other factors, such as environmental contamination and vector transmitted mechanisms, play a role in the presence of similar ABR fecal coliforms across tested animals.

05.11.04 Dietary Restriction Suppresses Tumor Formation in a Drosophila Model of Cancer

Joseph, Ahlander , Carla Horton, Harsh Patel, Jacob Yerton

Northeastern State University

Cancer is the second leading cause of death, second only to heart disease. Diet and nutrition is thought to play an important role in cancer risk. The purpose of our experiment was to observe the effects of diet on tumor development in a Drosophila model of cancer. Caloric restriction dramatically reduced the cancer rate from 95% in the high calorie diet to 22% in the low calorie diet. In a second experiment, we altered protein to carbohydrate ratios while maintaining a constant caloric content. We discovered that a high protein, low carbohydrate diet produced a 100% cancer rate, while a low protein diet reduced cancer incidence to 50%. These results suggest that amino acid restriction, rather than simple caloric restriction, has the ability to reduce cancer formation in Drosophila. This model system can be used to discover the biological mechanisms behind the effects of diet on cancer progression.