CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Shilpa P. Argade

Project Number

S0402

Project Title

Genetics and Biochemistry of Sialylation in Vibrionaceae

Abstract

Objectives/Goals

Sialic acids (Sias) are a family of nine-carbon sugars that play diverse biological roles, including the host-pathogen interaction. Specifically, many bacteria decorate themselves with Sias, a phenomenon related to virulence in several human pathogens. Bacterial #hijacking# of host Sia-binding proteins via #molecular mimicry# may be responsible for the virulence of Sia-decorated pathogens. Vibrionaceae is a family of bacteria that have been shown to possess the gene cluster responsible for Sia biosynthesis. This experiment set out to determine whether Vibrio species express high levels of Sias, explore the complexity of Sias among positive strains, and evaluate the genetic basis for Sia-decoration in Vibrionaceae.

Methods/Materials

The Thiobarbituric-acid (TBA) assay was used to screen through 56 strains of Vibrionaceae representing 14 different species for their total Sia contents. Sia values were normalized to protein content by the Bicinchoninic-acid (BCA) assay. Strains with high levels of Sias were further analyzed by a sensitive DMB-HPLC method with fluorescence detection. To determine the presence of O-acetylation, samples were profiled with and without mild base treatment. A transposon mutant whose transposon landed upstream the hypothesized Sia biosynthetic gene cluster was obtained. DMB-HPLC and LC-MS analysis was used to compare the mutant and WT for Sia expression.

Results

Among all strains of Vibrionaceae, Vibrio Parahaemolyticus 190-2004 had the highest amount of Sia (24.84 pmol Sia/ug protein). The DMB-HPLC profiles showed several peaks, suggesting the presence of Sia derivatives, such as Legionaminic and Pesudaminic (Pse) acid and O-acetylated species. In the WT vs. mutant experiment, the LC-MS analysis of DMB derivatives showed the presence of Pse in the WT, but not in the mutant.

Conclusions/Discussion

This study shows that ten strains of Vibrionaceae had high levels of Sias. DMB-HPLC analysis confirmed the presence of several related species of Sias along with O-acetylation. The mutant showed no Sias by DMB-HPLC and was confirmed by LC-MS analysis, thus supporting the genetic basis of Sia biosynthesis. These experiments document the discovery and genetic basis for Sia-decoration in Vibrionaceae. They begin the process of establishing a biological model that may help us understand the mechanisms of Sia molecular mimicry in host-pathogen interactions.

Summary Statement

This project proves Sia expression in Vibrionaceae, confirms the genetic basis of Sia biosynthesis, and shows the possible role of Sia in host-pathogen interactions.

Help Received

Used lab equipment at UCSD under supervision of Dr. Amanda Lewis and Dr. Victor Nizet.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Steven Chau; Steve Chung

Project Number

S0403

Project Title

Comparative Analysis of Mouse Liver Proteome by One Dimensional and Two Dimensional Gel Electrophoresis

Abstract

Objectives/Goals

To use 1 Dimensional SDS-PAGE along with 2 Dimensional SDS-PAGE to separate proteins in order to see which of the two methods yields a higher resolution of protein.

Methods/Materials

1 Dimensional SDS-PAGE refers to a technique used to count different types of proteins within a sample. Sodium Dodecyl Sulphate, a part of the running buffer, to denature proteins. These denatured, linear molecules are able to pass through the pores in the polyacrylamide gel, but will become trapped according to their molecular masses. After running buffer is added to the polyacrylamide gel, the protein samples are loaded into the gel electrophoresis chamber using a microcapillary pipet. Opposite electrical charges either end of an electrophoresis chamber pull the proteins through the gel at rates dependent on molecular mass.

In 2 Dimensional SDS-PAGE, the same protein mixtures used for the 1 Dimensional SDS-PAGE, mouse liver protein obtained from five weeks old animals, were used. The samples were applied on a specialized strip called an immobilized pH gradient strip and then separated based on their isoelectric points using high voltage. The proteins, located at different parts of on the strip depending on their isoelectric points, were then subjected to second dimensional analysis of the molecular mass using SDS-PAGE. With both Dimensions, the separated proteins were then analyzed using an image analysis system.

Results

When comparing 1D and 2D gel electrophoresis, we found that 2D gel electrophoresis has higher resolving power for different proteins present in a crude mixture. Compared to an average number of 16.5 protein bands obtained by 1D gel electrophoresis, we obtained 367.33 protein spots on an average for the same sample when separated in two dimensions. This is a difference of over 350 proteins, meaning that adding the second dimension increased the number of proteins detected by over 2100%.

Conclusions/Discussion

SDS-PAGE with two dimensions does indeed allow for the detection of more proteins of a given proteome. Two dimensional gel electrophoresis, where proteins are initially separated by isoelectric focusing followed by their separation based on molecular mass, provides a much better resolution. Because the separation was based on two different properties of the protein molecules, 2D SDS-PAGE give a better resolution of individual protein molecules present in the mixture, an over twenty-fold increase.

Summary Statement

This project aims to compare the resolutions of two types of protein resolving techniques in order to determine the more useful method.

Help Received

Used lab equipment at Keck Graduate Institute laboratory under the supervision of Professor Bulbul Chakravarti and Professor Deb Chakravarti.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Eric Eulau; Jonathan Waxer

Project Number

S0404

Project Title

Mercury Levels in Fish

Abstract

Objectives/Goals

The objective is to determine if the amount of mercury within a fish can be altered by various cooking techniques: poaching or barbecuing.

Methods/Materials

Tuna, Mahi-Mahi, Shark, Tuna Albacore Blender, Plastic Bags, Aqua Regia (HNO3 & HCL), water, Leeman Labs PS200 Automated Mercury Analyzer, Leeman Labs PS200 Data System, Okidata Microline 320 Printer, 200-mL graduated plastic cups (P-cups), Centrifuge tubes, Permanent Drying Tube, 60mL VOA Vials, Skillet, Barbeque

The fish were obtained from separate grocery stores including Vons and Albertsons.

Results

Raw Shark and barbecued shark contained .8 mg/kg of mercury. Poached shark contained .73 mg/kg of mercury. Raw mahi mahi contained .17 mg/kg, barbecued contained .15 mg/kg, and poached contained .13 mg/kg. Raw tuna contained .35 mg/kg, barbecued contained .24 mg/kg, and poached contained .16 mg/kg. Raw tuna albacore contained .90 mg/kg, barbecued contained .79 mg/kg, and poached contained .71 mg/kg.

Tuna albacore had the most overall mg/kg of mercury when it was raw and grilled, while shark had the most overall when it was poached. FGL Lab supplied us with a method to discover the mercury levels within our various samples of fish.

Conclusions/Discussion

As stated in our research, fish which are higher on the food chain have a higher level of mercury within them because they are feeding on other fish. Overtime, the mercury levels increase with the older the fish becomes. Unfortunately, our hypothesis was incorrect because barbecuing was not the most effective cooking technique, it was poaching. Although, with the results our objective was still obtained. The results were interesting to see because one would think shark would have the most mercury within them since all they do is feed on other fish, but in reality tuna albacore exceeded our sample of shark. This is interesting because our research mentioned that oceans bordering high polluting cities have a higher mercury amount than compared to the other oceans around the world. Tuna albacore quite possibly could have had the highest mercury amount because of this fact.

Summary Statement

We are trying to discover whether or not mercury can be reduced in fish by various cooking techniques.

Help Received

David Terz, the representative of FGL Lab, took our samples of fish and put the samples through the various tests to conclude the total amounts of mercury .

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)
Nelli Ghazaryan

Project Number
S0405

Project Title
BRCA1 Methylation in Sporadic Breast Cancer

Abstract

Objectives/Goals
To determine the stage in cancer in which there is a loss of BRCA1 expression, what the loss of this expression is due to. And what the effects of this loss are on the developement of sporadic breast cancer.

Methods/Materials
Throough Immuno Histo Chemistry, Hemotoxin & Eosin staining, Laser Capture Microdissection we will examine our collected multicutural cohort of patients, anaysizing tumor, lymph node and normal breast tissue for each. Using a nested PCR approach we will distinguish whether the patients have a loss of the BRCA1 protein or not.

Results
Distinctions between the patients who had a higher tumor grade percentage and the BRCA1 loss of expression were seen, as well as the effects of the BRCA1 methylation on the growth of tumors.

Conclusions/Discussion
INCONCLUSIVE DATE

At this point many of the procedures and protocols are being optimized for study and patient samples are being garnered.

Summary Statement
This project is about looking at BRCA1 loss abd nethylation and their correlation with the developement of sporadic breast cancer.

Help Received
Research was done at USC Norris in the labaratory of Dr. Michael Press, under the mentorship of Dr. Melinda Epstein

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Aryeh B. Hillman

Project Number

S0407

Project Title

Activity Based Proteomic Profiling of Lysophosphatidic Acid Treated Cancer Cells

Abstract

Conclusions/Discussion

Ovarian cancer is a debilitating disease lacking effective treatments. A key feature of the disease is elevated levels of the mitogenic lipid lysophosphatidic acid (LPA) found in the ascities fluid surrounding tumors. LPA evokes a wide array of pro-tumorgenic effects in cells and was recently shown to stimulate the expression of a cancer-associated protease, urokinase type plasminogen activator (uPA). To discern whether LPA treatment resulted in active uPA, I applied a novel proteomic technique, activity-based protein profiling (ABPP), that specifically monitors the amount of protein activity rather than abundance. I utilized ABPP to examine the effect of the bioactive lipid LPA on uPA in a human ovarian cancer cell line SKOV-3. To achieve this I first developed a new strategy for analysis of secreted proteins and then determined that treatment of SKOV-3 cells with LPA does indeed result in increases of active uPA. In addition to this finding, I also detected elevated uPA activity upon treatment of structurally distinct forms of LPA that vary in acyl chain length. This finding has not previously been reported and demonstrates the power of ABPP to identify changes in the functional state of low abundance enzyme activities.

Summary Statement

I sought to characterize the effects of certain lipids on the expression and activity of enzymes implicated in cancer metastasis.

Help Received

Used laboratory equipment at The Scripps Research Institute in La Jolla, California under the supervision of Dr. Benjamin Cravatt

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)
Katie A. Hintz

Project Number
S0408

Project Title
One with Blood

Abstract

Objectives/Goals
For my science fair project I want to test the affect of which foods raise your blood sugar the fastest. I found this interesting because my dad was recently diagnosed as a diabetic so he has to watch what he eats much more carefully. This could help people understand which foods to eat if they have some type of diabetes. I plan to have my dad fast for ten hours so that all the other foods are out of his system and test him to see what his blood sugar is. Then give him one serving of a type of food. Then after an hour or so check his blood pressure and calculate the change in levels. I plan to do this with several different servings of different types of foods.

Methods/Materials
Different types of food, "True Track Smart system" with lancets and TrueTrack test strips, clock, measuring cups, Human- 59 year old male, information sources of foods.

Results
My hypotheses is only some what correct. In most cases, foods with 15-30 grams of sugar and 20-100 carbohydrates raised blood sugar levels from 3 to 150. However in some cases, such as Pear which has 18 grams of sugar and 26 carbohdrates, the blood sugar decreased instead of rising. Also some foods with low sugar raised the blood sugar a lot proving my hypothesis wrong. An example of this is the test on Hotpockets. With low sugars and carbohydrates the blood sugar level was raised between 35 and 45.I found that the affect of the carbohydrates and calories affect the blood sugar sometimes more than the amount of sugars.

Summary Statement
I tested foods to see which ones cause a person's blood sugar to rise within an hour and then another hour.

Help Received
My Dad volunteered to be the test subject.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Sravya R. Keremane

Project Number

S0409

Project Title

Biochemical Analysis of Mechanisms of Cold Tolerance in Citrus: Effects of Abscisic Acid

Abstract

Objectives/Goals

To study the effect of abscisic acid root drench on levels of expression of different cold tolerance genes. If transcription increases with addition of abscisic acid then it may be possible to use abscisic acid root drench during periods of freeze to prevent the death and loss of citrus plants. Freeze damages are common to citrus industries in California and Florida. California citrus industry lost about a billion dollars in the winter of 2007 because of freeze damages.

Methods/Materials

Twenty Mexican lime and sour orange plants were treated with root drench of abscisic acid and placed in both 4^0 C and 24^0 C. Leaf samples were taken after 2 hours and 48 hours from both the treated and control plants. Total RNA was extracted using Qiagen RNeasy kit and cDNA was made using oligo dT primer and superscript II reverse transcriptase from Invitrogen. Quantitative real-time Polymerase Chain Reaction (qPCR) was done using SYBR greenER qPCR mix from Invitrogen. Expression of four genes were analyzed in separate PCRs using specific primers for detecting transcripts of abscisic acid binding factor 3 (ABF3), Inducer of CBF expression (ICE I), citrus low temperature a (CLTa), and a house keeping gene, aspartate trans-carbamylase (ATC) as an internal control. The results were analyzed using 2 hour and 48 hour samples from each plant. A standard curve was constructed using serial dilutions from a cloned plasmid of ABF3 transcript (Mexican lime).

A fragment of ABF3 gene was amplified by PCR from both DNA and cDNA of Mexican lime and sour orange using specific primers. These products were cloned and sequenced. An alignment of DNA and cDNA was made using ChromasPro, Clustal and Gendoc programs.

Results

Abscisic acid treatment increased the levels of expression of three different cold tolerance genes, ABF3, ICE1 and CLTa, in both greenhouse and cold conditions. Comparison of sequences of ABF3 in DNA and transcripts revealed the presence of an intron in cold susceptible Mexican lime, but not in cold tolerant sour orange.

Conclusions/Discussion

Abscisic acid root drenching resulted in increased levels of expression of all three cold tolerance genes in both Mexican lime and sour orange. These results suggest the usefulness of abscisic acid in enhancing cold tolerance in citrus. Further confirmation of these results is required, but even a modest increase in cold tolerance would substantially reduce the loss due to cold damage.

Summary Statement

Analyzing the effect of Abscisic Acid root drench on levels of expression of selected genes in citrus with the objective of understanding mechanisms of cold tolerance.

Help Received

Used lab facilities at the USDA Citrus and Date Germplasm Repository under supervision of Dr. Richard Lee.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Thomas G. Kwong

Project Number

S0410

Project Title

The Prevalence of Genetically Modified Organisms (GMO) in Everyday Plant Products

Abstract

Objectives/Goals

The purpose of this experiment is to test a handful of produce from a local grocery store to see how commonly prevalent genetically modified foods are. I predict that the majority of plant products not labeled GMO-free will not show signs of genetically modified DNA. This type of experiment has value because the science of genetically modified foods is still in its infancy and thus all the factors have not fully been researched. This experiment is illustrating a similar situation, but due to lack of resources demonstrates only a handful of plant products.

Methods/Materials

To do this, deoxyribonucleic acid (DNA) is extracted from each food sample tested in my experiment. The most frequently used DNA promoter and terminator in GMO insertions are then amplified in a polymerase chain reaction (PCR) and displayed using electrophoreses.

Results

After conducting the experiment the results showed a complete and total lack of genetically modified DNA in all of my samples.

Conclusions/Discussion

I predicted that approximately half of my samples would show GMO presence, but unfortunately this was not true at all. After performing electrophoreses, none of my samples showed GMO positive bands. Also, all my samples showed the presence of plant DNA and both my positive and negative control showed their respective positive and negative GMO bands, indicating to me that my technical process functioned correctly and thus that my results were trustworthy. Thus, my hypothesis was proven incorrect.
Despite the successful execution of my experiment and the clear results, I am inclined to doubt the accuracy of my results because approximately 60% of all plants grown today have at least some trace of genetically modified DNA material. My results would mean that all five samples fell under the 40% of non-GMO plants; furthermore, I tested four soy products, and approximately 81% of the current global soybean crop is genetically modified, decreasing the likelihood that all my soy samples would be GMO-negative.

Summary Statement

My project is about testing for the presence for genetically modified DNA in plant products.

Help Received

Mother helped borrow lab equipment.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)
Jeffrey K. Lio

Project Number
S0411

Project Title
The Effect of Alpha3 Integrin on Neuroblastoma Cell Survival

Abstract

Objectives/Goals
The objective is to determine whether the A isoform of the alpha3 integrin (alpha3 A) has an effect on short-term survival of neuroblastoma.

Methods/Materials
Alpha3 A was shuttled from the bacterial expression vector bluescript to the mammalian expression vector pcDNA3.1 (alpha3 A pcDNA3.1). NB5 was transfected with alpha3 A pcDNA3.1 and immunostained with anti-alpha3 antibody. NB& ov23 was transfected with alpha3 A pcNA3.1 and GFP (NB7 alpha3 A). Using a fluorescent microscope, the number of surviving NB7 alpha3 A in each window were recorded and images were taken daily.

Results
The NB5 alpha3 A pcDNA3.1 fluoresced after they were immunostained, whereas the immunostained NB5 transfected with empty vector pcDNA3.1 did not, indicating that neuroblastoma transfected with alpha3 A pcDNA3.1 did not express alpha3 integrin. NB7 ov23 cells transfected with alpha3 A pcDNA3.1 showed a decreased survival compared to that of NB7 ov23 transfected with empty vector pcDNA3.1 and the entire plate died after about one week.

Conclusions/Discussion
NB7 alpha3 A pcDNA3.1, which was confirmed to express alpha3 integrin, showed decreased survival compared to that of NB7 ov23 transfected with empty vector pcDNA3.1. Thus, the reinsertion of alpha3 A integrin into NB7 ov23, which is a cell line of NB7 that had lost its expression of alpha3 integrin, has a negative impact on the short-term survival. This suggests that the reinsertion of alpha3 integrin may inhibit tumorgenesis and metastasis in neuroblastoma.

Summary Statement
Reinsertion of alpha3 integrin isoform A into neuroblastoma cells had a negative impact on short-term cell survival.

Help Received
Lab equipment and materials at the UCSD Moores Cancer Center were provided by Dr. Dwayne Stupack, Associate Professor of Pathology. I worked in the lab under the supervision of Dr. Stupack and Dave Mikolon, the lab manager.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Monica S. Liu

Project Number

S0412

Project Title

Selective Amplification of Rare Mutations in Tumor Cells Enriched from Whole Human Blood

Abstract

Objectives/Goals

While the detection of mutated genomic DNA from cancer cells circulating in blood may be an early indicator of metastasis and may improve tumor staging, the task of detecting a few mutated cells in the presence of a large excess of wild-type cells requires a sensitive and selective assay. This study aimed to develop a novel polymerase chain reaction (PCR)-based approach to detect circulating melanoma cells harboring a common point mutation in BRAF, a cytoplasmic kinase in the MAPK (mitogen-activated-protein-kinase) signal transduction pathway.

Methods/Materials

A novel two-step PCR assay was developed to detect BRAF mutations in both cell mixtures and in blood samples spiked with tumor cells. In the first step, primer binding to wild-type BRAF was competitively blocked by a locked nucleic acid (LNA) oligonucleotide. In the second step, the LNA blocking approach was combined with a allele-specific primer that selectively amplified mutant DNA. The assay's sensitivity was tested on cell lines both homozygous and heterozygous for the mutation; both point and tandem mutations were also tested. To determine the clinical utility of this method, human blood was spiked with a defined number of melanoma cells (10 to 10,000 cells/mL blood). After negative epithelial cell enrichment and whole genome amplification were performed, genomic DNA from the enriched tumor cells was amplified by the aforementioned two-step PCR assay.

Results

This novel two-step approach easily detected ten BRAF-mutated melanoma cells mixed with 100,000 wild-type cells. In addition, this approach could readily identify mutant DNA from as few as ten melanoma cells circulating in one mL of human blood. DNA amplification was dose-dependent and highly reproducible.

Conclusions/Discussion

Since this approach facilitates sensitive detection of BRAF-mutated genomic DNA in circulating tumor cells, this assay may predict metastasis early, improve tumor staging, and identify candidate patients for therapeutic agents specifically targeting the MAPK pathway. By utilizing genomic DNA as a direct, inherently stable detection marker, this assay may be a viable alternative to reverse-transcription PCR (RT-PCR) techniques whose clinical applicability is limited by false positives from illegitimate mRNA transcription. Lastly, this highly selective and sensitive approach may be applicable to common point mutations implicated in other cancers.

Summary Statement

This study describes a novel real-time PCR-based assay that can predict metastasis and improve tumor staging by detecting as few as 10 melanoma cells circulating in one mL of human blood.

Help Received

Used lab equipment at Harbor-UCLA Medical Center under the supervision and mentorship of Dr. Michael Kolodney.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

R. Andrew Martens

Project Number

S0413

Project Title

The Effect of Proteases on Various Common Foods

Abstract

Objectives/Goals

The goal of this experiment was to determine what common foods contain a substantial amount of protein. I hypothesized that tofu would be the most protein-rich food because previous research showed that the ratio of protein compared to fat is very high in soybeans, the main ingredient in tofu.

Methods/Materials

The amount of protein contained in the food samples was determined by digesting the sample in bromelain, and comparing the food's mass before and after digestion. Materials included Bromelain, 21 test tubes, a balance, a Buchner Funnel, food samples, and a rocking table machine.

Results

For the first two carrot samples, none of the samples were digested and the third sample of carrot became waterlogged, gaining 0.5g. For the egg, one sample gained 0.3g and other two samples dropped 0.2g each. Spaghetti had gains of 1.5g, 1g, and 1.2g. Chicken lost 0.1g, 0.5g, and 0.4g in each trial. Lean beef saw similar results, losing .04g, 0.6g, and 0.1g. Beef fat displayed no digestion in the first two samples, but lost 0.1g in the third trial. Tofu was overall the most effectively digested, with 0.6g, 0.8g, and 0.6g drops.

Conclusions/Discussion

The tested hypothesis was correct in predicting that carrots, fat, and spaghetti would not be digested by the proteases, while chicken, lean beef, egg, and tofu would display significant digestion. The only surprise in the data came from egg, which must contain proteins indigestible by bromelain. These results have useful application in the modern world. Protease digestion can determine the protein content in most common foods. With protein being important to athletes, it is useful to know which cuts of meat have more protein for their amount of fat. As seen in the experiment, lean beef and chicken both contain a good amount of protein, while beef fat does not. Most importantly, although it comes from plants, tofu has by far the highest amount of protein. People wishing to fortify their diets with protein will probably find tofu to be the best source. In the future there could be several ways to elaborate on the concepts tested in this experiment. Instead of having food be the manipulated variable, different proteases could be tested to determine their effectiveness in digestion. Temperature, pH, and other factors may also have effects on digestion that could easily be tested with the resources available in a lab.

Summary Statement

This project is about the protein content of various common foods.

Help Received

My Father, Dr. Craig Martens, helped me contact his colleague, Dr. Patrick Farmer, who lent me his lab and equipment for the experiment.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

William C. Martin

Project Number

S0414

Project Title

The Effects of the 4EBP P-Element in Drosophila melanogaster

Abstract

Objectives/Goals

The objective of my project is to examine the effects of the 4EBP P-Element in Drosophila melanogaster. I believe that the P-Element will increase lifespan when expressed and have an affect on the fly's metabolic rate.

Methods/Materials

I set up two parts to my project, a starvation resistance lifespan, and a series of metabolic readings on flies under dietary restriction. The lifespan involved starving the flies on a diet containing no nutrition, which made stressful living conditions for the flies hoping to induce 4EBP. My metabolic assays involved testing flies with and without the P-Element, and examining their change in protein and triglyceride levels under high and low protein diets by using a microplate reader.

Results

In the starvation resistance lifespan, I discovered that flies with the P-Element lived longer than flies without it, and that the flies with the P-Element lived longer on low protein. Also, the females lived longer with the 4EBP than males. In my metabolic assays, I discovered that flies with the P-Element had lower levels of protein on both diets, which meant that the P-Element inhibited translation. Also, flies under high yeast diets had lower triglyceride levels than flies under a low yeast diet.

Conclusions/Discussion

In conclusion, my hypothesis was correct. 4EBP proved to be induced in times of stress and it did increase the lifespans of the flies throughout the experimental process. A very interesting thing that came up was that females were more affected, which could have to do with the inhibition of fertility. Last, I can conclude that the flies with the P-Element had lower protein levels than flies without the P-Element under both a low yeast and high yeast, which means that 4EBP does indeed inhibit translation.

Summary Statement

My project is about discovering a method for increasing human lifespan by experimenting with Drosophila melanogaster and the effects the 4EBP P-Element has on it.

Help Received

Used lab equipment at the California Institute of Technology under the supervision of graduate student Brian Zid.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Alejandra Mendiola

Project Number

S0415

Project Title

Evaluation of Background Mitochondrial DNA Levels in the Household

Abstract

Objectives/Goals

It is not known whether mtDNA background levels are so high as to create complex mixtures with the criminal's mtDNA and prevent his/her identification. The purpose of this study was to evaluate the levels of background mtDNA on common household objects.

Methods/Materials

For my project I examined ten objects from the household and swabbed them at different time periods such as before cleaning, 1 day, 1 week, and then after 2 weeks without cleaning. Ten surfaces were the bedroom light switch, bathroom left faucet, bathroom right faucet, bedroom drawer, Inside Door Knob of Bedroom, Bedroom Window,Telephone in Living Room, Bedroom Outside Door Knob, Bedroom Closet Knob, Computer Keyboard in Bedroom, Negative control (tweezers), including the paternal and maternal mouth swabs. After collecting the samples the mtDNA was isolated by removing all of the cotton swab and subjecting it to a Chelex extraction. After extraction we used the thermal cycler to amplify the mtDNA. The amplified product was then analyzed by agarose gel electrophoresis stained with ethidium bromide so that we can compare it to the DNA Quantladder; 100-1000base pairs. The last step is to hybridize the product thus determining an individuals mtDNA type.

Results

In this study : 40% of pre-cleaning samples contained mtDNA;
50% of the 1 day samples contained mtDNA;
60% for the 1 week samples contained mtDNA;
and the 2 week samples were inconclusive as to containing mtDNA (Chelex may have poor). Also, 50% of all of the samples collected contained mtDNA. Sample 7b (one day telephone) contained mtDNA, but gave no typing results. Otherwise, all mtDNA containing samples (16 total) produced typing results. 13 of the 16 typed samples were mixtures. Of the mixtures, 11 were consistent with a mixture of the paternal and maternal references.

Conclusions/Discussion

The Hypotheses of my study are:
1) The amount of mtDNA on an object will be directly proportioinal to the amount of handling of the object.
2) Without cleaning the surface for a longer amount of time the more mtDNA will be collected.
3) Objects that are used by everyone will have mixtures of mtDNA.

Summary Statement

Evaluating the levels of background Mitochondrial DNA on common household objects.

Help Received

Used lab equipment at CSULA under the supervision of Dr.Roberts and Professor Johnson

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Megan K. Morikawa

Project Number

S0416

Project Title

Alternative Means of DNA Preservation: Dry Storage on Qualitative Filter Paper

Abstract

Objectives/Goals

The purpose of this project was to explore and optimize a dry preservation technique for the storage of DNA. It was designed to correspond with the forensic analysis and to develop an easy and affordable way to send DNA samples via mail or store in the lab without electricity. It was hypothesized that DNA preservation on qualitative filter paper disks at room temperature would yield positive PCR results for the Cytochrome Oxidase Subunit I Gene(COI).

Methods/Materials

Experiment 1:Utilizing qualitative filter paper to store purified genomic chimp (Pan troglodytes) DNA and directly amplify with Polymerase Chain Reaction (PCR).
Experiments 2 and 3:Extracting genomic DNA from mouse(Peromyscus leucopus) tissue through Protease and PBS cell lysis procedures. Experiment 4: Testing for positive recovery of DNA stored on sterilized qualitative filter paper medium (removing the PCR process).
Experiment 5:Testing for positive PCR with disks by using various methods of washes for the sterile application of filter paper preservation (troubleshooting PCR process).
Experiment 6:Storing DNA at various concentrations for a week, resuspending samples, then sending through PCR.

Results

Experiment 1 showed that the qualitative filter paper somehow inhibited the PCR process. Tests using blank autoclaved disks added to the normal PCR solution even inhibited the PCR process. Experiment 4 showed that it is possible to store DNA on 2mm disks of qualitative filter paper and then re-suspend DNA for use in electrophoresis or PCR. Experiment 5 showed that DNA concentration of 10ng/ul of Peromyscus leucopus was not sufficient for PCR reaction. PCR was working effectively and amplified the COI gene. Results from experiment 6 show that DNA can successfully be stored for a week, be resuspended, and amplified for PCR. Safe resuspension of two days yielded positive PCR results.

Conclusions/Discussion

My hypothesis is proved partially correct: DNA can be stored on the filter paper. When it came to the PCR process, electrophoresis results showed strong indicators that the physical presence of the qualitative filter paper inhibited the process of PCR. Three conclusions are met: DNA can be successfully stored on the qualitative filter paper medium, stored DNA must undergo a re-suspension in order to be useful, and if DNA will yield positive PCR results when aqueous, it will yield positive results when stored on filter paper.

Summary Statement

This project was designed to explore and optimize a dry preservation technique for the storage of DNA.

Help Received

Mother helped construct board; Supervisor Dr. Vavra (biology teacher) gave general guidence on experiment design; Dr. Oliver Ryder of C.R.E.S. provided some materials and offered technical guidance

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Vasilios A. Morikis

Project Number

S0417

Project Title

Dancing Helices in Vacuum: A Computational Study of Peptide Molecular Dynamics

Abstract

Objectives/Goals

Biomolecules are not rigid; they fluctuate and participate in a variety of motions. A common protein or peptide secondary structure is an alpha-helix. Certain amino acids, like alanines, have propensities for alpha-helical structures. The objective of this study is to answer whether or not the length of a poly-alanine peptide affects its structural stability.

Methods/Materials

I have used computational tools to construct the following 5 polyalanine peptides of variable lengths. All peptides are perfect alpha-helices, because I fixed their backbone torsion angles to their theoretical values. All backbone hydrogen bonds are in place. The peptides are A5, A8, A11, A15, and A18, with 5, 8, 11, 15, and 18 alanines, comprising of 1-5 alpha-helical turns. I have performed molecular dynamics (MD) simulations in vacuum at 273K to study the unfolding of these peptides. The MD simulation for each peptide was 100 ps long. For the longest peptide, A18, an additional 1 ns simulation was performed. The software I used is DEEP VIEW for peptide design, VMD with NAMD interface for molecular dynamics, MOLMOL for analysis of MD trajectories.

Results

Structural analysis consists of calculations of hydrogen bonds and Ramachandran plots, using snapshots from the MD trajectories. The peptides A5, A8, and A11 unfold within 10 ps. A15 unfolds after 20 ps and A18 partially unfolds during 100 ps. The longer peptides unfold slower. The termini of the peptides unfold first. A18 shows that the unfolding is progressive from the end to the middle. During the 1 ns MD trajectory of A18, the alpha-helix unfolds and partially refolds.

Conclusions/Discussion

The longer peptides unfold slower, because they have larger number of hydrogen bonds. A18 has the largest number of hydrogen bonds and therefore unfolds slowest. The termini of the peptides unfold first, because the 4 first and 4 last amino acids have capability for only 1 backbone hydrogen bond each. The middle amino acids have capabilities for 2 backbone hydrogen bonds each. This is consistent with experimental data that suggest helices are stable in the middle and fraying at the termini. The longest peptide, A18, does not fully lose structure during the 1 ns of the MD trajectory. I have shown that peptides (and by extrapolation proteins in general) are dynamic entities, they fluctuate, their hydrogen bond patterns form and deform, and their structures partially unfold and refold.

Summary Statement

I have used computer simulation to demonstrate that peptides and proteins are dynamic.

Help Received

I am grateful to my mentor Dr. Dimitrios Morikis.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Adriana M. Mujal

Project Number

S0418

Project Title

Role of Lipid Metabolism in C. elegans Innate Immune Response

Abstract

Objectives/Goals

Fats have traditionally been considered rich sources of energy and major components of cell membranes. Recent studies, however, have established roles for fatty acids in the immune response # roles of which our experimentation explored. We hypothesized that firstly, the C. elegans immune response involved specific modulation of lipid metabolism, and that secondly, this alteration of gene expression was important for an effective immune response.

Methods/Materials

Wild-type C. elegans were infected with pathogenic Pseudomonas aeruginosa, and quantitative RT PCR analysis was used to determine shifts in the expression of lipid metabolic genes.

RNA interference treatments were then used to knock down the expression of candidate genes identified in the above RT analysis. Treated worms were placed in survival assays against the pathogen Pseudomonas aeruginosa and observed for differences in survival rate.

Results

From the RT PCR data, we observed a significant down-regulation of the mitochondrial ß-oxidation and glyoxylate pathways as well as differential regulation of specific lipid binding proteins in response to infection, and an up-regulation of peroxisomal ß-oxidation.

Currently from our screen of survival assays, we have identified seven specific genes that appear to have an effect on the C. elegans immune response, as with reduced expression, the survival rate of the nematode is altered.

Conclusions/Discussion

These changes in gene expression of various fatty acid metabolic pathways lent support to our hypothesis that the infection response provokes a specific modulation of the fat metabolism in the worm.

The data collected from the survival assays suggests that lipid metabolism does indeed possess a fundamental role in C. elegans innate immunity, and due to conservation of these metabolic pathways in plants and animals, might function similarly in mammalian innate immunity.

Summary Statement

This project explores the potential roles of specific fatty acids within innate immunity, employing C. elegans as a model organism to do so.

Help Received

Used lab equipment in the Tan Lab at Stanford University under the supervision of Madhu Nandakumar.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Laura A. Negron

Project Number

S0419

Project Title

How Closely Related Are Humans to Other Species?

Abstract

Objectives/Goals

I analyzed protein sequences from different species in order to trace the similarities and differences between humans and other species. I believed that, after analyzing five different protein sequences, I would conclude that they are very close to identical and that Homo sampiens have more in common with other species than one would expect.

Methods/Materials

After searching "Myoglobin Homo sapiens" in the NCBI/Genbank, there was a list of different myglobin proteins from which to choose. I chose the protein NP_976312 and translated the sequence into the FASTA format. I then inserted the protein sequence into the NCBI/Protein-BLAST program in order to find similar proteins in other species. I chose four proteins from amongst the displayed matrix: EAW60065.1, P32428, PO2193 and 1MYHA. After translation into the FASTA format, I inserted them into CLUSTALW. To these four sequences I added my original FASTA sequence, NP_976312. ClustalW then created a multiple sequence alignment of the sequences, placing then in a column in preparation for analysis. I counted the differences in amino acids by noting changes in letters, which represent different amino acids.

Results

The multiple sequence alignment of the five different proteins reveals results contrary to my expectations. The protein EAW60065, belonging to the human species, is most similar to NP_976312. Protein 1MYHA, from Sus scrofa (wild boar), is the second most similar sequence. It is followed by PO2193 and P32428, in that order. The least similar protein belongs to the Ondatra zibethicus species. However, even the least similar protein sequence had a small percentage of amino acid differences, the sequences being 86% similar.

Conclusions/Discussion

While these results do not prove that humans are closely related to any of the tested species, it does prove that humans have things in common with the most trivial of species. Through this analysis of proteins, I have learned that many amino acids make up a single protein and each is important. My experiment partially proved my hypothesis because the sequences were very similar, but disproved my hypothesis because they were not identical. My project emphasized the purpose of amino acids within protein sequences, and displayed their influence in the resulting protein sequences.

Summary Statement

This project's goal was to see how similar humans are to other species.

Help Received

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Christopher H. Nho

Project Number

S0420

Project Title

Eelgrass: A Study on Botanical Genetics

Abstract

Objectives/Goals

My objective was to test if ribulose 1, 5 bisphosphate (RuBP) would act as a universal gene for eelgrass and its close genetic relatives. Success would be determined by biogeographic and habitat comparison between the species.

Methods/Materials

Use the National Center for Biotechnlogy Information's (NCBI) blast tool to search RuBP sequences for multiple plant species that have a genetic similarity of 90% and higher. Compare these genomes in phylogenetic trees that can be made in "Clustal W". Make sure the sequences contains only the RuBP sequence. Analyze results.

Results

There are mixed showings. Although habitat shows a significant sensible relationship between the species, the geographical location has almost no comprehendible relationship.

Conclusions/Discussion

The mixed results reveal two discoveries. The first is that there is a glimmer of hope for RuBP. The native habitats do show success but it is daunted by the sister graph of biogeography. This is where the second, and most urgent realization was made. There is little research that has gone into genetics and plants. The Human Genome Project continues to thrive and catalogue, whereas only 10% of the world's plants have been barcoded for DNA. If more plants were available to test, more connections could have been made. Unfortunately, "could" remains only a hypothetical word until more work is to be done.

Summary Statement

The RuBP gene gives mixed messages about its reliability as a universal plant gene; however, it highlights the lack of research that has gone into botanical genetics.

Help Received

San Diego Super Computer Biology Workbench for access to Clustal W; National Center for Biotechnology Information for genome database

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Alex L. Nothnagel

Project Number

S0421

Project Title

Chemical Analysis of Glycosyl Composition of Cell Walls from Lower Land Plants

Abstract

Objectives/Goals

What is the glycosyl (sugar) composition of cell walls from lower land plants? Answering this question was the purpose of this project because little research has been done in this area. The hypothesis stated that the glycosyl composition of cell walls from lower land plants would be more like the glycosyl composition of cell walls from dicot plants rather than cereal monocot plants. The prediction was that if cell walls from a variety of lower land plants were extracted and tested for their glycosyl composition, the composition would reflect a greater content of pectin (typical of dicots) than of glucuronoarabinoxylan (typical of cereal monocots).

Methods/Materials

The methods used to test the hypothesis involved taking leaf tissue from various plants, then grinding it up and extracting lipids, starch, and other materials from the tissue. After that, imidazole and NaOH were used to extract cell wall polysaccharides from the tissue, giving three fractions (imidazole-soluble, NaOH-soluble, and NaOH-insoluble) that could be cleaved to their component sugars and then analyzed by gas chromatography.

Results

The data revealed that all of the samples had galacturonic acid, galactose, and arabinose, sugars more typical of pectin than glucuronoarabinoxylan. Some of the samples contained an unusual sugar, 3-0-methyl-rhamnose.

Conclusions/Discussion

The hypothesis was supported because the cell wall contents of the lower land plants were more like dicot cell walls than cereal monocot cell walls. Future work of interest might focus on further study of the occurrence and function of the unusual 3-0-methyl-rhamnose sugar, which is present in at least some lower land plants but seems to have not yet been found in angiosperms, the flowering and most advanced land plants.

Summary Statement

This project is about investigating whether cell walls have changed during the evolution of land plants.

Help Received

Dr. Eugene Nothnagel provided assistance and guidance in the use of laboratory instruments and chemicals.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Kyle R. Rothschild-Mancinelli

Project Number

S0422

Project Title

Breaking the Double Helix: Effects of Solar UV Radiation on Super-coiled DNA

Abstract

Objectives/Goals

The objective of this project was to determine if solar radiation levels are high enough to damage healthy DNA. Specifically I tested to see whether a super-coiled plasmid (pUC19) would nick or break under the UV radiation in Kenya. In Kenya during the austral summer the UV radiation levels are high, so one can expect that there is also a higher percentage of damage done to the DNA in cell directly exposed to the solar radiation.

Methods/Materials

I exposed the pUC19 to some of the highest natural UV radiation levels in the world, a Kenyan summer. Before I went to Kenya, I exposed the pUC19 to UV in a sterilization hood to see if it would nick or break. The pUC19 under the UV hood nicked and broke. I then exposed five quartz cuvettes containing the pUC19 to the Kenyan solar radiation for a full day on January 4, 2007 and repeated it again on January 7, 2007. Back in California, I ran three controls (lab bench, frozen, and exposed to airport x-ray scanners) and the 10 samples in a 1.2% agarose gel.

Results

The control test in the gremecidal UV hood showed some nicking after one hour of exposure. In the feild tests the results proved there was nicking and breaking of the pUC19 in the 10 samples, while the controls remained super-coiled. On a cloudy day the results proved that there was nicking, but on a sunny day there was nicking and breaking.

Conclusions/Discussion

My results proved there was nicking and breaking of the pUC19 in the 10 samples, while the controls remained super-coiled. I conclude from the results that the natural levels of UV on the earth are high enough to damage super-coiled DNA.

Summary Statement

I determined if an engineered super-coiled DNA plasmid (pUC19) could stay intact under natural levels of UV radiation.

Help Received

Dana Rogoff isolated the plasmid, and helped me in the use of the equipment. Kevin Hand assisted me with the light readings, and Lynn Rothschild provided me with the opportunity to conduct this experiment.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Kanan K. Sindhu

Project Number

S0423

Project Title

Testosterone Depletion and Mitochondrial Damage in Skeletal Muscle: A Mechanistic Study

Abstract

Objectives/Goals

The objective was to study whether testosterone depletion would cause oxidative stress and mitochondrial damage.

Methods/Materials

Methods: Protein levels were determined and western blotting was carried out, which consisted of separation of the proteins on SDS-Acrylamide gels, blocking, reacting with the primary antibodies, washing, reacting with the secondary antibodies, reacting with the HRP conjugated substrate, developing and fixing of the film, and analysis by densitometer.

Materials: Gastrocnemius muscle samples from male mice, Tris-HCl, homogenizer, Refrigerated Centrifuge, Lysis buffer, Bio-Rad kit, polyacrylamide gels, PVDF membranes, 5% dry milk , T-TBS, primary antibodies, secondary antibodies , enhanced chemiluminescent reagent, photographic films, laser densitometer, developer

Results

The protein expression of the gp91phox subunit of NADPH oxidase was markedly induced in the castrated samples, an indicator of oxidative stress. Supplementation with physiological testosterone levels resulted in a significant decrease of the protein. Supplementation with supraphysiological doses of testosterone had no effect on the protein compared to the castrated group. Mitochondrial damage was assessed by monitoring COX (Cytochrome C Oxidase) in the post-mitochondrial fractions. COX is present on the inner mitochondrial membranes and due to mitochondrial damage, would leak into the cytosol. The enzyme protein was significantly higher in the cytosolic fractions of the castrated samples as compared with the controls. Supplementation with physiological doses of testosterone prevented COX from leaking into the post-mitochondrial fractions, suggesting that it prevented mitochondrial damage whereas supplementation with supraphysiological testosterone levels failed to ameliorate mitochondrial damage.

Conclusions/Discussion

Testosterone depletion by castration resulted in a marked induction of the superoxide radical producing enzyme, NADPH Oxidase, and mitochondrial damage as assessed by the release of COX. Supplementation with physiological doses of testosterone ameliorates NADPH Oxidase and mitochondrial damage. These results point to potential implications of androgen therapy in elderly, hypogonadal, human immunodeficiency virus-infected and diabetic men. Treatment with supraphysiological levels of testosterone also caused mitochondrial damage and oxidative stress.

Summary Statement

Testosterone depletion causes oxidative stress and mitochondrial damage.

Help Received

Used lab equipment and samples at Charles Drew University under the supervision of Dr. Ram Sindhu

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Carol Y. Suh

Project Number

S0424

Project Title

Integrated Microfluidic Device for the Development of Human Embryonic Stem Cells

Abstract

Objectives/Goals

Stem cell technology can help pave the way for personalized medicine, but current methodologies prevent from doing so. Human embryonic stem cell cultures are contaminated with animal products, preventing transplantations. Lack of understanding of stem cells in their microenvironments hinders tissue engineering and accurate drug screening.

Methods/Materials

In order to address these problems, an integrated microfluidic device that can sustain the growth and development of human embryonic stem cells (hESCs) was developed. The device was fabricated by soft-lithography. HSF1 hESCs were cultured inside the device with mouse embryonic fibroblasts (MEFs) and cultured media.

Results

Human embryonic stem cells were able to grow inside the microfluidic device. The morphology of the stem cells matched that of conventional methods. The undifferentiated nature of the embryonic stem cells was confirmed through immunostaining with AP, DAPI, Oct-4 and SSEA-4. Stem cell growth curves matched conventional methods and were robust.

Conclusions/Discussion

Human embryonic stem cells were efficiently cultured in a microfluidic device. This device can maintain hESC self-renewal and pluripotency in a microenvironment similar to in vivo conditions. hESC colonies were stained for SSEA-4, Oct-4, AP, and DAPI. This microfluidic cell culture device can later be used for high-throughput drug screening and the creation of animal free culture systems.

Summary Statement

This project is about developing a microfluidic stem cell culture device that can later be used for high-throughput drug screening and the creation of animal free culture systems, leading to personalized medicine.

Help Received

Used lab equipment at University of California, Los Angeles under the supervision of Dr. Hsian-Rong Tseng and Kenichiro Kamei.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Ryan Tam; Daniel Yeh

Project Number

S0425

Project Title

A Screen for Mutants in Drosophila melanogaster Affecting Triglyceride Levels: Year 2

Abstract

Objectives/Goals

Through the use of triglyceride assays and protein assays, we intend to isolate new genes that will cause both an increase and decrease in triglyceride levels in the fruit fly Drosophila Melanogaster. If the lines with the overexpressed gene shows an increase in the triglyceride level, it means that those genes regulate the triglyceride levels. Through this study, we can see how these overexpressed genes may affect the fat metabolism and regulation of Drosophila, and connect them to obesity and diabetes in humans.

Methods/Materials

For the triglyceride assays, we used approximately 32 different samples of fly lines, homogenzing 8 male Drosophila fruit flies with Tween 20 PBS Buffer and protease in a big microtube. After an incubation and a centrifugation step, we place 100 uLs of the supernatant into a fresh tube, and eventually place them into various microplate wells, with which we add triglyceride reagant to. After another incubation step, we then put it into the microplate reader at 500 nm to read the triglyceride level results. The protein assay helps to verify these results, and we add a green protein reagant to each sample. Afterwards, a spectrophotometer set at 562 nm helps to read the results, and the Microsoft Excel program can develop the R value and standard curve equations necessary to determine the sample concentrations.

Results

Out of the many different fly lines tested, our triglyceride assay showed that the #5# line was the most reproducible phenotype through its notable deviation from the average and consistent results. This year#s study involves two different fly lines, Creosome 5 and Creosome 7 crossed with the white control and daughterless driver of the UAS-GAL4 system. Preliminary crosses have shown that the #5# line, once again, is the most reproducible phenotype, through the use of triglyceride and protein assays.

Conclusions/Discussion

Through the use of the protein assay and the Creosome, White and daughterless crosses, we were able to validate our triglyceride assay in proving that the overexpressed #5# line is most intriguing. Thus, we intend to isolate the progeny of the #5# line for future experimentation as we believe its gene will regulate increased triglyceride levels. We can further identify this gene using the plasmid rescue step, and then we will be doing a lifespan analysis in which we test these fly lines under different nutritional conditions.

Summary Statement

Through the use of triglyceride assays and protein assays, we intend to isolate overexpressed genes that will cause both an increase and decrease in triglyceride levels in the fruit fly Drosophila Melanogaster.

Help Received

My team used lab equipment at the California Institute of Technology and worked under the guidance of our mentor, Brian Zid. Parents gave us support.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Vinay Tripuraneni

Project Number

S0426

Project Title

Systems Genetics of the Hippocampus: A cis-QTL for Tmem19 on Chromosome 10 May Modulate Hippocampal Size and Function

Abstract

Objectives/Goals

The hippocampus is involved in many neurological processes as well as disorders. The hippocampus is known to have a direct effect on spatial orientation; it significantly atrophies in pathologies such as Alzheimer's Syndrome and Schizophrenia.

Methods/Materials

In this study, hippocampal volume was estimated in 216 BXD RI genetic reference population of mice using stereological techniques. The data obtained from the stereological analysis was then subjected to bioinformatical analysis.

Results

It was found that hippocampal volume is a highly heritable trait (h^2 = .30), suggesting that a genetic mechanism must modulate hippocampal size. Interval mapping and cluster mapping revealed suggestive Quantitative Trait Loci (QTLs) on chromosomes 9, 10 and 13.

Conclusions/Discussion

Alternatively, more than 2 genes could modulate hippocampal size, and quantitative trait analysis may not be computationally powerful enough to identify the epistatic interactions that are occurring. Data correlation to microarray and phenotype databases revealed that hippocampal volume correlated to Protein Kinase C (PKC) activity and spatial orientation as measured by the Morris water maze.Tmem19, a highly expressed gene transcript, revealed a strong cis-QTL on chromosome 10, suggesting that it is not only modulating its own expression, but may modulate and be the transcription factor for other genes that control hippocampal size and function.

Summary Statement

This project investigates the genetic basis of memory.

Help Received

Used laboratory equipment at Beth Israel Deaconess Medical Center under the supervision of Dr. Glenn Rosen.

CALIFORNIA STATE SCIENCE FAIR
2007 PROJECT SUMMARY

Name(s)

Tiffany L. Tsiou

Project Number

S0427

Project Title

Expression of Genes Associated with Orthodontic Tooth Movement and Root Resorption

Abstract

Objectives/Goals

Objective: Although cDNA microarrays are a powerful tool of analysis, false positives signal are frequently encountered due to intrinsic problems with the methodology. The objective of this study is to confirm the changes in gene expression obtained from the microarrays by using real-time PCR.

Methods/Materials

Method: RNA obtained from molars and surrounding tissues of 0 day (control) and 5 days (experimental) rats subjected to orthodontic forces resulting in tooth movement (low force) and tooth movement with root resorption (high force). RNA was converted to cDNA using Reverse Transcription and used for real time PCR analysis using primers for some of the genes identified using the microarrays.

Conclusions/Discussion

Conclusions: There was a strong correlation between the data obtained from the microarrays and the data obtained from the real time PCR. We have identified some genes possibly associated with the resorption. However, a direct correlation between root resorption and the genes identified needs to be established.

Summary Statement

The identification of genes associated with root resorption formed by orthodontic tooth movement.

Help Received

Dr. Reyna my mentor taught me the lab techniques and supervised my work in the lab and my PI, Dr. Zeichner-David helped me with the concepts, experiment design, and interpretation.