

ABSTRACTS- DÍA DE INVESTIGACIÓN DE CIENCIAS NATURALES- UPRH-2019

Network- Based Discovery of Brassinosteroid Regulation of Plant Growth and Stress Responses in *Arabidopsis thaliana*

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Brassinosteroids (BRs) are phytohormones that play an important role in the growth, development and stress response in plants. Many biological processes, like cellular differentiation and reproduction, are regulated or mediated by these hormones. BRs also affect the response of plants to environmental stimuli. The BR signaling pathway includes several kinases (BRI1 and BIN2) which regulate activity of transcription factors including BES1 and BRZ1 to promote plant growth. Mutant plants that have lost the ability to synthesize or detect BRs exhibit unique phenotypes because, due to the lack of BR, they don't have a normal growth or response to their environment. In this project, we use mutant lines of *Arabidopsis thaliana* in which the mutation affects the expression of candidate genes identified by phospho-proteomics as differentially phosphorylated in bin2 mutants. We conducted a series of four phenotyping assays with these mutants, which includes BR response assays, using two types of BRs (brassinolide and brassinazole), and stress response assays, testing different stressful conditions (sucrose starvation and drought conditions). The goal of this study is to try to understand the function of BR signaling, by analyzing how the different mutants of *A. thaliana* respond to BRs and stressful environments, which gives us information on the importance of this hormone in plants.

Characterizing Signaling Specificity in Two Diverging *Pseudomonas aeruginosa* Two-Component Signal Transduction Systems

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Two-component signal transduction systems, or simply two-component systems, are signaling pathways that allow bacteria to respond to their environment. These systems typically contain a histidine kinase receptor that transmits a signal to a response regulator by phosphorylating it. This event triggers a cellular response, thus consisting of two parts: histidine kinase receptor and response regulator. Two-component systems are prevalent across bacteria as an effective way to sense a diverse range of signals. Despite prevalence of this pathway, the mechanisms that allow for the evolution of new two-component systems remain largely unknown. For this project, we are studying two different two-component system pathways in *P. aeruginosa*, an opportunistic bacterial pathogen. The two different systems, PfeRS and PirRS, arose from a gene duplication event, thus are an excellent model for understanding divergence in two-component system pathways. PfeRS and PirRS have been shown to respond to the presence of extracellular siderophores, iron-chelating compounds. We are interested in

characterizing the activation of both systems by understanding possible crosstalk between components in PfeRS and PirRS pathways. By characterizing both systems, we hope to better understand the mechanisms that led to their divergence. In order to understand crosstalk, we created several gene deletions throughout both pathways in the *P. aeruginosa* genome to understand signaling specificity. Using Beta-galactosidase assay, higher beta-galactose activity suggested a lower specificity in the systems and increase crosstalk. In addition, we studied system divergence through a computational approach by analyzing genomic sequences in multiple *P. aeruginosa* strains. Using several hundred *P. aeruginosa* patient samples, we searched for signs of positive selection in PfeRS and PirRS. Data was consistent with a higher rate of divergence in histidine kinase and response regulator in both pathways, which further supports our hypothesis of actively diverging pathways.

Quality Assurance of Comet Population for NEOCam

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The Near-Earth Object Camera (NEOCam) is a, in proposal, space-based observatory designed to carry out thermal infrared survey in search for asteroids and comets, having on interest those objects that make approaches of less than 1.3 AU. Data taken by the NEOWISE mission is used for survey simulation and further optimize the detection cadence. Detection of comets by NEOWISE, or any other telescope, tends to be troublesome because of the nature of these objects. For this reason, comets tend to be fainter and fuzzier. Thus, the NEOWISE Moving Object Pipeline Subsystem (WMOPS), which automatically detects objects from data, fails to recognize a small but significant number of comets. Quality assurance for over 180 recently discovered comets were performed, about 33% were not detected by WMOPS. Another analysis with a total of 586 comets, shows that long-period comets can be detected further astronomical units away than the short-period comets. It also shows that for every time a comet is visible, an average of 97.5% is visible in Band 2 ($W_2=4.6\mu\text{m}$) and 66.7% in Band 1 ($W_1=3.4\mu\text{m}$).

Light-Induced Excited Spin State Trapping in Thiazole-Based Fe(II) Complexes

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Certain complexes of d4 - d7 metal ions exhibit spin crossover (SCO)¹ between the low spin (LS) and high spin (HS) electronic configurations, induced by changing temperature, pressure, or irradiation with light.¹ Our earlier work has shown that the spin states of tris-homoleptic Fe(II) complexes with diimine ligands can be predicted based on the N...N distance in the free ligand. Complexes with $d(\text{N-N}) < 2.78 \text{ \AA}$ and $d(\text{N-N}) > 2.93 \text{ \AA}$ adopt the LS and HS states, respectively, while complexes with $2.78 \text{ \AA} < d(\text{N-N}) < 2.93 \text{ \AA}$ exhibit SCO.² In the present work, we investigate known SCO Fe(II) complexes with 2,2'-bithiazole (2bt), 3-(thiazol-2-yl)pyrazole (3tpH), and 4,4'-bithiazole (4bt),³ in order to assess the possibility of light-induced excited spin-state trapping (LIESST) effect, which has never been probed in these materials. Our studies showed that (1) $[\text{Fe}(\text{3tpH})_3](\text{ClO}_4) \cdot 3\text{tpH}$ exhibits an abrupt hysteretic spin transition with $T_{1/2} \sim 160 \text{ K}$ and a LIESST effect with relaxation at $T_L \sim 70 \text{ K}$; (2) $[\text{Fe}(\text{2bt})_3](\text{ClO}_4)_2$ undergoes an LS \leftrightarrow HS transition associated with the loss of solvent at $\sim 360 \text{ K}$, after which the desolvated material exhibits an abrupt hysteretic SCO at $T_{1/2} \sim 230 \text{ K}$ and a LIESST effect with relaxation at $T_L \sim 80 \text{ K}$; (3) $[\text{Fe}(\text{4bt})_3](\text{ClO}_4)_2$ shows a gradual SCO with an onset above 300 K and $\sim 30\%$ fraction of the HS state at

400 K, suggesting that the higher stability of the LS state in this material is likely to greatly reduce the accessibility and lifetime of the metastable LIESST state.

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On the role of naturalized species on local food-webs in Puerto Rico: the rules of engagement between the Cuban Treefrog, *Osteopilus septentrionalis*, and the Puerto Rican Racer, *Borikenophis portoricensis*

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The Cuban Treefrog, *Osteopilus septentrionalis*, is a species native to the western region of the Caribbean. Its native distribution includes Cuba, the Cayman Islands, and the Bahamas. A few species of birds and reptiles have been reported to prey on adults and juveniles of *O. septentrionalis* in its native geographic distribution and areas where this species has been introduced (e.g., Florida and St Croix, U.S.A.). In Puerto Rico, this species was introduced in the early 1950s, and it is now frequently found in coastal areas in western, northern and eastern Puerto Rico, and some municipalities further inland. In this study, we document the first accounts of predation of *O. septentrionalis* by the Puerto Rican Racer (snake), *Borikenophis portoricensis*, from northern Puerto Rico. Also, we document preliminary results on the prey-predator interaction between several individuals of *O. septentrionalis* and an adult *B. portoricensis* under laboratory conditions. In the presence of the predator, an adult individual of *O. septentrionalis* showed an anti-predatory behavior, which consisted of raising its body in its four legs and inclined it dorsally facing towards the predator as to appear a prey larger in body size to the eyes of the predator. The snake captured the frog, which elicited several high-pitched release-calls, only to be ingested by the snake later on. In a separate event in the laboratory, more than five adult individuals of *O. septentrionalis* were added sequentially to the terrarium, and the snake captured and ingested each one of them. The behavioral response of the frogs included the release-call but also used all four limbs to press against the head and mouth of the snake to avoid ingestion. We kept the snake in the terrarium for observation during several weeks, and the snake never showed ill-effects attributed to the prey. Presumably, the toxins secreted by the skin of *O. septentrionalis* have negligible to no effect on this individual of *B. portoricensis*, and the snake already identified this frog as a natural prey-item. Our accounts in the laboratory support observations of predation events involving *O. septentrionalis* and *B. portoricensis* documented from the wild. Therefore, this study adds to our knowledge on trophic relationships in the Puerto Rican wildlife, and we suggest that *O. septentrionalis* has become a more-significant prey-item to native species like *B. portoricensis* than it is frequently acknowledged in Puerto Rico, and thus, this frog has become a regular member of local food-webs.

Effects of Artificial Light at Night on the Behavior and Performance of the Monarch Butterfly Caterpillar, *Danaus plexippus*

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The worldwide expansion of artificial light at night (ALAN) and its alarming rate of increase makes it an imperative issue to study effects of this anthropogenic disturbance on the natural world. It has been shown that ALAN has negative impacts including disturbing the circadian rhythms of herbivory in nocturnal insects. However, there is a lack of studies on how this disturbance on circadian rhythms affects diurnal insects. I studied the effects of ALAN on a diurnal insect's behavior and performance. My study system consisted of monarch caterpillars and common milkweed. These organisms are ideal to study effects of light pollution on diurnal insects species because milkweed often grows in disturbed habitats that area exposed to ALAN. I conducted an experiment to examine the effects of ALAN on feeding frequency and habitat selection, specifically how high individuals perched on their host plants. I conducted a second experiment to examine effects of ALAN on larval performance, in which I measured effects on days to pupation (of 2nd instar larvae) and pupal weight. I found that the feeding frequency of caterpillars at night was 91% higher under ALAN than under ambient light. Additionally, there was a marginally significant effect of ALAN on feeding frequency during daytime; caterpillars under ALAN fed 58% more often than caterpillars under ambient light. In contrast, I found no effects of ALAN on habitat selection. In the performance experiment, there was no significant effect of ALAN on the developmental rate of caterpillars. However, there was a marginally significant effect of ALAN on pupal weight such that the pupae of caterpillars exposed to ALAN weighed 8% more than the pupae of caterpillars exposed only to ambient light. The increased feeding at nighttime under ALAN could possibly be caused by disturbance to circadian rhythms of herbivory. A potential explanation for why this feeding carried over into daytime is that ALAN may have stimulated the production of hormones that promote feeding and remain in the body for a lengthy period of time. The increase on pupal weight may have been caused by the increased feeding frequency we observed in the behavioral experiments. This study is likely the first to show that ALAN increased the nighttime feeding of a diurnal insect. It is imperative to study any effects of human disturbances, like ALAN, on diurnal insects especially those like the monarch butterfly that are undergoing population declines.

Reproducing the Metabolic Conditions of Epigenetic Archaeal Adaptation

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Epigenetic mechanisms comprise of changes in an organism that do not occur due to mutations in the genetic sequence. Chromatin protein methylation is a common epigenetic mechanism believed to exist only in the Eukaryotic domain. However, epigenetics has recently been identified in archaeal thermoacidophile *Sulfolobus solfataricus* (S.so) specifically in strains subjected to adaptive laboratory evolution that acquired new heritable traits of super acid resistance (SARC) and mutation rate reduction. These traits were found to be non-mutational and were ascribed to chromatin protein methylation state. In S.so, SAM pools were depleted during growth in extreme acid. Acid stress is linked to oxidative stress, which inhibits the one-carbon and Vitamin B12 pathways that are essential for producing SAM. This implicates a metabolic mechanism that generated the SARC strain's chromatin undermethylation

and subsequent traits. In order to test the hypothesis that SAM pool depletion facilitated SARC adaptation, we had to recreate SAM depletion in the absence of acid stress. Methionine analogs cycloleucine and ethionine were used to inhibit the SAM synthesis enzyme, methionine adenosyltransferase (MAT). After SAM Extraction and HPLC Analysis, a 50% SAM pool depletion was obtained in ethionine treated cultures, similar to SARC strain pools previously quantified. Ethionine treatment also increased mutation rate threefold suggesting that undermethylation of chromatin proteins, rather than SAM pool depletion, more likely led to genome integrity in the adapted archaeal strains.

Phosphorylation of the Tumorhead Protein during *Xenopus laevis* Development

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Xenopus laevis (*X. laevis*) is an African clawed frog commonly used as an animal model in Developmental Biology studies. It contains a protein by the name of Tumorhead (TH), which has been proven to be important in ectodermal cell proliferation and neural tissue differentiation. Previous data acquired through mass spectrometry analysis showed that TH is phosphorylated at Serine residue 431 (S431). Western blot analysis with an antibody specifically designed to detect TH phosphorylated in S431 (p-TH), showed three distinctive bands for the phosphorylated protein throughout development. One of them appears consistently through all studied stages, another can be seen only in unfertilized eggs, and the last one appears after the mid blastula transition. These bands prove that p-TH is a maternal protein, and it continues being produced and used during embryonic development. After obtaining the developmental profile for p-TH, we began to investigate where the phosphorylated protein is located. In order to determine this, we performed immunostaining on fixed *X. laevis* eggs and embryos with the phospho-specific antibody mentioned above, and a secondary antibody with an attached fluorophore that allows visualization through fluorescence microscopy. In this study, we aim to discover whether changes in phosphorylation affect TH protein localization and function. The addition of a phosphate group has previously been shown to cause translocation of various proteins to the nuclei. Therefore, we hypothesized that p-TH has a nuclear sub-cellular localization. Our results show that p-TH is indeed found in the cell nuclei within the somites, during later stages of development. Based on these results, we are trying to determine if the phosphorylation of TH triggers its translocation to the nuclei, or if it has a different effect on TH. Understanding the role of TH phosphorylation will provide insights of its function and regulation through *X. laevis* development.

New mutations in Teosinte Branched 1 (Tb1) in *Triticum aestivum* to increase wheat tillering and yield

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The objectives of my project are to identify mutations in genes that could improve the agronomic yield of wheat by increasing the number of productive tillers. The increase in yield is important both for farmers to remain competitive in a global market and to meet the growing demand for food and feed. Our general objective is to increase the yield of wheat flour (*Triticum aestivum*) and durum wheat (*Triticum turgidum* ssp. Durum) by searching for mutations in genes that increase tillers. We are working

with the Teosinte Branching 1 (TB1) gene located on the chromosome of group 4 of flour wheat. Since wheat flour is hexaploid, examining the impact of TB1 requires identifying and following TB1 mutations in genomes A, B and D. TB1 is a transcription factor that suppresses the growth of lateral branches and activates spikelet development or inflorescences. In my experiments I am analyzing the effects of TB1 mutations on the growth of flour wheat. Mutations of the genome TB1 A, B and D were created by mutagenizing the population with EMS. A cross was made between a Cadenza plant that contained a stop codon mutation in the TB1-A and D genome gene with plants that contained mutations of the TB1-B genome in Alpowa. A greenhouse study found that the tendency of homozygous double mutant groups TB1 has increased the tiller. In the long term, the goal is to generate new alleles and allelic combinations so that TB1 develops genotypes to prepare for transfer to breeding programs.

Assessment of Different Transfection Protocols of SIRT6 in Primary CNC

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Many neurodegenerative and neuropsychiatric pathologies, such as Alzheimer's Disease, ALS, Huntington's Disease, anxiety and depression disorders, among others, have been linked to oxidative imbalance (1). High levels of ROS have been reported to lead to lipid, protein and DNA damage, resulting in cell death (1). Protein sirtuin 6 (SIRT6) is a histone deacetylase and mono-ADP-ribosylase that is a part of the cell's DNA repair machinery (2). In a situation of oxidative stress SIRT6 has been shown to promote DNA repair (3, 4). The protective potential of SIRT6 against oxidative stress could be of importance for the abovementioned pathologies. In order to ultimately study the potential of SIRT6 in safeguarding cortical neurons from oxidative stress, successful transfection of this gene needs to be achieved. We tested three different protocols using two different commercially available chemical transfection reagents, as well as lentiviral transfection, in primary cortical neuronal cultures in order to determine which protocol yields the highest efficiency while also having the lowest toxicity. We will assess transfection efficiency by GFP co-transfection and toxicity by looking at cell survival. Once the optimal transfection method is determined, transfected neurons could be subjected to different oxidative stressors, in order to assess SIRT6's potential in safeguarding cortical neurons against oxidative stress or damage.

The Role of Cofactors in Tau Pathogenicity and Seed-Competent State

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Tauopathies such as Alzheimer's Disease and frontotemporal dementia are progressive neurodegenerative diseases characterized by the presence of intracellular tau protein aggregates. A conformational change in the tau protein causes a switch from its inert form to a pathological and self-assembly form. Currently, there is no known cause of how and why these conformational changes develop. Cofactors, such as heparin in vitro and nucleic acids in vivo, could play a significant role in tau protein structure inducing its conformational swap to the pathological form. Once tau new structure is formed, it serves as a template leading to a state of self-assembly and replication, known as tau seed-competent state. At this state, seeding active tau is able of recruiting naïve tau proteins forming

intracellular aggregates and allowing pathology to begin. The use of enzymes capable of degrading cofactors such as heparinase and nucleases, has been proposed as a method to analyze the agent responsible for tau pathological state. In vivo, pathological P301S mouse brain purified tau fibrils were treated with nucleases to test their effect on tau pathogenicity. P301S mouse brain fibrils treated with benzonase, a nonspecific nucleic acid degrading enzyme, resulted in a significant reduction of tau seeding activity. This remarks that tau pathological and seed-competent state depends on nucleic acids presence. Moreover, in vitro heparin induced fibrils significantly lost seeding activity once treated with heparinase. Showing that, once the cofactor is removed, tau pathological state is greatly reduced. These findings allow to achieve a better idea of tau aggregation basis, which could lead to future improvements in the understanding and diagnosis of tauopathies.

Deterministic and Stochastic Compartment Models for Total Body Irradiation

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Sponsored by NIH-MARC U-STAR and the Department of Physics and Electronics at the University of Puerto Rico-Humacao

The objective of this research is to develop algorithms and computational codes (deterministic and stochastic) to mimic a clinical radiotherapy procedure TBI (Total Body Irradiation). The Jones model of radiation-induced myelopoiesis is modified by adding new compartments for mutated and cancerous cells populations. This proposed carcinogenesis model is mathematical described by five non-linear coupled differential equations. Numerical and graphical solutions are obtained for U.S. (8 fractions, 4 days, 1320 cGy) and Canadian (6 fractions, 3 days, 1200 cGy) TBI regimens. To obtain stochastic solutions, transition rates that mediate movement of cells among all compartments are replaced for random numbers. The developed algorithms and computational codes allow us to quickly update a planned TBI regime after the patient's treatment was interrupted for a length of time (due to a natural event or blackout). It is also shown that U.S. and Canadian TBI regimens killed about the same percentage of malignant cells. The stochasticity procedure shows in average a mortality of about 83% of the malignant cells in agreement with the deterministic solutions obtained for the US and Canadian TBI regimens. The proposed carcinogenesis compartmental model (deterministic and stochastic) was solved for the TBI US and Canadian regimens. Developed algorithms allow for a quickly update of an interrupted TBI regimen, and to make a comparison among different TBI regimens used worldwide. Interestingly enough, computational simulations (deterministic and stochastic) of the TBI US and Canadian regimens showed about the same percentage of the cancer cells killed after the treatment is completed.

Copper Catalyzed Decarboxylative Heck Reaction of Vinyl Bromides with Electron Deficient Carboxylic Acids

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The Heck-Mizoroki reaction has found wide applications in the construction of C-C bonds. These protocols offer efficient access to a variety of biologically active molecules. The decarboxylative Heck reaction can use carboxylic acids coupling partners in place of the traditional aryl halides. However,

these methods usually lack atom economy and rely on precious metals like palladium as the catalyst. Copper can be an attractive catalyst for this type of reaction since it's a first-row transition metal, highly abundant and low-cost. The combination of a copper catalyst and readily accessible carboxylic acid coupling partners makes this reaction of high interest in synthetic chemistry. This work will focus on the methodology development of a copper catalyzed decarboxylative Heck reaction between electron deficient benzoic acids and vinyl bromides. Currently, catalyst, temperature and bases have been screened. Future work will focus on increasing the yield of the reaction by evaluating the ligands, solvents and additives.

Investigating the Antibacterial Effects of Biological Pigments from Flowering Plants

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Today, bacterial resistance to antibiotics is a significant public health threat. Finding cost-effective compounds against resistant bacterial strains is critical. Plants contain many phytochemical compounds that can be studied for many purposes. Within the petals of flowers are many biocompounds that give flowers their scents, colors, sun protection, among other properties. The diversity of pigments found in flowers deserve being studied in depth since there is a controversy about the antibacterial properties of flower pigments, their antioxidative properties in the aid of bacterial survival, and their influence in the virulence of bacteria, while others state that pigments possesses antibacterial properties. For this project, we have selected four species of native tropical yellow flowers and red flowers, respectively known to possess medicinal properties according to traditional medicine. Three different extractions (50mg/mL and 25mg/mL) in acetone, isopropanol, or water were done to determine which solvent would extract the most pigments. The antibacterial properties of the crude extracts were tested by the Agar Disk Diffusion Assay against *M. luteus* (yellow pigment producing bacteria), *S. marcescens* (red pigment producing bacteria) and *E. coli* (none pigment producing bacteria). It was found that few extracts, mostly the ones from red flowers showed significant bacterial inhibition, specifically the pigments at a 50mg/ml concentration. Nonetheless, we decided to carry out distillations of the flower petals in a mixture of 50/50 water/isopropanol to isolate different biomolecules by their critical points. Later on, we repeated the agar Disk Diffusion Assay and for our surprise, isolated biocompounds from the flowers showed now greater inhibition zones. Ft-IR and NMR were taken to characterize the different extracts confirming the chemical biomolecules which possess antibacterial properties. From these experiments we conclude that there are certain biocompounds in flowers with antibacterial properties. It is necessary to carry out ascertained methodologies for the extraction of biocompounds. In addition, we conclude that plants have many naturally synthesized compounds from which we do not know their biomedical applications. In the near future we plan to find the interactions between the bacterial and flower pigments in correlation to synergism and antagonism activity.

Aspectos comparativos de la reproducción de los Columbiformes en la UPR-Humacao pre y post Huracán María

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El grupo de las palomas (Columbiformes) está representado en el campus de la UPR-Humacao por cuatro especies. A saber: la Rolita (*Columbina passerina portoricensis*), la Tórtola cardosantera (*Zenaida aurita*), la Tórtola aliblanca (*Zenaida asiática*) y la Paloma turca (*Patagioenas squamosa*). Desde el 2013 hasta el presente (2019) se ha estado estudiando la reproducción de las mismas. El 20 de septiembre del 2017, el Huracán María paso sobre Puerto Rico con vientos sostenidos de más de 155 mph (categoría 5), que causaron la destrucción o alteración de hábitat de muchas especies, lo que afectó, de forma sustancial, a algunas poblaciones de aves. Tomando en consideración los datos que teníamos previo al huracán, el monitoreo posterior a la tormenta (búsqueda de nidos bisemanalmente), nos permitió determinar el impacto de la tormenta en la reproducción de las palomas. Durante el 2018 los intentos reproductivos de la Paloma turca se redujeron en un 90%, los de la Tórtola aliblanca en un 87% , los de la Rolita en un 70% y no se encontraron nidos de Tórtola cardosantera. Durante el 2018 notamos cambios en el uso de vegetación para reproducirse en las especies estudiadas. No obstante durante el 2019 hemos observado una recuperación de la gran mayoría de las especies. Hasta julio del 2019 se habían encontrado 59 nidos de Tórtola aliblanca, 10 nidos de Tórtola cardosantera, 17 nidos de Paloma Turca y un nido de Rolita. A tales efectos las dos especies de tórtola se han recuperado en su totalidad, las turcas casi han duplicado los intentos reproductivos de años previos al huracán y la única especie, que no parece haberse recuperado es la Rolita. Mucha de la vegetación que produce comida para las especies estudiadas, fue seriamente afectada por el huracán y es probable que una reducción en los recursos alimentarios haya sido el factor principal en la reducción de intentos reproductivos durante el 2018. Para el 2019, la mayoría de la vegetación se notaba recuperada y es probable que esto haya influenciado en que la propagación de las palomas haya alcanzado los niveles que se encontraron previos al huracán.

Aspectos comparativos de la reproducción de la Reinita de Puerto Rico (*Coereba flaveola*) en la UPR-Humacao pre y post huracán María

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La Reinita de Puerto Rico (*Coereba flaveola*) es considerada el tipo de ave más común y abundante de Puerto Rico encontrándose desde bosques hasta hábitats urbanos. Esta ave, se le considera una de las más beneficiosas por la gran cantidad de insectos dañinos que consume y la amplia gama de plantas que poliniza. El ave construye dos tipos de nidos. Unos para dormir y otros para reproducirse . Se pueden encontrar nidos de esta especie a través de todo el año. Durante el 2014 y 2015 se estudió el anidamiento de esta ave en la UPR-Humacao. El método utilizado lo fue buscar en la vegetación del campus nidos del ave, semanalmente. En septiembre de 2017 azotó a Puerto Rico el huracán María. A tales efectos se utilizó la metodología previamente mencionada para determinar el efecto del fenómeno atmosférico en la reproducción del ave. Durante el 2014 al 2015 se encontraron 435 nidos de reinita ($X = 217$ nidos/año), con un pico en la reproducción entre mayo y junio. No obstante, de septiembre a diciembre de 2017 se encontraron solamente tres nidos de aves todos utilizados para dormir. Durante el 2018 se encontraron tan solo 14 nidos, la mayoría entre septiembre y noviembre. Hasta septiembre del año en curso se han encontrado tan solo 29 nidos, lo que indica que la especie, a dos años del huracán,

no se ha recuperado en su totalidad. El huracán causó que la gran mayoría de la vegetación en el campus perdiera su follaje incluyendo sus flores. Es posible que la falta de alimento haya sido uno de los factores principales para que esta ave haya reducido sus intentos reproductivos durante el 2018. Seguimos los trabajos de campo para determinar cuánto tiempo le toma a la especie recuperarse en su totalidad.

Analyses of Brain Regional Volumes in Alzheimer's Disease Mouse Models Using Non-Linear Symmetric Normalization Tools in ANTs

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Alzheimer's disease affects tens of millions of people worldwide. Post-mortem analyses of the brains of Alzheimer's patients reveals two major histopathological hallmarks, (1) the accumulation of extracellular beta amyloid plaques ($A\beta$) and (2) intracellular neurofibrillary tangles (NFTs). NFTs are associated with the loss of neurons, whereas $A\beta$ is linked to dysfunction of neuronal synapses, cerebrovascular deficits, and inflammatory activity.

In addition to the above post-mortem hallmarks, in vivo magnetic resonance imaging (MRI) studies reveal structural differences between the Alzheimer's brain and unaffected healthy subjects. This includes thinning of the cortical mantle, shrinking of the hippocampus, and enlargement of the lateral ventricles, which carry cerebrospinal fluid (CSF).

However, a link between $A\beta$ or NFTs and these in vivo MRI hallmarks remain unclear. In this study, we applied Advanced Normalization Tools (ANTs) and Symmetrical Normalization to assess structural differences between control nontransgenic (nTg), TgCRND8, and 5xFAD mice harboring both amyloid precursor protein (APP) and presenilin mutations.

The Role of MUSA1 during Somitogenesis in *Xenopus laevis*

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MUSA1 is an F-box protein, the substrate recognition component of the SCF ubiquitin ligase, whose role is to bind substrates and target them for proteasome degradation. Others have shown that MUSA1 regulates chromosome segregation in mice during oocyte meiosis, as well as being a negative regulator during muscle growth in adult mice. The role of MUSA1 in the African clawed frog, *Xenopus laevis*, development is still unknown. We do know, oocytes contain mRNAs and proteins needed for early stages of development, known as maternal component; while the zygotic component is produced after the mid-blastula transition when the expression of the zygote starts. Our in situ hybridization studies reveal MUSA1 mRNA is located at the animal pole of the egg and early cleavage stages, then disappears and reappears in the somites of the tailbud and tadpole. Immunostaining confirm the presence of MUSA1 protein in the oocyte, early cleavage stages and somites, with a distinctive nuclear signal. We have also observed a nuclear signal in the epidermal cells, which leads us to assume that MUSA1 protein in this location is derived from the maternal component since we did not detect the mRNA in the epidermal layer. The protein presence in the somites (transitory tissue that give rise to muscle and

dermis) makes us question if MUSA1 protein has a role in somitogenesis and/or muscle development. Muscle tissue in the frog is derived from somites that become mature through a process called somitogenesis. This process takes place during organogenesis, after the fertilized egg cleaves and the embryo establishes the three germ layers during gastrulation. In this study, we aim to understand the role of MUSA1 during *X. laevis* somitogenesis through a loss-of-function approach. The knockdown of MUSA1 by morpholino injections allow us to determine the role of a protein by comparing the phenotype it gives us with a normal phenotype. The embryos were injected with morpholino on only one side producing an embryo with a control half (normal development) and an experimental half (development in the absence of MUSA1). The downregulation of MUSA1 produced an abnormal growth of the somites and disruption of the intersomitic boundaries, as seen by immunostaining the injected embryos with markers that allow visualization of the somitic tissue through confocal imaging. We have also performed a western blot analysis to obtain information regarding the development stages where the MUSA1 protein is present and its abundance over time. The western blot data reveals that the MUSA1 is maternally expressed, decreases during gastrulation, and is present during somitogenesis. The next step will be to perform a gain-of-function approach, where we can establish the phenotype produced when MUSA1 is overexpressed.

Para-aminobenzamidine Spacer Arm Morphology Classification

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Membrane based chromatography has become one of the most powerful techniques available for the isolation of biological molecules. These membranes provide a more easily accessible surface area for protein binding and the ability of being further optimized by controlling the length of spacer arms and ligand densities. Functionalized cellulose nanocrystals have been intensively studied as a suitable affinity membrane material due to its low cost, renewability, and excellent mechanical properties. The goal of this study is to computationally identify an optimized combination of spacer arms length and density for cellulose nanocrystals affinity membranes by means of a molecular dynamics simulation. This project includes the implementation of a cellulose polymer and crystal editor, the optimization of force fields for this model, and a set of simulations where densities and lengths of affinity ligands were varied. These affinity ligands were developed by combining carbon based spacer arms of different lengths (5-atoms, 7-atoms, and 14-atoms) and para-aminobenzamidine; while force fields and partial charges were adapted to CHARMM and computed by GAMESS respectively. Systems were minimized in vacuum at NV conditions, solvated, and simulated at NTP conditions during 20 ns at 1.0 fs under periodic boundary conditions. In order to identify the presence of these structures through our set of 33 simulations, we proposed the analysis of the applicability of various unsupervised machine learning algorithms to generate a classification mechanism. Methodology includes the representation of the spacer arm coordinates as a graph, as a spiral parametric function, and as a set of points in a three-dimensional space. Results have demonstrated that a twisting behavior is present in simulations including low concentrations of 14-atoms spacer arms. Leaning behavior is observed through all simulations of less than 60% of concentration, while straight behavior is present on all simulations with concentrations greater than 60%. Therefore, the proposed optimal spacer arm will depend on the concentration of the system. 5-atom and 7-atom spacer arms have proven to be stable and interact freely at any concentration. 14-atom spacer arms on the other hand, should be used in concentrations near 40% were they are optimally interacting. Concentrations above or below this point will not be optimal for

affinity membranes purposes. Unsupervised machine learning algorithms have proven to be efficient at the time of visualizing the agglomeration of groups present in simulations. Future work includes the optimization of these algorithms for more in-detail visualizations and to model the interaction of the proposed affinity membranes in presence of proteins.

Using a Raspberry Pi for Weather Sensor Monitoring

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The Raspberry Pi is a low cost single-board computer. For this work, it was configured as a portable web server that can remotely acquire data. In the Raspberry Pi microcomputer, a Raspbian OS has been installed, the official supported operating system, that is Linux based and it allows the writing of Python codes. It is possible to interface different kinds of sensors with this microcomputer through GPIO. Temperature, humidity and motion among others sensors have been tested for further implementation. The system must measure the remote signals, store the data in a database, and allow the users to remotely access through a web server. For database management, SQLite was configured. The main objective of this project is to provide a monitoring mechanism through a web server that can control an action depending on the sensors outcome.