CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Disha Bahl; Jeremy Wang

Project Number

S1501

Project Title

Taraxacum Officinale Root: An Antibiotic

Abstract

Objectives/Goals

Taraxacum Officinale, otherwise more commonly known as Dandelion, is a large species of flowering plants belonging to the family, Asteraceae. The purpose of our experiment is to find whether taraxacum roots have antibacterial properties and to see the effectiveness of different concentrations in killing bacteria. We predict that taraxacum roots have antibacterial properties and that the increase in concentration will cause the rise in effectiveness of killing bacteria.

Methods/Materials

First, we prepared the different concentrations of dandelion root extract by soaking different amounts (0.25g, 0.5g, 0.75g) of powdered dandelion root in 10 mL of each solvent (isopropyl alcohol, hexane, water). Then we centrifuged the tubes to form a pure extraction. After dipping the filter papers in the resulting extracts, we allowed them to dry, and then placed them on top of the bacteria plates along with the neutral control (plain discs), negative control (solvents), and positive control (iodine). We then incubated them for 24 hours and measured the zone of inhibition.

Results

The Iodine created an 11-15 mm range zone of inhibition on both bacteria and yeast. However, none of the discs dipped in hexane or water extractions produced area of inhibition rings. Only the dandelion root extracted by isopropyl alcohol produced area of inhibition rings. The 0.25g to 10 mL concentration formed 1-4mm rings, the 0.5g to 10mL concentration formed 2-3mm rings, and the 0.75g to 10mL concentration formed 5.5-7mm rings.

Conclusions/Discussion

Through our experiment, we conclude that antibiotic properties exist in strong concentrations of dandelion root extract, when isopropyl alcohol is the solvent. The 0.75g dandelion roots to 10 mL isopropyl alcohol extraction was the most effective at killing yeast, Bacillus Subtilis, and E. Coli. After conducting multiple t-test analysis, we concluded that this proved our hypothesis correct for all the bacteria tested. Both 0.25g to 10mL, and 0.5g to 10mL extractions showed minute traces of antibiotic properties, however after further t-test analysis, we concluded that there was no statistical significance. In all concentrations tested of hexane and water extractions, no antibiotic properties were observed in any of the bacteria plates. After further t-test analysis, we confirmed that our observations were statistically valid.

Summary Statement

A study aimed at proving the effectiveness of Taraxacum Officinale root as an antibiotic.

Help Received

Mother helped with taping board

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Ben Bence; Christopher Paghasian

Project Number

S1502

Project Title

Does Copper Encourage Pseudo-nitzschia to Grow and Contain More Domoic Acid?

Abstract

Objectives/Goals

The project tested if increasing the amount of copper in a culture of Pseudo-nitzschia would encourage its growth and thus contain more domoic acid. It was hypothesized that the culture with the highest amount of copper would grow the most and so produce the most domoic acid. It has been found that drainage pipes can add copper to the ocean, which Pseudo-nitzchia feed on. Pseudo-nitzchia also produce domoic acid, which has been known to poison and kill marine wildlife.

Methods/Materials

Three cultures of Pseudo-nitzschia were grown, one grown in distilled water with no added copper, another that was exposed to a low amount of copper, and a third that was exposed to a high amount of copper. These cultures grew over the course of 72 hours. The cultures were then put through an ELISA test and read through a spectrophotometer which read their absorbance.

Results

The culture that produced the most domoic acid was the culture that was injected with a low dose of copper. It had an average of 1142.13 ppb. The culture that grew in autoclaved seawater with distilled seawater had the lowest average at 952.55 ppb. The average ppb of the culture that grew in the water exposed to a high dose of copper had an average of 1089.38 ppb.

Conclusions/Discussion

It was found that the culture that was exposed to a low amount of copper grew the most and produced the most domoic acid. The results suggest that drainage pipes add subtle amounts of copper to the ocean, and those amounts are enough to encourage Pseudo-nitzschia to grow and make the ocean contain more domoic acid.

Summary Statement

Three cultures of Pseudo-nitzschia were grown, one with a low dose of copper, one with a high dose of copper, and one that was not exposed to copper, and the culture exposed to a low dose of copper contained the most domoic acid.

Help Received

Lab equipment was used at Moss Landing Marine Laboratories under the supervision of Moss Landing Marine Laboratories student April Woods

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Sarah S. Chang

Project Number

S1503

Project Title

Phosphorescence of the Sea

Abstract

Objectives/Goals

The objective is to determine if longer or shorter exposure to light and/or darkness affects the length of time bioluminescent dinoflagellates, specifically the species Pyrocystis fusiformis, sustain bioluminescence.

Methods/Materials

Pyrocystis fusiformis was ordered from Empco and divided equally into 6 tubes and placed in 3 different lighting conditions. Two tubes were exposed to 12 hours of light and 12 of darkness, 2 tubes to constant light, and 2 tubes to constant darkness. After establishing a baseline, microorganisms were observed over a 10 day period in a controlled environment at 8 am and 8 pm and the amount of time they maintained bioluminescence was recorded.

Results

In the first box which was consistently exposed to light, Tubes 1 and 2 maintained their glow for an averaged 3.9945 seconds longer than the baseline of 7.885 seconds at 8 am and -1.0955 seconds less than the baseline at 8 pm. At 8 am the bioluminescence from Tubes 3 and 4 in the Light/Dark box could be observed for 8.1945 seconds longer than the baseline of 13.185 seconds and at 8 pm -1.034 seconds less than its baseline. The box kept in darkness, containing Tubes 5 and 6, lasted 1.928 seconds longer than the baseline before becoming exhausted and at 8 am for 0.3785 seconds longer.

Note: Modifications conducted to the experiment in the time between submitting the application and the California State Science Fair will possibly lead to new results.

Conclusions/Discussion

In the experiment, data proved that Pyrocystis fusiformis are able to sustain their bioluminescence for the longest amount of time when given suitable time in the light and darkness. Too much time in the light or dark will result in a shorter time before organisms become exhausted.

Summary Statement

My project was to determine how the effects of different exposure to light affect the length of time Pyrocystis fusiformis can maintain bioluminescence.

Help Received

Borrowed equipment from school, mother ordered microorganism online

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)
Eric S. Chen

Project Number
S1504

Project Title
Discovery of Novel Influenza Endonuclease Inhibitors to Combat Flu Pandemic

Abstract

Objectives/Goals
The objective is to discover novel influenza endonuclease inhibitors as leads for a new type of anti-flu medicine that is effective against all influenza viruses including pandemic strains.
New anti-flu medicines are urgently needed as current drugs are losing their effectiveness due to emerging resistant strains. Since the influenza endonuclease is well-conserved and essential for viral propagation, inhibitors of this enzyme can potentially block any influenza virus and reduce the chance of developing resistance.

Methods/Materials
I used ROCS software to construct pharmacophore models and performed virtual screening of large compound libraries with over 450,000 chemicals. I set up a fluorescence-based enzyme assay to validate the virtual screening hits as endonuclease inhibitors. In parallel, I used TACC Ranger supercomputers to run molecular dynamics (MD) simulation of influenza endonucleases and FTMap software to perform solvent mapping. Molecular docking experiments of new inhibitors to the enzyme were performed by using the Glide module in Schrodinger software. I also examined structure and activity relationship using analogs of the new inhibitors.

Results
Through the pharmacophore model-based virtual screening, I identified 237 hits of potential endonuclease inhibitors, and among them, six compounds were confirmed to have potent inhibitory activities. They exhibit structural diversity and belong to five distinct classes. Two compounds were found to block influenza propagation with negligible cell toxicity. In addition, MD simulation and solvent mapping construct a comprehensive map of binding pockets and druggable hot spots within the endonuclease active site. Molecular docking of the new inhibitors to the endonuclease active sites provides valuable information for designing even more potent inhibitors.

Conclusions/Discussion
I have successfully identified a number of new, potent and structurally diverse endonuclease inhibitors with great potential to be developed into new anti-influenza drugs. The structural analysis also laid the ground work for further optimizing the new inhibitors. Therefore, my findings will help combat influenza and save lives. A patent was filed on my discoveries.

Summary Statement
By combining computational research and biological assays, I identified novel and potent influenza endonuclease inhibitors and performed comprehensive structural analysis, which laid the ground work for developing new anti-flu medicine.

Help Received
Used computers in Dr. Rommie Amaro's lab at UCSD; used lab equipment in Dr. Gen-Sheng Feng's lab at UCSD.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)
Jasmeet S. Dhaliwal

Project Number
S1505

Project Title
Biofuel from Microalgae

Abstract

Objectives/Goals
The objective of this project is to determine if microalgae from a local pond would be a viable source for producing biofuel using direct transesterification. Also, how would the hexane extraction method compare to the chloroform-methanol method.

Methods/Materials
Materials: Algae from a local pond, n-hexane solution, deionized water, 1:1 solution of chloroform & methanol, 5% solution of sulfuric acid, Bio Flow Chamber, Laboratory blender, centrifuge machine, Vortex mixer, hot bath, separation glass funnel, 10 mL graduated cylinders, 100 mL beakers, 150 mL conical flasks,45 mL plastic vials with conical bottom, Electron compound microscope, electronic scale, referigerator, gloves, small forceps, parafilm, labeling tape,sw permanent marker
Procedure: Collect 1 liter of algae sample and wash it with deionized water. Make a paste of the algae using a blender. Centrifuge the algae paste at 5,000 rpm for 8 minutes. weigh the algae mass after discarding the supernatant. For the hexane method, add 30 mL of n-hexane solution and mix thoroughly using hand motions and vortex mixer. Pour the contents into a separating funnel and let the funnel stand vertically for 10 minutes. Open the bottom valve of the funnel to collect dark color liquid (mixture of algae oil and hexane . Transfer the liquid into glass tubes and put the tubes in a hot bath at 65ºC for 20 minutes. Take the glass tubes out and measure the volume of the liquid. For the chloroform-methanol method, add 30 mL of 1:1 solution of chloroform & methanol and 35 ml of 5% sulfuric acid and follow the same steps.

Results
The hexane method resulted in extracting very small amount of oil out of the wet algae mass; the oil got stuck to the sides of the separating funnel and could not be measured. The chloroform-methanol method resulted in oil mass ranging from 45 to 75% of the wet algae mass.

Conclusions/Discussion
The hexane is not efficient in extracting any oil out of the wet algae mass. The chloroform-methanol method is much more effective in extracting the oil from the wet algae mass. The yield of the oil increased with the increase in the mass of the algae.

Summary Statement
My project is about extraction of oil from microalgae (wet mass) using direct transesterification method and comparison of hexane and chloroform-methanol extraction methods.

Help Received
My father helped me perform and supervise the experiment and my mother helped me finish the board. In addition, Dr. Lauer from CSUB provided guidance in using the lab equipment and methods.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)
Raghu V. Dhara

Project Number
S1506

Project Title
A Novel Pentameric Model of the T4 Bacteriophage Genome Packaging Motor and a Means of Disrupting Its Mechanism

Abstract

Objectives/Goals
The first objective of this project is to determine the exact structure of the protein complex that comprises the T4 bacteriophage's molecular motor. The second objective is to provide a mechanism by which the model proposed in step one would package the DNA.The final objective is to discover a molecule that would effectively disrupt motor function and disable the virus. This project has immense potential in medicine, as the drug molecule proposed in phase three can be refined to produce more effective antiviral drugs.

Methods/Materials
Phase one was accomplished using rotation matrices, Java code, molecular visualizers such as VMD, and a previously proposed conformation as a starting point; with these tools, a stable, feasible structure that met all criteria, both theoretical and experimental, was designed. Phase two used biomolecular computer simulation software like NAMD and Chimera. The molecular cap from phase three was found using molecular docking software, namely AutoDock Vina.

Results
Based on the analysis of data from molecular visualizers,I propose a novel configuration for the T4's motor. It resembles a cone without its apex, commonly known as a frustum. Using this frustum shape, molecular modeling, and mathematical analysis, I offer a new model for the translocation of genetic material through the virus, known as the "frustum-impulse" model after the motor's shape and primary physical principle of operation. Finally, human phospholamban protein, or PLN, looks to be a feasible molecular cap that completely inhibits motor operation.

Conclusions/Discussion
We have concluded that the shape of the viral packaging motor is a frustum, that the model for translocation is the frustum-impulse mechanism, and that PLN can effectively disrupt the T4 motor function. Still, much work needs to be done: frustum impulse must be tested experimentally and the phospholamban cap should be examined more closely to determine its drug potential. In any event, this project has advanced our understanding of nature's most mysteries pathogens and offered a possible means of addressing numerous illnesses that plague our society.

Summary Statement
This project attempts to obtain the structure of a viral genome packaging motor, offers a model for how the motor functions, and provides a possible way to disrupt its mechanism.

Help Received
Worked with UCSD NanoEngineering Department with Professor Gaurav Arya

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Gabrielle A. Evey

Project Number

S1507

Project Title

Potential Pathogens: A Surface Comparison of the Occurrence of Gram-positive and Gram-negative Bacteria

Abstract

Objectives/Goals

25 million people in the United States and Canada have a phobia of using public toilets. The objective is to identify the bacteria in public restrooms to show what the common person may be exposed to. The hypothesis is stated as, if the toilet seats and faucet knobs are swabbed from public restrooms, then the toilet seats will contain the most bacterial organisms that provide the greatest opportunity for gram-positive and gram-negative pathogenic infections.

Methods/Materials

Based on last year's project, all toilet seats contain gram-positive Staphylococcus when grown nutrient agar. This year, MacConkey agar was used to find gram-negative growth. 50 toilet seats were swabbed, placed on MacConkey agar, and were incubated for 48 hours at 98ºF. Growth was Gram stained and viewed under a microscope. 50 faucet knobs were swabbed for comparison. Faucet knobs were swabbed onto nutrient agar, incubated for 48 hours, and transferred onto MacConkey and Mannitol Salt agar. These were grown for 48 hours and growth was Gram stained and viewed under a microscope. Additional tests on the bacteria, including catalase and oxidase tests, were performed.

Results

100 total surfaces were swabbed during this project.
50 of 50 toilet seats contained Staphylococcus (Staph), 4 of 50 contained Escherichia coli, and 1 of 50 contained Klebsiella pneumoniae.
50 of 50 faucet knobs contained Staph, with 34 of 50 containing Staph aureus, and 23 of 50 containing Staph epidermidis. 2 of 50 faucet knobs contained Haemophilus influenzae, 2 of 50 contained Escherichia coli, 1 of 50 contained Proteus, and 1 of 50 contained Pseudomonas.

Conclusions/Discussion

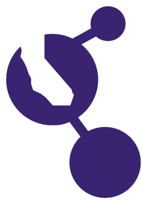
This data refuted the hypothesis. Faucet knobs contained the most variety of bacterial growth. Faucet knobs are touched by hands, which touch the eyes, nose, and mouth. These areas are optimal for bacterial transfer, which poses a higher potential for infection. Bacterial spread can be prevented by turning off knobs with a paper towel. In an additional study, bacteria was placed onto nutrient agar that contained hand sanitizer. Bacterial growth was completely inhibited, so hand sanitizer reduces possible infection. Unless one has an open sore on the buttocks or thighs, toilet seat bacteria cannot enter the body to cause infection. This data suggests that toilet seat covers are unnecessary and are not protecting the body.

Summary Statement

When toilet seats and faucet knobs are swabbed from public restrooms, faucet knobs grow the most variety of bacterial organisms.

Help Received

Parents purchased materials and drove to obtain samples; The Edwards AFB Medical Clinic technicians allowed the use of their materials and aided in research and the conduction of the project.



CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Elan E. Filler

Project Number

S1508

Project Title

Investigating an Outbreak of Cryptococcus gattii Infection

Abstract

Objectives/Goals

When inhaled, the fungus Cryptococcus gattii causes life-threatening meningitis and pneumonia in humans and animals. Two species of Cryptococcus, C. neoformans and C. gattii, cause infection. These two species are not routinely distinguished from each other in clinical laboratories. Currently, there is an outbreak of C. gattii infection in California. Previously, I discovered that C. gattii grew on two species of trees near two outbreak cases in South Central Los Angeles, but these results were preliminary. This year, my objectives were to 1) further define patients with infection caused by C. gattii; 2) map the location of patients with C. gattii infection; and 3) further delineate the environmental sources of C. gattii.

Methods/Materials

I analyzed 48 de-identified patient isolates of Cryptococcus for the presence of C. gattii by plating them onto CGB agar. Next, I swabbed 56 trees and collected 39 soil samples from 17 different sites in South Central Los Angeles near the C. gattii outbreak cases. To isolate and identify C. gattii, I plated these samples onto NGS agar and then onto CGB agar.

Results

Of the patient samples, 25% were positive for C. gattii. Surprisingly, the majority of the outbreak cases were tightly clustered within a two kilometer radius in South Central Los Angeles. My environmental sampling revealed that Cryptococcus species was present in 23 tree and soil samples from 11 locations. Of these samples, 6 contained C. gattii. Notably, all were isolated from locations that were in the same area as the outbreak cases.

Conclusions/Discussion

In conclusion, I discovered that there is an alarming cluster of C. gattii outbreak cases in South Central Los Angeles. My results verify my hypothesis that C. gattii grows on trees that are in the same area as the outbreak. Therefore, C. gattii is endemic in this region and is the likely source of the outbreak.

Summary Statement

I discovered a Cryptococcus gattii outbreak in patients clustered in South Central Los Angeles and found that the likely environmental source of this outbreak is the trees, P. canariensus, L. styraciflua, and M. excela.

Help Received

Dr. Deborah Springer at Duke University oversaw project; physicians in LA County provided de-identified patient isolates; father drove me to sampling sites; LABioMed provided space and equipment for lab work.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Joel Herman; Alec Zhang

Project Number

S1509

Project Title

The Effect of UV Wavelength on the Mutation Rate of Escherichia coli

Abstract

Objectives/Goals

The purpose is to compare the mutagenic effects of UV-B and UV-C light at equivalent intensities on Escherichia coli.

Methods/Materials

A bacterial tryptophan reverse mutation assay was used to measure the mutagenicity of UV-B and UV-C radiation. E. coli WP2, which require tryptophan for growth due to a point mutation, were inoculated into minimal growth media and exposed to equal intensities of UV-B or UV-C light for various times. Growth of E. coli WP2 on minimal media requires reversion of the point mutation, therefore, the number of colonies is a measure of the mutagenicity of the UV-B or UV-C exposure.

Results

With no exposure to UV light, an average of 12 colonies was observed after 48 hours incubation on minimal media, which represents the background rate for reversion of the tryptophan mutation. With UV-C the maximum number of colonies (mean = 436, standard deviation = 31), was observed with 15 seconds exposure at 45 mWatts/cm2. With UV-B exposure at the same intensity, the maximum number of colonies (mean = 359, standard deviation = 62) was observed at 3:00 minutes.

Conclusions/Discussion

The maximum mutagenic effects of UV-B and UV-C irradiation on E. coli were not significantly different, but the maximum number of mutations with UV-C was obtained at a much lower exposure. This study was done to investigate the potential for mutations in bacteria that survive UV-C decontamination systems, such as those used to disinfect water, due to receiving a sub-lethal exposure, and to determine if UV-B might have lower potential for mutations in bacteria that survive decontamination. Our results suggest that UV-B and UV-C do not differ in their mutagenic potential in bacteria that survive UV decontamination.

Summary Statement

We used a reverse mutation assay to compare the mutagenic effects of UV-B and UV-C radiation in E. coli, to determine if UV-B has lower potential for causing mutations in bacteria that survive UV decontamination.

Help Received

One of our fathers (Mr. Herman) obtained permission for us to conduct our experiments in a microbiology laboratory at his company, supervised our laboratory work and taught us basic bacteriological techniques. My parents and biology teacher helped us proof-read and edit our poster and binder.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Melissa M. Holtzen

Project Number

S1510

Project Title

The Consequences of E. coli Infected Fruit Flies

Abstract

Objectives/Goals

My hypothesis is that fruit flies that eat E. coli, and fruit flies that walk directly on E. coli will become contaminated and will be able to spread the bacteria to apples.

Methods/Materials

I performed a bacterial transformation with E. coli and the pGLO plasmid. Then I infected fruit flies with the transformed E. coli two different ways. I infected the fruit flies internally by putting the E. coli in the flies' food and I infected the flies externally by have them walk directly on E. coli colonies. I sterilized the internally infected fruit flies with ethanol, but did not sterilize the externally contaminated flies. Then I plated them both on an LB/amp/ara agar plate. I put some of the contaminated flies on apples and let them contaminate the apples. I tested the apples b plating them on an LB/amp/ara plate.

Results

The flies that ate the E. coli and the flies that walked on the E. coli colonies both become contaminated and were able to spread the bacteria to the apples.

Conclusions/Discussion

The bacteria glowed because of the transformation with the pGLO plasmid. The flies glowed when I plated them on the LB/amp/ara because of the E. coli contamination. The apples glowed on the LB/amp/ara plate because the flies transferred the bacteria either through their feces or larvae or through their external contamination.

Summary Statement

My hypothesis is that fruit flies that eat E. coli, and fruit flies that walk directly on E. coli will become contaminated and will be able to spread the bacteria to fruit.

Help Received

None

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Kamran M. Jamil

Project Number

S1511

Project Title

Autism and Gut Microbiome: Is There a Link?

Abstract

Objectives/Goals

Autism spectrum disorders (ASD) now affect 1 in 88 children in the U.S and cost $35 billion annually. The hypothesis is that functional interface of genes & environment is metabolism, and that a persistent alteration in metabolism during critical period of neurodevelopment is responsible for ASDs. The gut microbiome contains up to 10^15 bacteria which produce an array of bioactive metabolic products capable of entering systemic circulation & can have profound effects on host metabolism, and immune function in many organs, such as brain. Recent research suggests that gastrointestinal microflora composition may differ between ASD & non-ASD children & an increase prevalence of Clostridia, Bacteriodetes and Sutterella species in ASD. Hypotheses: Significant metabolic changes occur in ASD mice compared with control mice. Stool metabolic profile can be utilized as a screening tool for early detection of ASD.

Methods/Materials

C57BL/6J mice were used. They were exposed in utero to saline, or a simulated viral infection by injection of synthetic ds RNA (Poly I:C) 3mg/kg on E12.5 into pregnant dams (Maternal Immune Activation) to mimic ASD.Stool samples were collected from 4 mth old male controls & ASD (6 mice each).The conc. of 75 polar metabolites were quantified by hydrophilic interaction liquid chromatography&scheduled multiple reaction monitoring on Mass Spectroscopy. Metabolomics is a research field with methods for analysis of low molecular weight compounds in biological systems. Data was analyzed using univariate/multivariate statistical tools implemented by MetaboAnalyst 2.0.

Results

Strong metabolic group differences between ASD &control mice were found:
a) The danger-associated metabolites were increased in autism microbiomes such as nucleotides & deoxynucleosides (GTP,Deoxyadenosine, Inosine, Hypoxanthine, and cAMP), sulfur-containing metabolites (Taurine) & tryptophan, nicotinamide & serotonin precursors.
b)The health-associated metabolites were decreased in the autism microbiome such as vitamin cofactors (Thiamine, Nicotinamide), nucleotide & Krebs cycle precursors (L-Aspartate).

Conclusions/Discussion

An increase in deoxynucleotides & other nucleotides in ASD mice also supports the purinergic theory of autism which is developed by my mentor Dr Naviaux, which teaches that autism is the outcome of ecogenetic factors that lead to persistent increases in neuroinflammation, gut & metabolic abnormalities.

Summary Statement

The study points toward a relationship between gut bacterial metabolic products and ASD mice and opens new avenues of research for advancing knowledge on the consequences of dysbiosis with the potential for identifying novel microbial related drug targets. The stool metabolic profile can also be utilized as a

Help Received

Lab equipment (bacterial cultures, extraction, HILIC and mass spectrometer) were all property of Dr Naviaux's laboratory at UCSD. Dr Kefeng Li taught me how to use HILIC and mass spectrometry. I have taken animal research workshop at UCSD.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Kriti Lall

Project Number

S1512

Project Title

Mutating E. coli with the arxA gene: Creating a Novel, Practical Solution to the Global Arsenic Water Problem

Abstract

Objectives/Goals

Arsenic, a poison found in water, exists in environment in mainly two states: arsenite (carcinogenic and water-soluble) and arsenate (easily removed from water), with arsenite being most predominant. Extremophilic bacteria like MLHE-1 have a gene called arxA, which enables them to change the toxic arsenite into less-toxic arsenate.

The goal of my project is to determine if E. coli strain K-12 can be transformed to contain the gene arxA from MLHE-1. If so, will the new strain recombinantly express the protein from the arsenite oxidase gene? I hypothesized that the E. coli strain K12 can be transformed to contain arxA, and when induced, K12 will express arxA. This mutated E. coli strain is an ideal choice for practical arsenic water bioremediation.

Methods/Materials

MLHE-1 DNA was extracted, and the arxA gene was amplified using PCR. Restriction digests were conducted, and the plasmid and the insert were ligated. E. coli underwent transformation via heat shock, and was plated onto LB-lac-ampicillin plates, and surviving colonies were subcultured. Recombinant protein expression analysis and an SDS-PAGE Gel was conducted.

Results

In my ligation gel, cut plasmid moved faster than the uncut plasmid, and the ligations moved faster than the uncut plasmid. After the transformation, E. coli cells grew on LB-lac-ampicillin plates, indicating insertion of the plasmid. In the SDS-Page Gel, I saw only 1-2 bands (not the expected barcode-like protein patterns) probably because the samples were too dilute, and this part of the research is a work in progress.

Conclusions/Discussion

The first part of my hypothesis was supported. As seen by my ligation and transformation results, the plasmid with the arxA gene was inserted into E. coli. The second part of my hypothesis is currently inconclusive and a work in progress, since the sample run in the SDS Page Gel is too dilute. The next step is to concentrate the sample and conduct the gel again. If the E. coli expresses the protein, the induced sample should have one more band than the uninduced sample, representing the arxA gene.

Summary Statement

This research focused on creating a new strain of E. coli with a gene called arxA, that converts arsenite (toxic & hard to remove from water) to arsenate (easy to remove from water), and opens up a possible way to remove arsenic from water.

Help Received

Used lab equipment at Schmahl Science Workshop under the supervision of Dr. Aru Hill.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Deborah Lee; Odelia So

Project Number

S1513

Project Title

How Effective Are the Three Most Popular Teas: Black, Green, and Oolong Tea in Preventing Tooth Decay?

Abstract

Objectives/Goals

Our teacher told us a story about how her dentist observed that even though American people pay more attention to dental hygiene, they seem to be more prone to tooth decay, whereas those from Asia and Europe seemed to be less prone to tooth decay. Upon further research, we realized that Asian and European countries drank tea, whereas America leaned more towards coffee. We are avid tea drinkers ourselves, especially green tea. The story made us wonder if our beloved green tea and possibly other types of tea would have a cavity prevention property.

Methods/Materials

We wanted to simulate the environment of the mouth, so we used Lactobacillus Acidophilus, commonly found in the mouth and known to digest sugar consumed through food and produces lactic acid to decay teeth. We picked 10 teeth per tea. We thought that 10 would be a good sample size in order to draw conclusions and obtaining virgin molar teeth plucked within the age of 15-22 was difficult, we were forced to choose the most effective and efficient number. We soaked each tea in 2 cups of boiling water in the designated time labeled on the back of the tea bag. We took photos manually and digital x-rays for each of the teeth, which was difficult because we needed to take 5 consecutive days of the time of the dentist in order to compare our data at constant increments. We took the photos outside in natural lighting and measured the distance from the lens to the ground to make sure that all the teeth were the same sized photo.

Results

After compiling our data onto a table and graphing the average, we saw that the increase of decay was directly correlated to the amount of fluoride each tea contained. Black tea was most effective in preventing tooth decay with an average of 1.46 mm2, green tea was second most effective with an average of 4.0mm2 of decay, and oolong came in least effective with 4.05 mm2 of decay.

Conclusions/Discussion

Our data supported our hypothesis; black tea was proven to be the most effective in preventing tooth decay with the least average of decay, 1.46 mm2. We deduced that the amount of decay had a direct correlation to the fluoride levels present in each tea. However, there were some factors that we did not account for, such as the uniform alignment under the camera lens as well as the individuality factor of the teeth because the chemical makeup of each tooth depend on the lifestyle of the person and eating habits.

Summary Statement

Our project is about the effect of the three most popular teas in preventing tooth decay.

Help Received

We used the digital x-ray at Smile Family Cosmetics and Dentistry, under the supervision of Dr. Rottjakob. We obtained teeth from Dr. Patel, and Dr. Follmar. Dr. Rottjakob assisted us by analyzing the decay on each tooth. We borrowed an incubator from Bret Harte Middle School under supervision of Ms.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Andy S. Meyers

Project Number

S1514

Project Title

Algae: The Living Oil Factory: Year 2

Abstract

Objectives/Goals

My hypothesis is: If I expose algae to an electric field, then it will separate from the medium and lyse the cell membrane and release the biomass and lipids which can be used as a biofuel.

Methods/Materials

Method: 1. Set up algae lab using Tetraselmis chuii in 1.5 liters of medium using photobioreactor and cultured 95 liters of algae in medium over seven months.2. Harvested 2254 ml of algae and continued to remove water to create 490 ml of concentrated algae for testing.3. Conducted range tests varying voltage, electrodes and distance to narrow down variables. 4. Exposed concentrated algal medium to electric field. Trial #1 & #2: Placed 80mL of concentrated medium in 30cm trough at 15 volts. Trial #3: Placed 50 mL of concentrated medium in 10cm trough at 15 volts. Allowed electric field to run for 30 minute intervals for three hours. At each interval, took sample and observed and photographed it under microscope at 40x, 100x, 400x and 1000x magnification. After three hours, removed treated algae and placed in graduated cylinder to settle.5. Analyzed sample in terms of percent flocculated and percent of cell membranes lysed.
Materials: Culturing: Photobioreactor, Tetraselmis chuii sample, culturing nutrients, salt. Harvesting: Pans, buckets, custom-made settling tubes. Testing: Power supply, electrodes, leads and wire, 30 cm and 10 cm custom-made troughs, microscope, containers.

Results

Flocculation begins to occur within the first 30 minutes of exposure and takes up to 2 hours for total flocculation. About 10% of the cells appeared to be ruptured in the first 30 minutes, about 35% -50% after three hours. Oil was captured at an average of 1.5% of the algae concentrate or 15% of the wet biomass.

Conclusions/Discussion

Hypothesis was correct. Electric field aids harvesting algae from medium and lysing cell for biomass to be released and oil to be extracted. Electric field is more efficient in harvesting than settling. Shorter distance led to higher amps, higher wattage, higher cost but similar results. Opportunity to optimize electric field as higher amps cost more but did not yield better results.

Summary Statement

When algae is exposed to an electric field, the cells flocculate and the membrane can be lysed.

Help Received

Consulted with Dr. Stephen Lyon; mother helped harvest algae; borrowed microscope from a hospital.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Adrian Miller; Michaela Sanchez

Project Number

S1515

Project Title

Fecal Coliform: A Study of Water Contamination in the San Lorenzo River

Abstract

Objectives/Goals

Our goal is to identify and measure the presence of fecal coliform bacteria in the San Lorenzo River, with collected data to be used to answer our investigative questions: Our goal is to identify and measure the presence of fecal coliform bacteria in local water supplies, with collected data to be used to answer our investigative question: What is the main source of fecal coliform in the San Lorenzo River? We hypothesized that fecal coliform would be present at levels safe enough for swimming. We predicted that human waste is a contributing factor to the fecal coliform levels and that the cleaning up of the campsites would reduce the amount of contamination.

Methods/Materials

We have been monitoring in four different locations about once every week. We have taken samples in the San Lorenzo River in two different locations starting directly under the Covered Bridge in Covered Bridge Park in Felton, California. Our next three locations are upstream from the Covered Bridge at 50 meter intervals. We use sterile whirl-pak bags to collect water samples, and then we take them to the lab and perform membrane filtration. After filtration, we put the filters on petri-pads saturated with m-FC media inside petri dishes and incubate them at 44.5ºC for 24 hours. We have been using Escherichia coli as a positive control, and we run phosphate buffer through the membrane filtration system, as a blank, proving there is no outside contamination.

Results

There is fecal coliform presence in the river at all four of our sample locations. Comparing data taken before and after the clean up of the campsites, we saw a significant drop in contamination levels after the clean up.

Conclusions/Discussion

The water at all four locations is safe for swimming. The clean up of the homeless camps appeared to help decrease the amount of fecal coliform in the San Lorenzo River at the Covered Bridge Park.

Summary Statement

We have been identifying and measuring the presence of fecal coliform bacteria in the San Lorenzo River to determine whether a clean up of homeless campsites along the river helped decrease the amount of fecal coliform contamination.

Help Received

Jennifer Slaughter, Water Quality Specialist, answered some of our questions through emails and gave us a tour of her lab and a demonstration of professional water contamination testing; Mother helped with transportation; Mrs. Orbuch provided supplies, storage space; Mr. Hearn provided lab space

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Meghan Nealon; Elaine Romano

Project Number

S1516

Project Title

Emiliania huxleyi Response to Euphotic Zone Temperature Gradients

Abstract

Objectives/Goals

The purpose of the experiment was to study the effect of temperature on the growth of Emiliania Huxleyi under high-light intensity, mimicking conditions of stratified ocean waters in the euphotic zone. The hypothesis stated that if temperature gradients are established mimicking the Bering Sea (2 degrees Celsius), the Portuguese coast (20 degrees Celsius) and projected ocean temperatures (25 degrees Celsius) with standard light intensity, both warm and cold strains of Emiliania Huxleyi will experience no trend toward increased metabolic activity and biomass in conditions of projected ocean temperatures.

Methods/Materials

Prior to experimentation, a growth media for E. Hux to simulate seawater was produced at a marine biology lab. Two differing strains of base cultures of E. Hux (warm water and cold water) were placed in tanks with the produced media. These tanks were then placed into three baths maintaining three different temperatures. Over 4 to 5 days, samples from each tank were mounted daily on a wet plate and counted under a microscope. These numbers were recorded and photos from the microscope were collected as well. These procedures were repeated twice more for a total of three trials.

Results

Growth was experienced in all baths, and the warmest bath did not appear to be the ideal condition for all E. Hux, based off its lack of trend toward more growth in the warmest waters.

Conclusions/Discussion

The results would suggest that temperature is not a significant factor causing coccolithophore blooms. Instead they could be explained by more important factors, including increasing nitrate levels, mixed layer irradiance, and low silicate levels. Temperature has been ruled out of causing the blooms primarily because E. Hux are eurythermal species. Temperature gradients seemed to instead coincide with other more influential factors, such as water stability, and the presence of diatoms in larger quantities. This experiment may lead to a better understanding of the niche phytoplankton have in their ecosystem. From our results, a greater understanding of how E. Hux would respond to changing water conditions due to global warming and increased anthropogenic carbon dioxide levels could be developed. The data may also aid scientists understanding the causation of yet unexplained and seemingly random E. Hux blooms.

Summary Statement

We experimented to assess the role of varying temperature on oceanic blooms of the coccolithofore Emiliania Huxleyi.

Help Received

Obtained cultures and growth medium from Romberg Tiburon Laboratory, from graduate students Roy Bartel and Andrew Kalbach, completed experimentation in school chemistry lab.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Suzanne Salameh

Project Number

S1517

Project Title

The Effects of Different Yeast Concentrations and Algae on the Chemotaxis of Physarum polycephalum

Abstract

Objectives/Goals

Explore chemotactic responses of P. polycephalum in culture exposed to various amounts of yeast, algae, and then algae and yeast in combination. Will the plasmodial slime mold detect cues, collect and integrate information about its surroundings, and move towards the yeast? Perhaps the algae? Or will they migrate away?

Methods/Materials

- Culture the Physarum.
- Make Solutions with Varying Concentrations of Yeast (.1, 1, 10, and 100 mM concentrations.
- Prepare Plates with 8x2cm filter strips.
-Soak the labeled strips of filter paper in the appropriate cups containing the varying yeast concentrations.
-Place 2 strips of growing physarum below a growing Physarum culture.
- Transfer four such blocks, plasmodium-side down, onto the junction of the two filter paper strips.
-Observe plasmodium movement every hour for several hours.
-Repeat same procedure, with yeast and algae; then, algae alone.

Results

The Plasmodial slime molds migrated towards the higher concentration of yeast at 10mM and 100mM and their migration appeared less for lower concentrations of yeast like 1mM or .1mM solutions. This suggests that the chemical cues in the lower concentration solutions weren#t as strong as those of higher concentration, which may have led to a decreased chemotactic response by the slime molds. When the experiment was repeated under the same conditions for an algal mixture compromising of 5 different species (chlorella vulgaris, scenedesmus quadricauda, selenastrum capricornutum, ulothrix fimbriata, and volvox aureus), the slime molds grew away from the algae 44% of the time, grew towards both the control and algae 42% of the time, and towards the algae alone only 13% of the time.When the experiment was done a third time using yeast and algae, growth away from the algal mixture soared higher.

Conclusions/Discussion

This suggests that the slime molds are not particularly attracted to algae; in fact they may even be repulsed by them.If the slime molds were to be exposed to algae and live in an environment where that was there only nutritional source then they would most likely be transformed into a hard, dry, inactive mass called a sclerotium. It becomes a plasmodium again when favorable conditions return or in this case, when a new nutritional source such as yeast makes itself present.

Summary Statement

Explore chemotactic responses of P. polycephalum in culture exposed to various amounts of yeast, algae, and then algae and yeast in combination.

Help Received

Mother helped drive me to get desired equipment and father helped order plasmodial slime molds.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Sriram Somasundaram

Project Number

S1519

Project Title

A Novel Treatment for Biofilms Using Nanocurcumin, Chitosan, and nAg, and an Innovative Coating in Preventing Biofilms

Abstract

Objectives/Goals

Biofilms are strong bacterial communities that adhere to surfaces due to certain gene expressions in reaction to the environment. They are 1000 fold more resistant to antibiotics and communicate through quorum sensing. Biofilms commonly form on areas such as catheters, pacemakers, and prosthetic replacements, contributing greatly to the downfall of patients. My research proposes a combined treatment of nanocurcumin, nanosilver, and chitosan (nCnSC) to combat the strong bacterial defense. Additionally, I have developed a preventing coating onto a PTFE sheet that is a preventive measure against the formation of biofilms.

Methods/Materials

A wet-milling method was used to make nanocurcumin. The environmental indicator, sucrose, stimulated the growth of the biofilm of S. mutans. The MIC and the Disk Diffusion Assays were used to determine the antimicrobial effects. Results were analyzed both in the form of mm of inhibition and minimum inhibitory concentrations (µg/ml), and the control was Erythromycin. The anticoating was devised through novel manners. Three trials were conducted.

Results

Nanocurcumin was the strongest individual treatment (20. µg/ml), whereas chitosan was the weakest (200. µg/ml). nAg and curcumin had equal anti-microbial effects (50. µg/ml). nCnSC alone inhibited biofilm formation on an average of 7.5 mm and had the lowest minimum inhibitory concentration value of 10.µg/ml. The anticoating with the fluorinated oil and nCnSC had 9 mm of inhibition. The combined treatment worked better than any of the individual treatments, meaning that the compound successfully bonded into another stronger compound. Additionally, nCnSC and nanocurcumin had higher inhibition values than the antibiotic. Standard deviations and p value were calculated, and the data is not due to chance and is significant.

Conclusions/Discussion

My hypothesis was correct and my test results confirmed my hypothesis: The cumulative compound, nCnSC, will inhibit the biofilm of S. mutans, and the preventive anticoating will protect surfaces from biofilm formation. This compound inhibits the actual formation of biofilms and the biofilms in an advanced stage. Moreover, the compound can be manufactured as a Teflon film that is useful in preventing the formation of biofilms before they get to an advanced stage.

Summary Statement

My experiment shows that the cumulative compound of nanocurcumin, chitosan, and nAG will effectively inhibit the biofilm formation of Streptococcus mutans, and the preventive coating will protect surfaces from biofilm formation.

Help Received

I used the lab equipment at the Harker School under the supervision and mentorship of Dr. Gary Blickenstaff and Mr. Chris Spenner.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Isabel Torres

Project Number

S1520

Project Title

Effects of Ocean Acidification on Marine Calcifying Invertebrates

Abstract

Objectives/Goals

My objective is to determine how ocean acidification will affect Foraminifera, some of the world's most common marine microorganisms which make their shells out of calcium carbonate, by studying springs with high carbon dioxide content in the oceans of Yucatan, Mexico. My hypothesis is that there will be a higher abundance of foraminiferans per gram away from the springs than near the springs.

Methods/Materials

Sediment samples were collected in the center of and far from the carbon dioxide springs off the Yucatan Peninsula in Mexico. I weighed about 1-5 g of each sample and separated the sample by size fraction, using sieves with different sizes of holes. Using a compound microscope, I separated foraminiferans into the 6 most common species on a glass slide and counted the number of each species. I then calculated the number of foraminiferans per gram and percentage of each taxonomic group in each sample.

Results

There are statistically significantly fewer foraminiferans in the sediment near the springs than away from the springs. Some species, such as Discorbis rosea, are less common near the springs than away from the springs. Other species, such as Amphistegina gibbosa, are more common near the springs than away from the springs.

Conclusions/Discussion

As I hypothesized, foraminiferans are less abundant near the springs than away from the springs, most likely due to the high carbon dioxide levels and low pH levels at the springs. Thus, as carbon dioxide levels in the ocean rise and ocean pH decreases, due to ocean acidification, foraminiferans will become less abundant. Ocean acidification will affect calcifying organisms, such as forams, directly by requiring more energy for them to build their shells and skeletons and other organisms indirectly via food webs and other mechanisms.

Summary Statement

I show that forams are less abundant near high-carbon dioxide springs off Mexico, which suggests that forams will become less abundant as carbon dioxide continues to rise and ocean pH decreases, which is known as "ocean acidification."

Help Received

I used lab equipment at UC Santa Cruz under supervision of Dr. Adina Paytan. Graduate student Ana Martinez Fernandez collected sediment samples. Graduate student Kristin McCully helped me analyze my data and make my poster.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Sophia R. Vale

Project Number

S1521

Project Title

Navigation of Physarum polycephalum

Abstract

Objectives/Goals

Physarum polycephalum is a simple slime mold that crawls over agar and sends out pseudopodia, long projections, searching for food. Physarum can also navigate by leaving behind slime, a sticky trail of sugar and protein Although it has no nervous system, a previous study showed that Physarum uses a basic form of spatial memory to help it navigate (Reid, PNAS, January 15, 2013), using its own slime to avoid places it had been where there was no food. When completely surrounded by slime, it took Physarum much longer to find food because it could not use its own slime trail as a navigational marker. This study did not figure out how Physarum behaved when it encountered its own slime. My first goal was to reproduce the conclusion that slime slows down Physarum's search for food. My second goal was to watch Physarum by time lapse to see if it behaved differently when traveling on agar versus slime.

Methods/Materials

I grew Physarum on a 2% agar plate with oat flakes as food. I introduced a plastic barrier between the a piece of Physarum and its food. The time it took for the Physarum to navigate around the barrier and reach its food was measured. In one test, Physarum was placed on a fresh agar plate; in the other, it was placed on a plate covered with slime. In a second experiment, I made time lapse movies of Physarum crossing a slime barrier to reach its food source(one frame per 33 min).

Results

The mean time for Physarum to get to the food for the control (2% agar) was 39.7 hours with a s.d. of 1.5 hr for 3 trials. In the slime experiments, the mean time was 54.5 hours with a s.d. of 2.1 hr for 2 trials (Physarum failed to reach the oat in the third trial). On 2% agar, Physarum makes a fan shaped front edge that moves around searching for food. When Physarum reached a line of slime, it was not immediately repelled and could cross it. In about half of the trials, the Physarum behaved different from controls, traveling sideways along the slime instead of going straight ahead.

Conclusions/Discussion

Based upon the study of Reid, I hypothesized that Physarum surrounded by slime will take longer to get around a barrier than without slime. My results supported this hypothesis. From this result, one might think that the Physarum might be completely repelled by the slime. Instead I found that Physarum could enter into the slime but could not efficiently travel straight to its food.

Summary Statement

I studied how Physarum navigates to find food and how its uses information from its previous paths, marked by its slime trail.

Help Received

UCSF helped me to make agar plates. My Dad showed me how to make time lapse movies.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

David M. Zimmerman

Project Number

S1522

Project Title

Site-Directed Mutagenesis of S. oneidensis MR-1: A Novel Strategy for Genetic Engineering in Recalcitrant Microorganisms

Abstract

Objectives/Goals

Due to its respiratory vesatility, Shewanella oneidensis MR-1 is widely employed as a model organism for the study of electron-transport processes including subsurface bioremediation and electricity production in microbial fuel cells. However, MR-1's usefulness as a model organism is limited by its recalcitrance to techniques of genetic engineering developed for Eschericia coli. My objective was to implement a strategy for site-directed mutagenesis of the MR-1 chromosome in the absence of exogenous recombinase functions; to evaluate and optimize its utility for the construction of point substitutions and large deletions by examining strand-, site-, and sequence-specific effects.

Methods/Materials

Flask-cultures of MR-1 were harvested in mid-log phase, made electrocompetent, and snap-frozen for cryostorage. These were thawed and electroporated with DNA oligonucleotides (oligos) that contained the desired sequence alterations (conferring drug-resistance phenotypes) flanked by regions of homology to the target loci. Recombination frequencies were determined by plating on selective media while controlling for basal mutation rate, with subsequent restriction-fragment analysis to confirm presence of the intended mutations.

Results

Point substitutions were achieved at frequencies of 10^{-8} to 10^{-7}. Silent modifications designed to evade methyl-directed mismatch repair (MMR) enhanced this efficiency by ~10-fold ($p < 0.05$) in isolation, but had a negative impact on recombination frequency when in the presence of other similar modifications. Although the antibiotic resistance assay was not sufficiently sensitive to discriminate oligo-mediated deletions from the spontaneous mutation frequency, PCR amplification revealed that a minority of the drug-resistant isolates had incorporated the intended deletion.

Conclusions/Discussion

Ongoing experiments involve the use of ssDNA purified from PCR products to mediate insertional mutagenesis (e.g., of marker cassettes), obviating the need for mutations that confer selectable phenotypes in themselves. Taken together, these results open the door to development of a greatly expanded molecular toolkit for genetic manipulation of Shewanella spp. and provide novel insights into the mechanistic basis of Red-independent recombination.

Summary Statement

I developed and optimized a recombineering strategy, independent of host/exogenous recombinase functions, for genetic manipulation of the bacterium S. oneidensis MR-1; this technique has broad applicability to other recalcitrant microbes.

Help Received

Used laboratory facilities at the University of Southern California under the supervision of Prof. S.E. Finkel.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Austin Jones; Ian Jones

Project Number

S1595

Project Title

How Sterile Are Frozen Foods? The Effects of Defrosting on Bacterial Growth in Peas

Abstract

Objectives/Goals

We hypothesized that when peas were defrosted, bacterial growth would increase and there would be a direct correlation between the duration of defrosting and bacterial growth.

Methods/Materials

Three replicate pea samples were defrosted for each different treatment and refrozen until grinding and plating on Luria Broth agar plates. After 42 hours, growth was recorded by counting the number of colonies on each plate. Data was analyzed in Open Office.

Results

Bacterial growth during the first four hours of defrost time was generally minimal, but after the four hour mark, growth spiked and cultures contained hundreds of colonies.

Conclusions/Discussion

In our experiment, we found that, as predicted by our hypothesis, bacterial growth had a direct relationship with defrosting time. A longer period of defrost time correlated to more bacterial growth.

Summary Statement

We tested how defrosting affects bacterial growth in peas.

Help Received

Dr. Malhotra showed us a plating technique, but her culture was not used in the results.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Cory Hard; Michael Rincon

Project Number

S1596

Project Title

Biocontrol of Candidas albicans via Extracellular Chitinase

Abstract

Objectives/Goals

We hypothesized that the extracellular chitinase would be an effective antifungal agent against C. Albicans

Methods/Materials

Materials:
S. Marcescens (C. Biological), Petri Dishes, C. Albicans (C. Biological), Inoculating Loop, LB base, Fume Hood, Cornmeal base, Incubator, Fluconazole (2mg/ml), Shaker Plate, $(NH_4)_2SO_4$, 75% saturated, Autoclave, .5 McFarland Standard, DI H_2O, P20 and P1000, Microwave, 75% Ethanol, Centifuge, Critrate, Phosphate Buffer (pH 5.8), Analytical and Tabletop scales

Methods:
Preparation for 200 ml LB agar, Pouring plates, Inoculation of S. Marcescens onto the LB agar plates, Starting a Liquid Growth Culture, Extracting the Supernatant, Producing Chitinase Crude Extract, Growing Candidas Albicans, KB Disk Diffusion Test

Results

Our hypothesis was somewhat correct. At 48 hrs our Chitinase C.E. had the highest Zone of Inhibition, same as our Fluconazol, which was our standard. Though, the S. Marcescens Supernatant had the highest Average Zone of inhibition at 48 hrs.

Conclusions/Discussion

Discussion:
Our hypothesis was somewhat correct; the S. Marcescens supernatant was very effective against C. Albicans, creating clear zones of inhibition almost every trial. Alternatively, the chitinase crude extract was not effective as often, but did have some large zones of inhibition. Compared to the fluconazole, the S. Marcescens supernatant was a better antifungal agent against C. Albicans.
The crude extract of chitinase didn#t have a high average ZOI, but it did show potential with its 12 mm ZOI.

Conclusion:
This experiment showed that the supernatant of Serratia Marcescens does contain an antifungal agent equal to, if not better, than fluconazole.

Summary Statement

Our project was designed to see if Extracellular Chitinase would be an effective antifungal agent.

Help Received

Dr. Malhotra let us use her classroom and equipment at Thousand Oaks High School, she also helped us get access to the chemicals we needed.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)
Emmanuel P. Chan

Project Number
S1597

Project Title
Use of FTA Paper for the Transportation of Plasmodium Infected Blood Sample: A Feasibility Study

Abstract

Objectives/Goals
The use of FTA paper to transport biological specimens is important for remote areas to get access to laboratory services. Although some research studies have shown that nucleic acids of some microbial agents can be maintained for a long time on FTA paper, it is not clear whether the stability of these microbial DNAs can be maintained under various environmental conditions, such as high heat treatment. Here, the feasibility of FTA paper to transport Plasmodium falciparum DNA was examined.

Methods/Materials
FTA paper containing P. falciparum infected blood was subject to treatment at different temperatures for 24 hours, or at high temperature for up to 5 days. A field study was also carried out by sending FTA paper containing DNA of the parasite to different regions of the world. Quantitative real time PCR was used to measure the change in amplifiable DNA isolated from these treated FTA papers

Results
Results showed that there was no statistical significant change in amplifiable DNA when FTA paper containing the parasite was incubated at room temperature, 370C, 550C and 700C for 24 hours. Even when the FTA paper containing the infected blood was incubated for 5 days at 700C, there was no significant drop in amplifiable DNA. When FTA papers containing DNA of the parasite were sent to Cleveland, Toronto, Hong Kong and Shanghai, there was also no significant difference in amplifiable DNA isolated from these samples. However, based on linear regression analysis, a weak correlation was observed between the duration of postal transit and decrease in amplifiable DNA on the FTA papers. In addition, no amplifiable DNA was detected in two samples sent to Asian regions, suggesting other factors may affect the stability of the parasite DNA on the FTA paper.

Conclusions/Discussion
Results support the use of FTA paper to transport Plasmodium infected blood for clinical diagnostic uses. However, more studies are needed to delineate other factors which may compromise its use.

Summary Statement
To determine whether FTA is suitable for transporting Plasmodium infected blood sample for clinical diagnostic uses

Help Received
Scientists for Zoologix, Inc supervised and trained me in carrying out the research

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

D. Tre Risk, III

Project Number

S1598

Project Title

Waste Not, Want Not: Reducing Aquifer Depletion through Increased Recycled Water Consumption (Year 2)

Abstract

Objectives/Goals

In the Coachella Valley, the golf industry consumes an enormous amount of water. Golf courses need to have well-manicured, visually pleasing water features, which also acts as a reservoir for nightly watering and a source of nutrients for aquatic life. They frequently use aquifer water to achieve this. However, this resource is limited; the other two water sources are Colorado River water and Reclaimed water which is treated waste water. My goal was to mix different percentages of Reclaimed, Aquifer, and Colorado River water to find a solution that encourages little to no algae growth. I duplicated the work done during last years project and added a survey of golf course superintendents.

Methods/Materials

I ran 11 various combinations of water sources (from the Colorado River, the Aquifer, and Reclaimed Water). 3 tests of each sample type were made. I sampled each water combination for a total of 33 tests and examined the samples for algae growth. This was out of my budget so I developed a color system to measure algae growth.

I sent out a survey to 300 golf course superintendents in my area and questioned them on the different water sources that they use in their ponds and lakes.

Results

Algae started growing in the second week of the tests and continued throughout the study. At the end of the six week period the following levels of algae growth were noted:

100% Aquifer(Aqu)4.3; 100% Reclaimed(Rec)2.0; 100% Colorado (Col)5.7; 33% Aqu/33% Rec/33% Col 2.3; 50% Aqu/20% Rec/30% Col 3.0; 30% Aqu/50% Rec/20% Col 2.7; 20% Aqu/30% Rec/50% Col 3.7; 50% Aqu/30% Rec/20% Col 2.7; 60% Aqu/20% Rec/20% Col 3.3; 20% Aqu/60% Rec/20% Col 2.3; 20% Aqu/20% Rec/60% Col 5.0

Conclusions/Discussion

Colorado River water and its high percentage combinations allowed the highest levels of algae growth. Reclaimed water is highly treated and as a result, it hinders the algae growth the most.

Reclaimed water was not available to most of the golf courses who responded to my survey; CVWD is currently working on making this available to more golf courses. Reclaimed water not only proved to be effective as an added mixture to control algae growth but is also a plentiful resource during golf season. Therefore reclaimed water is at a peak at the same time water usage is highest on the courses. Currently there is not enough use for our existing reclaimed water so the excess water is actually dumped into the desert.

Summary Statement

Can algae growth be minimized by using water sources other than Aquifer water?

Help Received

Coachella Valley Water District provided water samples.

CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

Claire E. Ha

Project Number

S1599

Project Title

The Biggest Loser: Silkworm Edition

Abstract

Objectives/Goals

The objective of this experiment was to determine whether 4 grams of bacteroidetes, 2 grams of bacteroidetes, or no bacteroidetes causes the most weight loss. My hypothesis was the silkworms consuming 4 grams would lose more weight than the silkworms consuming 2 grams and no bacteroidetes since bacteroidetes cause weight loss.

Methods/Materials

After I evenly distributed thirty silkworms into fifteen containers by placing two in each container and separating them with dividers, I labeled one side of a container N-1 and the other N-2 (no bacteroidetes 1, no bacteroidetes 2), continuing until N-10. I did the same with the L (low) and the H (high). I weighed each silkworm#s initial weight. I cooked the food by boiling and mixing water with the artificial mulberry powder, microwaving, and storing the food in the refrigerator. I cooked two more batches: one with 2 grams of bacteroidetes, and one with 4 grams. I sliced the hardened food into pieces that weigh 0.5 grams and gave a piece of food to each silkworm. The next day, I weighed the silkworms. I cleaned containers by removing the contents, rinsing, and drying the container. I gave one piece of food to each silkworm. For eleven days, I fed, cleaned, and weighed the silkworms.

Results

The resulting averages illustrated that since Day 1, the silkworms exposed to 4 grams of bacteroidetes gained the most weight, gaining an average of 1.44 grams over the eleven days, the silkworms exposed to 2 grams of bacteroidetes gained the least weight, gaining an average of 1.28 grams, and the silkworms exposed to no bacteroidetes were in between, gaining an average of 1.31 grams.

Conclusions/Discussion

The data rejects the hypothesis that the silkworms consuming the 4 gram bacteroidetes food will lose more weight than the silkworms consuming the 2 gram food or the no bacteroidetes food since bacteroidetes cause weight loss. Although the amounts of bacteroidetes given to the silkworms were increased this year, the results this year were similar to those of last year: the high bacteroidetes silkworms gained the most weight, the low bacteroidetes silkworms gained the least, and the no bacteroidetes silkworms were in between. The similar results led me to hypothesize that bacteroidetes are most effective if used in moderate amounts rather than excessive amounts.

Summary Statement

The objective of this experiment was to determine whether 4 grams of bacteroidetes, 2 grams of bacteroidetes, or no bacteroidetes causes the most weight loss in silkworms.

Help Received

Mother bought supplies; father helped with graphs; teacher gave feedback.