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BOOK OF ABSTRACTS

IEEE EMBS
University of Puerto Rico at Mayagüez

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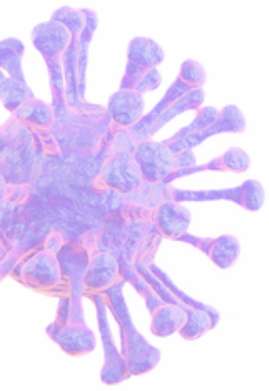


2ND ANNUAL BIOX SYMPOSIUM

Concurrent Sessions

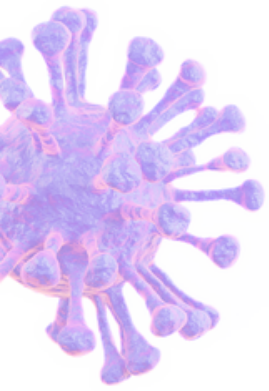
1:30 to 2:45 PM
204 Stefani Building

Osvaldo G. Ríos Fernández

Humanization of yeast genes of the mitochondrial copper delivery pathway to identify pathogenic mutations in rare mitochondrial disorders

Category: Biochemistry and Molecular Biology > Genomics

Copper is an essential cofactor of cytochrome c oxidase (CcO), the terminal enzyme of the mitochondrial respiratory chain that powers cellular energy production. The delivery of coppercto this enzyme is a complex process requiring multiple proteins and loss-of-function mutations in many of these proteins result in fatal infantile disorders. Motivated by the highly conserved nature of the copper delivery pathway proteins, here we aim to develop a “humanized yeast” system to rapidly test the pathogenicity of spontaneous mutations reported in these patients. Towards this goal, we have cloned ten evolutionarily conserved human genes of the mitochondrial copper delivery pathway in a yeast expression vector. Deletion of their corresponding yeast genes results in respiratory growth defect and decreased respiration. We hypothesize that expression of the conserved human protein in their corresponding yeast knockout would restore its respiratory growth and mitochondrial respiration. The successful completion of our work will not only validate the functional conservation of these genes but also offer a facile system to provide rapid molecular diagnosis of rare mitochondrial disorders caused by mutations in these genes.



2ND ANNUAL BIOX SYMPOSIUM

Concurrent Sessions

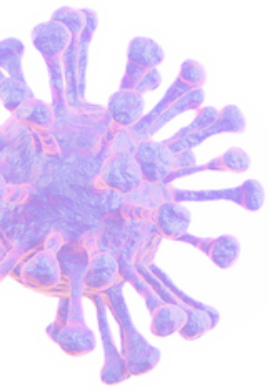
1:30 to 2:45 PM
205 Stefani Building

Julio E. Ocana Ortíz

Engineering Highly Thermostable Cas12b via De Novo Structural Analyses for One-Pot Detection of Nucleic Acids

Category: Biochemistry and Molecular Biology > Proteomics

Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) in complex with a CRISPR associated (Cas) protein is a rising biogenic technology tool, mainly used for the purpose of gene editing through the Cas9 endonuclease. As a response to the COVID-19 pandemic, a Reverse Transcription Loop-Mediated Isothermal Amplification (RT-LAMP) reaction, was coupled with the CRISPR/Cas highly specific diagnosis tool, in the development of a rapid one-pot detection of nucleic acids, such as those of SARS-CoV-2. The technique was clinically validated through 40 positive and 40 negative Hepatitis C (HCV) serum samples. Resulting in a 97.5% specificity and 88.8% accuracy, making us believe it has the potential to become a universal method for infectious diseases detection. This was developed by means of the Cas12b protein, thanks to its enhanced trans-cleavage capability. In this work, a Cas12b from Brevibacillus sp. (a bacteria found in hot springs), that can withstand temperatures up to 60°C, was engineered with the purpose of increasing that threshold to 65°C. With the aid of software such as Hotspot Wizard and DeepDDG, multiple amino acids in the wild-type BrCas12b (WT) sequence were identified as possible “hot spots”, for what these were selected to be substituted by another one. By means of Site-directed mutagenesis, 49 variants of the WT-BrCas12b were produced, purified, and tested in terms of specificity, cis-cleavage, and trans-cleavage activity. From these, a quadruple mutation (RFND) exhibited a higher thermostability, while serving its purpose in one-pot detection of nucleic acids up to 67°C. Because RT-LAMP provides faster and more accurate amplification at temperatures close to 65°C, the increment in the BrCas12b thermostability represents a significant value, that would allow detection of nucleic acids even with low copies numbers of a patient sample.



2ND ANNUAL BIOX SYMPOSIUM

Concurrent Sessions

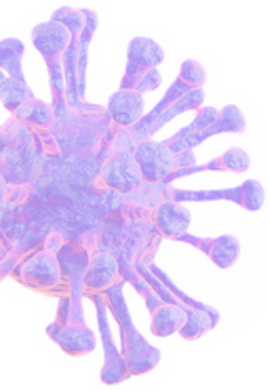
1:30 to 2:45 PM
203 Stefani Building

Lyana M. Rivera Negrón

Isolation of Cardiac Endothelial Matrix-Bound Vesicles as Biomarker Models for EV-biosensor Development

Category: Electronics and Devices > Medical Devices

Endothelial extracellular vesicles (endoth-EVs) expressing CD144+ are a new biomarker associated with the prognostic and diagnostic of cardiovascular diseases. Endoth-EVs are present in body fluids, including saliva, blood, and sweat. In addition, endoth-EVs are found within the cardiac endothelium extracellular matrix, known as matrix-bound vesicles (MBVs). Currently, endoth-EVs are isolated and detected via labor-intensive techniques such as EVs isolation and detection kits and ELISA, limiting their study as a complementary diagnosis marker in monitoring cardiovascular disease. We hypothesize that MBVs isolated from endothelial tissues (endoth-MBVs) will be CD144+ (a marker for endothelial cells), playing a key role as an EV-model in the development of endothelial EV-biosensors.The overarching goal of this project is to develop an EV-biosensor for the selective detection of Endoth-EVs CD144+ using a wearable-friendly electrochemical technique. To accomplish this, we first must isolate endothelial EVs from the cardiac matrix endothelium (endoth-MBVs) and characterize them as CD144+ to use them as EV models for biosensor construction. We have developed a method to decellularize cardiac endothelial tissue to endothelial - ECM. The vesicles were isolated using ECM digestion and then quantified with methods validated for extracellular vesicles. Finally, an immunoblotting technique (dot blot) was used to detect CD144 in the isolated endoth-MBVs. The results confirmed the presence of CD144+ protein in the isolated endoth–MBVs. This project provides evidence of the isolation of CD144+ MBVs that will be used as a target model for engineering the endothelial-EV biosensor.



2ND ANNUAL BIOX SYMPOSIUM

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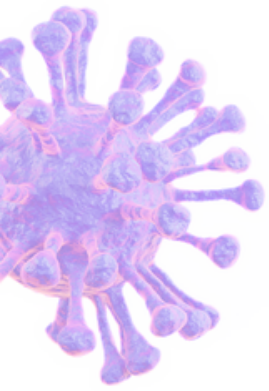
204 Stefani Building

Malcom Díaz García

Cancer Cell Characterization Through Machine Learning Applied to Electrochemical Impedance Spectroscopy

Category: Electronics and Devices > Medical Devices

Cancer is still considered a leading cause of death worldwide, despite the emergence of novel treatments such as cell therapies. Early diagnosis is key in cancer treatment, however early detection faces a unique set of challenges. Unlike other malignancies, circulating tumor cells (CTCs) aiming to colonize distal sites can evade detection by the immune system, and symptoms do not necessarily show early on. Thus, there is a need to improve detection of CTCs, through a system that can accurately differentiate them from healthy cells. Electrochemical Impedance Spectroscopy (EIS) is a technique that has been used in past experiments involving confined cells, which has revealed a distinctive impedance response at specific frequencies. Our present work proposes the use of Machine Learning, specifically the Random Forests (RF) algorithm, to generate classification models from impedance magnitude and phase angle response obtained from EIS that can distinguish between HeLa, MDA-MB-231, and MCF12A cell lines, and identify the most important frequencies for classification. Given that cells lines can elicit unique responses to specific frequencies, we hypothesize that RF can yield accurate classification models and the most important frequencies for it. To test this hypothesis, a fabricated microfluidic device was employed to trap HeLa, MDA- MB-231 and MCF12A cells in a micropore and apply a frequency sweep at AC voltages 30mV, 60mV, 90mV, 120mV and 150mV. The impedance magnitude and phase angle were screened for outliers and arranged in pairs of cell lines to make data comparing between each pair, using MATLAB. In R, pairwise RF models of the three cell lines were generated. Results show that accurate models can be generated to classify between pairs of cell lines at the tested voltages. The most important frequencies for model accuracy were in the order of 105Hz and 106Hz. It is worth noting that MCF12A are healthy mammary epithelial cells while MDA-MB-231 are advanced cancer mammary cells. Therefore, accurate RF models that distinguished between the two is indicative that EIS is a viable technique for cell line discrimination, which agrees with the established hypothesis. Essentially, coupling EIS with RF classification models proves an important achievement towards engineering a system that can detect CTCs from healthy cells, applicable to clinical settings, such as blood biopsies.



2ND ANNUAL BIOX SYMPOSIUM

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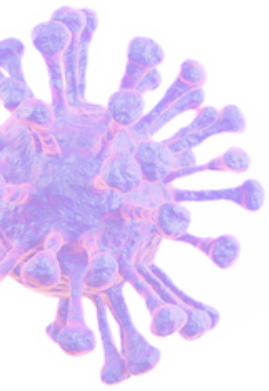
1:30 to 2:45 PM
205 Stefani Building

María Soto Medina

MSC's Metabolites in Extracellular Vesicles Isolated by Adsorption on TiO2 as Specific Predictors of MSC Manufacturing

Category: Cell Biology and Tissue Engineering > Stem Cell Engineering

The use of Mesenchymal stem cells (MSCs) as cell therapy in humans has great clinical potential in regenerative medicine. The manufacturing process of MSCs must comply with the required cell quality to satisfy safety and clinical needs. Methods to monitor MSCs growth at different scales remain underdeveloped or labor-intensive, making it difficult to scale-up the cell manufacturing process. MSCs metabolites are key predictors of cell culture status and are used to monitor cell proliferation in bioreactors. Extracellular vesicles (EVs) are carriers of the metabolites produced by MSCs or cells. Therefore, the objective of this project is to use TiO2 particles to adsorb EVs present in the liquid phase medium, subsequently analyze the metabolites using techniques such as Liquid chromatography-mass spectrometry (LC–MS) and use it as in line tool to scale-up the MSCs manufacturing. We initially evaluated the EVs adsorption on the metallic particles by adjusting a suspension of TiO2 in mQH2O (0.0125 mg anatase TiO2/mg mQH2O). The suspension was centrifuged, and the liquid phase was discarded. A solution containing the EVs samples (1.00x1012 exosomes/mL, exosome standards) was thoroughly stirred with the solid phase at room temperature for 15 minutes. The resulting suspension was centrifuged, and the two phases were separated. The solid phase was washed 4 times with filtered DPBS, and a method for detection of EVs adsorbed on the solid phase was employed. For the EVs detection method, we used the Coomassie blue staining assay to detect proteins present in EVs potentially adsorbed by TiO2 particles. However, the results were unsatisfactory because no signal was obtained from EVs adsorbed on TiO2 solid phase. Then, we used a fluorescent imaging approach using EVs carrying Green fluorescent protein (GFP) under the microscope. The results suggest that TiO2 adsorbs and concentrates EVs in areas of high particle conglomeration.



2ND ANNUAL BIOX SYMPOSIUM

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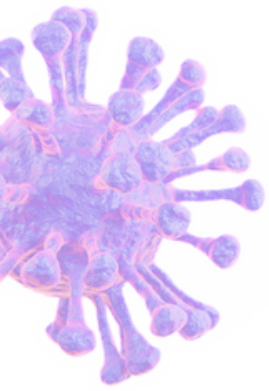
1:30 to 2:45 PM
203 Stefani Building

Luis Burgos

Endothelial Matrix-Bound Vesicles as Signaling Factors for Stem Cell Differentiation

Category: Cell Biology and Tissue Engineering > Stem Cell Engineering

Endothelial cells (ECs) are critical for biomedical research; however, ECs are not widely available. Mesenchymal Stem cells (MSCs) are a promising autologous source of ECs, but there is a need for suitable substrates for in-vitro differentiation. Matrix Bound Vesicles (MBVs) are extracellular matrix (ECM) signaling factors with tissue-specific biomolecular cargo (i.e., proteins, microRNA) that can replicate a cell-fate response like the ECM of origin. It's hypothesized that MBVs from endothelial tissue are CD144+ (EC marker) and can influence the differentiation of MSCs towards ECs. The overarching goal of this research is to evaluate endoth-MBVs as substrate-enhancer for MSCs differentiation. Endothelium tissue was scrapped mechanically from the porcine inner heart. Decellularized-ECM (dECM) was produced by automated decellularization in a bioreactor using sodium deoxycholate 4%w/v. dsDNA content in dECM was quantified. Then, MBVs were released from dECM by digestion, purified through size exclusion chromatograph, qEV columns (IZON), and finally quantified using an EV Validated kit (EXOCET, SBI). MBV characterization was carried out by Nanoparticle Tracking Analysis (NTA) for particle size distribution. An Immunodetection technique was used to detect CD144 in isolated MBVs. Proposed decellularization method achieved significant dsDNA reduction. DNA quantification assays showed 4.15 dsDNA µg/ECM mg on decellularized endoth-ECM. EV quantification method detected 5.00x107 MBVs/µL. NTA determined 264.0+/-12.5 nm as the mean particle size of MBVs. Finally, the immunoblotting assay revealed that isolated MBVs have the CD144 biomarker. Purified endoth-MBVs are CD144-positive, making them a suitable endoth-ECM signaling factor to tissue engineer a substrate for MSCs differentiation to ECs.



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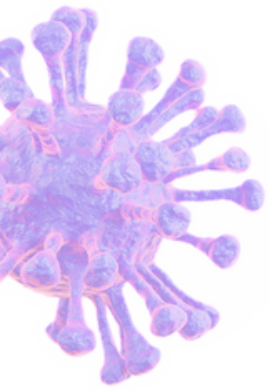
204 Stefani Building

Valeria Herrero Martínez

Isolation and Characterization of Lethal Factor Interacting Partners Using Human Lung T7 Phage Display cDNA Libraries

Category: Biochemistry and Molecular Biology > Chemical Biology

The lethal factor (LF) protein is an important virulence factor of Bacillus anthracis, a Gram- positive sporulating bacterium and a biological agent enzootic to several countries in America and Asia. B. anthracis has also caused human outbreaks in Zimbabwe and Russia and has been historically used in warfare. Although LF depends on the activity of the protective antigen protein to gain access to the cytoplasm, it is arguably the most significant tripartite unit as it cleaves regulators such as mitogen-activated protein kinase kinases (MAPKKs), therefore disrupting signaling pathways involved in the conversion of extracellular stimuli into intracellular responses and leading to cell apoptosis. There are three exposure routes to the pathogen: cutaneous, gastrointestinal, and inhalation pathways, of which the latter is the most alarming manifestation of the disease, with mortality rates up to 90% if left untreated. Previous records show that inhalation anthrax induces inflammation of the mediastinal lymph nodes, necrotizing pneumonia, and hemorrhagic symptoms. Thus, this investigation seeks to answer whether the LF-wild type protein (LF-wt) and LF-active site mutant (LF-mut) interact with peptide substrates other than MAPKKs in lung tissues; the mutant form of the protein possesses an inactive catalytic site, which allows for the interaction and isolation of peptide candidates with affinity for the active site. LF interacting lung peptides were isolated and amplified using the T7 phage display system where genetically modified T7 bacteriophages display human lung (HL) peptides on the capsid surface. The phage system, combined with biopanning selection tests, allow us to isolate LF-HL peptide interactions to further characterize the cellular pathways of the LF protein. It was found the initial library contained 2.2X1010 plaque forming units, which was reduced to 5.5X103 phage candidates specific for wild-type LF and 5.5X103 candidates for mutant-type LF after the first round of biopanning. Additionally, 20 individual interacting partners were amplified for LF-wt and LF-mut. Candidates were further selected with two additional biopanning rounds. Finally, 20 candidates from the third biopanning were amplified. The isolation of these interacting lung peptides will serve to characterize novel LF substrates and develop biosensors and therapeutic blocking agents.



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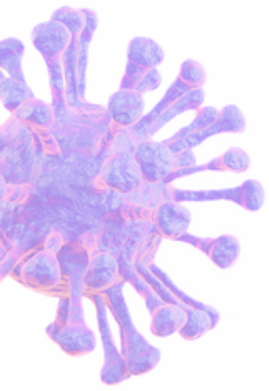
203 Stefani Building

Valeria Figueroa Stuart

Gene Expression Commonalities Between Autism and Schizophrenia in Postmortem Brain Tissue Through BioOptimatics

Category: Computational and Systems Biology > Bioinformatics

Schizophrenia (SCZ) and Autism Spectrum Disorder (ASD) are neurodevelopmental disorders that cause social and cognitive disabilities and share various symptoms and potential causes. This study aims to understand the underlying etiology between SCZ and ASD through their joint gene expression analysis. This analysis involved mathematical optimization formulations compiled in an R suite called OBAMA (Optimization-Based Analysis of Multiple Arrays) developed by our group. Through OBAMA, four genes with joint maximum relative expression changes were identified: RGS1, HSPA6, RNU4-2, and CCL4. Their associated biological pathways and cell processes are detailed next. RGS1's function is to regulate the activity of G-Protein Coupled Receptors by activating GTPase, which prevents GDP from changing to GTP. Therefore, the receptor remains inactive while this occurs. RGS1 was found underexpressed in ASD and SCZ. Since RGS1 is a negative regulator of GPCRs, it can be inferred that a low concentration of RGS1 can lead to an increase in the activity of GPCRs. This increase in activity of this receptor in the brain can lead to overstimulation, which has been associated with seizures. Seizures are, indeed, a common symptom of both ASD and SCZ. CCL4 is known for its proinflammatory effects at sites of infection or injury. The development of dysregulated immunity pathways that give way to ASD and SCZ could potentially be connected to a maternal immune response caused by an Influenza infection during the first trimester. The high levels of maternal cytokines can trespass the placenta and affect the distribution and quantity of microglia present during fetal development. This can be seen as a possible reason for overexpression of CCL4 and dysregulated immunity responses. A similar route could link the RNU4-2 gene to ASD and SCZ. RNU4-2 is involved in the splicing pathway, essential for the development of mRNA and thus protein synthesis. The formation of binding domains essential to this process is blocked by the dysregulation of C-reactive proteins, which are dysregulated in ASD and SCZ patients due to neuroinflammation. Maternal immune response signaling for the release of these proteins during pregnancy, blocking the splicing pathway in the fetus, could be the trigger for the development of ASD and SCZ. The gene HSPA6 (Heat Shock Protein Family A Member 6) is responsible for encoding Heat Shock Proteins (HSPs) which act as chaperones and have important roles in cell signaling, apoptosis, and protein homeostasis. Dysfunctions in HSPs are linked to neurodegenerative diseases like ASD. Several brain regions, like the cerebellum, showed a significant increase in microglial activation in ASD patients compared to those without. The inhibition of HSPC1 could relieve symptoms of neurodegenerative diseases, while the overexpression of HSPA1 can prevent neuronal apoptosis by restoring protein homeostasis.



2ND ANNUAL BIOX SYMPOSIUM

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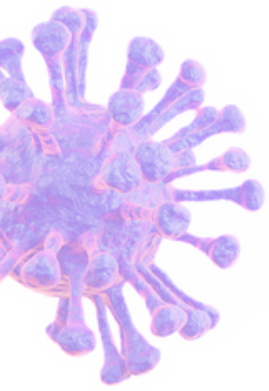
204 Stefani Building

Jean M. Trinidad Rivera

Isolation of Urea Metabolizing Bioprospects by Functional Analysis of Metagenomic Libraries from Different Ecosystems in Puerto Rico

Category: Microbiology > Environmental Microbiology

Urea is a common by-product of many industrial processes, frequently used as a nitrogen-based fertilizer in agriculture, which is also present in large quantities in chicken manure. It ends ups entering various ecosystems via the discharge of wastewater by leeching from agricultural soils or chicken manure, causing eutrophication. Some methods exist to treat urea contamination, such as enzymatic degradation, thermal hydrolysis, and phytoremediation. Urease is a nickel-dependent metalloenzyme that catalyzes the hydrolysis of urea to ammonia and carbon dioxide. While urease is one of the most common enzymes used to degrade urea, there is a need to find novel activities capable of performing similar functions more efficiently. This study aims to perform a functional analysis of metagenomic libraries (ML) obtained from various ecosystems in Puerto Rico to find novel bioprospects capable of metabolizing urea. The functional analysis was performed on 4 ML; Dry Forest at Gúanica (DF; 679,644 clones), Añasco River at Añasco (AR; 65,250 clones), Guajataca Water Reserve at Isabela (GWR; 2,250,000 clones), and Playuela Beach at Cabo Rojo (PB; 1,200 clones). ML were grown in LB broth with chloramphenicol for 4 hours at 37oC. Then, each library was inoculated in Urea media and grown at 37oC for 48-72 hours. The ML positive for urease production was serially diluted, plated on LBA with chloramphenicol, and incubated for 24-72 hours. Individual clones were inoculated in urea media and incubated for 48-72 hours to further score for clones with urease activity. Only the DF library tested positive for urease production out of the four libraries screened, and of all individual clones evaluated, 61% showed urease activity within 48hrs. We are monitoring more individual clones for urease activity to further determine the genes associated with urease production via Tn-mutagenesis. Finding novel ureases or urea-metabolizing-like enzymes would positively impact our ability to treat urea-contaminated environments, such as agricultural lands, chicken farms, and processed industrial wastewater.



2ND ANNUAL BIOX SYMPOSIUM

Concurrent Sessions

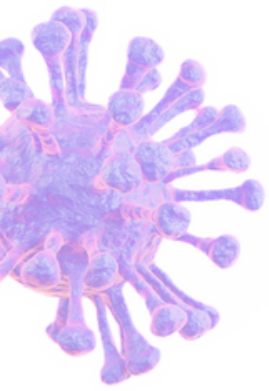
1:30 to 2:45 PM
205 Stefani Building

Jessica Paéz Díaz

Generation of High Molecular Weight Metagenomic Libraries from the digestive tract of Holothuria glaberrima

Category: Biochemistry and Molecular Biology > Genomics

Several non-mammalians species can regenerate their organs or appendages. Understanding these mechanisms, novel translational research can be developed and applied to organ and transplant technology. Sea cucumbers (Echinoderms) such as Holothuria glaberrima can eviscerate their gastrointestinal system when exposed to severe environmental conditions, regenerating the lost tissue in approximately twenty-eight days. Since gut microbiota could play a role in the regeneration process, it's necessary to access the cultivable and uncultivable microbiota. Most microbes cannot grow in traditional laboratory media, the emergence of culture-independent approaches, such as metagenomics, allow the unraveling of microbial diversity and its functional traits. This study focuses on generating high molecular weight metagenomic libraries from the gut microbiota of H. glaberrima. Direct DNA extractions from three sections of the digestive tract of H. glaberrima: complete evisceration (C), the washed intestine (WI), and the contents from the wash (CW), were used to develop metagenomic libraries (ML). DNA fragments of 40kbp were isolated by sizing selection and were gel-purified using gelase. The DNA fragments were blunt-ended by end-repair and further ligated with the vector PCC1FOS into concatemers. These ligated DNA-vector were packaged into the Lambda phage using MaxPlax, and the appropriate phage:bacteria (Epi300TM) ratio was determined by serially diluting the packaged phages. Four metagenomic libraries were generated, one from the complete evisceration sample (C-ML), contents from the washed intestine sample (CW-ML), and two from the washed intestine (WI-ML). The total metagenomic clones generated from the H. glaberrima isolated DNA from the gut microbiota, were approximately 4.04x105 (this is equivalent to 1.61x104Gbp of genetic information). The number of clones obtained were distributed as: 1.32x103, 5.63x104, and 3.47x105 from C-ML, CW-ML, and WI-ML respectively. The generation of these metagenomic libraries represents an opportunity to study and characterize the microorganisms present in the digestive tract of the. Most importantly, identify metabolic activities that are related to the regeneration process.



2ND ANNUAL BIOX SYMPOSIUM

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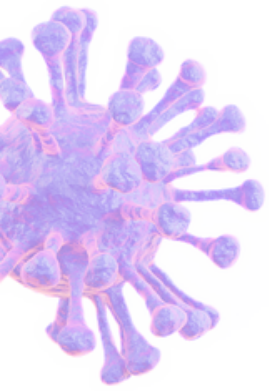
1:30 to 2:45 PM
203 Stefani Building

Gabriela Meléndez Martínez

Extraction of Large Insert Metagenomic DNA from the Sea Cucumber Holothuria glaberrima Eviscerated Gut

Category: Biology and Molecular Biology > Genomics

The Daneo rerio (zebra fish), and amphibians such as Ambystoma mexicanum (axolotl) are just some examples of species that have the ability of organ or appendage regeneration. The sea cucumber's, Holothuria glaberrima, regenerating capabilities allow the replacement of its entire digestive system 28 days after evisceration. Apart from genetic factors, it has been proposed that microbiota could contribute to this ability; thus, studying the microbiota in the H. glaberrima digestive system could unveil microorganisms that promote organ regeneration. There are non- culturable microorganisms unable to grow with traditional and laboratory culture techniques. Culture independent approaches, such as metagenomics, allow for the access and study of unculturable microorganisms, which compose more than 95% of most environments. The generation of metagenomic libraries depends largely on the size, purity, and concentration of the DNA extracted. This study aims to generate an effective direct DNA extraction method of the H. glaberrima digestive system for further metagenomic library generation and microbiome analysis. The freeze and thaw mechanical lysis method was used to extract large insert (40kbp) sea cucumber DNA (DNAsc) of four H. glaberrima samples: the complete (C) evisceration and fecal (F) content, washed intestine (IL), and the liquid obtained after washing (CL). Combined mechanical, enzymatic, and chemical approaches for the extraction alongside Z-buffer (phosphate-based buffer with Tris-HCl, KCl, and MgSO4 that cleaves disulfide bonds) were used for cell lysis and nucleic acid accessibility of the samples. The use of lysozyme RNase with the Sodium Dodecyl Sulfate (SDS) detergent and the Guanidine Thiocyanate (GITC) chaotropic agent, were used for the final lysis reaction. A mixture of chloroform-isoamyl alcohol was used for further protein contaminant removal, followed by DNAsc precipitation and salt removal using absolute isopropanol and 70% ethanol respectively. The concentration and purity of the DNAsc was determined espectrophotometrically, and the DNAsc was assessed in 1% agarose gel with 1X TAE as a running buffer. The highest DNAsc concentration was obtained from the C (54.5 – 1,301 ng/µL) sample, followed by IL (16.2 – 1,202.9 ng/µL), F (68.7 – 307 ng/µL), and CL (16.8 – 92.6 ng/µL). The purity analysis parameters used were 260/280 (~1.80 expected ratio). Only sample F fell outside parameters, with an average value of 1.52. The electrophoresis showed high molecular weight (40 kb) in all the DNAsc samples barring F. This indicates that the direct DNA extraction method was successful in yielding DNA of high concentration, molecular weight, and purity in samples C, CL, and IL; this has helped us generate a total of four high molecular weight metagenomic libraries. Finally, these libraries will be sequenced to obtain their taxonomical profiles and initiate functionality testing.



2ND ANNUAL BIOX SYMPOSIUM

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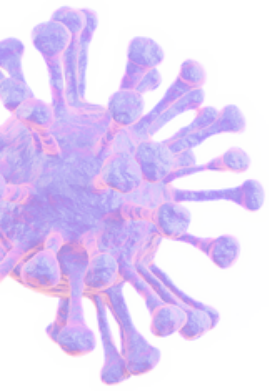
1:30 to 2:45 PM
204 Stefani Building

Alexxa C. Cruz Bonilla

The Impact of M2-polarized macrophages on the oncogenic activity of hedgehog signaling in triple negative breast cancer cells

Category: Cell Biology and Tissue Engineering > Cancer Biology

Hedgehog (Hh) signaling activity is highly upregulated in about 30-40% of tumor specimens and it has been associated with poor prognosis in breast tumors of the triple-negative sub-type. Hh signaling activity has been linked with the phenotype of tumor-associated macrophages (TAMs) in tumors, yet its oncogenic role within the context of triple-negative breast cancer (TNBC) is not well-understood. We hypothesize that TAMs support the oncogenic activity of Hh signaling in TNBC in a paracrine manner. Hh signaling activity was examined in monocytes, TAMs, and MDA-MB-231 (TNBC cell line) through qRT-PCR and Western Blot. The qRT-PCR results showed no significant difference in the levels of GLI1 and SMO genes in TAM monocultures +/- SHH ligand, indicating the absence of canonical Hh signaling activity. The SHH ligand was only expressed in tumor cells but not in TAMs. Tumor cell growth was examined in a co-culture system when increasing TNBC to a set TAM quantity, with a 2:1 and 1:1 ratio. These ratios were also observed under -/+ NVP-LDE225 (NVP) treatment; a Hh pathway inhibitor. Macrophage retention in the co-cultures was analyzed in comparison to the TAM monocultures, these demonstrated no statistical difference across all conditions. All experiment replicates of n=3 that were performed demonstrated replicability amongst all samples. Initial examination of growth rates indicates that NVP does not affect the TAM and TNBC monocultures; having a non-significant difference when analyzed through a One-Way Anova. Utilizing Dunnet's multiple comparison test, the results showed a decreasing tendency in the tumor proliferation rates between the co-cultures treated -/+ NVP and when compared to the TNBC monocultures. In the absence of NVP, both 2:1 and 1:1 co-culture, the difference in proliferation rate was significantly higher ($p<0.0001$) than in the TNBC monocultures. Where the 1:1 co-culture -NVP conditions had a $p<0.0001$ and +NVP a $p=0.0020$, decreasing the proliferation rate when in treatment. Overall, results pointed to an increase in TNBC growth when in direct contact with TAMs and lower proliferation rates in co-cultures under NVP treatment. Utilizing the same parameters established for the co-culture system, a tri-culture model with a fibroblast cell line is currently being tested. Future work also includes replicating into the three-dimensional platform to better understand the role of cell-to-cell contact and the metabolic processes that occur in vivo.



2ND ANNUAL BIOX SYMPOSIUM

Concurrent Sessions

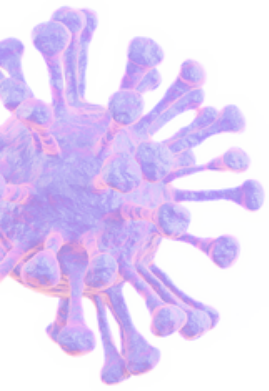
1:30 to 2:45 PM
205 Stefani Building

Luis Mañan Mejías

Fitting Computational Growth Model to Experimental Coarctation of the Aorta

Category: Computational and Systems Biology > Systems Biology

Coarctation of the aorta (CoA) is a congenital cardiovascular disease which causes stenosis in the proximal descending thoracic aorta [1]. Surgical correction is common, yet the heterogeneity of patients makes further clinical studies difficult [1]. A lumped-parameter growth model [2] can be modified to match existing experimental hemodynamic data from CoA rabbits [3]. Predicting changes in cardiovascular parameters can help understand and treat long-term morbidities after correction. Experimental data for the control group from the rabbit model was allometrically scaled and input into the current 6-compartment model, with an additional inductor to match aortic flow. The systemic arteries were divided into three capacitors for the flow split along the aorta, allowing the 8-compartment model to simulate a coarctation [4]. Parameters for circuit model were optimized to fit experimental data, including reported mean blood pressure gradient for the latter. Long-term CoA morbidities can be modeled in lumped parameter circuit to understand patient risk. Additional compartments for the upper body and ascending and descending aorta are necessary o fit the characteristic blood pressure gradient. Fitting growth model over time can provide unique insights into the diagnosis and treatment before and after correction.



2ND ANNUAL BIOX SYMPOSIUM

Concurrent Sessions

1:30 to 2:45 PM
203 Stefani Building

Javier Moscoso Cabrera

Solar Energy Systems and Health

Category: Engineering, Physics & Mathematics > Electronics

Proyecto Luz Verde UPRM is an initiative that aims to raise awareness, educate, and design photovoltaic solar energy systems in Puerto Rico. The team consists of undergraduate students and members of the IEEE Power and Energy Society student association. They offer educational workshops and informational brochures on the benefits of photovoltaic systems, good maintenance practices, components, handling and safety measures, social, economic, environmental impacts, among other aspects. Their mission is to guide and raise awareness about energy consumption and its impact locally and globally, and to empower people on the path to self-management and transition towards energy security through sustainable energy. The first implementation of the solar gazebo is planned at the University of Puerto Rico - Mayagüez Campus, with the goal to go beyond and achieve its implementation in communities outside the campus. The structure will be resistant to hurricanes and earthquakes and will consist of a 1.44 kW solar system on solar panels on the roof with batteries. The team is open to feedback and collaboration.