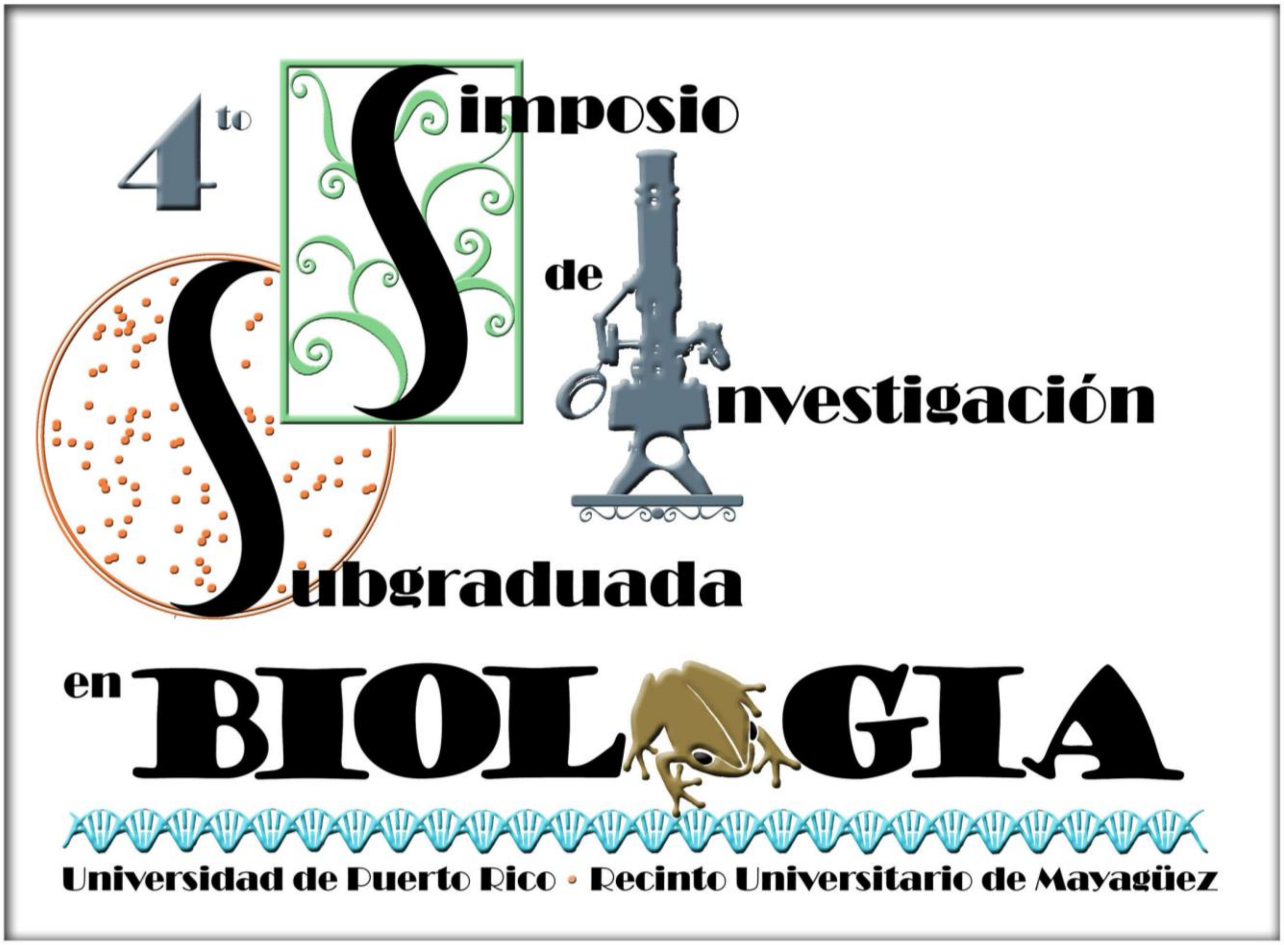

4to Simposio de Investigación Subgraduada en Biología

Universidad de Puerto Rico • Recinto Universitario de Mayagüez

sábado, 3 de mayo de 2014
Edificio de Biología
Recinto Universitario de Mayagüez

Biología
Universidad de Puerto Rico Mayagüez

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¡BIENVENIDOS AL CUARTO SIMPOSIO DE INVESTIGACIÓN SUBGRADUADA EN BIOLOGÍA!

Nuevamente el Departamento de Biología del Recinto Universitario de Mayagüez se une para celebrar y reconocer la diversidad y la labor investigativa de nuestros estudiantes subgraduados. Nuestro departamento alberga unos 1,400 estudiantes, de los cuales aproximadamente el diez por ciento se envuelve en el diseño y la ejecución de proyectos científicos en diversas ramas de la biología. Con la divulgación de los resultados de sus investigaciones, dentro del contexto de la comunidad cívica y científica, nuestros estudiantes completan el método científico.

Este Cuarto Simposio de Investigación Subgraduada tiene como propósito continuar proveyendo el espacio para consolidar el conocimiento adquirido durante la experimentación científica en el laboratorio y poner en práctica las destrezas de comunicación oral científica. Este año, reconociendo la reciprocidad y el potencial de colaboración entre biología y arte, se abre un certamen de exposiciones artístico-científico de nuestros estudiantes y colegas.

Como en años anteriores, el comité organizador agradece profundamente el apoyo del Departamento de Biología-Recinto Universitario de Mayagüez, Role Model-H.H.M.I. (subvención de Howard Hughes Medical Institutes) y su Directora, Dra. Nanette Diffoot Carlo. También deseamos agradecer el apoyo y colaboración de los todos los mentores de investigación de los estudiantes presentadores y de los colegas que fungen como jueces en la evaluación de los trabajos presentados. Además, queremos agradecer profundamente a nuestros estudiantes graduados y a las asociaciones estudiantiles de nuestro Departamento por su ayuda durante la celebración del simposio. Finalmente, nos gustaría reconocer la colaboración del Sr. Ramiro Vidal por la preparación de la página electrónica para someter los resúmenes y las inscripciones y al Sr. Martín Rosas por hacer disponible la infraestructura para el proceso de recibir las presentaciones. Además, nuestro agradecimiento al Dr. Carlos Muños por la preparación de la portada para el libro de resúmenes y a nuestras secretarias en el Departamento de Biología por su apoyo y colaboración: Brenda Soto, Mitzy Zavala, Alicia Collazo, Magda Bermúdez y Mary Jiménez.

Comité Organizador

David Logue-Presidente

Dimaris Acosta

Sandra L. Maldonado Ramírez

Vivian Navas

Luis A. Ríos Hernández

María M. Vargas Rodríguez

Jeanine Vélez Gavilán

Itinerario Cuarto Simposio de Investigación Subgraduada
3 de mayo de 2014

8:00	Registro
8:30	Bienvenida: Auditorio de Biología (B-392)
9:00	Primera Sesión Plenaria Dr. Lisa Gieg Auditorio de Biología (B-392)
9:30	Merienda
9:45	B 180 Ecología Microbiana
	B 181 Génetica No Humana
	B 182 Medicina
	B 280A Comportamiento
12:00	Almuerzo
1:00	Segunda Sesión Plenaria Dr. Eugenio Santiago Auditorio de Biología (B-392)
1:45	Sesión II
	B 180 Bioquímica
	B 181 Simbiosis
	B 182 Medicina Genética
	B 280A Depósito de Genes Microbianos
	B280C Ecología de Plantas
3:30	Merienda
3:45	Sesión III
	B 180 Evolución
	B 181 El Poder de los Microbios
	B 182 Ecología Animal
	B 280A Genética Humana
5:00	Premiación y Clausura Auditorio de Biología (B-392)
6:00	Foto del Grupo de Participantes

Presentaciones científicas

OVER-EXPRESSION OF HSCEN1 USING *ESCHERICHIA COLI* IN A 30L BIOREACTOR

Acevedo Rivera, Yesenia M.1 and Belinda Pastrana2

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Abstract

Centrins are calcium-binding proteins that belong to the EF-hand superfamily; they are also considered to be eukaryotic signature proteins. Up regulated expression of *Homo sapiens* Centrin 1 (Hscen1) has been observed in pancreatic and prostate cancer, suggesting it could be potentially used as a cancer biomarker for diagnostic and prognostic purposes. To date, there are NO pancreatic cancer biomarkers clinically available. This is the fourth cause of cancer death in the United States and Puerto Rico. Our aim was to over-express Hscen1 using *E. coli* BL21 (λDE3) STAR cells and scale it up to a 30L BIOSTAT® Cplus bioreactor for future biophysical studies and further research and development. Temperature, pH, dissolved oxygen and agitation parameters were controlled during the fed-batch culture process. The E. coli cell culture was induced with isopropyl β-D-1-thiogalactopyranoside (IPTG) for a tightly regulated protein expression. Bacterial growth was monitored by measuring optical density (OD) at 550nm. In order to verify protein over-expression, an SDS-PAGE was performed. As a result of the bioprocess, 40 grams per liter cell culture yield was obtained. Together, these results suggest a successful fermentation process was achieved.

RELATIONSHIP BETWEEN GLAUCOMA AND GENE LOXL1

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Abstract

Recent studies have shown a relationship between Exfoliation Glaucoma Syndrome (XGS) and polymorphisms found on the gene Lysil oxidase-like 1 (LOXL1). Puerto Ricans are valuable candidates to elucidate the role of LOXL1 in XGS due to the high incidence of glaucoma and the high European ancestry on the island. A population genetics study was done to determine frequency of LOXL1 variants associated to XGS in Puerto Rico. A single non-synonymous single nucleotide polymorphism (rs3825942) in LOXL1 associated with XGS was genotyped using Real-Time PCR from randomly sampling 385 Puerto Ricans from different regions. Allelic frequency was determined by cities and by geographical regions. The high-risk allele (G) believed to increase susceptibility to XGS was found to be less frequent (38%) in Puerto Ricans compared to the low-risk allele A (62%). The high-risk G allele is found at a frequency of 82% in Europe and 86% throughout the world. Thus, its frequency of 38% in Puerto Rico should be regarded as low. We conclude that the low frequency of the allele may have been the consequence of a founder effect during the colonization of Puerto Rico by Europeans. We further conclude that the high incidence of exfoliation glaucoma in Puerto Rico may be due to some other genetic variant being in a higher-than-expected frequency.

NUTRIENT IMPACT ON THE CILIATE COMMUNITY OF *TILLANDSIA UTRICULATA*

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Abstract

Biological interactions and nutrients are important factors regulating community structure and ecosystem stability. “Top-Down” theory suggests that predators play a key role in structuring trophic webs, whereas the “Bottom-Up” theory postulates that trophic web dynamics are regulated by nutrients in the ecosystem. Previous studies demonstrated a “Top-Down Effect” in the phytotelmata of tank bromeliads, *Tillandsia utriculata*. However, it is unknown whether the opposite model is also valid in such a simple micro ecosystem that undergoes monthly fluctuations in humidity, phosphate, and nitrate concentrations (Santiago-Vera, 2013). If “Bottom-Up Effects” are prevalent in this natural microcosm, then there will be differences in ciliate species richness, composition and abundance in treatments with higher nutrient concentrations in contrast to the controls. We constructed artificial bromeliads to emulate spatial heterogeneity of the natural microcosm, and performed a randomized complete block design with 4 treatments (control, phosphate, nitrate, and phosphate/nitrate). After ten days, the samples were fixed on Lugol’s and enumerated. There were significant differences (ANOVA) in ciliate species richness and abundance among the control and the other treatments. In terms of species composition, there were no differences in the dominant species (NMDS) between treatments. Thus, both “Top-Down and Bottom-Up Effects” play an important role in this simple trophic web. The next step would be to identify the relative weight of these concomitant effects in *T. utriculata* across time since this information could serve to understand changes in large scale trophic webs in the same habitat.

ISOLATION OF UV-C RADIATION RESISTANT BIOPROSPECTS FROM PUERTO RICO

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Abstract

There are three types of ultraviolet (UV) radiation: UV-A and UV-B, which reach Earth’s surface, while UV-C remains at the upper atmosphere. Human UV-C exposure can occur because of the recent fragmentation of the atmosphere; this causes complications because it is lethal and really harmful to cells. To date, many researches have been aimed to detain different types of radiation-induced illnesses, but none have been focused on the search of UV-C resistant microorganisms. In fact, scientists are using microorganisms as biological models for solving similar biomedical challenges. Our research goal is to find cultivatable bacteria in natural ecosystems of Puerto Rico that resist UV-C. This was achieved by growing previously isolated radiation resistant (RR) candidates from the Cabo Rojo’s Hypersalines Microbial Mats and Guanica’s Dry Forest. RR candidates were exposed to UV-C for periods of 45, 90, and 135 seconds using a laminar flow hood as a UV-C source. After the exposure, bacteria were grown at 37ºC for 24 hours, and covered in aluminum foil to avoid DNA repair by photo-reactivation enzymes. The bacterial survival percentage was determined and plotted. Three bacterium, named R4red, R4red/orange, and Bac. Mat, were found to have a higher survival percentage than that of the control group bacteria *Escherichia coli*. R4 red had the highest survival rate which was of 10%. Work is in process for isolating and testing of more candidates using this system. The RR bioprospects isolated will be analyzed in order to detect the gene(s) responsible of their UV-C resistance.

DIFERENCIAS EN NUTRIENTES DE *PILOSOCEREUS ROYENII* INFECTADA POR *H. PUNGENS*

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Abstract

Los nutrientes dentro de una planta pueden alterar las funciones de la misma y su desarrollo dentro del ecosistema. En el caso de la cactácea columnal endémica *Pilosocereus royenii* su nutrición puede verse afectada por el posible bloqueo de agua y nutrientes causado por el insecto parasítico *Hypogeococcus pungen*. Para conocer la nutrición de la cactácea *Pilosocereus royenii* se obtuvieron 16 muestras de tejido de tallo: 12 saludables y 4 de tejido infectado. También se obtuvieron 6 muestras de agallas provenientes de individuos infectados. A cada una de las muestras se le realizó un estudio químico para obtener el porciento de cada nutriente por individuo en estudio. Dentro de los nutrientes observados en la cactácea se encontraron N, K, Ca, P, Mg, Mn, Zn, B, Al y S. Se encontró que de once elementos estudiados, cinco fueron significativos ($P < 0.05$) y tres fueron marginalmente significativos ($0.10 > P > 0.05$). El conocer dichos datos puede ser de utilidad en la conservación de la especie, ya que se pueden crear estrategias para lograr una mejor absorción de nutrientes esenciales a pesar del patógeno. Se debe tomar en consideración que estos datos pueden verse afectados por diversos factores tales como: composición del suelo, calidad de agua y tipo de planta. Además es la primera vez que se conduce este tipo de estudio en *Pilosocereus royenii* por lo que no existen valores de nutrición designados a la especie. Una investigación posterior podría ser realizar ensayos con fertilizantes o estudios de suelo.

FRECUENCIA DE MUTACIONES EN EL GEN FGG EN LA ISLA Y SUS IMPACTOS A LA SALUD

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Abstract

El gen FGG que codifica para una de las subunidades de fibrinógeno, una proteína importante en el proceso de coagulación. Mutaciones en FGG pueden afectar la velocidad de la coagulación y aumentar el riesgo de padecer de trombosis venoso. Tras estudiar los 55 individuos puertorriqueños secuenciados en el Proyecto Mil Genomas, identificamos 38 haplotipos distribuidos en cuatro familias que se distinguieron por tres polimorfismos de los cuales ninguno se encontró en la región codificante del gen. Entre ellos rs1800792, en la región promotora del gen, ha sido asociado a linfoma no-Hodgkin, a un contaje reducido de plaquetas en méjico-americanos, y, en mujeres, influye sobre el nivel de las lipoproteínas de alta densidad y el índice de masa corporal. Además, rs1049636, en la región 3' no traducida, ha sido asociado a bajos niveles de fibrinógeno gamma. Finalmente, una variante de rs2066861 ha sido asociada a un riesgo incrementado de trombosis venoso. La frecuencia de estos tres polimorfismos y de los haplotipos que distinguen fue investigada en residentes de los pueblos de Lares y Río Grande, en donde se observaron dos haplotipos que no fueron encontrados en los individuos de Mil Genomas. Además se observó un desequilibrio Hardy-Weinberg en Río Grande, pero no en Lares, para rs2066861. Este análisis se estará realizando en muestras representativas de la región norte, sur, este y oeste de Puerto Rico. Hasta el momento, no se ha encontrado ningún haplotipo que difiera de los encontrados en los puertorriqueños del Proyecto Mil Genomas.

DEGRADATION OF JET FUEL BY BACTERIA ASSOCIATED WITH *UCA RAPAX*

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Abstract

Mangrove forests are considered very important dynamic ecotones between terrestrial and marine habitats inhabited by various microorganisms and marine invertebrates. Due to the ever-growing intrusive human activities on these ecosystems, their destruction and pollution has increased throughout time. Therefore, interest has shifted to discovering alternative forms of bioremediation. The fiddler crab, *Uca rapax*, is a small deposit-feeder invertebrate that inhabits tropical mangroves whose diet consists mainly of detritus. Such diet demands a particular microflora capable of producing enzymes that are capable of degrading complex polymers and pollutants, such as hydrocarbons, found in the detritus. Previous experiments were done to identify these bacteria and later test their capacity to degrade complex hydrocarbons. Some were found to successfully degrade cellulose, alginate, toluene and diesel. Jet fuel is a mixture of hydrocarbons consisting of 90%-100% of kerosene C9-C16 and 0%-3% of naphthalene. Because this is a less complex mixture than diesel, it was hypothesized that these microorganisms could use these molecules as an energy source. This was tested through a qualitative method where bacteria were inoculated in petri dishes with 100 µl of jet fuel as the only source of hydrocarbon in 25 ml of agar medium with selected minerals. Preliminary results show that 27% from the isolated bacteria are capable of catabolizing this mixture of hydrocarbons, the bacterial genera included: *Bosea, Streptomyces, Bacillus, Actinobacter* and *Photobacterium*. Further screening will be done to test more genera previously identified bacteria.

GENOMIC JIGSAW PUZZLES: ASSEMBLY OF THE CARIBBEAN *AMAZONA* GENOMES

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Abstract

As a prime example of a locally crowd funded scientific endeavor, *de novo* sequencing of three Caribbean parrots of the *Amazon* genus was done using next generation technology. The three parrots sequenced were *A. vittata*, *A. ventralis* and *A. leucocephala*, the Puerto Rican, Dominican and Cuban amazons, respectively. *De novo* genome assembly is a computationally complex task in genome projects that generates an initial map of the unknown genomic sequence. The use of overlaps in sequence and quantifiable genetic markers assist in the assembly by fingerprinting the DNA. Thus, sequences of variable length can be aligned with each other, progressively making a map. To construct a map of the Caribbean *Amazona* genome, markers that are being used mainly include ESTs and variable number of tandem repeats DNA (VNTRs). Computational tools used to attack the assembly problem include mainly statistics and graph theory for a resulting a network of BLAST alignments to additional reference species from the Aves class, as databased on NCBI. Using these tools coupled to wet lab techniques, one can estimate the length of any remaining gap in the chromosomal map. Results presented include the comparative assembly of the candidate chromosome 28 *Amazon* along with both local and global genomic parameters.

LOSS-OF-FUNCTION MUTATIONS IN CHROMOSOMES 14, 15 AND 22 IN PUERTO RICO

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Abstract

The Puerto Rican population, genetically complex, is descended of African, European, and Native American (Taino) ancestries. According to the 1000 Genome Project, Puerto Ricans as a whole have 74% European, 14% African, and 12% Native American ancestry. The continental origin of different chromosomal segments in Puerto Rico can be determined using ancestry informative markers and the program RFMix, developed at Stanford University. Thus, the origin of loss-of-function (LOF) mutations in Puerto Rico can be traced back. Using the 1000 Genomes Project database, we have found 57 LOF mutations that are only present in 1% of the global population that were also are found in the Puerto Rican population across chromosomes 14, 15, and 22. As a result of that search we also found 23 LOF that are exclusive to the Puerto Rican population. Of these, 35 form a premature stop codon in the coding sequence and 13 affect splicing. The diseases and conditions to which these LOF mutations are associated are being investigated. Analyzing these results draws attention to the importance of the association between LOF mutations, their ancestry, and both the population history of the parental populations and the demographic processes by which they arrived to Puerto Rico.

DISTRIBUTION OF EARTHWORMS BETWEEN NATIVE AND INVASIVE HABITATS

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Abstract

Invasive species are huge issue on ecological conservation. Invasive plants are capable of changing the components of the soil in an ecosystem. For example, when invasive plants move into an area they can alter environmental variables that may promote changes in the invertebrate community, which is a component of the forest food webs. Earthworms are an example of one of these components, and are responsible for the decomposition of leaf litter and other organic matter dispersed in the soil. In this way, they help maintain the ecosystem balance, contributing to nutrient cycling and are also considered ecological engineers. Exotic species of earthworms often destabilize this balance by increasing litter decomposition rates through consuming much of the organic matter at the soil surface and changing soil structure and chemical properties. Similar effects are observed in studies of invasive plants interactions and it is attribute to its nitrogen-rich leaf litter. However, interactions between invasive plants and the distribution or composition of earthworms has not been well-studied. We performed two set of surveys under one native habitats and 3 dominated by invasive species. A total of 425 earthworms were collected, representing 7 species and unidentifiable juveniles. Results suggest an indirect effect of the habitat on species richness through the understory vegetation. From the 7 species, 2 were found only in native habitat and one only found under habitats dominated by the invasive Dahurian Buckthorn.

DIVERSITY OF *MACROPHOMINA PHASEOLINA* ISOLATES COLLECTED FROM COMMON BEAN

Colom, Sara M.1, Ana Vargas, Yulia Trukhina, Consuelo Estevez2 and Timothy Porch2
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Abstract

Macrophomina phaseolina is a soilborne fungus that infects over 500 plant species globally. Understanding how the genetic and phenotypic diversity of this disease contribute to its virulence and pathogenicity is crucial for developing host plant resistance in the field. In our study, eleven *M. phaseolina* isolates or DNAs were collected including nine from various locations in the western region of Puerto Rico and two from Tanzania, Africa. The conserved ITS region of the isolates were amplified, sequenced, and compared to the ITS sequences of isolates, from GenBank, from other regions of the world. We amplified six SSR loci that had high polymorphism information content values from a previous study and conducted a greenhouse virulence study on three phenotypically diverse isolates using three bean genotypes that were considered susceptible, moderately resistant and resistant. Isolates demonstrated a variation of charcoal colored, grey and, or white hyphal growth when grown on potato dextrose agar, although the latter was only observed in the Tanzanian isolates. ITS region between our isolates and isolates collected from GenBank were highly conserved and the six SSR loci each had more than one allele reported.

COMPARATIVE GENOMICS OF PIGMENTATION GENES IN CARIBBEAN AMAZONS

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Abstract

Pigmentation genes can be found as homologous across all vertebrates, and account for differences in phenotypes, particularly in skin, eye, hair, and feather coloration. At the same time, these genes are often involved in a number of human and animal diseases such as cancer, oculocutaneous albinism, porphyria, attention deficit-hyperactivity disorder, depression, as well as other health conditions. We are trying to introduce Caribbean parrots as a model to study of genetics of pigmentation. Amazon parrots are rightfully considered among the most colorful of birds, but little is known about genetics basis of these important adaptive traits. In our study, we look at sequence differences in the Caribbean Amazons (specifically the Cuban, Hispaniolan and the Puerto Rican parrots) within pigmentation genes (OCA2, TYRP1, ASIP, MC1R, ALAS1, PCBD1, TPH2, MOCS2, and PTS) using the alignments between the reference genomes of other vertebrates (human, chimpanzee, gorilla, orangutan, rhesus macaque, mouse, rat, chicken, turkey, and zebra finch). We are searching for the presence of polymorphic alleles, especially those homologous to the human disease variants. Once such variant is found, it can be tested for polymorphism in the corresponding species. We believe that this approach can be instrumental in identifying potential genetic targets in animal models that can be used to study human condition, benefit medical research and public health.

STRUCTURAL CENTRALITY IN ADELAIDE'S WARBLER SONG

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Abstract

Many species of songbirds (Passreri) learn to sing repertories of discrete song-types, which they use it to attract female and defend territories. Learning ability is believed to vary among males, and to play an important role in female choice. Measuring this variation in the field, however, has proven difficult. We are testing an indirect measure of learning fidelity called ‘structural centrality’. Structural centrality measures the ‘typicality’ of a male’s rendition of a given song type. Models indicate that males who learn with high fidelity will tend to sing with high centrality. The goal of our study is to quantify structural centrality in a sample of songs from male Adelaide’s warblers (*Setophaga adelaidae*). We used the program Luscinia to measure structural distance for each of several song types from nine males. We then subjected the distance scores to Principal Coordinates Analysis, from which derived structural similarity. Preliminary results indicate that Luscinia’s dynamic time warping algorithm is a valuable tool for measuring structural centrality in bird songs.

POPULATION STRUCTURE AND VOCAL LEARNING IN *DENDROICA ADELAIDAE*

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Abstract

Comparative and gene expression studies suggest the important role of candidate genes like the FoxP2 in vocal learning for both humans and songbirds, but genetic studies in natural populations so far have been limited. Here, we report initial results from an ongoing study of the correlation between genetic variants and vocal learning ability in wild songbirds. We obtained blood and feather samples from free-living Adelaide’s warblers (*Dendroica adelaidae*) in the Cabo Rojo Wildlife Refuge and extracted their DNA. To develop our genetic approach, we used phylogenetic analysis to compare sequences form the closely related avian species, and then merged their FoxP2 regions to a consensus sequence used as a template to design universal primers. The fragment encompassing one of the FoxP2 exons as well as the mtDNA control region was amplified and sequenced for the first time in this species. Our results will enable further population studies as well as comparative and functional analysis of the FoxP2 in Adelaide’s warblers, and among other songbirds whose FoxP2 regions have been previously sequenced.

DIVERSITY IN THE CABO ROJO SALTERNS UTILIZING CULTURE-DEPENDENT METHODS

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Abstract

The use of the 16S rRNA gene sequence to establish phylogenetic relationships has long been the universal method in taxonomy. However the fact that the gene is highly conserved, sequence results cannot be used to differentiate closely related species. The recently developed method of Multilocus Sequence Analysis (MLSA) has been proposed as an alternative to differentiate closely related organisms at the species level. The method consists of using the sequence data of 3-7 concatenated housekeeping genes to form phylogenetic relationships. The purpose of this study is to analyze the archaeal diversity at different culture media conditions and utilizing MLSA as our main tool for strain characterization. We also compared the use of different solidifying agents (agar and agarose), water (artificial sea water and water from the Cabo Rojo solar salterns), and finally carbon source (pyruvate and glycerol). Samples were collected from the solar salterns of Cabo Rojo, Puerto Rico and grown in the aforementioned culture media variables. After obtaining pure strains, the next step is to utilize MLSA by amplifying the genes rpoB', atpB and EF-2 and construct phylogenetic trees with the sequence data obtained. Preliminary data showed that more growth was obtained in media containing agarose and water from the Cabo Rojo salterns; however we observed more diversity in media containing agarose and artificial seawater. Based on the sequence data obtained, we isolated a strain of *Rhodovibrio salinarum*, a non-sulfurous purple bacterium that appears to be resistant to ampicillin. This is the first time the organism has been reported to grow in the solar salterns of Cabo Rojo.

MORFOLOGIA DE LAS DIFERENTES ESPECIES DE OPILIONES DE PUERTO RICO

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Abstract

Relacionados a las arañas y los escorpiones, los opiliones también pertenecen a la clase Arachnida. En Puerto Rico se conocen solamente 13 especies de opiliones cuya identidad ha sido publicada. En esta investigación se estuvo observando especímenes colectados de diferentes partes de la Isla. A estos se les tomo fotografías de alta resolución para documentar las diferentes características morfológicas, y así poder comparar entre los diferentes especímenes. Durante el transcurso de la investigación han aparecido por lo menos tres especies nuevas.

DETERMINATION OF LD50 IN ADULT HONEY BEES ORALLY INFECTED WITH IAPV

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Abstract

Israeli acute paralysis virus (IAPV) has been associated with Colony Collapse Disorder (CCD) of honey bees. This disorder brings complications not only to apiculture but also and more importantly to agriculture because the pollination of many crops is significantly affected. To find an ideal dosage for the study of IAPV in controlled conditions, in this work we amplified the virus in microinjected pupae. Viral particles were then isolated and used to determine the lethal dosage, 50% (LD50) by oral feeding of caged adult honey bees. Two feeding experiments were carried out (group and individual feeding) using different concentrations of IAPV. In both experiments the LD50 resulted in 0.4 dilution of virus stock. Symptoms were clearly observed in the individual oral experiment in contrast with the group oral feeding experiment. The analysis of these data will allow us to design future experiments that can help us understand IAPV effects on honey bee health, both alone and in combination with other factors.

THE DIVERSIFICATION OF THE PAPAYA RING SPOT VIRUS (PRSV) IN PUERTO RICO

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Abstract

The Papaya Ring Spot Virus (PRSV) is a positive sensed, single stranded, filamentous two-strained virus. The PRSV-P stain infects papaya as well as cucurbits, while PRSV-W infects only cucurbits. The infection of papaya or cucurbit yields high loses within farm crops. Consequently, the diversification of PRSV in Puerto Rico is being studied to find a conserved region within the coat protein of the virus's genome that could potentially be utilized to target a transgenic plant that could silence such gene upon infection. RNA extractions and RT-PCR of *Papaya carica* and *Cucurbita moschata* leaves from different areas of Puerto Rico infected with PRSV are performed in order to isolate the virus from the leaf and to sequence the PRSV coat protein. Presently, we are in the process of sequencing samples in order to continue with the diversity studies.

PRESENCE OF UNIQUE LOSS-OF-FUNCTION MUTATIONS IN CHROMOSOMES 2, 19 AND 20i

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Abstract

Loss-of-function (LoF) variants have been useful for understanding complex diseases and identifying novel candidate genes. These mutations are typically inherited in a recessive manner and have the effect of disrupting the function of the protein encoded by the mutated gene. Puerto Ricans, a recently admixed population, are a complex genetic mosaic of European, African, and Native American ancestral populations, and thus represent a great opportunity to study interactions between ancestry-specific alleles. Using the 1000 Genomes Project catalogue we searched and studied the LoF variants in Puerto Rico for chromosomes 2, 19, and 20 that possessed a global allele frequency of 1% or less. We found 111 LoF variants and, of these, 58 resulted in a premature stop codon, 43 disrupted splice sites and 10 caused a reading frame shift. Moreover, we discovered that 38 of these variants were found exclusively in the Puerto Rican population. A considerable amount of these variants were found in genes that were associated with conditions such as diabetes, obesity, Bardet-Biedl syndrome and several types of nephropathies. A broader understanding of these variants, their continental origin and the processes in which they arrived in the Puerto Rican population is greatly needed. We are currently inferring the ancestral origin of these variants by means of RFMix, a program developed at Stanford University that uses ancestry informative markers to identify the original parental population of chromosomal segments in an admixed population.

TARGETING THE CHEMORESISTANCE IN ENDOMETRIAL AND OVARIAN CANCER CELL LINES

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Abstract

Endometrial and ovarian cancer were the most common and most deadly gynecological malignancies in the US, respectively. Despite the advancement of single-agent and combined-agent chemotherapy regimens for these cancers, most tumors eventually develop resistance. Therefore, strategies to enhance the sensitivity of tumor cells to common chemotherapies are needed. Adenosine is known for its tissue-protective role in numerous organ systems. Recently, our lab has shown that adenosine's activation of the adenosine A1 receptor (ADORA1) promotes the integrity of epithelial cells in the endometrium. Studies in breast and colon cancer have shown that cancer cells are more sensitive to chemotherapy agents when they exhibit more epithelial-like features. Thus, we hypothesized that the treatment of cancer cells in combination with ADORA1 agonist, N6-cyclopentyladenosine (CPA), would cause cells to be more sensitive to paclitaxel, a standard chemotherapy agent. To test our hypothesis, we assessed ADORA1 expression by quantitative RT-PCR and cell viability to drug treatments, using MTT assays, in a panel of endometrial and ovarian cancer cell lines. Two endometrial cancer cell lines, HEC-50 and KLE, and an ovarian cell line, HEYA8, showed significant sensitivity to paclitaxel (= or <0.5nM) in combination with 10uM CPA as compared to paclitaxel alone. CPA alone did not induce cell death, which suggests CPA sensitizes cells by another mechanism. These preliminary results suggest that the use of CPA may be a rational approach to sensitize cancer cells to chemotherapy agents. More pre-clinical studies are needed to determine the efficacy this strategy may have in cancer patients.

CROHN'S DISEASE, TUBERCULOSIS, AND A MISSENSE POLYMORPHISM IN PUERTO RICO

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Abstract

Recent studies have found a relationship between genetic variations at the immunity-related GTPase family M gene (IRGM) and common inflammatory bowel diseases such as Crohn's disease (CD), as well as resistance to tuberculosis. This may be so because IRGM regulates autophagy formation in the presence of an intracellular pathogen. Hence, selection for resistance to tuberculosis, a very common fatal disease in Puerto Rico during the first half of the 20th century, may have raised the frequency of the allele that render our body susceptible to CD. In particular, rs72553867 is a missense polymorphism that replaces threonine for lysine at position 94 of the protein. It is far more common in Asia (18%) than in Europe (4%) or Africa (1%) and, according to the 1000 Genomes Project, its frequency n Puerto Rico is 9%. We investigated if this finding was consistent across the Puerto Rican population. This study consisted of extracting DNA samples of 10 individuals in 20 municipalities across the island each in order to perform a direct SNP-Genotyping Taqman Assay to test for the presence of the CD susceptibility A allele. We have found an uneven distribution of this allele with a higher frequency in the north and central regions of Puerto Rico and only the municipalities of Utuado and Vega Alta showing homozygous. The overall frequency was estimated at 10.4%. The distribution of the allele is consistent with a Native American origin.

VARIATION IN THE CALL STRUCTURE OF THE ENDANGERED PUERTO RICAN AMAZON

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Abstract

Parrots are known for their ability to learn vocal signals. These signals have many functions such as defending a territory, finding a mate, or recognizing group members. Since vocal signals are culturally learned, they may vary through populations. The Puerto Rican Parrot (*Amazona vittata*) conservation project currently has two different facilities that occur in two natural populations where these parrots are bred. To maintain genetic diversity, individuals are translocate from one facility to another. The success of these translocations may depend on the ability of a newly introduced individual to integrate to a new social environment. Since vocal signals are a crucial aspect of a population's social environment, any variation in these signals may act as potential barriers for an individual to successfully interact with its new environment. To see if there is variation in the vocal signals of these parrots, we looked for differences in their call structure. Individuality in vocal signals was measured in the wild population of Puerto Rican Parrots from the Rio Abajo Aviary in Arecibo, Puerto Rico. Recordings of the contact calls of several individuals were obtained and analyzed. The Luscinia program was used to measure the vocalization of the individuals using several variables including, bandwidth, amplitude, peak frequency and many others. We expected to obtain individual vocal dialect variation in the contact calls of the Puerto Rican Amazon. A deeper understanding of the acoustic communication of these parrots will help managers determine ways to contribute to the conservation project of the Puerto Rican Amazon.

EFFECTS OF OCEAN ACIDIFICATION ON MARINE CRUSTACEANS

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Abstract

Global atmospheric CO_2 concentrations are increasing, causing changes in seawater chemistry including decreasing its pH. We hypothesize that these acidic conditions would affect growth and development of larval stages of *Artemia* sp. (brine shrimp) and *Metacarcinus magister*. We measured growth of *Artemia sp. nauplii* exposed to sea water representing current CO_2 conditions (400 ppm) and CO_2 conditions projected for the year 2100 (1000 ppm). Growth of brine shrimp nauplii was measured in length, during five days of exposure. Then we monitored molting and survival of crab larvae (zoea) of the Dungeness crab *Metacarcinus magister* fed brine shrimp diets exposed the CO_2 treatments. Brine shrimp growth was affected and by day five were significantly smaller. Survival rates appeared lower for zoea fed high pCO_2 brine shrimp, but no statistical significance was found. Molt duration was longer for zoea fed high pCO_2 brine shrimp, but showed no statistical significance. Ocean acidification has the potential to affect many marine species, including those that are commercially important.

SEARCH FOR BIOFILM PRODUCING GENES IN METAGENOMIC LIBRARIES

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Abstract

Biofilms are aggregate structures of polysaccharide matrixes that protect bacteria from their environment. Ailments as pneumonia and pink eye are caused by biofilm producing organisms. Also, textile industry has found use in biofilms for production of edible films and food preservation. There are current efforts to identify and analyze genes involved in biofilm formation. The emergent discipline of metagenomic has allowed the study the genetic composition of any environment using culture-independent approaches. Information extracted from metagenomic libraries (MtgL) has been used for studying new sources of energy, research for health treatments including antibiotic resistance and production. The main focus of this research is to detect and identify biofilm formation genes present in MtgL from different environments in Puerto Rico. A total of six MtgLs (2-cave, tropical forest, microbial mats, water reservoir, river) were cultivated in broth medium, transferred into 96-ELISA microwell plates (approx. 400clones/well, duplicated) and incubated for a week at 37oC. The samples were screened for biofilms formation using a staining method, and the data compared to positive and negative control Pseudomonas aeruginosa and Escherichia coli Epi300 respectively. The data showed positive samples only in the microbial mat MtgL screened (purple halo formation) in 10% of the wells tested (3,200 clones). Genetic material is being extracted from the stained cells and subsequent transformation into isogenic *E. coli* cells will be performed to individual re-test for biofilm formation. This data supports using metagenomic for functional purposes, and allows the possibility of finding novel genes in biofilm production.

GENETIC DIVERSITY IN MYOCARDIAL DISEASE SUSCEPTIBILITY LOCI ACROSS PUERTO RICO

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Abstract

The Local Genome Diversity Studies (LGDS) is a project that aims to collect DNA from the samples of saliva, from all the 78 municipalities of Puerto Rico, with the purpose of using them for the identification of the admixture present in the modern population of Puerto Ricans. The information that this admixture can provide us can be very useful for the identification of genetic disorders and diseases. My project is based on the identification of the LTA4H gene, whose rs2247570 and rs2660898 alleles of African ancestry could encode for heart attack problems in the Puerto Rican population. In order to show this association, I helped organizing collection of samples from five different municipalities (Loíza, Fajardo, San Lorenzo, Naguabo and Humacao) located on the eastern part of the island, and carrying the most of the African admixture based on the earlier studies. For each sample, we extracted the DNA and prepared them for the concentrations suitable for the nReal Time PCR. We showed that the selected gene was, indeed, present in the Puerto Rican population with higher African ancestry. However, we also found that the gene was distributed among Puerto Ricans that have higher European ancestry. Future directions of the study include selecting five different municipalities from around the island in order to make a map of myocardial infarction incidence in the island with the purpose of contributing to the development of a personalized medicine and to determine whether or not the gene that we selected is more frequent in Puerto Ricans with African ancestry or in Puerto Ricans with European ancestry.

MOLECULAR CHARACTERIZATION OF AN ALPHA GLUCOSIDASE FROM *HALOQUADRATUM* SP.

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Abstract

There are few reports about gene regulation in halophilic Archaea, especially with genes related to carbohydrate metabolism. Also there are no reports describing the properties of an extremely halophilic alpha glucosidase (maltase) from the Archaea. Enzymes from haloarchaea inhabiting in hypersaline environments has been used for biotechnological process. Because α-glucosidase is involved in the last step of the starch degradation it can be used biotechnologically to fuse sugars with biological materials. A putative gene encoding for a α-glucosidase was detected by bioinformatics in the genome of the extremely halophilic archaeum *Haloquadratum walsbyi*. Primers were designed and an amplicon of 3000 bp was obtained by PCR. The structural gene was then cloned in the expression vector pET28b, which was transformed into *Escherichia coli* Rosetta™. Large amounts of a soluble but inactive form of the enzyme were produced upon its induction with IPTG 1mM. Activation of this enzyme was obtained at a high salinity of 3M NaCl. The α-glucosidase exhibited maximal activity at pH 6.0. Optimal temperature for the α-glucosidase activity and stability was 40ºC. Additional induction for expression of the protein and full purification of it is currently in progress.

COMPARISON OF THE ANTI-PROLIFERATIVE ACTIVITIES BETWEEN DIBENZYL DISULFIDE AND ITS ESTROGEN DERIVATIVES AGAINST COLON CANCER CELLS

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Abstract

Presently, cancer is the second greatest cause of death in developed countries. Chemotherapy and other therapies have been widely used to treat cancer and have proven to improve survival rates. However, undesirable side effects may result in termination of treatments by the patients. This creates an urgent need for the development of new, effective and safer drugs to treat cancer. Evidence suggests that dibenzyl disulfide (DDS) extracted from *Petiveria alliacea* has anti-proliferative properties against several cancer lines. It is believed that it acts as a good drug candidate for the development of therapies against different types of cancer. Using the DDS as a lead compound with anticancer properties, we hypothesized that derivatization of the compound with an estrogen should improve the potency of the compound against HT-29 cells (colon cancer cell line), since these cells overexpress the estrogen receptors. The purpose of this study is to test the cytotoxicity of the newly synthesized DDS-estrogen and DDS-estradiol complex against colon cancer cells (HT-29). The anti-proliferative activity will be tested by MTT assay, growth curves and expressed in terms of IC50 values. The cytotoxicity of the new synthesized compound will be compared with the cytotoxicity of the pure dibenzyl disulfide and the two estrogens used.

CATALOGING ENDEMIC PUERTO RICAN PLANTS THROUGH DNA BARCODING

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Abstract

DNA Barcoding allows easy identification of species and the study of biological diversity in organisms. This makes a whole catalog of genetic diversity possible and accessible to everyone. The plant species can be identified at genetic level and using small or damaged specimens. In addition to this, it is important for the conservation of species diversity to avoid the impact of global climate change in genetic diversity. Another important aspect of DNA Barcoding is to determine whether there was no fraud (in the case of the market) or even use of protected species. This project is focused on using DNA Barcoding in endemic Puerto Rican species. The primers used in this project are rbcl, MatK and MatK KIM which have already shown success with a variety of samples. The expected results are to have a catalog of the genetic diversity of endemic Puerto Rican plant species.

ELECTROTAXIS OF EPIDERMAL GROWTH FACTOR RECEPTOR INDUCE METASTASIS OF CANCER CELL

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Abstract

Electrotaxis, directed cell migration in current electric fields, is an important biological phenomenon that plays a role in cancer metastasis. Investigations related to underlying signaling mechanisms will lead to a better understanding of an electrically guided cancer cell migration and suggested start to unveil its potential implication in metastasis. MDA-MB-231 cell research has associated the migration of this cancerous cell with the polarization of the epidermal growth factor receptor (EGFR) in response to an electric field. The MDF-12A cell line has been shown to be affected by the electric field, when exposed to 30 minutes in electric field at ~4 miliamp. The focus of this investigation is to study the possible polarization of the Epidermal Growth Factor Receptor in metastasis using three different cells lines of cancer; MCF-7, MDA-MB-231 and MDF-12A. Cells will be grown on 1%, Omini Pur Agarose (CAS 9012-36-6) and then exposed to an electric field of ~4 miliamp for 30 minutes. Using immunoassays migration of the cells and the position and concentration of EGFR will be studied.

YEASTS ASSOCIATED WITH MIGRATORY BIRDS IN BOQUERÓN, PUERTO RICO

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Abstract

Birds are usually associated with the transport of microorganisms. These serve as vectors of yeasts, among other microbes, throughout the planet carrying them in their feathers or as part of their intestinal flora. Some of these yeasts can be potential pathogens to humans. The potential for transport and spread of some pathogenic microorganisms by migratory birds is an issue that affects public health. Yeasts are one of the least studied microorganisms in birds. A recent study revealed, that the most frequently encountered species are *Hanseniaspora guilliermondii, Candida albicans, Saccharomyces cerevisiae* and *Aureobasidium pullulans*. The aim of this study was to investigate the presence of yeasts in the intestinal flora and the plumage of migratory birds that arrive to Boquerón, Puerto Rico. For this purpose, 200 samples of yeast were isolated in Sabouraud Dextrose Agar from the migratory birds *Anas discors, Fulica americana* and *Aythya affinis*. Samples were collected at the Cabo Rojo National Wildlife Refuge from November 2013 to January 2014 during the hunting season. The 28s rDNA gene was amplified for 115 strains, using the primers NL1 and NL4. The bands of the PCR products were 680bp, which was the expected size for the D1/D2 region. The PCR products were sent to sequence at the High Throughput Genomic Unit, University of Washington in Seattle.

TAXONOMICAL REVIEW AND PHOTOGRAPHIC KEY OF PENTATOMIDAE (HEMIPTERA) OF PUERTO RICO

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Abstract

Entomological collections have very valuable information ranging from evolutionary biologist to agronomists. The importance of this information underlie on the availability for further research. Hemiptera, also known as true bugs, presents a wide morphological variability and is considered the fourth mega diverse order in insecta. Pentatomidae has a striking variation in ecological roles, being of particular interest on agronomy sciences. However, few studies on taxonomy and distribution on this family have been developed in Puerto Rico. Therefore, the purpose of this study is to generate a complete inventory of Puerto Rican pentatomids, and also update their taxonomic status. So that, approximately 100 specimens deposited in the INVCOL collection in the UPRM were used in order to make the first photographic compilation of pentatomids of Puerto Rico, by using a Digital Imaging Integrate System. Besides, their species status was updated using current taxonomic keys. This valuable information was uploaded on the worldwide available specify data base, putting this biological information at the service of the scientific community.

RELATIONSHIP BETWEEN CROHN'S DISEASE AND INTERLEUKIN 23 RECEPTOR GENE

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Abstract

Crohn's disease is a chronic inflammatory disorder that can affect any part of the gastrointestinal tract. It has no cure, but its detection is important to improve the patient's quality of life by maintaining the condition in a remission state. The main cause of Crohn's disease remains unknown; however, variations in genes such as IL-23R have been associated with this disease. IL-23R is a gene that codes for the Interleukin 23 Receptor which interacts with inflammatory mediator molecules. rs11209026 is a single nucleotide polymorphism (SNP) in the IL-23R gene. Two alleles of this polymorphism confer either protection or susceptibility to Crohn's disease. The allele that confers susceptibility (G) is predominant among Africans (100%) and Europeans (94%), and because these are the main ancestries of Puerto Ricans, this polymorphism may be predominantly seen in Puerto Rico. The aim of this study is to determine the frequency and geographic distribution of rs11209026 in Puerto Rico. The allelic frequency of rs11209026 was assessed by genotyping 296 saliva samples collected from different municipalities of Puerto Rico using the Real-Time PCR (RT-PCR). The results illustrated that the allele that confers susceptibility (G) predominates in the Puerto Rican population having a frequency of 0.94, while the allele that confers protection (A) only presented a frequency of 0.06. The G allele is distributed throughout Puerto Rico, reaching its highest frequency in the south region and its lowest frequency in the center region of the island.

CHARACTERIZATION OF AUTOTROPHIC MICROBES FROM SOLAR SALTERNS IN CABO ROJO

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Abstract

Carbon and Nitrogen are the most important elements for life and therefore their cycles are very important as well. Autotrophic ammonia oxidation was thought to be restricted to a group called ammonia-oxidizing bacteria found in the Bacteria domain. However, Archaea, which are commonly known for thriving in harsh environments, have some mesophilic groups that can oxidize ammonia autotrophically. The recent isolation of a marine crenarchaeote able to grow autotrophichally by aerobically oxidizing ammonia to nitrite confirmed the existence of ammonia oxidizing archaea (AOA). In AOA one of the enzymes responsible for CO2 fixation is the acetyl CoA carboxylase found in the citric acid cycle metabolic pathway. Nonetheless, little is known about carbon fixation at hypersaline environments, or if members of the Halobacteriales can perform this process. Water samples from the solar salterns of Cabo Rojo, Puerto Rico were used for the isolation and identification of possible carbon – fixating organisms. Isolated organisms were grown in Synthetic Crenarchaeota media modified with 5.0%, 15.0%, and 25.0% (w/v) NaCl. Genomic DNA extractions were performed using conventional methods and were used as template in PCR amplifications of the 16S rRNA with archaea specific primers. We found organisms that are able to grow autotrophically. Studies of the 16S rRNA gene sequences suggest that there is a diverse group of haloarchaea capable of growing under these conditions. However, in order to find genes that encode and express putative ammonia monooxygenase regions in situ, further work needs to be done.

DECODING ASIAN CITRUS PSYLLID TASTES: UTILIZING VISUAL AND TACTILE CUES

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Abstract

The Asian citrus psyllid (ACP), *Diaphorina citri* Kuwayama (Hemiptera: Liviidae), is the vector of the most devastating citrus disease, huanglongbing (HLB), associated with the phloem limited bacteria candidatus *Liberibacter* spp. The ACP and the HLB have a nearly worldwide distribution and are decreasing production and ultimately killing the tree. It is of paramount importance to understand the cues that *D. citri* use for host identification. A promising technique is the use of traps developed by Dr. Russ Mizell of the University of Florida, which will attract ACPs utilizing a range of visual and tactile cues: textures, colors, and entry holes with distinct light reflectance. The psyllid is attracted to the yellow surface of the trap; then it is directed to the entry hole by a black or yellow textured line; and falls in a vial with alcohol for preservation. A variety of these traps were tested at a *Citrus limon*, lemon orchard in Juana Diaz, PR, and Gabia, PR, along with yellow sticky traps to monitor ACP abundance over time. Preliminary trials indicated that traps with yellow or a smaller area of black tops and with 2 black sidelines and yellow vertical holes captured the most psyllids per week. Although more research is needed, Mizell traps provide a novel method for monitoring ACP populations and insight to ACPs visual and tactile cues for host discovery. These traps could also be enhanced to include an entomopathogen dispenser to further control ACP and HLB.

ASELLARIA JATIBONICUA IN THE TERRESTRIAL ISOPOD *LITTHOROPHILOSCIA CULEBRAE*

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Abstract

The trichomycetes are microorganisms associated with the gut of arthropods. They are an ecological group composed of protists (Ichthyosporea) and fungi (Kickxellomycotina) that converged in a similar life style evolutionary solution with key adaptations to their gut environment. Isopods in particular harbor fungal members belonging to the Asellariales. One essential aspect of the ecology of the Asellariales is to understand the environmental conditions associated to the isopods. For instance, the different environmental fluctuations of temperature, water precipitation and humidity affect the isopods lifestyle and thus, the life cycle of these fungi. In this study we observed seasonality of Asellariales associated to the terrestrial isopod *Litthorophiloscia culebrae* (Moore 1901) with a low prevalence in the dry seasons and a higher one in the wet seasons. We have found *L. culebrae* in different forests of Puerto Rico, including Río Abajo, Guajataca and Toro Negro and in different urban localities in Mayagüez. For this reason, we intend to compare the behavior of these organisms and the prevalence of its fungal symbionts in these different localities. Isopods were collected in the University of Puerto Rico, Mayagüez campus and dissected in the laboratory the same day. Slides were made in ddH2O and then fixed with 0.05% lactophenol-cotton blue. In addition, during this study period we found another trichomycete in the same host, *Parataeniella* sp. (Ichthyosporea: Eccrinales), which represents a first record for Puerto Rico.

PRESENCE OF LOSS-OF-FUNCTION MUTATIONS IN CHROMOSOMES X, 10, 18, AND 21IN

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Abstract

A variety of studies have indicated that all humans carry several types of genetic variants with the ability to disrupt protein-coding genes, collectively they are known as loss-of-function (LoF) mutations. These genetic mutations are usually inherited in a recessive manner and cause either the complete loss of a protein or a reduction in its ability to accomplish their work and may lead to the development of many disorders. By using the genomic data published by the 1000 Genomes Project catalogue that contained 55 Puerto Ricans, we were able to identify LoF mutations with a global allele frequency of 1% or less within chromosomes X, 18, and 21. We found 23 LoF variants and, of these, 14 resulted in a premature stop codon, 6 disrupted splice sites, 4 caused a reading frame shift, and 10 where exclusive in Puerto Rico. Some of the variations found in our population are involved with several disorders including insulin resistance, diabetes, childhood obesity, and many others. Because the Puerto Rican population have the influence of three different ancestral populations, it is probable that a relation between a given ancestry and specific alleles exists. We are currently inferring the ancestral origin of these variants using ancestry informative markers (AIMs) in order to identify the original parental population of chromosomal segments in our population.

ISOLATION OF TOXIN COMPONENT INTERACTING PARTNERS USING T7 PHAGE DISPLAY TE

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Abstract

Biological warfare has been the cause of thousands of deaths worldwide proving its efficiency by causing terror. Since the use of *Bacillus anthracis* spores on 9/18, as a biological agent, research trying to understand the biological mechanism of this bacterium Lethal factor (LF) toxin component has increased. The cleavage performed by LF to the mitogen activated protein kinase results in a cascade of reactions ending in cell apoptosis. Moreover, the damage caused by LF suggests novel interactions with other unknown proteins. The T7 Phage Display (PD) is a technique that allows the identification of protein-protein interactions. This research focuses on the isolation of novel LF interaction partners by PD. Using LF as target, rounds of biopannings were performed with human premade cDNA libraries from stomach expressed on the surface of a bacteriophage (T7). The cDNA present in the LF interacting partners isolated was amplified, sequenced and analyzed *in silico*. A total of 8 putative LF interaction partners were isolated. *In silico* data of some of the candidates suggest interactions with proteins with affinity to nucleic acids like zinc finger proteins, and transcriptions factors. While new interaction partners is been analyzed, this results will increase the understanding of the functions of proteins with LF for the development of therapeutics in biomedical research.

ANTIFUNGAL PRODUCTION IN ACTINOBACTERIA ASSOCIATED WITH THE EXOSKELETON AND THE INTESTINE OF THE TERMITE *NASUTITERMES COSTALIS*

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Abstract

Actinobacteria are known for their ability to produce secondary metabolites that exert antimicrobial functions and can form symbiotic associations with insects to protect them. We know that termites possess Actinobacteria in their exoskeleton, although their exact role is still under study. In the exoskeleton, we suspect a defense function against pathogens as reported in other social insects. Pathogenicity of the fungus *Beauveria bassiana* has been reported in many arthropods, including termites. During this study we tested the antifungal capacity of Actinobacteria associated with the termite *Nasutitermes costalis*, which is a common arboreal termite in Puerto Rico. Actinobacteria were isolated and identified from the exoskeleton of *N. costalis* in a previous study, of which the majority of isolates belong to the genus *Streptomyces*, known for its antibiotic production. We selected 15 isolates based on their phylogenetic position from our previous analyses. We evaluated their antifungal capacity against the entomopathogenic fungus *B. bassiana* through bioassays. Cell growth was determined through optical density to standardize the inoculum. Isolates were cultivated in Yeast Maltose Extract Agar for 72 hours at 25° C. Our preliminary results show that *B. bassiana* growth was inhibited. The strain W1SI96 [3], isolated from the termite's intestine, was the one that showed the most inhibition; therefore it is possible that this strain plays a key protective role. Further investigation on this strain is warranted.

DETECTION OF PARV4 AND B19 DNA IN HEART, LIVER AND LUNG TISSUE BY PCR

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Abstract

Human Parvovirus 4 (PARV4), a member of the Parvoviridae family, was recently discovered in humans. It has not yet been linked to any particular disease, but its prevalence in immunocompromised patients suggests its involvement in diseases. In previous studies, diverse solid tissue sample analyses have shown higher viral prevalence in myocardium, lung and liver tissues. In order to determine the presence of PARV4 along with Parvovirus B19V (B19), a member of the same family that infects humans, tissue samples from the myocardium, lung and liver will be collected. Viral DNA extraction and a PCR of all samples will be performed using specific primers for PARV4 genotypes 1 and 2 and all three B19 genotypes, which will be followed by sequencing. Risk factors that may be associated with certain diagnoses and viral presence will be evaluated. In accordance with prior publications, we expect to find higher prevalence of PARV4 in the liver, followed by myocardium and lung tissues. We expect B19 to prevail over PARV4. This will be the first study assessed to detect both viruses in tissues of the Puerto Rican population. Study results may help in relating cardiac, hepatic and pulmonary diseases to PARV4 and/or B19 presence.

HONGOS MICELIALES ASOCIADOS A EQUIPO ACUÁTICO

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Abstract

El uso de equipo deportivo es frecuente entre los deportistas. El equipo de Natación de la Universidad de Puerto Rico del Recinto de Mayagüez hace uso de respiradores (*snorkels*) y gorras durante su entrenamiento y este equipo luego es almacenado. Luego de observar el crecimiento de hongos en varias de estas piezas se colectaron muestras del hongo utilizando hisopos estériles. Estas muestras fueron estriadas en platos Petri conteniendo Agar de Papa y Dextrosa (PDA). Después de una semana de incubación a 25°C se transfirieron los crecimientos a Agar de Papa y Dextrosa y Agar con Rosa de Bengala para ser incubados por siete días 25°C. Los hongos purificados fueron caracterizados a partir de cámaras húmedas y preparaciones semi-permanentes. Se identificó a *Rhizopus stolonifer* de las muestras del gorro de natación y a *Cladosporium* spp asociado al *snorkel*. Estos datos serán provistos al equipo de Natación de la Universidad de Puerto Rico del Recinto de Mayagüez para que tomen medidas cautelares y se evite el crecimiento de estos hongos, los cuales tienen potencial como patógenos oportunistas.

FUNGI TRANSPORTED BY MIGRATORY BIRDS IN BOQUERÓN, CABO ROJO

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Abstract

Bird migration occurs every year in winter from areas where food resources diminish to areas of higher resources. Most of these birds come from Canada or the United States down to the Caribbean or Central America, making them long-distance migrants. The objective of this investigation is to establish what kind of filamentous fungi migratory birds transport to Puerto Rico. During the hunting season 2013-2014 at Refugio de Boquerón, Cabo Rojo we sampled birds captured by hunters. Species sampled belonged mostly to *Anas discors* (blue wing teal), but others were represented: *A. americana, A. clypeata, A. plathyrhynchos, A. bahamensis, Aythya collaris, A. affinis* and *Gallinula chloropus*. Samples were taken from the cloacae with a sterile cotton swab, which was then placed in Sabouraud media with antibiotics until processed in the laboratory. Down feathers were also sampled and incubated in wet chambers. Fungal isolates were sub-cultured into SDA and identified by morphology under light microscopy. We collected a total of 344 bird samples, from which 124 fungal isolates were obtained. So far, we have identified 60 isolated filamentous fungi in the genera *Cladosporium, Aspergillus, Fusarium, Pestalotia, Penicilluim, Mucor, Cylindrocladium* and *Paecilomyces*. Some of these genera have species that are considered pathogenic to humans; thus, it is important to continue further identification of these isolates. We have identified genera commonly found associated with birds in Europe, such as *Cladosporium, Aspergillus, Fusarium, Penicilluim*, but differ from others including *Alternaria, Botrytis, Talaromyces*, and *Rhizopus*, yet to be identified in our samples.

CELLULOSE-DEGRADERS BIOPROSPECTS FROM *CARACOLLUS MARGINELLA*'S GUT

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Abstract

The *Caracollus marginella* is a pulmonate mollusk native from some Caribbean Islands and Central America. Their capability to adapt to different food resources in the environments that colonize is greatly due by microflora present in the gut. Other pulmonary mollusk have gut microbial flora capable of degrading xenobiotics and complex carbohydrates, showing great biotechnological potential. This research focuses on isolate and characterize cultivable microbial flora from the gut of *C. marginela* and explore for biotechnological potential. Specimens of *C. marginella* were collected from the north and west part of Puerto Rico and dissected to extract the gut. Cultivable analysis was performed to the gut microflora by placing pieces of the open gut on agar plates with casein, nutrient agar and Luria Bertani, and further incubation for 24-48hrs at 25°C, 32°C and 37°C. The gut's isolates will be characterized microbiologically (macro and microscopically), and functionally test for degradation of cellulose were performed using cellulose agar plates. A total of thirty two colonies were chosen based on its morphology. Microscopically, the analysis revealed 15 Gram-positives, and 8 Gram-negatives where 12 were bacilli, and 11 with coccid morphology. Also, eight yeast-like prospects and one possible fungi were identified. The cellulose degradation test showed positive results in 15 of the 30 isolates tested. The data provide insights in the study of the snail microbiome, and will be of benefits in formal applications in the biofuels field.

UNRAVELING THE RESISTOME OF MICROORGANISMS IN COMPOST USING METAGENOMICS

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Abstract

The outbreak of infectious diseases by antibiotic resistant (AR) microorganisms is destroying the first line of medical defense in the world. Recent research has discovered a relationship between the AR genes in pathogens with those found in microbial communities of natural ecosystems. While classic microbiology studied microorganisms using culture-dependent approaches, scientific data shows that approximately 99% of microorganisms cannot be cultivable. Metagenomics is a culture-independent approach based on the isolation of environmental genomic material aimed to study the cultivable and the uncultivable microorganisms. The research aims was to generate metagenomic libraries from composts and explore for AR. Two metagenomic libraries from composts, a vegetable waste (VW), and a human-biosolid (HB), were generated using direct DNA isolation. High molecular weight (40kbp) and end-repaired DNA was electro-eluted, ligated into the fosmid vector pCC1FOS and transduced to *Escherichia coli* Epi300-T1R. The VW and HB libraries contain 30,000 and 10,000 clones respectively. The Minimal Inhibitory Concentration (MIC) of ampicillin against the cultivable host used for cloning the compost DNA was determined. The clones with ampicillin resistant activity were isolated by a selection on culture media with 1X, 2X and 5X MIC. Thousands of clones in HB library (too numerous to count) showed AR in 1X and 2X but only six clones showed AR to 5X. These results represents significant progress in the discovery of the resistome in HB environment; information directly related to the big problem for treatment of AR bacteria. Work is in progress to identify the gene(s) responsible for the resistance activity.

FUNGI FOUND ASSOCIATED WITH MIGRATORY BIRDS FEATHERS ON THE WEST COAST OF PUERTO RICO

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Abstract

Dermatophytes are parasitic fungi that use keratin as substrate as a means to grow and proliferate that cause a wide arrange of conditions. They are of clinical importance because this fibrous protein is a key component in hair, nails, skin and other structures which are found in reptiles, mammals, amphibians and birds. Their presence on many classes of organisms is of great importance, because it creates an opportunity to study these fungi. It would help in many ways such as early diagnosing the different kinds of dermatophytosis and their hosts, it would also help in studying the transmission of these organisms via migratory animals, the effect it has on local fauna of the migrating area and if these fungi are host-specific. The focus of these investigation is to study the dermatophytic fungi present in migratory birds on the west coast of Puerto Rico associated with their feathers. The fungi were isolated from samples taken from birds hunted in the Boqueron Refuge, Cabo Rojo during Dec 2013-Jan 2014 hunting season. Feather samples were placed in Petri dishes on paper filters with 1mL of distilled water. They were incubated for weeks due to the lack of nutrients in order to force fungi to only use keratin as substrate to grow. The fungi identified by morphological characteristics so far belong to the genera *Penicillium, Aspergillus* and *Fusarium*. No dermatophytes have been identified yet. The investigation is currently on going and using molecular phylogenetic analysis the identification will be narrowed to species.

STUDY OF LCT GENETIC VARIATIONS AND THE EFFECT OF RS2322659 ON POPULATIONS

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Abstract

The protein coded by the LCT gene is a member of the family 1 of glycosyl hydrolases with lactase activity. LCT phenotypes are highly variable due to the large number of polymorphisms in the gene, some of them related to lactose resistance. The C allele of the LCT polymorphism rs2322659 has a worldwide structured distribution with frequencies hovering 70 to 80% in Northern European populations, 40 to 50% in Asian populations, and only 20 to 26% in Sub-Saharan African populations. Puerto Rico has a highly admixed population involving three parental populations: European, Sub-Saharan African and Native American. Two of them went through bottlenecks before arriving to Puerto Rico. The European ancestry in Puerto Rico is largely the product of a few men who migrated to Puerto Rico during the 16th century. On the other hand, proto-Native Americans survived for 5000 years in the Bering Strait during the Ice Age before colonizing the World approximately 15,000 years ago. Thus, the frequency of alleles brought to Puerto Rico by Europeans or Asian populations, such as the rs2322659 C-allele, may have been subject to genetic drift and increased or decreased dramatically. Our SNP rs2322659 was tested throughout the population and compared with the date obtained with the date obtained from The 1,000 Genome Project our final allelic frequencies from all 5 regions only varied 5%. To further our findings we must compare these frequencies with the ancestry of each individual in order to observe each alleles distribution pattern.

COMPARISON OF FUNGAL DIVERSITY FROM *OPLONIA SPINOSA*, AN ENDEMIC PLANT FROM GUAJATACA AND ISABELA, PUERTO RICO

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Abstract

Fungal epiphytes infects the leaves surfaces while endophytes causes infections within tissues of healthy plants. The infection could be parasitic or symbiotic depending on the host plant. A study on *Oplonia spinosa* was conducted to identify epiphytes and endophytes associated to different populations of this endemic plant in Puerto Rico. For the comparison between locations in Guajataca and Isabela, healthy leaves were surface sterilized using ethanol (70%) and sodium hypochlorite (0.15%). For endophytes, sterilized leaf fragments sectioned in apex, center and base and inoculated in Potato Dextrose Agar and incubated for two weeks at 22°C. To isolate the epiphytes leaf printing method in Malt Extract Agar was used. *Nigrospora, Pestalotiopsis* and various coelomycetes were among the most common genera recovered in Tomato Juice Agar and Carrot Agar. After completion, this study will provide data on the presence of fungal epiphytes and endophytes in both plant communities.

A NOVEL TECHNIQUE TO MEASURE RELATIVE CYTOCOMPATIBILITY OF MULTIPLE SUBSTRATES

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Abstract

Normal tests for cytocompatibility entail the seeding of cells on substrates in multiwell cell culture plates. In these experiments, substrates are normally placed flat in the wells and cells are deposited on these plates. Clearly, cells have no option but to attach to and grow on these substrates and lysis occurs only if these substrates are extremely cytotoxic. In this research project, a novel method of testing cytocompatibility is presented. Cells are seeded in a custom-designed stainless steel well in medium that is in contact with various substrates which are placed vertically, in slots, around the well.. In the present study, the breast cancer cell lines MCF-7 and MDA-MB-231, as well as the normal epithelial breast cell line MCF-12A were cultured and affinity tests of these cells to aluminum oxide, titanium alloy, polyethylene, and polydimethylsiloxane (PDMS) substrates were performed. A specific number of cells were seeded in the well and incubated at 37 ºC for 4 days. The number of cells attached to the various substrates, after the incubation period, were measured using a hemacitometer and Cellometer® Auto T4 instrument. Some preliminary results are presented.

G-PROTEIN COUPLED RECEPTOR REGULATION OF HUMAN MYELINATION

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Abstract

Pharmacological induction of oligodendrocyte differentiation from endogenous oligodendrocyte progenitor cells (OPCs) represents an important step in the treatment of demyelinating diseases. We have found that muscarinic acetylcholine receptor M3 (CHRM3), a g-protein coupled receptor, act to delay oligodendrocyte differentiation from OPCs in vivo and that antagonizing can induce oligodendrocyte differentiation. We hypothesized that inappropriate activation of CHRM3 would impair oligodendrocyte differentiation and may, thereby, contribute to chronic disease. In this study, neonatal mice were treated with a muscarinic receptor agonist, Oxotremorine-M, between postnatal days 4 and 9 and oligodendrocyte differentiation assed by immunohistochemistry. Treated mice showed a decrease in myelination in the corpus callosum, and exhibited a lower density of CC1+ mature oligodendrocytes compared to saline injected controls. To study the underlying signal transduction of CHRM3, we examined the gene expression profile of G-protein subunits in human OPCs. G-protein β- subunit 4 (GNB4) was highly expressed by human oligodendrocytes and dynamically upregulated during differentiation. To assess the role of GNB4, fetal human OPCs were infected with lentivirus that overexpresses GNB4. In vitro GNB4 induced significant oligodendrocyte differentiation and, following transplantation into shiverer hypomyelinating mice, induced more rapid differentiation. GNB4 overexpression increased myelination and a higher proportion of transplanted cells developed into mature CC1+ oligodendrocytes in the corpus callosum. These data suggest that inappropriate CHRM3 activation may contribute to chronic disease and that GNB4 plays an important role in OPC fate and differentiation. Future studies will be aimed at establishing a causal link between CHRM3 and GNB4.

USING SONG NETWORKS TO CHARACTERIZE SINGING MODES IN ADELAIDE'S WARBLERS

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Abstract

Characterizing sequences of animal signals is a critical step toward understanding their adaptive functions. Network theory may provide a useful toolkit for visualizing and quantifying signal sequences, and for comparing sequences across contexts, individuals, populations, and species. Individual male Adelaide's warblers (*Setophaga adelidae*) sing repertoires of approximately 30 song types. A previous study that used traditional methods to characterize song-type sequences concluded that males use two distinct singing modes. We generated song transition networks based on long recordings taken from the same population used in the previous study. Our analysis largely supports the conclusions of the previous study. However, the new analysis provides significantly more detail than the older work, facilitates quantification of singing patterns, and generates intuitive and comprehensive visualizations of singing behavior. We suggest that network theory is a promising tool for the investigation of animal signal sequences.

VACCINIA AND MYXOMA VIRUSES AS EFFECTIVE VECTORS FOR ONCOLYTIC THERAPY

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Abstract

Cancer incidence in canine and feline populations is comparable to that in humans. A paucity of safe and economic treatments along with the similarity between mechanisms of tumorigenesis in dogs, cats, and humans, make these animals excellent models for the study of new oncolytic therapies, such as vaccinia (VACV) and myxoma (MYXV) viruses. These viruses effectively infect and kill cancerous cells, and can be modified to attenuate their pathogenicity or promote anti-tumor immunity. In the case of VACV, K1L and M2L genes were deleted (VACV.1) to increase safety while conserving effectiveness by allowing the cell to generate an anti-viral response. Whereas genes for interleukin-15/interleukin-15Rα fusion protein and tdTomatoRed were inserted in the MYXV genome (MYXV.1) to provide the cell with the means to generate an anti-tumor response. The safety of VACV.1 was assessed after infecting mice with a high dose of the virus. The survival curve and histopathology indicated attenuation by showing 100% survival for the VACV.1 group and meningitis present only in the VACV group. Two cancer cells and a non-cancerous canine cell line were infected with MYXV.1, and cell death was assessed. Sequencing showed 99% identity between the designed and amplified sequences, confirming correct insertion of tdTomatoRed and IL-15/IL-15Rα genes. Fluorescent microscopy confirmed tdTomatoRed expression post-infection. MYXVR and MYXV.1 showed cytopathic effects in all three cell lines but a significant selectivity toward cancerous cell death. In conclusion, VACV was attenuated and MYXV.1 showed selectivity toward cancerous cell infection and lysis.

GENE ANNOTATION AND CHARACTERIZATION OF REARRANGEMENTS IN THE EVOLUTION OF THE PUERTO RICAN PARROT (*AMAZONA VITTATA*)

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Abstract

The Puerto Rican parrot (*Amazona vittata*) genome data has become recently publicly available and the manual annotation of the parrot chromosomes has begun. To advance the description of the protein-coding genes and other important protein and gene features, we started focusing on chromosome 8 from the latest genome assembly (http://genomes.uprm.edu/parrot). Some annotation resources and tools used for this work are: Stand-alone Blast, Blast from NCBI, Gene Model Checker, BLAT, Ensembl and MEGA 6. We started by identifying 500 scaffolds of the parrot genome matching to the chicken chromosome 8, 186 of which with an E-value equal to zero. Chicken (*Gallus gallus*) and zebra finch (*Taeniopygia guttata*) chromosome 8 sequences were used as templates for annotation and when these proved unuseful, other annotated bird genomes such as those of the turkey (*Meleagris gallopavo*), collared flycatcher (*Fidecula albicolis*), budgerigar (*Melopsittacus undulatus*), and scarlet macaw (*Ara macao*) were used. During the process scaffolds with translocations of chromosomes 8 and 9 were found in consistency with those recently described for the scarlet macaw. The length of the chromosome in the Puerto Rican parrot is unknown. We have found several chromosomal rearrangements and manually annotated in full 115 genes in eight of the scaffold. The length of the completed analyzed sequences adds to 9.8Mb. Another 10.5Mb coming from seven different scaffolds are in the process of annotation. These results allow us to see the mode of conservation of genes throughout evolution and to build a detailed map of the Puerto Rican parrot chromosomes.

ARE *HELICONIA* BRACTS DETERMINISTIC MICROCOSMS? CILIATE COMMUNITY CONVERGENCE

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Abstract

The effects of climate change on biodiversity is currently fueling modeling studies about microbial community structure in diverse habitats such as phytotelmata. One example is the bracts of *Heliconia*, which retain rain water and produce varying amounts of nectar and have a significant amount of digestible nutrients capable of sustaining life. Yet the limited source of nutrients delineate the composition of ciliates proficient to survive. Thus, *Heliconia* phytotelmata represents a good model to study how ciliate communities respond to a changing environment in terms of nutrients and water composition, particularly in short time scales. The micro ecosystem also allows us to test Clement's deterministic succession theory, in which communities converge towards a common structure determined by environmental conditions. If community convergence is deterministic in *Heliconia* bracts, then there will be similar ciliate community structure within these flowers bracts, under similar ontogenic stages and inflorescense size, across four *Heliconia* species. A total of 15 samples were collected from four species of Heliconias gathered from Maricao (*H. caribea, H. wagneriana, H. bihai* and *H. strictairie*) that differed in terms of inflorescence size and ontogenic development. Based on preliminary data, there are numerical differences across species, across inflorescence developmental stage and size. This information may serve as baseline knowledge to test community convergence under nutrient, and moisture stressors, particularly since these parameters will be affected by the upcoming climatic change.

EVALUATING RELATIVE CONTRIBUTION OF GENETIC AND ENVIRONMENTAL FACTORS TO BACTERIAL PROFILES IN PARROT SPECIES

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Abstract

The genetic differences among species, as well as their ecological and geographical separation all contribute to the complexity of microbial and viral meta-communities. Recently, next-generation sequencing has allowed us to bypass many challenges in culturing representative isolates in order to identify taxonomic groups. The first is called community profiling, which includes a group of methods that are based on the direct amplification and analyses of a conservative DNA marker. An example of this is to use the small subunit ribosomal RNA gene to generate profile(s) of microbial communities. Studies have already employed this approach to describe the diet of a variety of animals. Quantitative gene concentration analysis can reveal both species-specific and habitat-specific metagenome fingerprints that reflect specific genetic determinants, as well as physical and biological characteristics of the sampled environments. However, it is not clear how much of the metagenome is determined by the environment, and how much by the genetics of the species. In our experiment, we are trying to standardize the environment to see if and how much of the difference between the species is determined by the genetic differences. Fecal samples are collected from 22 different parrot species kept at a private farm and fed exactly with the same diet. These samples are used to obtain genomics DNA , and profiled using or the Ion Torrent PGM at the Caribbean Genome Center where bacterial diversity can be assessed by 16S rRNA amplicon sequences and analyzing sequencing reads on the phylum, class, order, family, and genus levels.

LUSCINIA AS A TOOL TO DETERMINE SINGING CONSISTENCY IN ADELAIDE'S WARBLER

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Abstract

It has been hypothesized that singing consistency is a sexually selected trait in song birds. Here, the term "consistency" refers to the acoustic similarity between renditions of a specific song-type. We used the acoustic analysis program Luscinia to study singing consistency in male Adelaide's Warblers (*Setophaga adelaidae*). Our goal is to test the hypotheses that (1) consistency is positively related to song-type use, such that the most common song types are also the most consistent, (2) consistency varies among males, and (3) consistency is positively related to trill performance. Preliminary analyses indicate that Luscinia is a useful tool for measuring structural consistency.

STRESS DOWN-REGULATES VITAMIN D RECEPTOR EXPRESSION IN ENDOMETRIOSIS MODEL

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Abstract

Endometriosis is defined as the presence of endometrium tissue outside the uterus, including the gastrointestinal tract and is characterized by peritoneal inflammation, infertility and chronic pelvic pain. Since stress can affect the immune system and recruitment of inflammatory cells it may contribute to this condition. The vitamin D receptor (VDR) is associated with anti-proliferative and anti-inflammatory properties and is expressed in the cycling endometrium. Previous studies have shown that stress can exacerbate endometriosis in a rat model and there is evidence that stress can disrupt VDR. AIM: Investigate the impact of stress on VDR in an animal model of endometriosis. METHODS: Endometriosis was induced in female Sprague-Dawley rats by suturing uterine horn tissue next to the intestinal mesentery; sham rats had sutures only. Rats were exposed to an uncontrollable or controllable stress protocol for 10 days. At sacrifice (day 60) all rats were examined for cysts. Colon and uterine tissue were analyzed for damage and myeloperoxidase levels. The VDR expression was measured by immunohistochemical analysis. RESULTS: Endo-stress rats developed more and bigger cysts than endo-no stress rats. Uncontrollable stress resulted in higher colonic damage ($p<0.05$) and uterine MPO compared to no stress, while controllable stress showed no difference. Endometriosis animals had increased VDR expression in uterus stroma nuclei and glands which was decreased by stress ($p<0.05$ vs. controllable stress; $p<0.05$ vs. sham, in glands only). CONCLUSION: Stress exacerbates development of cysts in an animal model of endometriosis and also promotes down-regulation of VDR expression. 1R15AT006373 (CBA) and R25GM082406 (SH).

GENOMIC ANNOTATION OF CHROMOSOME 28 OF THE PUERTO RICAN PARROT

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Abstract

Genome decoding has proven to be a useful tool to understand the evolutionary history and biology of a species. Annotation of the Puerto Rican Parrot (*Amazona vittata*) genome can have an impact for the better understanding and preservation of the species. Genome annotation consists of finding genes and other important genomic elements in a sequenced genome. I am part of a group of students using computational informatics approaches to discover and identify all genes in the Puerto Rican Parrot including their arrangement throughout the genome. Our group works specifically on the parrot chromosome that is homologous to the chicken chromosome 28. By using genomic tools commonly found online that contain information from other avian species, we have decoded several genes found in 18 scaffolds of the ALLPATH assembly. These scaffolds cover 4.9Mb of sequence whereas the chicken chromosome 28 is only 4.7Mb long. Finding the genes in this chromosome and defining their structure can help in further research of the Puerto Rican Parrot by predicting biochemical roles, biological function, regulation, genetic interactions, and expression. Important similarities and differences have been found relative to the parakeet *Melopsittacus* undulates this comparative approach has promise to identify many genomic landmarks like we have done with other similar species before.

CRYSTALLIZATION OF RHBI HIS-TAG

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Abstract

Hemoglobin I (HbI) from *Lucina pectinata* is a model hemeprotein used to understand H2S interactions with hemeproteins. To attain this protein at high scale, recombinant protein hemoglobin I (rHbI) with a Histidine tag was obtained. Kinetically studies showed similar behavior between HbI and rHbI, therefore, the latter is suitable as the native protein analog. Structurally, only SAX-WAX data has been obtained which support that there is no structural change. To ensure this and further explore the effect of His-Tag in rHbI, crystal patterns are needed. Crystallization is the process in which molecules of a solution arrange themselves in a natural manner to form a crystal. Crystallization of rHbI His-tag was conducted by the hanging drop vapor diffusion and counter diffusion techniques at room temperature. Buffers from the Hampton Research Screening Kit 1 and Triana™ Crystallization Kit with pH variations were used as precipitant agents in the screening. The protein sample was prepared at different concentrations with cyanide as a ligand. Crystal formation was observed in buffers containing calcium chloride, sodium acetate, or lithium sulfate. Further optimization is required to enhance crystal quality for X-ray diffraction.

BACTERIAL CULTURES OF AMERICAN BULLFROG AGAINST *BATRACHOCHYTRIUM DENDROBATIS*

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Abstract

Bacterial symbionts are widespread in nature, but the mechanisms of their establishment and maintenance in vertebrate hosts is not well understood. The host may regulate its microbiota on the skin to prevent pathogen colonization and to promote beneficial communities than can supplement host functions such as immune defense. Amphibian microbiota can influence how they are infected by the emerging chytrid fungus, *Batrachochytrium dendrobatidis*. The American bullfrog (*Lithobates catsbeianus*) has shown immunity to this pathogen. This frog is invasive in North America, and once established, it spreads the pathogen to other amphibian species. We hypothesize that these microbial defenses change throughout amphibian development and are regulated by host skin defense peptides. Our data show that skin peptides play a role in bacterial selection. This study compares the effects of tadpole and adult skin defenses on bacteria collected from their skin. Results gathered so far have shown a correlation between skin peptide concentration and bacterial development. At higher peptide concentrations there is less microbe growth, but we did find some exceptions to this. Our data also shows adults have less infection loads than tadpoles. The next step in this research is to test these microorganisms against *B. dendrobatidis*. We expect that the host selects for antifungal bacteria at both stages, but host regulation may be strongest post-metamorphosis, when frogs become susceptible to the disease. We can utilize these results to help manage other amphibian species through bio-augmentation.

DESCRIBING THE UNIQUE MICROBIOME OF AN ENDEMIC AND ENDANGERED MARINE MAMMAL

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Abstract

The Antillean manatee (*Trichechus manatus manatus*) is an aquatic mammal that lives in the Caribbean Sea. This species occupies a specialized niche, since it is the only mammal whose major food source is sea grass, which contains high levels of cellulose and salt. Ingested cellulose is mainly digested in the cecum and the anterior portion of the colon of this species, by the aid of specific microorganisms, a process similar to only a small number of terrestrial herbivores. We set out to describe this unique bacterial community using next-generation sequencing technology. First we extracted DNA from *T. manatus* feces, and then sequenced 16S RNA using eight primers that separated the genes, which encodes four different hyper-variable regions measuring approximately 150bp each. An Ion Torrent Personal Genome Machine was used to obtain multiple reads for the four hyper mutation regions. Highly similar sequences were grouped into Operational Taxonomic Units (OTUs), which were compared to 16S databases. The community of the manatee microbiome will be described in terms of species presence, relative abundance, and phylogenetic relationships. This research may help to identify novel and unique mechanisms involved in the process of the degradation of the cellulose by an endemic and endangered marine mammal.

LIGNIN DEGRADATION ASSAY USING CONGO RED BY MANGLICOLOUS FUNGI FROM BAHÍA SUCIA, CABO ROJO, PR

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Abstract

Lignolytic fungi in mangrove ecosystems are the main organisms involved in carbon recycling from lignin. Fungi have specific enzymes involved in lignin degradation, such as lignin and Mn peroxidases, and laccases. Previous studies have shown that lignolytic fungi can also degrade polycyclic hydrocarbons (PAH's). In order to study lignin degradation in mangrove ecosystems, we isolated fungi from wood and decaying leaves in Bahía Sucía, Cabo Rojo. The azo dye Congo Red has similar chemical structure to lignin, thus serving as proxy for degradation studies of the latter. Decolorization of the dye over 20 days for eight different fungal isolates was studied. Fungi were cultured in a liquid medium with Congo Red at 28°C, 150 rpm. As a positive control for Congo Red degradation we used *Asperguillus flavus*, which is already known to degrade this dye. Congo Red decolorization was measured by absorbance at 490 nm. Fungal growth was measured by dry weight biomass. Maximum decolorization of Congo Red was observed in two isolates: a *Pencillium* sp. Isolate and an unidentified isolate with 99.80%, while the minimum degradation was observed in a *Fusarium* sp. isolate with 81.19% of medium decolorization. *Pencillium* sp. generated 0.050g of biomass, *Fusarium* sp. generated 0.066g and the unidentified isolate generated the most biomass (0.100g) under the experimental conditions. We can conclude that the isolates have the capacity to degraded lignin and might also be able to degrade PAH's. Further studies will characterize specific ligning-degrading enzymes.

MITOCHONDRIAL GENOME TO DETERMINE POPULATION STRUCTURE IN THE SHINY COWBIRD

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Abstract

The shiny cowbird, *Molothrus bonariensis*, is an obligate interspecific brood parasite, meaning it always lays its eggs in the nests of other bird species. This behavior can cause severe damages to host populations by reducing the survival of the hosts' nestlings. Recent observations (T. Nakamura, unpublished data) suggest there are two distinct populations of cowbirds, that look and sound different, and most importantly, parasitize different hosts. Population models used for management decisions currently assume that there is only one population. The models' predictions, and thus conservation actions, would be dramatically different if there are in fact two populations. We evaluated this hypothesis by examining the DNA of shiny cowbird samples that were collected from two areas in southwest Puerto Rico (Lajas and Cabo Rojo). The mitochondrial genome was amplified and sequenced utilizing Ion Proton technology, and the sequencing results were evaluated for genetic distance between the populations. Our results will provide valuable information about shiny cowbirds in Puerto Rico, informing yellow-shouldered blackbird conservation efforts.

SEARCHING FOR FUNGAL BIOPROSPECTS CAPABLE OF METABOLIZING 2,4,6 TRINITROTOL

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Abstract

Fungi are characterized for their cell wall made of chitin, tubular structures and saprophytic capabilities. Its morphological diversity and physiological versatility are also distinguishing traits. Fungi have been used for environmental applications in bioremediation, being capable of degrading complex molecules and hydrocarbons. In this research, fungal bioprospects where tested for 2,4,6-trinitrotoluene (TNT) degradation. The fungal candidates were inoculated on potato dextrose broth supplemented with 2ppm TNT, except the negative control. The plates were incubated for two weeks, collecting samples every three days. Each sample was analyzed using High Performance Liquid Chromatography (HPLC) with a mobile phase of 70% water and 30% methanol. The peak on the chromatogram corresponding to TNT appeared 7.2 minutes approximately after injection for each sample. According to these results, three candidates were capable of degrading TNT at different rates. Although there was a reduction of TNT, peaks associated with TNT degradation products did not appeared, suggesting that the bioprospects might assimilate TNT. According to morphological characterization, two bioprospects may belong to the *Aspergillus* and *Trichosporon* genus. Molecular characterization involved genomic DNA extraction, and amplification of 18S rDNA and the internal transcribed spacer (ITS) regions by PCR. The amplicons were further sequenced and *in silico* evaluated. The ITS analysis suggests that the bioprospects belong to the *Trichosporon asahii*, *Aspergillus sydowii* and *Aspergillus nomius* species. Ongoing experiments are being performed to understand the bioprospects usage of TNT, and further molecular characterization.

ROLE OF PALMITOYLATION IN PROTEINS ASSOCIATED TO AUTISM SPECTRUM DISORDER

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Abstract

Palmitoylation is a post-translational modification that introduces a palmitate group in cysteines present in proteins. Palmitoylation has shown to alter protein function and subcellular localization. Neuroligin genes (NLGNs) contain one to three conserved cysteine residues in their intracellular domain, which could serve as possible palmitoylation sites. Mutations in these genes have been thoroughly associated to Autism Spectrum Disorder (ASD). Interestingly, a study revealed that a patient carries a non-synonymous single point mutation in NLGN4 that introduces a cysteine at position R704 (R704C), which could serve as a new palmitoylation site near the cell membrane. We aimed to study if cysteines in NLGN4 are palmitoylated and how the palmitoylation affects the stability and expression of this protein in hippocampal neurons. Results confirmed that NLGN4 Wild Type (WT) is palmitoylated and that mutation R704C does add a new palmitoylation site. Transfection of hippocampal neurons with WT and mutants of NLGN4 was performed and changes in morphology were seen. These results suggest that palmitoylation may regulate localization of NLGN4 in neurons and could have a function in synapse. Studying palmitoylation effects on neuronal synapses and identifying differences in expressed proteins can provide new insights into ASD and other neurodevelopmental disorders. This study could also serve as possible target for pharmacological manipulation and the development of new ways of treatment.

USING NETWORK THEORY TO DESCRIBE SONG SYNTAX IN ADELAIDE'S WARBLER

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Abstract

All human languages are characterized by a property called “lexical syntax.” Lexical syntax describes a set of acceptable orderings of elements that also provide information when given individually. It appears to be rare in non-human animals. If we consider a given bird song as an independent and complete unit of information, then birds that consistently sing their song types in an ordered manner could be said to exhibit lexical syntax. We tested for this type of lexical syntax in male Adelaide's warblers (*Setophaga adelaide).* One lag sequential analyses of morning singing from four individuals indicated non-random song-type delivery. We developed networks to visualize our data. These show that before dawn, males sing in 'switch mode,' quickly switching from one song type to another. After dawn, however, they sing in 'repeat mode', singing each type many times before switching. We then integrated male-male interactions to understand the function behind the different ordering of elements. Preliminary analyses indicate that song order changes when a male is answering to another male and that some songs types are used to transition into an interactive state. To further understand song syntax, future analyses will describe how song performance levels changes between the interactive and non-interactive states and will relate this to song order.

LOSS-OF-FUNCTION MUTATIONS IN CHROMOSOMES 13 AND 16 IN PUERTO RICO

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Abstract

Puerto Rico has a contained, well defined population product of an admixture between Europeans, Africans and Native Americans. Two bottleneck processes occurred in the demographic histories of these parental populations: proto-Native Americans were stranded in the Bering Strait for 5000 years before colonizing the New World, and only a small group of European men distributed their genes among Puerto Ricans in the 16th century. The founder effect of these bottlenecks may have increased the frequency of detrimental mutations. On the other hand, Africans were brought to Puerto Rico from all over Sub-Saharan Africa and, as the most diverse world population, may have the highest number of detrimental mutations at low frequency. Thus, a higher frequency of mutations of European and Native background should be expected in Puerto Rico, but a higher number of mutations may be of African origin. We aim to identify loss-of-function mutations in Puerto Rico using the 1000 Genomes Project database. The continental ancestry of the mutations can be determined using ancestry informative markers and RFMix Program developed at Stanford University. We classify them according to the conditions associated with the mutated genes. We have found 169 loss-of-function mutations in chromosome 13, of which 19 are present in Puerto Rico and 5 are exclusively found here. A higher number but a similar pattern is observed in chromosome 16, with 431 loss-of-function mutations, 55 of which are present in Puerto Rico and 8 are exclusively found here. The determination of the continental origin of these mutations is underway.

QUALITATIVE AND QUANTITATIVE ANALYSIS OF CELL PROLIFERATION RESTRICTION DUE TO METAL TRACE ELEMENTS

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Abstract

Metals such as titanium and its alloys are often used for bone replacement in orthopedic biomedicine due to their excellent biocompatibility. Ti-6Al-4V is a titanium alloy mostly used as implant material for bone reconstruction. This alloy is considered to possibly release vanadium (V) ions that are known to cause cytotoxic effects. The V-free gamma-TiAl alloy has shown to be an excellent biocompatible alloy with high corrosion resistant properties. hFOB cells were cultured on both Ti alloys thermally oxidized at temperatures of 121°C, 500°C, and 700°C. A MTT Assay technique was used in order to compare the viability of hFOB cells at a qualitative level, while atomic absorbance spectroscopy using graphite furnace (GF-AAS) was used to evaluate vanadium traces from Ti-6Al-4V. The presence of V trace elements was observed in media from cell cultures onTi-6Al-4V treated at temperatures from 500°C and 700°C. Data obtained suggests a direct relationship with V presence and increase in degree of cell death of hFOB cells cultured on Ti-6Al-4V alloy. Further studies of V-free alloys are highly recommended in order to obtain the best biocompatible material for orthopedic implants.

HIGH FREQUENCY OF WARFARIN SENSITIVITY GENE VARIANTS IN PUERTO RICO

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Abstract

CYP2C9 is a cytochrome P450 enzyme coding gene located in chromosome 10. The enzyme is involved in the NADPH-dependent electron pathway and in the oxidation of many compounds such as steroids, cholesterol, and fatty acids. The enzyme contributes to the metabolism of drugs used for a variety of treatments, such as epilepsy, inflammation, blood clotting and diabetes. Variations in the sequence of the gene alter enzyme effectiveness. A survey of the variants of this gene in the Puerto Rican sample set of the 1000 Genome Project showed two polymorphisms predicted by Polyphen to be probably (rs1799853) or possibly (rs1057910) damaging. Whereas rs1057910 is at a frequency of 4%, rs1799853 is at a 17% frequency, which is highest for all world population sampled by the 1000 Genome Projects. Both polymorphism are non-synonymous and have been associated to warfarin and non-steroidal anti-inflammatory drugs such as ibuprofen. Median-joining network analysis identified two haplotype groups, each possessing one of these polymorphisms. Both groups were predicted to be composed of haplotypes of European origin, as these polymorphisms are absent an Africa and only rs1057910 has a low frequency in Asia. For next semester, I will study the geographic distribution of these polymorphisms in Puerto Rico.

ANALYSIS OF SSR PRIMERS FOR USE IN THE ASSESSMENT OF PAPAYA IN PUERTO RICO

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Abstract

Papaya is one of the leading tropical fruits in the market. Specifically, it is the third major tropical fruit and future projections state that by 2014 it will have a 16% of the total world tropical fruit production. Papaya is mainly cultivated in subtropical and tropical regions. It is a diploid organism with nine pairs of chromosomes, a sequenced genome of 372 Mb, a gestation time of nine-fifteen months, and continuous flowering throughout the year. The fact that it has a sequenced genome has encouraged the development of Papaya genetic markers, such as simple sequence repeats (SSRs). SSRs have a variety of uses and can be used to determine different strains of Papaya at a molecular level. The level of genetic diversity in a species provides the basis for which natural selection can act upon and the diversity of the crop accounts for their survival when exposed to a diverse array of abiotic and biotic factors from the biosphere. Currently, no assessment of the genetic diversity of papaya has been done in the island of Puerto Rico. The goal of this project is to analyze SSR primers, and their corresponding PCR conditions, are optimal for the evaluation of papaya diversity in the island. Five known diverse papaya strains were chosen to act as standards for the evaluation. We will present the optimal amplification conditions of different SSRs that then could serve as a basis for determining diversity of this tropical produce in Puerto Rico.

EXPRESSION AND LOCALIZATION OF FLIGHTIN AND TRANSGENIC CMYBP-C IN *DROSOPHILA*

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Abstract

Cardiac myosin binding protein C (cMyBP-C) of vertebrate cardiac muscle and Flightin (Fln) of insect indirect flight muscle (IFM) are thick filament proteins that have been demonstrated to fulfill essential roles in thick filament function and sarcomere integrity in their respective muscle systems. It has been demonstrated that Fln fulfills an essential role in defining the structural and biomechanical properties of IFM thick filaments in *Drosophila melanogaster* and that cMyBP-C fulfills a similar role in vertebrate cardiac muscle. cMyBP-C and Fln possess several functional similarities: i) they contribute to thick filament stiffness and influence thick filament length, ii) in vitro they bind to a common site in the coiled-coil region of myosin II, and iii) their function is regulated by phosphorylation. cMyBP-C is of considerable clinical interest because mutations in its gene are a common cause of hypertrophic cardiomyopathy. To test the hypothesis that Fln and c-MyBP-C are functionally homologous, Drosophila transgenic lines that express cMyBP-C in the IFM in the presence or absence of Fln were created. This study is aimed at optimizing a protocol for immunofluorescently staining dissected *Drosophila* IFM to determine the sarcomeric localization of cMyBP-C. We determined that performing the protocol directly on a Plus Slide that had a circle drawn with a hydrophobic PAP pen improved retention of myofibrils. This procedure will allow us to quantify and qualify differences in cMyBP-C and Fln expression and localization to determine if there is competition for a common myosin binding site when both cMyBP-C and Fln are expressed.

GENETIC DIVERSITY IN REFRACTIVE ERROR SUSCEPTIBILITY LOCI ACROSS PUERTO RICO

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Abstract

In the NSF-supported Local Genome Diversity Studies (LGDS) undergraduates collect DNA from saliva samples of individuals from all 78 municipalities of Puerto Rico, with the purpose of identifying and studying patterns of admixture present in the genomes of modern population of the island. Under the direction of the P.I-s ad the graduate students, the undergraduates carry out sample collection, DNA extraction and genotyping. They use data from the 1,000 Genomes Project to identify evolutionarily relevant, locally polymorphic genetic variants, related to genetic disorders and diseases. These markers are used to develop individual projects within the LGDS cycle. My own project is based on the GJD2 gene, a gene strongly associated with myopia refractive error in European populations. Working in collaboration with the Interamerican School of Optometry, the aim is to identify the prevalence of the rs524952 SNP (Single Nucleotide Polymorphism) in the Puerto Rican population and associate it with myopia-affected individuals by selecting a representative range of samples, ranging from low refractive error to high refractive error, for genotyping. In the second phase of the project LGDS samples will be used to assess the prevalence of the refractive error susceptibility SNP across Puerto Rico. The findings of my study will contribute to the local development of a personalized medicine on the island.

SEARCHING FOR ESTROGEN METABOLIZING BIOPROSPECTS

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Abstract

On recent years high levels of contamination with estrogen over water bodies have caused a worldwide feminization of fish and human health problems that triggers diseases such as Alzheimer's, low sperm count and cancer. In order to address this problem we propose cultivable (CA) and non-cultivable approaches to search for bioprospects capable of metabolizing estrogen. Here we present the data acquired from the CA. The CA screening of a soil sample was performed using M9 minimal salt medium 17α-ethynylestradiol and 17β-estradiol as the sole carbon sources, where growth indicates the possible metabolization of estrogen compounds. The candidates isolated were characterized microbiologically, in order to determine the identity of the microbe responsible for the activity. After monitoring one soil sample a total of 22 cultivable bioprospects grew on M9 media enriched with estradiol; indicating possible metabolization of estrogen. Macroscopically the majority of the bioprospects showed white or cream pigmented colonies, most of which are opaque but translucent and transparent were also present. Microscopically most of the organisms are Gram-positive bacilli and one Gram-negative bacterium. Primary screening showed that out of the 22, 18 could only metabolize 17β-estradiol, 1 could only metabolize 17α-ethynylestradiol and 3 could metabolize both estrogens. This research can lead to novel procedures for estrogen reduction via enzymatic reaction in water treatment plants keeping the hormone from reaching water bodies or human consumption.

ISOLATION AND PURIFICATION OF AGARASES FROM THE CABO ROJO SALTWORKS

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Abstract

Agar is a polysaccharide contained in the cell walls of red algae and is composed of agarose and agaropectins. Agarases are the catalytic enzymes responsible for the hydrolysis of agar. These products of the hydrolysis of the agar have applications in the different kind of industries. Although many agarases have been isolated from bacteria in saline environments, recent investigations point that Archaea are also capable of agar degradation. The purpose of this study is to isolate prokaryotic strains having agarase activity from saline environments in the Island. Water samples have been obtained from marine (3.5% - 5.0% NaCl), saline (10.0% - 15.0% de NaCl) and hypersaline environments (20.0% - 25.0% NaCl) in the Cabo Rojo, Saltworks. Fifty-one isolates were obtained from the sampling and fifteen of these isolates indicated agarase activity. Isolates where characterized based on physiological, molecular and morphological properties. These samples were then filtered using a 0.45µm nitrocellulose membrane. Membranes were inoculated in a two different modified version of the Synthetic Crenarcheota medium. Isolated strains were grown in medium with yeast extract and without it using agar and agarose like solidifying agent, to demonstrate their capability of agarase production in media with or without nutrients. Analysis of a 16S rDNA amplicon revealed that the isolates belong to the Archaea and Bacteria domains. This study can contribute in describe the agarase diversity which can help develop different applications of the enzyme. Can contribute too to understanding the function of the enzyme agarase in saline environments from Cabo Rojo, PR.

STRUCTURAL CLASSIFICATION OF ADELAIDE'S WARBLERS' SONG TYPES

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Abstract

Like many songbirds, male Adelaide's Warblers (*Setophaga adelaidae*) sing repertoires of discrete song-types. Visual inspection of sound spectrograms is the traditional method of classifying song-types. There are, however, some problems that can arise when using human-based categorization, including variation among observers, and the introduction of unintended biases. Compared to visual classification, computational classification has the potential to classify songs faster and more consistently. Luscinia is new a database-oriented bioacoustics program that can classify songs based on acoustic features that it extracts from recordings. We subjected a set of Adelaide's Warbler songs to both visual classification and to automated classification using Luscinia's dynamic time warping algorithm. The main goals of our study are to compare Luscinia's categorization with our own visual classification scheme, and evaluate the pros and cons of classification in Luscinia relative to visual classification methods. Preliminary results indicated that Luscinia is a time-consuming, but effective way to classify song-types in this species.

DETERMINATION OF THE INHIBITORY CAPACITY OF ACTINOBACTERIA AGAINST *CANDIDA*

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Abstract

Humans were not the first organisms to use microbes to deal with pathogens. This is thought to be a common host defense mechanism. The extensive literature about social insects (such as ants, bees, wasps and termites) developing mutualistic associations with antibiotic-producing Actinobacteria supports this idea. Our sources of natural products against antibiotic-resistant bacteria in nosocomial infections are coming to an abrupt stop. The discovery that many insect species form associations with microbes to protect themselves from pathogens has spiked the interest in this research area. Actinobacteria are Gram-positive, filamentous bacteria that are ubiquitous in soil and produce the majority of known antibiotics. In this research we want to study the inhibitory capacity of Actinobacteria associated with *Nasutitermes costalis*, which is a common termite in Puerto Rico, against the pathogenic fungi *Candida albicans* and *Candida guilliermondii*. *Candida* species are among the most frequent nosocomial pathogens, contributing significantly to morbidity and mortality. We have previously isolated and identified Actinobacteria from the exoskeleton and intestine of *N. costalis* and most of our isolates belong to the genus *Streptomyces*, well-known antibiotic producers. We evaluated the inhibitory capacity of 9 *Streptomyces* strains against *C. albicans* and *C. guilliermondii* fungi through bioassays. Our results show growth inhibition of 77.7% and 55.5% of *C. albicans* and *C. guilliermondii*, respectively. The Actinobacteria with more capacity of inhibition were W1SE179 [1] against C. albicans and D1SI287 [14] against *C. guilliermondii* with 18 mm and 20 mm of inhibition halo, respectively. These effective inhibitors could provide an alternative source for antifungal compounds.

GENETIC VARIABILITY OF THE METABOLIZATION OF COPPER IN GENE ATP7B

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Abstract

Wilson's disease is an autosomal recessive genetic disorder caused by a deficiency in copper metabolism, which henceforth accumulates in body tissues such as the liver or brain. Neuropsychiatric and hepatic symptoms are observed in subjects suffering from this disease. However, symptoms may be misdiagnosed as psychiatric or hepatic problems such as dementia or cirrhosis, with subsequent mistreatment and aggravation of the disease. Wilson's disease has been associated to mutations located on the ATP7B gene, which codes for a copper transporter to the bile and ceruloplasmin, the major copper-carrying protein in blood. In most cases (60%) subjects are homozygous for a loss-of-function mutation in this gene. Otherwise, the subject may be heterozygous (30%) or carry no detectable mutation in ATP7B (10%). Two mutations have been found in a subject from southwestern Puerto Rico which appears to be heterozygous for Wilson's disease and slightly affected by copper transportation deficiency. One of them is an A-to-G transition at position 2731 of the mRNA based on GenBank accession number NM_000053.3. This mutation abolishes a splice site. Another mutation located at position 3551, seems to co-segregate with the 2731 mutation, but is located within an intron and believed to have no effect. We have established a major part of the genealogy of the subject and will be studying closely related family members that may be suffering from this condition to confirm the association of these mutations to the disease. We will also study the frequency of these mutations in different regions of Puerto Rico.

DEMOGRAPHIC STUDY OF MET POLYMORPHISMS ASSOCIATED TO AUTISM IN PUERTO RICO

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Abstract

Autism Spectrum Disorders (ASD) is a highly diverse group of brain developmental conditions. It involves different levels of disability, from barely noticeable, to severe, affecting one in every 110 children born in the United States. These disorders have been increasing in frequency in Puerto Rico. ASD are highly heritable, 90% being determined by genetic factors. MET is commonly known as an oncogene, however, the ancestral alleles of three SNPs located in the promoter and in the first intron have been associated with an increasing chance of developing ASD: rs1858830, rs38841, and rs38845. To further understand these disorders and their increasing risk in the population we first analyzed these SNPs in the Puerto Rican subjects of the 1000 Genomes Project databases. We observed a general distribution across these samples and the three principal ethnic groups that compose the population, Europeans, Africans and Amerindians. All the haplotypes were present in Puerto Rico; specifically, the one composed of the three ancestral alleles was in 10% of the subjects. Then, we genotyped 357 samples from 20 towns across the Island with rs38845 to study its distribution in different areas of Puerto Rico. The results showed a frequency of 64% for the ancestral allele, 49% of the population being heterozygote and 40% being homozygote. Further studies of these three SNPs, their Hardy-Weinberg Equilibrium, and linkage disequilibrium will give us a clearer view of their distribution in the Puerto Rican population and further our knowledge of the increasing risk of children developing Autism Spectrum Disorders.

GENETIC DETERMINANTS OF HAIR AND EYE COLOR IN PUERTO RICANS

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Abstract

Genetic markers have been used to predict phenotypic characteristics like eye color and hair color, but eye color is difficult to predict since many loci are involved, and different alleles come from different continents. We set out to determine variation and frequency in loci known to influence hair and eye pigmentation in Puerto Rico. Using custom TaqMan® essay panel, we genotyped six single nucleotide polymorphisms (SNPs): four from the OCA2 gene and two from the MC1R gene that are all previously associated with eye and hair color. In the preliminary study using 40 samples from the municipality of Santa Isabel, we found higher genetic variation in OCA2 than in MC1R. In the current study, we created a diversity panel using DNA from 432 saliva samples collected with the help of the Local Genome Diversity Studies (LGDS) in Puerto Rico, specifically focusing on the East side of the island where a high concentration of African ancestry has been found. Despite the common misconceptions of Puerto Ricans having all the same eye and hair color, genetic tests reveal the existence of variation in the genes. We will genotype samples from municipalities across the island to obtain a clear picture of genetic variation on these pigmentation genes that have been associated with a higher risk of melanoma and obesity. If this test is successful, our findings can be applied in forensic investigations.

ARTE

RETRATO DE NATURALEZA

Categoría: Pintura, Dibujo y Serigrafía

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Resumen

En esta obra busqué juntar los temas de la biología y el arte mediante la figura humana (representando tanto la biología y el arte del retrato) y las plantas, creando un híbrido entre ambos conceptos. Realizado a lápiz de color en papel 9”x12".

MOVING SANDS

Categoría: Otra

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Resumen

Foraminifera are small organism that live in the sea, estuaries, salt marshes and also in lagoons. They are form of shells of different minerals possessing a variety of shapes and sizes. Also they have become throughout time an essential key for understanding the past and present environment. This piece of art made in crochet represents this little world diversity that the naked eye cannot see.

NUESTRA NATURALEZA NO ES LA VIOLENCIA, SI NO LA CONCIENCIA

Categoría: Pintura, Dibujo y Serigrafía

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Resumen

A través de la historia, el ser humano siempre ha tenido mucha dificultad en la convivencia con miembros de su propia especie y otros organismos. Este sentido de mayordomía inculcado por una cultura mayormente patriarcal ha creado en la raza humana un complejo de superioridad ante toda la vida en este planeta. El poder que nos ha brindado la ciencia nos ha cegado y, de una mano llena de soluciones, se ha convertido en una causante de muchos problemas. Hemos violado y manipulado los recursos de una manera inconsiderada, destruyendo y promoviendo todo lo que nos llevará a un inevitable fin, como lo son la injusticia, pobreza, contaminación, enfermedad… Es nuestro deber utilizar nuestro conocimiento, la ciencia para enmendar nuestros errores y poder convivir en este planeta. En esta obra voy a expresar el conflicto ecológico análogo a un tema muy pertinente, el abuso que la mujer recibe por parte de la sociedad. Decidí ligar ambos temas ya que en muchas culturas se personifica a todo lo que es natural como un ente con sexo femenino. Esto lo haré mediante el uso de la figura de *Lady Justice* como el sujeto principal de la obra. Esta es por muchos vista como una personificación alegórica de la justicia, la cual es mujer, y representará a su vez a la naturaleza. Esta a su vez se presentará arrodillada pero en forma de resistencia ante su abusador. Por medio de los colores, sombras y dimensiones se difuminarán ambos temas en la obra.

EVOCATIVE DIPTERA

Categoría: Pintura, Dibujo y Serigrafía

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Resumen

Es una pintura/*collage* sobre lienzo. La pieza central de la obra es una mosca (*gadfly*). Mientras que a su alrededor se encuentran tres hormonas relacionadas a la atracción y/o tensión sexual; ya que el tema de la misma es la atracción y las hormonas que la provocan.

PROVOKING A CATALYST

Categoría: Pintura, Dibujo y Serigrafía

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Resumen

Es una pintura/*collage* sobre lienzo. El tema de la misma es la atracción y las hormonas que la provocan. En la misma se encuentran unos ojos colocados en el centro bajo una franja verde, para así mostrar el efecto que puede tener una mirada penetrante en el juego que es la atracción. Mientas que en la parte inferior derecha se encuentra una araña y cerca de ella se observan las representaciones de las hormonas de estrógeno y testosterona; mientras que en la parte superior izquierda está representada la oxitocina.

AROUSING NEURONS

Categoría: Pintura, Dibujo y Serigrafía

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Resumen

Es una pintura/collage sobre lienzo. El tema de la misma es la atracción y las hormonas que la provocan. En la misma se puede ver la representación de dos neuronas y como en el punto de su encuentro está la oxitocina. A través del lienzo se encuentran otras representaciones de distintas hormonas asociadas con la atracción. Tales como el estrógeno, la testosterona, cortisol, estradiol, serotonina y vasopresina. Mientras que en la parte inferior izquierda hay una leona con sus dientes expuestos de una manera innegablemente agresiva algo parecido a algunas reacciones químicas y la tensión provocada por la atracción.

ESPONJAS DE AGUAS LLANAS DE PUERTO RICO

Categoría: Ilustración Científica

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Resumen

Dibujo de línea con tinta china; estilo de rayado, de varias esponjas que se encuentran en las aguas llanas de Puerto Rico.

BIOMAS ESTRATIFICADOS

Categoría: Otra- Vestimenta

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Resumen

En este trabajo, se buscó representar los biomas y sus conexiones biológicas. Se colocaron los biomas del bosque lluvioso, seguido por el bosque seco, la sabana, la pradera, el desierto y, por último, la tundra. Todo esto se realizará en un vestido largo donde se encontrarán los biomas terrestres y en la capa se colocaría el esquema de la continuidad de los ríos. El traje representando los biomas terrestres se confeccionará teniendo en cuenta el orden en q se encuentran ubicados los biomas, uniendo algunas características para representar interacciones entre ellos. Éste llevará un sombrero representando una nube sobre unos árboles que representan el bosque lluvioso, lo que conllevaría la parte superior del traje. Luego, continuaría con el bosque seco que se representaría con hojas secas, verdes y 4 soles. Esto da a entender que este bioma se ve afectado por los cambios solares y como los arboles por temporada pierden sus hojas o están totalmente cubierto de ellas. Este traje continuará con una sábana representada en la falda del traje y, sobre éste, irá una falda amarrada con una correa con rayos representando que el disturbio de las sabanas son los rayos que causan incendios. En esa falda amarrada seguirán el desierto y la tundra que sería el último bioma a representar. Se van a utilizar materiales reciclables para algunas partes del traje. Pintar la piel para representar algunas interacciones entre biomas, tal como algunos animales que habiten en los distintos biomas.

ESCARABALLISMO

Categoría: Pintura, Dibujo y Serigrafía

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Resumen

Escarabajo negro, pequeño, dibujado con la técnica de puntillismo utilizando tinta y plumilla.

HOJA DE ÁRBOL DE MARÍA

Categoría: Ilustración Científica

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Resumen

Ilustración científica

NACIMIENTO NATURAL

Categoría: Pintura, Dibujo y Serigrafía

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Resumen

Es una representación de como la naturaleza es la madre de todo ser que abarca en nuestro planeta y como debemos ser agradecidos por todo lo que nos provee.

TRASFERENCIA

Categoría: Punta seca

Leyshla Matos
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Resumen

La transferencia de información existente en el ser humano.

ECO DEMUDO

Categoría: Pintura, Dibujo y Serigrafía

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Resumen

Cuentan los vientos que las nubes nómadas naufragaron en el Caribe aquella primavera del 92; cuando vieron germinar el 7 de abril a un chico inusualmente curioso y observador. Las nubes fascinadas con dicha criatura decidieron arraigarse aquella islita borinqueña para ver al joven forjarse como todo un escrupuloso microbiólogo. Después de dos décadas el joven puertorriqueño se ha ido desarrollando en un ser mucho más complejo y creativo, una materia espontánea, llena de ideas, decidido a crear su propia dimensión utópica, donde expone y salpica sus ingenios, inquietudes y plasma su única verdad. En esta orbita, expondré mis grabados, aquellos que me llevaron a encontrarme con mis manos. Hoy espero que puedas descubrirte en mí y con una humilde gratitud te doy la bienvenida a Eco Demudo, mi espacio interactivo donde las nubes se convierten en papel y el universo es mi tinta. Con un soplo de estrellas te abrirás paso a mis fantasías, a mis delirios, así que si decides echarle un ojo solo te pediré que “escapes de la razón y que te sumerjas en mi ilusión”.

DIOSPYROS BLANCOI

Categoría: Ilustración Científica

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Resumen

Esta es una ilustración de la fruta mabolo, antes de completar su etapa de maduración y caer del árbol.

DIVERSIDAD DE ATROPODOS EN EL BOSQUE ESTATAL DE TORO NEGRO

Categoría: Fotografía y Cortometrajes

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Resumen

Colección de fotografías de aproximación ilustrando la diversidad de especies de artrópodos encontrados en el Bosque Estatal de Toro Negro.

ATABEY

Categoría: Pintura, Dibujo y Serigrafía

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Resumen

Acrílico y relieve en papel sobre madera de 24''x36''. Representación de la naturaleza autóctona puertorriqueña, entrelazada con la Diosa Atabey y la mujer como fuente de vida.

LIFE UNDER THE MICROSCOPE

Categoría: Pintura, Dibujo y Serigrafía

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Resumen

A painting illustrating the beauty of the microcosm world under a microscope.

DEFINING TRAITS OF THE COLEMBOLLA ORDER

Categoría: Ilustración Científica

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Resumen

Se describe los caracteres particulares dentro del orden Colembolla, como estos varían por especie, últimamente el movimiento y funcionamiento de la furcula. Tamaño de la obra 18"x24" medio mixto.

"MADERA, EMBARAZO"

Categoría: Pintura, Dibujo y Serigrafía

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Resumen

La obra es de un estilo que se fusiona con el arte surrealista que va más allá de la tranquilidad que la consume y la naturaleza que la acoge a la hora de manifestarse en esta pintura. La obra se distingue por representar a la mujer en su etapa de gestación como la madre naturaleza. La mujer es un árbol seco, que a lo lejos puedes ver una cara sonriendo, con un fondo verde y amarrillo para representar la naturaleza. La pintura es en acrílico sobre papel. Su tamaño es de 11 pulgadas. X 14 pulgadas. La pintura es parte de una serie llamada "Madera" reproducida por este servido.

MATA DE GUINEO

Categoría: Ilustración Científica

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Resumen

Ilustración científica de una mata de guineo, en acuarela sobre papel. Aproximadamente 7”x11”.

EL MOSQUITO

Categoría: Pintura, Dibujo y Serigrafía

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Resumen

Ciclo de *schistosoma mansoni*

LA ROSA NEGRA

Categoría: Pintura, Dibujo y Serigrafía

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Resumen

La Rosa Negra es una obra de origen surrealista, debido a que fue sacada directamente de un sueño. Sin embargo, sería más justo enmarcarle dentro del estilo artístico del expresionismo. El aspecto biológico en la obra es claramente visible ya que los elementos involucrados lo son la fauna (ave) y la flora. Que además muestra el proceso de copulación en un sentido metafórico. La obra mide un pie cuadrado (12x12) y está realizada en acrílico sobre *canvas board*.

GRACIAS POR SU PARTICIPACION Y APOYO