

# **11th Annual Spring Student Research Symposium**



**March 23rd, 2013  
St. Croix Campus  
College of Science & Mathematics  
University of the Virgin Islands**

# Eleventh Annual Spring Student Research Symposium

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Saturday, March 23, 2013  
University of the Virgin Islands  
St. Croix Campus, U.S. Virgin Islands

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**Event Organized by:**

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*Emerging  
Caribbean  
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Emerging Caribbean Scientists (ECS) Programs increase research training and promote excellence for STEM (science, technology, engineering, and mathematics), psychology, and nursing students at the University of the Virgin Islands.



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## **Mycobacteriophage Cluster Assignments by PCR Complicated by Genome Diversity**

**Denniqua Benjamin<sup>1</sup>**

Joel F. Schildbach<sup>2</sup>, PhD (mentor)

<sup>1</sup>University of the Virgin Islands and <sup>2</sup>Johns Hopkins University

Mycobacteriophage are a group of bacteriophages or viruses that can infect Mycobacterial species. Mycobacteriophage were originally isolated from the *Mycobacterium smegmatis* and *Mycobacterium tuberculosis*. Presently over 2,500 have been isolated from environmental and clinical sources and nearly 400 phage genomes have been sequenced. Mycobacteriophage genomes are organized into clusters. Definitive assignment is by alignment of the entire genome with genomes of known phages. The 2011-2012 Phage Hunting class at Johns Hopkins University isolated 25 different phages. Attempts were made to place the different phages into clusters. Two different methods were used but produced conflicting results. High titer phage lysates used for PCR was developed by the students. A primer set developed by Victoria Hohenstein was used. The phages were amplified and selected reactions were treated and sequenced using a PCR primer. After conducting the series of tests, two lysates were successfully placed into sub clusters. Lysate 4 seems to have been contaminated with Lysate 14. Lysates 2 and 7 came up with inconclusive results because of the presence of multiple bands for multiple primers. The remaining lysates remain of question. Because of this we are led to believe that the primers that were developed are not as specific as we would have hoped.

This research was conducted at Johns Hopkins University and was funded by NIH RISE grant 2R25GM061325 and the Genentech Foundation.

## **High Levels of Sedimentation Hinder Lesion Recovery in the *Porites astreoides***

**Lavida Brooks**

Dr. Marilyn Brandt (mentor)

University of the Virgin Islands, St. Thomas, USVI

Coral reefs are of great importance to human and animal life. They protect the shorelines, serve as an economic plus and are providers of shelter and food to many animals. Unfortunately, coral reefs are easily harmed and destroyed by human activities, including activities that lead to increased sedimentation. This study investigated the impact of sediment run off on *Porites astreoides* (the mustard coral). The question of this study was “Would increased levels of sedimentation lead to lesion recovery or mortality?”

The test subjects were collected from John Brewers Bay, St. Thomas, VI. Each coral was randomly assigned into one of three treatment groups: 1) with 0 ml of sediment (control), 2) a group with 5 ml of sediment, and 3) a group with 15 ml of sediment. Small ( $< 3 \text{ cm}^2$ ) lesions were created on the added to the corals and the assigned amount of sediment was added to the corals and photographs taken every two days between November 14<sup>th</sup> 2012 and December 13<sup>th</sup> 2012 for future analysis. Photographs were taken at these times in order to analyze the progression rates of recovery or mortality. Using the program Image J to analyze the photographs, the area and the perimeter for the lesions were measured.

The data collected showed that coral mortality was more prominent in the 15ml group. As for the control and the 5ml group, signs of lesion recovery were observed. We concluded that these corals would be able to survive in areas with between 0-5 ml of sediment. For future study we plan to examine the impact of sedimentation levels between two intervals 0-5ml and 5-15ml and analyze the potential for thresholds of lesion recovery and or mortality rates.

This research was funded by the NIH MARC Grant #5T34GM008422.

## **Drug Use and Academic Experiences of Youth in the Custody of Human Services**

**Shareece Cannonier**

Aletha Baumann, PhD (mentor)

University of the Virgin Islands, St. Croix Campus

The purpose of this study was to examine the drug use of youth as it relates to history of substance use, results of urine analysis, truancy, history of suspensions/expulsions, and number of grade retentions of 189 youth who were in the custody of the Department of Human Services in 2008. The US Virgin Islands can benefit from having fewer adolescents who use drugs. More productive adolescents may decrease the crime rate and add more productive adults to the US Virgin Islands population. Data were gathered by the Virgin Islands Department of Human Services in 2008 and are completely anonymous. The data was analyzed to assess the relationships among history of substance use, results of urine analysis, truancy, history of suspensions/expulsions, and number of grade retentions. 27.50% of adolescents reported using drugs before. For the urine analysis, 17.50% adolescents tested positive for a drug. There was a significant correlation between all variables. The strongest was found between drug use and truancy.

## **Analysis of twenty species of the USVI fishery for overfishing**

**Tasha Corneille**

Angela Dikou, PhD (mentor)  
University of the Virgin Islands

Currently 44, 16, and 6 % of fish stocks are fully to heavily exploited, overexploited and depleted, respectively, worldwide. Overfishing is the depletion of fish from the population to such an extent that it can't be replenished naturally. Overfishing may occur as recruitment or/and growth overfishing. Recruitment overfishing is the removal of the fish from the population before it matures whereas growth overfishing is the depletion of larger size fish from the population such that fewer larger fish are represented in the catch. Fisheries management addresses overfishing for the sustainability of biological productivity through conservation of marine ecosystems.

To determine whether or not overfishing is occurring at the USVI, data for 20 out of approximately 70 species of a port biosampling database [1980-2009] was analyzed and values of critical fish lengths ( $L_{mat}$ : length at maturity;  $L_{\infty}$ =infinite length) were obtained from FishBase. Specifically, trends in average fish size in the catch; differences in average fish size among gear types; and contrasts of critical fish size values of the catch with those reported at Fishbase for relevant populations were evaluated. Significant trends in average fish size were revealed through regression analysis; significant differences in average fish size among gear types were revealed through one-way Analysis Of Variance; contrasts between fish size critical values were evaluated graphically. During the thirty year period, mean fish size decreased for two species (mutton snapper,  $R^2_{adj.}=0.48$ ,  $p=0.0004$ ,  $Y=15529.84-7.57*X$ ;; Spanish hogfish,  $R^2_{adj.}=0.99$ ,  $p=0.0331$ ,  $Y=7948.8-3.82*X$ ); increased for three species (longspine squirrelfish,  $R^2_{adj.}=0.23$ ,  $P=0.0023$ ,  $Y=-1103+0.65$ , spotted trunkfish,  $R^2_{adj.}=0.37$ ,  $P=0.0065$ ,  $Y=-3141.3+1.67*X$  and white grunt,  $R^2_{adj.}=0.48$ ,  $P=0.0281$   $Y=-3128.16+1.72*X$ ); and remained unaltered for the rest of the fifteen species. However, contrast of critical values of  $L_{mat}$  and  $L_{\infty}$  from FishBase indicated that Spanish hogfish and spotted trunkfish may be subject to recruitment overfishing regardless of the negative and positive trends, respectively. Differences in mean fish size among different gear types were species-specific. In particular, there was significantly lower mean fish size for 6 out of 17 species caught with fish traps compared to the other fishing gear types. Mis-matches between the direction of trends in mean size of fish in the catch and contrasts of critical length values of fish with minimum, maximum and average values of fish length in the catch, indicate probable creeping overfishing.

Examination of the whole suite of species in the future may assist in highlighting the magnitude of creeping overfishing in USVI fisheries and prompt appropriate adjustment of regulatory tools, such as protected areas, gear restrictions, and species-specific restrictions, by the Department of Planning and Natural Resources, if necessary.

Funding for this research was provided by the National Science Foundation (NSF) HBCU-UP grant #HRD-0506096.



## **Evaluation of Drought Tolerance in 3 Native Tree Species with Landscape Potential, a Biometric Approach**

**Kalunda Cuffy**

Dr. Thomas W. Zimmerman and Michael Morgan (mentors)  
Agricultural Experiment Station, University of the Virgin Islands

The US Virgin Islands possesses a seasonally dry climate; therefore, plants need to be drought tolerant. Plant species native to the USVI tend to tolerate drought better than the showy and exotic ornamental plants people like to use for landscape plantings. The objectives of this study were to assess drought tolerance, determine growth rates and calculate the amount of water necessary to produce plants of a size suitable for landscape planting, for three native tree species. The native tree species were Dog-Almond (*Andira inermis*), Torchwood (*Jacquinia arborea*) and Bay-rum (*Pimenta racemosa*). Three weekly watering regimes were established: field capacity,  $\frac{1}{2}$  and  $\frac{1}{4}$  field capacity. Every week, for 28 weeks, height and stem diameter of the plants were measured. Plants were harvested at the end of the study and separated into leaves, stems and roots, dried and weighed and subjected to statistical analysis. Although no tree dropped its leaves due to water stress, there was some wilting between watering periods, particularly as plants increased in size. *A. inermis* proved to be the least drought tolerant, followed by *P. racemosa*. The small coastal tree *J. arborea* tolerated water stress the most. For most of the study, plant growth of all species was best under a watering regime of  $\frac{1}{2}$  field capacity, until plant growth reached a sufficient size to demand more water. The planting of drought tolerant native tree species around buildings and in public spaces conserves both water and local biodiversity.

This research was funded by the USDI-USGS through the Virgin Islands Water Resources Research Institute.

## **Graphetonics**

### **Jewel Cumberbatch**

Dr. Wayne Archibald (mentor)

Univeristy of the Virgin Islands

The long-term objectives of this research are to understand doping mechanisms in graphene and to develop a quantitative understanding through computational modeling and simulations. In support of the structuring of graphene, we will have a robust computational and modeling effort to determine the required periodicities, symmetry classes, and expected band gaps for the graphene structures to be created. This effort will also be used to validate experimentally measured results. The entire proposed effort is designed to be an iterative process that goes from graphene synthesis, through materials characterization, to analysis, and back to synthesis. For superlattices formed by multiple alternating vertical layers of graphene and silicon carbide, conventional transfer-matrix methods will be used to analyze the band structure. For the planar structured graphene, the tight-binding or density-function methods will be used.

This research is supported by NSF grant award # 1238839. This presentation is funded by NSF HBCU-UP Grant Award No. HRD – 0506096.

## **Designing an Effective Scheduling Algorithm**

**Lauritz David Jr.**

Dr. Marc Boumedine (mentor)

Univeristy of the Virgin Islands

Many institutions, businesses, and organizations require scheduling to keep it on track with daily, weekly, monthly, and even yearly tasks. Scheduling is the action of sorting, organizing, and structuring required demands into available resources. In some situations there are constraints on the demands, which can only work for particular resources. There are two types of constraints, soft constraints and hard constraints. Hard constraints must be met for the demand to be scheduled, but the soft constraints are requests that are satisfied for convenience. For example a college schedule would have hard constraints such as the amount of seats in the class, but soft constraints such as the time the class was held. To implement this into a program, research was done to find the optimum algorithm for getting the best results in a reasonable amount of time. The *Tabu Search* algorithm was chosen because it was simple and effective. When completed it would check possible solutions and choose the one that satisfies all hard constraints and the most soft constraints thus producing a satisfying schedule. First a priority queue program organizes the demands from most constraints to least. Next, a blank schedule is created for the beginning of a binary tree. As the tree branches out the first level of branches attempts to add one demand to the blank schedule, and creates another level of branches for each instance where the demand can fit in the schedule. Each branch is called a node. Before the tree continues branching a cost function is added to determine which node satisfies most of the soft constraints without violating any hard constraints. The tree continues branching and adding demands into available resources, but only following the branch with the best cost until all the demands have been placed creating a complete schedule. As a student at the University of the Virgin Islands and learning that it's made its schedules by hand also sparked an interest in seeing the possibility of writing a scheduling program and later apply it to the UVI classes. Now that the program is in the testing stage not only should the program be able to schedule UVI classes but it would also find the near optimal solution, satisfying most of the constraints.

This research and presentation was funded by NSF HBCU-UP (Grant Number HRD – 0506096).

## **Effect of 4-CPA on Fruit Set and Yield of Heat Tolerant Tomato Cultivars**

**Shamali Dennerly**

Dr. Dilip Nandwani (mentor)

Agricultural Experiment Station, University of the Virgin Islands

Tomato (*Solanum lycopersicum* L.) is a favored commercial crop for most producers in the US Virgin Islands and is grown for fresh market sales. Higher temperatures in summer in the Virgin Islands are a challenge for flowering and low fruit set in tomato crop. We conducted a study on the effect of 4-Chlorophenoxy acetic acid (4-CPA) on the heat tolerant cultivars of tomato in the Virgin Islands tropical climate conditions. Two cherry tomato cultivars “Terenzo” and “Summer Cherry” evaluated in the greenhouse in summer season. Higher yields obtained in both cultivars treated with 4-CPA and no structural deformities in fruits observed. Marketable fruit weight was higher in treated plants of two cultivars evaluated. Fruit set and ripening was early in treated plants. No significant difference in acidity (pH 4), brix (7%) and firmness (6 ibf) recorded in treated and non-treated fruits. The preliminary results suggest that 4-Chlorophenoxy acetic acid may have the potential to increase fruit set and yields in tomato crop grown in the summer season.

This research was funded by the USDA-NIFA (Insular area funds) program to Agriculture Research Station (AES).

**Comparative Study to Determine the Water Quality Parameters of  
Bioluminescent Mangrove Lagoon and Salt River Bay, St. Croix, USVI**

**Anthonios Doliotis** , Lynisha Farrel, Anthonio Forbes, and Shelsa Marcel  
Dr. Bernard Castillo II and Kynoch Reale-Munroe (mentors)  
University of the Virgin Islands

Located on St. Croix, US Virgin Islands, Salt River Bay National Historical Park and Ecological Preserve contains both historic ruins and a diverse ecosystem. Salt River Bay is known for its mangrove forests and coral reefs. Bioluminescent dinoflagellates can be found throughout the entire bay. The dinoflagellates responsible for bioluminescence are small unicellular protists. Bioluminescence results from the conversion of chemical energy to light energy. Bioluminescence appears to be most concentrated in Mangrove Lagoon, which is located east of the bay. The main objective of this study was to determine and compare water quality parameters of Mangrove Lagoon and Salt River Bay. Water quality parameters, namely dissolved oxygen, salinity, temperature, pH, and turbidity were collected using a YSI data logger within the bioluminescent Mangrove Lagoon and Salt River Bay. Salinity and temperature are the two water quality parameters that this research project focused on and the results acquired were compared to known bioluminescent bays in literature. Results showed that the average salinity in Salt River Bay was 36.47 ppt and 37.98 ppt in Mangrove Lagoon, while the average temperature was 29.86°C in Salt River Bay and 30.30°C in Mangrove Lagoon.

This research was funded by NSF HBCU-UP Grant Award No. HRD – 0506096.

## **Molecular Detection of *Ehrlichia* in Virgin Islands Ticks**

**Denese Dorival**

Dr. Jennilee Robinson  
Univeristy of the Virgin Islands

The *Ehrlichia* organism is a gram negative bacterium which tends to infect dogs and other such animals. The *Ehrlichia* species which infect these dogs include *Ehrlichia canis*, *Ehrlichia chaffeensis*, *Ehrlichia ewingii*, and *Ehrlichia ruminantium*. *Ehrlichia* is transmitted by ticks *Rhipicephalus sanguineus*, better known as the Brown Dog Tick, and *Amblyomma americanum* better known as the Lone Star Tick when they bite on the animal. Upon entry the bacteria intergrates itself within the white blood cells of the animal. Previous research on ticks found in the Virgin Islands has led to the discovery of the *Ehrlichia* DNA in those ticks. During the Spring 2013 semester, a PCR assay will help identify the specific species of *Ehrlichia* found in those ticks. To carry out this research, ticks (*Rhipicephalus sanguineus*) were obtained from a local veterinary clinic. The samples were chopped and subject to DNA extraction. Polymerase Chain Reaction (PCR) was used to amplify the DNA samples and electrophoresis was performed to see if there was any *Ehrlichia* DNA present. The results show that *Ehrlichia* is present in a few of the ticks that were processed, however species identity is not yet known. Research is still being done to identify the species. *Ehrlichia* has clinical importance because the pathogen can be transmitted to humans through tick bites and is capable of causing ehrlichiosis. Also, since there is a natural inclination of dogs to be bitten by ticks, Virgin Islands dogs are also at risk of being infected. The results of this research could become useful to the public health sector of the Virgin Islands, where both humans and dogs are concerned.

This research and presentation was funded by the NIH MBRS-RISE  
Grant Award No. GM061325.

## **Evaluation of First and Third Generation Sorrel for Plant Vigor**

**Kenya Emanuel** and Khalid Matthew

Thomas W. Zimmerman, PhD (mentor)

Agricultural Experiment Station, University of the Virgin Islands

Sorrel, *Hibiscus sabdariffa*, has autogamous flowers that self-pollinate prior to flower opening resulting in inbred varieties. Cross pollination of inbred plants normally results in hybrid with vigor and outperforming both parents. Two varieties of red sorrel, 'TTB' and a 'KDN' were use as parents. 'TTB' are late flowering with a crimson fruit and 'KDN' is day-neutral with red fruit. The objective was to study two parental sorrel lines and the F1 and F3 progeny to evaluate plant vigor for production. Controlled pollinations, between the two varieties, were used to develop the F1 hybrids which were grown out for the second generation. Selection of plants from the F2 population, second generation, was used to obtain seed for the F3 progeny. Plant vigor was determined by measuring plant height and number of branches at two week intervals as well as recording when floral buds became visible. Data was analyzed using ANOVA and mean separation using Tukey test. Though the F1 population of 'TTB' x 'KDN' had a trend being taller than the parents, it wasn't significant for plant height and branch development. The F3 populations were significantly taller than the F1 and parent varieties. The F1 and F3 'TTB'x'KDN' plants initiated flowers at the same time as 'TTB' which was two weeks later than 'KDN'. However, the F3 line of 'KDN'x'TTB' initiated flowers at the same time as 'KDN' indicating a new day neutral variety. Hybrid vigor can be obtained from specific controlled crosses in sorrel. The day neutral characteristic can be recovered in F3 population where 'KDN' was the female parent.

This research was funded through USDA-NIFA- Insular Tropical Grant funds and USDA-SCBG from the VI Department of Agriculture.

## **Data Mining Database Design for Qualitative Research Analysis**

**Nichole Etienne**

Kostas Alexandridis, PhD (mentor)  
University of the Virgin Islands (St. Thomas Campus)

Qualitative research has become a means of gathering a wealth of data. Data may include social interaction, computer interaction, blogs or even information from websites. With that data comes the need for tools to analyze the complex structure. Data mining has the ability to convert field (qualitative) work into database (advance) through the use of mining statistics and algorithm. Data mining is an interdisciplinary field which refers to the process of extracting and analyzing the content and value of information from existing datasets and databases. From the existing information, associations are made through text mining (extracting or categorizing information within semantic categories) and identifying statistically important connections between attributes, among attribute states, and across states and attributes in the database. This results in the discovery of patterns of interconnectivity within and across data variables and their states. This research looks at the design and implementation of databases which connects qualitative information to quantitative for mining. Such will be implemented using SQL databases as well as the code. It will demonstrate the functionality of the database and the model. The importance of this research includes: benchmarking in the development of a modeling platform for more advanced scientific inferences; facilitating the emergence and discovery of complex patterns of associations within existing data structures, and linking parametric with non-parametric inference using machine learning and data mining tasks. Such analysis can aid the discovery and mining of complex patterns of relationships especially in large and seemingly unrelated relational database structures. Also, it is useful for generating useful analytical data (Real world data).

Partial funding for this research is provided by the NSF HBCU-UP HRD (award no. 0506096), the MBRS-RISE program (award no. GM061325), and the NSF VI-EPSCoR program (award no. 0814417).



**Assessing Change in Water Quality of Brewer's Bay, St. Thomas  
From 1978-Present**

**Lynisha Farrell**

Dr. Tyler Smith (mentor)  
University of the Virgin Islands

In the Virgin Islands, seagrass beds and coral reefs are valuable marine ecosystems that provide natural barriers for the shoreline, and food, breeding grounds, and nurseries for many familiar marine species. These habitats are impacted by terrestrial run off and sedimentation that impairs their ability to function effectively. To maintain healthy conditions these habitats must have the correct water quality (temperature, salinity, turbidity, water clarity, nutrients, chlorophyll, pH). In 1979 the Harry S. Truman Airport in St. Thomas USVI began construction to extend the runway by 726 meters length and 27 meters in depth into Brewers Bay. In 1978 to 1981 scientists measured the impacts the construction had on water quality and also provided a baseline of how the conditions were thirty years ago (Rogers et al. 1982). During 1978-1980 experimental stations were established at twenty different sites. The water quality parameters for turbidity, suspended matter, and transparency data were measured once a month at each station. Light transparency was measured twice in 1979 at the different stations using a Martek transmissiometer. The past objective of this experiment was to monitor and detect any changes to the water quality parameters of the seagrass beds and coral reefs. Preliminary historical results showed that extension of the runway changed the circulation patterns within Brewers Bay. However, there was not much of an effect on water quality, nor seagrass beds and coral reefs. The present objective of this experiment is to monitor the water quality parameters of sedimentation, water clarity, and a turbidity change from the 1980's to present. It is predicted that the water quality (sedimentation, water clarity, and turbidity) has declined since the 1980's. We will also monitor additional water quality parameters (pH and chlorophyll) to establish baselines for future investigations.

This research and presentation was funded by the NIH MBRS-RISE Grant Award No. GM061325.

## **Threats to Our Reefs: Establishing Baseline Data for Total Maximum Daily Loads (TMDLs) Development**

**Antonio Forbes** and Shelsa Marcel  
Dr. Bernard Castillo and Kynoch Reale-Munroe (mentors)  
University of the Virgin Islands

Terrestrial sedimentation is a large contributor to increased turbidity in relatively large bodies of water. Turbid waters have been known to negatively impact coral reefs by smothering the coral's exoskeleton and decreasing the availability of the sunlight used for photosynthesis by the coral reef's symbiotic partner; the zooxanthellae. In October of 2010, the United States' Environmental Protection Agency (EPA) published a list of impaired waters in the U.S. Virgin Islands, which indicated that the most common causes of pollution were sedimentation. As a result, Total Maximum Daily Loads (TMDLs) for turbidity from terrestrial sediment delivery has been targeted for development. Boiler Bay, located at the east end of St. Croix, USVI is the site of this study. Boiler Bay was selected as an ideal site to develop what baseline water quality parameters might be since it is undeveloped and free of direct sources of discharge, such as effluent or industrial. At the study site, we have deployed a YSI 6920 model sonde, approximately seventy feet away from its shoreline. The sonde collected water quality data, such as, temperature, dissolved oxygen, salinity, and turbidity data at an interval of five minutes over an eight-week period. Data collected from the sonde has shown that under ambient conditions, Boiler Bay meets the standards for optimal Nephelometric Turbidity Units (NTU) of no greater than 3 NTU. By using Boiler Bay as a standard of good quality water for other bodies of water around St. Croix, USVI, we can create a Total Maximum Daily Load (TMDL), in an attempt to safeguard our reefs.

This research was funded by NIH MBRS RISE Grant Award Number No. GM061325, as well as the United States Geological Survey-Water Resource Research Institute project number 2012VI220B.

## **Distribution of Disease in Shallow and Mesophotic Reefs**

**Akima George**

Marilyn Brandt, PhD (mentor)

University of the Virgin Islands

Coral reefs are very important to the Virgin Islands, but they are being affected by a myriad of stressors, including coral disease. Different reef habitats likely respond differently to these stressors based on the composition of their coral communities. This study examined the impact and dynamics of disease in mesophotic (> 30m depth) versus shallow (< 30m depth) reefs. We used a spatially-explicit individual-based model that could be programmed to represent the different community compositions of these two types of reefs. We hypothesized that disease would have greater impacts in the mesophotic reefs because of the mass-action principle that more hosts provide more opportunities for disease spread. Simulations were initiated with community compositions and disease levels recorded in the Territorial Coral Reef Monitoring Program's data set for mesophotic and shallow reefs and allowed to run for 10 years. Multiple simulations were run and outputs were compared between the reef habitats and to field data. Disease was found to have a more variable impact in the shallow reef systems where coral colonies were less dense.

This research and presentation was funded by the NIH MARC Grant #5T34GM008422.

## **Molecular Diagnostics can Detect and Identify Prokaryotic and Eukaryotic Pathogens in Terrestrial and Marine Organisms**

**Abrar Husein**

Jennilee Beth Robinson, PhD (mentor)

College of Science and Mathematics, University of the Virgin Islands

Molecular diagnostics, PCR and DNA analyses, can differentiate between prokaryotic or eukaryotic pathogens' unique DNA sequences. The proteobacterial order, Rickettsiales, contains numerous pathogens including medically important *Rickettsia* and *Ehrlichia* spp. transmitted by ticks. *Babesia*, a blood-borne protozoan parasite, is also transmitted by ticks. *Rhipicephalus sanguineus*, the brown dog tick, is ubiquitous and distributed worldwide. *R. sanguineus* transmits numerous pathogens, including disease-causing *Rickettsia*, *Ehrlichia* and *Babesia* to humans and animals. *R. sanguineus* was recently implicated in transmission of fatal Rocky Mountain spotted fever (*Rickettsia*) infections to humans. Previously, a *Rickettsia*-specific PCR assay amplified DNA fragments of various sizes from total genomic DNA extracted from *R. sanguineus* of V.I. canines. When visualized by gel electrophoresis, amplified DNA matches the expected length, 381 bp, of the *Rickettsia* *gltA* gene region targeted by this assay. To test my hypothesis that *R. sanguineus* in the V.I. are infected with *Rickettsia*, I gel-purified the PCR amplified ~381 bp DNA fragments. The purified DNA was submitted for direct DNA sequencing and cloned on a plasmid in *Escherichia coli* for analysis. Sufficient DNA was recovered from a volume of 50ul PCR reaction for purification and direct sequencing. Direct DNA sequencing was inconclusive due to contamination of purified DNA sample. Cloning attempt of the *gltA* gene failed in consequence of the *E. coli* being inactive. This experiment would have to be repeated to determine whether or not the *Rickettsia* *gltA* gene is present in the genome of *R. sanguineus*.

PCR-RFLP assays can quickly detect and differentiate between species that cause canine babesiosis. Species of *Babesia* are known to cause diseases in select hosts including dogs, cattle and humans. *B. canis* and *B. gibsoni* are the cause of severe disease and fatality in V.I. canines. Infections require different, high-risk treatments. Unfortunately, rapid diagnostics required to determine appropriate treatment are not available in the Virgin Islands. Therefore, I developed an assay that will rapidly detect and differentiate between agents of canine babesiosis. The assay (RFLP) uses restriction endonucleases to cut PCR-amplified DNA into different length fragments based on nucleotide sequence differences. Conserved PCR primers were selected to amplify 18S rDNA from all canine *Babesia* pathogens. Selected enzymes will generate unique fragment lengths for each pathogen, allowing species differentiation. Canine blood samples, infected with *Babesia*, would have to be obtained to test the validity of the developed PCR assay. An attempt was made to include a related hematozoan parasite of fish, *Haemogregarina*.

This research was funded by NSF HBCU-UP (Grant Number HRD – 0506096).

## **Utilizing Eye-Tracking to Determine Student Comprehension of Chemistry While Reading Online**

**Chantel Ible** and Murchtricia Charles  
Dr. Justin Shorb (mentor)  
University of the Virgin Islands

Over the years, eye-tracking has proven to be an essential resource for Human-Computer Interaction Researchers around the globe. Eye-tracking is a technique where a subject's eye movement can be measured in order to locate of his or her point of interest at any given time. Additionally, it allows researchers to observe the sequence in which the subject is looking from one location to another. This in return can permit observers to determine whether or not the movement of one's eye can be used to indirectly study the cognitive responsiveness of a student. The basis of this study is to utilize eye-tracking to determine whether Chemistry students have the ability to make conceptual connections between different representations of the same Chemistry information. Making use of microscopic, macroscopic and symbolic representations, we would be able to observe the variations in attention which the student give various representations to determine their understanding of the relationship between them. A novel approach to analyzing this data will be discussed along with preliminary data showing how relational connections can be extracted from eye-tracking sequences. This analysis is done using eigenvalue/eigenvector decomposition, also known as Factor Analysis.

This research was funded by grant number HBCU-1137472. Additional support provided by NSF HBCU-UP (Grant Number HRD – 0506096).

## Development of Water Quality Labs for General Chemistry at UVI

**Clyde Joseph** and Micadel Hazell

Dr. Justin M. Shorb (mentor)

University of the Virgin Islands

There are different styles of chemistry laboratories: some have been proven to be more effective at helping students to master the material. The four types of labs, as defined by Domin<sup>1</sup>, are expository, inquiry, discovery and problem-based. Up until this past year at UVI, all of the laboratories were expository or discovery styles. These use given procedures which students follow like a cookbook recipe. The inquiry and problem-based styles of lab make use of student generated procedures. Research has shown that having students generate their own procedures improves the ability for students to think creatively and retain information longer. In this work, a set of water quality tests were used as a foundation to design new laboratory exercises for general chemistry. The choice to incorporate water quality testing was decided based on the ubiquitous appeal water quality measurements have within our island territory. Laboratory exercises and their pedagogical design are discussed for measuring pH, turbidity, and salinity/Total Dissolved Solids.

Reference Cited:

1. Domin, D. S. A Content Analysis of General Chemistry Laboratory Manuals for Evidence of Higher-Order Cognitive Tasks. *J. Chem. Educ.* **76**, 109 (1999).

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## **Impact of Macroalgal Interactions on Coral Health Across the USVI**

**Matthew Kammann**

Dr. Tyler Smith and Jacquelyn M. Calnan (mentors)

Center for Marine and Environmental Studies, University of the Virgin Islands

An understanding of the impact of coral-algal interactions is critical to predicting future reef conditions. While competition between coral and macroalgae has been described as a fundamental process structuring reef communities, there is a lack of information on natural prevalence rates and species-specific impacts of competition on coral health. From 2009-2011, we conducted annual surveys of 28 study sites of the US Virgin Islands Territorial Coral Reef Monitoring Program (TCRMP) across a variety of depths (4 – 40 m) and distances from shore (0.1 – 18 km) in the U.S Virgin Islands. At each site we assessed benthic cover and coral health, including macroalgal interactions on each coral colony under transects. The prevalence of coral-macroalgal interactions increased with macroalgal cover ( $r^2=0.23$ ,  $p<0.001$ ). The overall prevalence of macroalgal interactions was 41%; however, there was high species-specific variability, from 59% (*Montastraea annularis* species complex) to 17% (*Scolymia* spp.). The vast majority of macroalgae interactions (97%) were caused by the algal species *Lobophora variegata* (36%) and *Dictyota* spp. (61%). In addition, the extent of colony affected by interactions was significantly greater for small colonies (<10cm) than large colonies ( $df=118$ ,  $p=0.0041$ ).

Funding was provided by the Territorial Coral Reef Monitoring Project, Virgin Islands Experimental Program to Stimulate Competitive Research (VI-EPSCoR). Support for this work also provided by the Vento Research Fund.

**Developing a PCR Protocol for the Greater Bulldog Bat (*Noctilio leporinus*)  
in the Northern US Virgin Islands**

**Thalia Lake** and Shanelle Farrington  
Dr. Alice Stanford (mentor)  
University of the Virgin Islands

Bats are a vital link in the food chain system. Some species control the mosquito population and others serve as pollinators. *Noctilio leporinus* (order Chiroptera), is commonly called the greater bulldog bat because of its features. *Noctilio leporinus* is the largest species of bats found in the Virgin Islands. It is suspected that the populations are declining due to natural and anthropogenic causes. This may lead to decreased biodiversity within the bat populations of the Virgin Islands. Population genetics data are needed in conservation planning to identify means of protecting our species and their habitats. Before we can assess genetic diversity, we must develop a Polymerase Chain Reaction (PCR) protocol for *N. leporinus* that can be used to generate population genetics data. We extracted nuclear DNA (deoxyribonucleic acid) from tissue that was excised from the bat's wing. We hypothesized that 55 degrees would be the optimal annealing temperature. For each primer, we tested a range of annealing temperatures of 55-63 degree Celsius to determine the best PCR protocol. The results were then visualized using gel electrophoresis. Conclusively, each primer has one particular temperature at which it works best. The protocol that was developed was successful using the primers at annealing temperatures between 55 degrees Celsius and 59 degrees Celsius.

This research was funded by the Vento Foundation and the National Science Foundation's HBCU-UP program (grant # HRD-0506096).



## **Applying Digital Normalization to Transcriptome Sequencing: Effects of Varying Coverage**

**Danny Lynch**<sup>1</sup>

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Advances in next generation sequencing (NGS) have led to a wealth of data being produced by the scientific community. These large data sets require new software pipelines to lower the cost of transcriptome assembly. Digital normalization, a single pass algorithm that reduces the size of shotgun sequence data sets, is one such tool. The purpose of this study was to determine if digital normalization could be effectively used to reduce RNA-Seq data sets while retaining sufficient information for accurate *de novo* assembly. We hypothesized that digital normalization at varying coverage values would produce assemblies similar to those obtained from processing non-normalized data. Using a yeast reference transcriptome and a known RNA-Seq read set, we digitally normalized the raw reads at varying coverage levels. We then assembled the original and normalized read sets and compared the resulting transcriptome assemblies with the reference. We found that at varying coverage values, the digital normalized assembly contained fewer errors than the non-normalized data for the yeast dataset's *de novo* transcriptome assembly. Furthermore, when the raw reads were aligned against each of the assemblies, it was discovered that the digitalized assemblies returned a 20% more accurate mapping than the non-digitalized assemblies. By more efficiently processing RNA-Seq data using digital normalization, it will be possible to assemble complete transcriptomes in a fraction of the current time. This increased knowledge will facilitate greater understanding of gene expression and function. Eventually, this could help improve direct patient care and future biomedical research endeavors.

This research was funded by National Science Foundation Grant #0939454. Support also provided by NIH's MBRS-RISE Grant #GM061325.

## **Threats to Our Reefs: Lionfish Invasion in St. Croix, USVI and GIS Mapping of Distribution**

**Shelsa S Marcel**

Dr. Bernard Castillo II and Prof. Kynoch Reale-Munroe (mentors)  
University of the Virgin Islands

The incursion of the invasive species of lionfish, *Pterois volitans*, in the Western Atlantic and Caribbean has been an issue of great scientific concern since their first detection in the Atlantic in 1992. November 28<sup>th</sup>, 2008 marked the first confirmed sighting of lionfish in the waters around our United States Virgin Islands territory, specifically St. Croix. Only four years later, St. Croix waters are being ravaged by proliferating populations of these indigenously Indo-Pacific lionfish. *Pterois volitans*' presence in the ecological system of our waters could have detrimental effects on native populations of fish, the local fishing industry, and the ecology of our coral habitats. In reaction to this invasion, there have been early dive attempts at search and recovery efforts of lionfish around the island of St. Croix, USVI. Our study aimed to create a GIS map of the spatial distribution and abundance of lionfish using the data from these dives, in response to the threat of the lionfish. The island was divided into six sectors, each sector serving as a dive spot for the collection of data on lionfish GPS location and abundance. GIS, Geographic Information System, was then used as a tool to plot the data onto a satellite map of the territory. The resulting map is a powerful tool useful for identifying spatial distribution and determining regions of abundance of lionfish around St. Croix, enabling analysis and solution development concerning this current threat to our reef.

This research was funded by NIH MBRS-RISE Grant Award No. GM061325.

## **Generation of an EFhd2 Null Mutant to Study its Association with the Microtubule-Associated Protein Tau**

**Shenee Martin**, Eva N. Rodríguez-Cruz, and Jaime Vaquer-Alicea III

Irving E. Vega, PhD (mentor)

University of Puerto Rico, Rio Piedras Campus, Department of Biology, San Juan, PR

The hyperphosphorylated microtubule-associated protein tau is implicated in the pathobiology of neurodegenerative diseases known as tauopathies. The identification of proteins associated with tau may provide insights that contribute to the understanding of tauopathies. Previous research work contributed to the identification of the novel protein EFhd2 as a tau-associated protein linked to tau-mediated neurodegeneration in tauopathy mouse models and Alzheimer's disease. However, the molecular requirements that facilitate the interaction between these two proteins are unknown. EFhd2 is a calcium binding protein of unknown physiological function. Biochemical analysis on this novel protein indicated that EFhd2 is phosphorylated by the protein kinase complex Cdk5/p25. Therefore, the aim of this project was to develop an EFhd2 null mutant that allowed us to evaluate whether or not the association between EFhd2 and tau protein and also the putative oligomerization of EFhd2 depends on calcium binding and phosphorylation state of EFhd2. A conserved aspartate residue known to be required for EFhd2 calcium binding activity was mutated to alanine. Additionally, another missense mutation was incorporated to exchange the identified serine residue, where EFhd2 is phosphorylated, to alanine. The mutant EFhd2 generated was defective in calcium binding activity and not phosphorylated by Cdk5/p25. A modified direct-ELISA was used to determine the interaction between the generated EFhd2 null mutant, wild type EFhd2 and recombinant tau. The results showed that mutating the phosphorylation site and calcium binding domain do not affect the self-oligomerization of EFhd2. The generation of the EFhd2 null mutant allows us to obtain insights into the molecular properties of the novel protein EFhd2 and its association with tau.

This research was funded, in part, by UVI NIH MARC Grant No. 5T34GM008422, NIH-NINDS SC1NS066988-03, and NSF- REU.

## **The Necessary Relationship between Persistence and Institutional Satisfaction**

**Darrell H. Mercer Jr.** and Tara J. Brim  
Dr. Konstantinos Alexandridis (mentor)  
University of the Virgin Islands

The ultimate goals of every person entering college are to graduate and earn their diploma. Earning a college degree enables enhanced career, financial and employment opportunities for the graduates. Data from the Bureau of Labor Statistics indicate that the unemployment rate for people with a Bachelor's degree is 4.5% whereas if a person solely has a high school diploma the rate is 8.3%. Similarly, on average, a person with a Bachelor's degree earns \$414 dollars more per week than a person with a high school diploma. However, everyone that goes to college does not graduate. According to U.S. Department of Education, the national college graduation rate is 57.3%. Black men and women graduate from college at a rate of 33.1% and 44.8% respectively. Persistence and institutional satisfaction as important factors associated with retention and graduation rates were looked at by the researchers. The more satisfied a student is with her/his academic institution, the more likely they are to persist in subsequent semesters, perform better academically, and ultimately graduate from college. Both quantitative academic and qualitative satisfaction criteria as potential factors influencing retention and graduation rates at the University of the Virgin Islands were looked at by the researchers. A mixed research methods approach was used by the researchers, and focused on the factor composition and the factor interactions as influencers of academic performance, retention and graduation rates. The importance of this research rests on the proposition that institutional academic interventions aimed at improving satisfaction and performance can have a beneficial effect to college and graduation rates at the University of the Virgin Islands.

Partial funding for this work is provided by NSF/HRD ERP award no. 1036183 and the MBRS-RISE Grant Award No. GM061325.

## Investigation of Filtering Metagenomic Sequencing Data on Assembly

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Digital normalization, a new heuristic approach that reduces sequencing data to a minimum while preserving maximum information. We hypothesize metagenomic data filtered by digital normalization successfully reduces the data volume without losing information. We mapped reads to reference genomes from the Human Microbiome Project (HMP) mock data set. We then performed metagenomic assembly on raw, normalized, and normalized partitioned reads. Next, we mapped the raw reads to the *de novo* assemblies and compared them to the reference to determine if information from the normalized reads was lost and/or if there was an advantage in the normalized assemblies. The mapping analysis show the digitally normalized assembly had 1.33% increase in reads mapping compared to the raw read assembly and retained information that would have been lost. The normalized and partitioned assembly only lost 2.49% of reads that mapped when compared to the non-normalized assembly results. The non-normalized assembly took 57 minutes to complete and used approximately 16.1 gigabytes of memory. The digitally normalized assembly took 8 minutes to run, 7.125x faster than the non-normalized assembly, and used 34 megabytes of memory, a 485% reduction in memory capacity. The digitally normalized and partitioned assembly finished in 11minutes (5.18x faster) and used 48 megabytes of memory, a 344% decrease in memory compared to the non-normalized assembly. This investigation shows that digital normalization can reduce redundant reads and their associated errors in metagenomic sequencing data, thereby significantly decreasing the time and computational resources required to perform *de novo* assembly without sacrificing sensitivity.

This research was funded by Michigan State University and the National Science Foundation Grant #0939454. Presentation is supported by the NIH's MBRS-RISE Grant #GM061325.

## **Papaya: The Influence of Sex on Plant Height and Production**

**Tyrone Pascal**

Dr. Thomas W. Zimmerman and Carlos Montilla (mentors)  
Agricultural Experiment Station, University of the Virgin Islands

The genders of papaya plants are male, female or hermaphrodite (bisexual) with the latter two as the main fruit-bearing types but information lacks on which sex is the most productive. The objective was to study the relationship between the female and hermaphrodite papaya gender and its effect on height and fruit production. Four varieties of importance to the US Virgin Islands, 'Maradol', 'TW', 'Tainung 5' and 'UVI' and four hybrids, FW x C, 'Maradol' x 'Tainung 5', 'Maradol' x 'Young Nong 1', and 'TW' x 'Tainung 5' were evaluated. The plants were transplanted into the field on April 4<sup>th</sup>, 2012. Data was collected monthly for ten months and included plant sex, plant height, height to first fruit and number of fruit set. Female papaya plants began to flower a week or two before hermaphrodite papayas. The females had a trend to be shorter than hermaphrodites over time. The height to the first fruit was significantly lower for female 'Tainung 5', 'Maradol' x 'Tainung 5', 'Maradol' x 'Young Nong 1'. Female trees had a trend for greater fruit set but female 'Tainung 5' set significantly more fruit than hermaphrodite plants. Even though differences were observed between female and hermaphrodite trees, these differences were minimal for most varieties and hybrids.

This research was supported by USDA-NIFA-Hatch.

## **Biometric Analysis of the Invasive Pacific Lionfish (*Pterois volitans*) in the Virgin Islands**

**Nalinie Ramnaraine**

Dr. Richard S. Nemeth (mentor)

Center for Marine and Environmental Studies, University of the Virgin Islands

Indo-Pacific lionfish (*Pterois volitans*) are precipitously invading the waters of the Caribbean and tropical Atlantic. Due to their population explosion and aggressive behavior, lionfish have the potential to become the most devastating marine invasion in history by significantly reducing the abundance of coral reef fishes and leaving behind a devastated ecosystem. It was first found in the US Virgin Islands in 2008 and is now becoming a common sight on most coral reefs. Lionfish are now being found on both St. Thomas and St. Croix. These two islands differ in the abundance and size of reef fish with St. Croix having much fewer and smaller fish than St. Thomas. In order to understand its potential impact on native fishes, we need to learn more about its biology and basic life history characteristics. The analysis of weight length data can be used to evaluate the condition of fish species. This condition factor is measure of the well-being or rate of consumption of reef fish. Our primary goal is to test the hypothesis that lionfish in St. Croix has a lower condition factor than lionfish in St. Thomas. This leads toward two objectives; (1) Mathematically relating the relationship between weight and length of lionfish in St. Thomas and St. Croix; (2) Measuring the variation from the expected weight (W) for length (L) of individual fish as indications of corpulence, well-being, or gonad development. Length and weight of sample lionfishes (***N* = ~90**) were obtained. The Fulton's Condition Factor ( $W/L^3 \times 100,000$ ) was done to determine the ratio between the observed weight and an expected weight dependent on the fish's length. According to the *ANOVA Analysis* that was obtained (***N* = 48**) the **average female length = 29.59 cm** and **average male length = 26.66 cm**; (***F* = 26.66, *P* < 1.46 x 10<sup>-6</sup>**). Weight analysis indicated (***N* = 90**) the **average female weight = 256.38 g**; **average male weight = 424.41 g**; (***F* = 26.66, *P* < 1.46 x 10<sup>-6</sup>**). *Studies are being continued to determine the length-weight relationships, condition factor, GSI among habitats. We are also interested in examining growth rates of lionfish in the territory. Factors that would be taken in consideration are age and length of lionfish. The age will be determined by examining the otolith obtained during dissection process.*

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**Evaluating the Abundance and Size Distribution of Indo-Pacific Lionfish  
(*Pterois* spp.) in the US. Virgin Islands**

**Nikita Thompson** , Charles Martin, and Nalinie Ramnaraine  
Dr. Richard Nemeth (mentor)  
University of the Virgin Islands

Over the last decade, the invasion of the Indo-Pacific lionfish have captured the attention of many scientists and researchers, due to the poorly understood ecological impacts the invaded species can have on the marine ecosystems and native organisms. Because of its voracious appetite and lack of predators, the invaded species' population is rapidly increasing; therefore, this may be challenging for managers when trying to control the population and reduce the potential negative impacts.

In the U.S. Virgin Islands, the lionfish sighting have become more frequent over the last few years. To aid USVI managers in the efforts to control the population and reduce the number of lionfish by targeting specific habitat types, this study will focus on evaluating the abundance and distribution patterns and size structure of the lionfish population. The goal is to identify habitats with the highest abundance of adult and juvenile lionfish and any drivers that the species may have in selecting specific habitat type. In this study, fish surveys were carried out in three habitat types – mangroves, seagrass beds, and coral reefs. Ten sites were randomly stratified by habitat type, and 25 x 4m transects were deployed and a roving dive was performed at each site. In addition to the surveys, a database compiled of information from the surveys as well as past and current lionfish sightings around the territory. Also, dissections were performed on lionfish specimens that were caught by researchers and recreational divers. This will, also, allow examination of the effects of habitat on lionfish demographics, such as growth and reproduction.

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# **Notes**

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### Judges

The event organizers would like to recognize the mentors and judges who have volunteered their time and energy to critique these student presentations. They have made a great contribution to the success of our students and this symposium. Thank you to the judges for your dedication to the advancement of young Caribbean scientists. You are greatly appreciated.

***Thank you to friends, family, and members of the wider community for attending and supporting student research at the University of the Virgin Islands.***



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