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11. Genetics

Northeastern State University

Abstracts from the 2015 Oklahoma Research Day

Held at Northeastern State University

05. Mathematics and Science

11. Genetics

05.11.01 Functional Analysis of Major Depressive Disorder Related Human Genes

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Major depressive disorder (MDD) is a mental disorder that affects about 10% of the population worldwide. The disease has been the leading cause of disability in recent decade, and is potentially fatal to some patients who may commit of suicide eventually. Previous studies have confirmed that MDD is a multi-gene involved disease, which shows the wide variants in both clinical manifestations and genetic variations. This retrospective study is to explore the types, genome locations, and functions of current reported MDD related human genes to investigate the potential mechanisms of MDD's multi-system phenomenon. The study found total 147 expressed genes that related to MDD, which include the genes involved in cellular structure formation and function, cellular enzymatic activities, and signal transduction pathways. Among them, multiple organs/tissues are also involved, which include genes expressed in liver, kidney, skeletal muscle, brain, eyes, and endocrine system. The finding of this study suggested that MDD patients might have multiple gene expression level changes, and therefore, might have the functional changes of multiple organs/tissues and systems. That may explain why most MDD patients always complain for multiple systemic symptoms, but do not demonstrate any structural abnormality in clinical examinations.

05.11.02 The Study of Blood-based Potential Molecular Markers for Major Depressive Disorder Diagnosis

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Major depressive disorder (MDD) is a mental disorder and affects multiple functions of the body. Previous studies showed that human peripheral blood cells shared more than 80% of the transcriptome with nine different tissues including brain, which indicated that circulating blood could reflect the states of health or disease within the brain. Currently, MDD diagnosis is based on clinical survey. There is no effective laboratory means to provide objective diagnosis for MDD. This retrospective study is based on previous reported, MDD-related gene profile to investigate the genes expressed in peripheral blood to explore the potentials of those genes as molecular markers. The results showed that there were 14 out of total 147 MDD related genes demonstrated statistical significance in their peripheral blood expression level difference between normal and MDD groups. Among them, 10 genes showed significant reduction of their expression levels in MDD patients' peripheral blood comparing to that in normal person while 4 genes showed remarkable increased expression levels. The results of this study will facilitate the development of potential peripheral blood MDD molecular markers, which will benefit the accurate diagnosis of MDD.

05.11.03 Sequencing of Plasmids Carrying Genes for Ofloxacin Resistance

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Antibiotic resistance in bacteria presents great challenges in the healthcare field. Infections that were once treatable have become bigger threats to the public health due to the presence of resistance genes in bacteria. The environmental sources of resistance genes and the mechanisms behind their spread are therefore important. We are interested in resistance to the antibiotic ofloxacin. Ofloxacin enters bacterial cells and inhibits the enzyme DNA gyrase. DNA gyrase prevents superhelical strain on the DNA during replication by acting as a swivel point. When DNA gyrase is inhibited the cell cannot replicate or repair its DNA and dies. Several resistance mechanisms are known, including efflux pumps that expel the antibiotic and mutations in DNA gyrase that render it insensitive. We are interested in resistance due to a plasmid-carried gene, qnrS. This gene encodes a protein that prevents ofloxacin from binding to DNA gyrase. Ofloxacin-resistant aeromonads were collected from sediments downstream of a wastewater treatment plant. Strains containing plasmids bearing qnrS genes were identified. We are sequencing plasmids from two of these strains using primer walking. The sequences obtained will be compared with qnrS-bearing plasmid sequences from other ofloxacin-resistant isolates from different dates and locations. This comparison should allow us to assess the number of different qnrS-bearing plasmids present and whether qnrS resistance genes are being transmitted between bact

05.11.04 Silencing of autophagy genes in Drosophila shows that the Ard1 gene plays a role in cell death.

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Our world is facing a cancer epidemic that is a threat to all societies and us personally. Ard1 is a protein encoded by a gene that is conserved in Eukaryotes and is directly linked to cancer progression and other human diseases. The Ard1 protein could be instrumental in regulating autophagy, a cellular pathway that deals with degradation and disposal of obsolete and unusable cellular constituents. Model organisms, such as Drosophila melanogaster can be used to study cancer and autophagy. Through genetic analysis, we switched off the Ard1 gene during eye development and eye surface areas were considerably smaller than the control flies. We hypothesized that the reduced eye size is because the cells were indeed dying. One way that cells can die is through the pathway of autophagy. To test whether Ard1 silencing causes autophagic cell death, we silenced autophagy genes Atg1 and Atg101 by RNAi. We found that by silencing these Atg genes, the phenotypes measured were actually larger, indicating a decrease in cell death and autophagy. These results support the idea that reduction in number of cells is due to overactive autophagy. Understanding the effects of the Ard1 gene could possibly lead to future treatments for the cancer epidemic in humans.