RCMI 2019 PROGRAM CONFERENCE

Collaborative Solutions to Improve Minority Health & Reduce Health Disparities

December 15–17, 2019 in Bethesda, MD | #RCMIconf

> ***The Research Centers in Minority Institutions (RCMI) Program*** *develops and strengthens the research infrastructure necessary to conduct state-of-the-art biomedical research and foster the next generation of researchers from underrepresented populations.*

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Editorial Message

We are delighted to publish the abstracts from the 2019 Research Centers in Minority Institutions (RCMI) National Conference held in Bethesda, MD on December 15-17, 2019. The conference highlighted excellence and innovation in basic, behavioral and clinical research, especially from programs sponsored by the National Institute of Minority Health and Health Disparities (NIMHD). Supported by a multi-institutional cooperative U13 award, the conference focused on advances achieved by RCMI investigators on research to reduce health disparities and improve minority health.

Through congressional mandate, the RCMI program was initiated by the National Institutes of Health (NIH) in 1985. The authorizing legislation called attention to the Department of Health and Human Services (DHHS) Secretary's Task Force annual report on the status of the health of the American people and noted the disparities in the health status between minority and majority Americans. The legislation also acknowledged the important role that minority educational institutions have traditionally played in training professionals who provide health care to the minority community. Based on this mandate, the primary goals of the RCMI program are (1) to enable minority institutions that offer doctorates in the health professions and/or health-related sciences to strengthen their research environment to become more competitive in obtaining support for the conduct of biomedical and behavioral research, and (2) to foster training and development of the next generation of researchers from underrepresented populations.

The 2019 RCMI National Conference was aligned with NIMHD's vision to advance the science of minority health and health disparities research by enabling all investigators showcase their research experiences on diseases that disproportionately affect health disparity and minority populations. The conference included plenary sessions, workshops, oral and poster presentations, and concurrent sessions. Over the three-day period, there were abundant opportunities for sharing research information, attending mentoring and professional development workshops, identifying collaborators and conducting networking activities.

More than two hundred participants submitted abstracts in areas related to basic and applied minority health and health disparities research, behavioral and social determinants of health, capacity building, clinical and translational minority health and health disparities research, community-based participatory research and research in special populations and sub-groups. We are pleased to share this work through publication of the conference abstracts.

Lastly we thank all our submitting authors and the Puerto Rico Health Sciences Journal for allowing us to share with the scientific community the knowledge and efforts of the RCMI investigators in eliminating health disparities and improving minority health.

Cordially,

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ORAL ABSTRACTS

| BASIC & BIOMEDICAL SCIENCE |

11.01.004

VERNONIA AMYGDALINA DELILE FOR PROSTATE CANCER THERAPY

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Jackson State University

Prostate cancer is one of the common cancers in males and its incidence keeps increasing globally. Approximately 81% of prostate cancer is diagnosed during the early stage of the disease. The treatment options for prostate care include surgery, radiotherapy, and chemotherapy, but these treatments often have side effects that may result to poor quality of life such as impotence or decrease bowel function. Our central goal is to test the anticancer activity of Vernonia amygdalina Delile (an edible medicinal plant that is relatively inexpensive, nontoxic, and virtually without side effects) for the prevention of prostate cancer using human adenocarcinoma (PC-3) cells as a test model. To address our specific goal, PC-3 cells were treated with Vernonia amygdalina Delile (VAD). Cell viability and cell morphology was analyzed by acridine orange and propidium iodide (AO/PI) dye using the fluorescent microscope. DNA damage was evaluated by the comet assay. Cell cycle arrest and cell apoptosis was evaluated by Flow Cytometry assessment. Nucleosomal DNA fragmentation was detected by DNA ladder assay. Data obtained from the AO/PI dye assessment indicated that VAD significantly reduced the number of live cells in a dose-dependent manner, showing a gradual increase in the loss of viability in VAD-treated cells. Similar result was previously obtained by the MTT assay. We observed a significant increase in DNA damage in VAD-treated cells compared to the control group. Flow cytometry data showed that VAD induced cell cycle arrest at the G0/G1 checkpoint. Flow cytometry data also showed that VAD induced caspase-3 activation in treated cells compared to the control group. We observed the formation of the DNA ladder in gel electrophoresis by induction of apoptosis in PC-3 cells treated with VAD. These results suggest that inhibition of cancer cell growth, induction of DNA damage, cell cycle arrest at the G0/G1 checkpoint, and apoptosis through caspase-3 activation and nucleosomal DNA fragmentation are involved in the therapeutic efficacy of VAD as anticancer candidate towards the prevention and/or treatment of prostate cancer.
Keywords: Vernonia amygdalina Delile, cell death, cell cycle arrest, apoptosis, prostate cancer

11.01.008

TARGETING MITOTIC REGULATORS IN BASAL BREAST CANCERS

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Purpose: While non-Hispanic white women (NHW) are more prone to develop breast cancers than Hispanic/Latino (H/L) and African American (AA) women, H/L and AA women have higher probabilities of dying from breast cancers. This is in part due to AA and H/L women with breast cancer being: (1) more frequently diagnosed with later-stage/grade and larger breast tumors, (2) more likely to develop hormone-receptor-negative (mainly triple-negative, TNBC: ER-PR-Her2-) breast cancers, and (3) to the aggressive nature of TNBC, which are more likely to be metastatic, refractive to anti-hormonal therapies and to relapse after chemotherapy than luminal subtypes. Our laboratory is investigating the molecular drivers of cancer disparities between AA, H/L, and NH by identifying transcriptional networks unregulated in Her2+ and TNBC. Methods: Because these subtypes display more centrosome amplification (CA), proliferation, and chromosome instability (CIN) than luminal subtypes, we performed several expression screens that identified the Cdk/Rb/E2F pathway as a major driver of CA/CIN in hormone-receptor-negative breast tumors. That allowed us to identify Nek2, SgoI, and TTK as critical drivers of CA/CIN in breast cancer cells. Results: Our data indicate that these kinases have novel functions since they signal survival, EMT, and invasion in TNBC cells and affect patient survival. We have confirmed the relationship between mitotic kinases and invasion with a tissue microarray of AA, H/L and NHW white women with breast cancers. Discussion: Our ultimate goal is to inhibit TTK, Nek2, and SgoI in TNBCs in order to prevent progression into metastatic stages or to specifically target metastatic cells.

11.01.001

KDM5B IS ESSENTIAL FOR PI3K/AKT SIGNALING IN PROSTATE CANCER

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MEHARRY MEDICAL COLLEGE (GL, TK, WL, SIC, MI, BRB, ZC), TENNESSEE STATE UNIVERSITY (SIC), YALE UNIVERSITY (QY), VANDERBILT UNIVERSITY (RJM)

The hyperactivation of the Phosphoinositide 3-kinase/Protein kinase B (PI3K/AKT) signaling pathway has been long recognized to make important contributions on the

development and progression of human diseases and cancers, but the key factors governing the PI3K/AKT signaling are still unclear. Phosphatase and tensin homolog (PTEN) antagonizes Phosphatidylinositol (3,4,5)-trisphosphate (PIP3)/AKT levels, and PTEN loss leads to the hyper-activation of AKT signaling and cancer growth. Lysine-specific demethylase 5B (KDM5B) controls the methylation levels of histone H3 lysine 4 and is frequently upregulated in human cancers including prostate cancer (PCa). Here, we show that KDM5B contributes to the PI3K/AKT signaling pathway in PCa in vitro and in vivo. Strikingly, KDM5B inactivation abolishes the hyper-activation of AKT signaling and decreases the proliferation in human PCa cells through reduction of P110α/P85 expression and PIP3 levels. By contrast, KDM5B overexpression significantly augments the AKT signaling. Furthermore, we demonstrate that conditional inactivation of Kdm5b in the mouse prostate reduces the P110α/P85 levels, blocks the hyper-activation of the AKT signaling, and suppresses the prostate tumorigenesis in Pten-null mice. These findings reveal that KDM5B acts as a key effector on regulation of the PI3K/AKT pathway, and further support that targeting KDM5B can be a novel and effective therapeutic strategy of controlling PC

11.01.039

METABOLIC CHANGE IN TNBC DUE TO LDHA & LDHB DOUBLE KNOCKOUT

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PURPOSE: Triple Negative Breast Cancer (TNBC) is an aggressive form of cancer that disproportionately affects African Americans and has a high mortality rate with no known cure. All solid tumors exhibit the Warburg effect and display an elevated glycolytic flux, accounting for increased levels of lactic acid production, which is believed to be driven by the various isoforms of the enzyme Lactate Dehydrogenase (LDH). LDHA and LDHB are highly expressed in MDA-MB-231 cells. Increased lactic acid secretion contributes to significant pro oncogenic malignant and metastatic processes. METHODS: Edited MDA-MB 231 TNBC cells with LDHA and LDHB double gene knockouts were provided by Snynthego from their engineered cell product, knockout cell pool. Clonal isolation was performed in the lab using Synthego's limiting dilution protocol. The effects of LDHA and LDHB double knockouts on genetic parameters in MDA-MB-231 cells were evaluated by examining whole transcriptomic influence on mRNAs and long intergenic non-coding RNA transcripts (lincRNA) using Affymetrix human 2.1-ST microarrays. Genome studies were complemented by metabolic analysis of mitochondrial function, lactic acid production, glucose consumption, and ATP production. RESULTS: The data provide evidence to suggest that there are alternative pathways to the production of lactic acid outside of LDH conversion of pyruvate to lactic acid. The transcriptome analysis shows specific genes that could be involved with an alternative route of lactic acid production in cancer cells. CONCLUSION: There is clearly enough evidence to suggest that acidity drives malignant processes using lactic acid as a means to control pH. Prevention of lactic acid production would be a formidable detriment to survival and metastasis of human malignancies, including TNBC.

11.04.002

HMGA2 ISOFORMS IN PCA-BONE MICROENVIRONMENT INTERACTIONS

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PURPOSE: Prostate cancer (PCa) is the second leading cause of cancer related deaths in American men. Compared to Caucasian men, African American males have a higher bone density, and mortality rate due to PCa bone metastasis. Recent studies have shown that high mobility group A2 (HMGA2), a non-histone chromatin binding protein, plays a critical role in promoting epithelial-mesenchymal transition (EMT) and metastasis. HMGA2 full-length/wild-type and truncated (lacking the 3'UTR) isoforms are overexpressed in several cancers, however, their distinct roles in metastasis have not been reported. Our laboratory focuses on tumor-microenvironmental interactions, particularly, how PCa cells interact with bone at the metastatic site. We hypothesize that HMGA2 isoforms may play differential roles at the bone metastatic site to increase paracrine cell migration. METHODS: LNCaP PCa cell line stably overexpressing either wild-type or truncated HMGA2 was co-cultured with low (100 mg) or high (200 mg) density hydroxyapatite (inorganic component of bone), followed by collection of conditioned media (CM). CM was added to parental LNCaP cells followed by analysis of paracrine cell migration across collagen-coated boyden chambers, paracrine cell proliferation using MTS assay, and signaling pathways by western blot analysis. RESULTS: Truncated HMGA2 co-cultured with hydroxyapatite led to increased paracrine phospho-ERK expression (but not phospho-AKT), and higher paracrine cell migration, compared to wild-type HMGA2, which could be antagonized by MAPK inhibitor, U0126. Conversely, wild-type HMGA2 co-cultured with increasing hydroxyapatite density promoted higher paracrine cell proliferation compared to truncated HMGA2. CONCLUSIONS: HMGA2 isoforms may differentially mediate PCa/hydroxyapatite interactions at the bone metastatic site.

11.04.005

APOE DEPENDENT EXERCISE-INDUCED ADAPTATION IN CARDIAC TISSUE

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PURPOSE: Apolipoprotein E (APOE) is a major cholesterol carrier. In humans, the APOE gene has 3 variants: APOE2, APOE3, and APOE4. The APOE4 isoform incurs a higher risk for cardiovascular and neurodegenerative disease relative to the more common APOE3 isoform. Exercise is a therapeutic strategy for preventing these debilitating conditions; however, recent studies indicate that the APOE isoform may show attenuated exercise-induced adaptations. We hypothesize that exercise-induced adaptive changes in APOE4 and APOE3 genotypes are associated with differences in mitochondrial function and oxidative capacity. The aim of this study was to identify protein networks that show APOE-dependent exercise-induced adaptive changes. METHODS: Transgenic APOE3 and APOE4 mice were grouped as sedentary and exercised. Mice in exercised groups were subjected to daily, forced treadmill running for 8 weeks. Cardiac tissue was processed for proteomic analysis using the S-trap method and data collected using 1D-LCMS on an Orbitrap-ELITE. Data were assigned using Proteome Discoverer 2.3 with Mascot Batch. RESULTS: Quantitative analysis identified 1199 proteins differentially regulated by exercise and/or APOE genotype. Several mitochondrial proteins (including ATP synthase-coupling factor 6, Cytochrome c oxidase, cytochrome c1, cytochrome b-c1 complex, and NADH dehydrogenase) were significantly different between genotypes under sedentary conditions or showed divergent adaptations with the exercise intervention. CONCLUSION: Our data shows APOE genotype has a differential effect on cardiac tissue protein expression in sedentary and exercised conditions, which may underlie differences in genotype susceptibility to cardiovascular and neurodegenerative disease.

11.05.001

PP1-TARGETING SMALL MOLECULES FOR HIV-1 INHIBITION

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Current antiretroviral drugs do not affect HIV-1 transcription, which needs to be inhibited to facilitate functional cure. Previously we identified 1E7-03 compound targeting protein phosphatase-1 (PP1) that inhibited HIV-1 in cell culture (IC50 is about 5 μM) and humanized mice (40-fold downregulation). However, poor metabolic stability of 1E7-03 (degraded in 30 min in mouse plasma) and some toxicity limited its future use as an antiviral drug. Here, we aimed to improve metabolic stability of 1E7-03 and decrease its toxicity. We performed structural optimization based on the identified labile sites and generated 52 analogs by replacing labile linkers with more stable substructures such as urea and piperazine. The HIV-1 inhibitory activity of the developed analogs was evaluated with one round HIV-1 infection with VSV-G pseudotyped HIV-1-Luc virus and fully replication competent HIV IIIB virus. We identified analog HU-1a as the best candidate with slightly better HIV-1 inhibitory activity (IC50 = 3.68 uM for SAM-75 and IC50=4.78 uM for 1E7-03) and lower toxicity (80% viability at 100 uM for SAM-75 comparing to 50% for 1E7-03). Importantly, SAM-75 was 100% stable after 6 hrs of incubation in mouse plasma, while 1E7-03 showed 80% degradation in 30 mins. Moreover, we confirmed that both HU-1a and 1E7-03 compounds primarily interacted with non-catalytic RVxF site of PP1 using novel "protein painting" approach that was combined with split NanoBit system. Thus we developed a novel optimized analog of 1E7-03, HU-1a, which retained the inhibitory mode of the lead compound and showed improved metabolic stability and reduced toxicity.

16.01.002

MACHINE LEARNING TO PREDICT WARFARIN DOSES IN HISPANICS

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Center for Collaborative Research in Health Disparities(RFM,ARL,JRM,BN,KC), University of Puerto Rico School of Medicine(ARS), University of Puerto Rico School of Pharmacy(JD)

PURPOSE: The utility of machine learning (ML) techniques for warfarin dose predictions in Hispanics has yet to be fully evaluated. This study compares seven machine learning methods to predict stable warfarin dosing in Caribbean Hispanics. METHODS: Participants were recruited from San Juan, Puerto Rico, which serves a predominantly Caribbean Hispanic population. Several ML methods were applied, including multivariate adaptive regression splines (MARS), artificial neural networks (ANN), random forest regression (RFR), support vector regression (SVR). Data were divided between 80% and 20% to train the predictive models. Model performance was determined using the mean absolute error (MAE) and percentage of patients whose predicted dose were

within ±20% of the actual stabilization dose. Performance metrics were compared between patients with normal, sensitive and resistant dose requirements. RESULTS: RFR outperformed all other methods, with MAE of 4.93 mg/week and 80.6% of cases with predicted doses within ±20% of actual patient's stabilization dose. Among those with normal dosing requirements, RFR performance was also better than the rest of models with MAE and predictions within ±20%. In the sensitive sub-cohort, both SVR and RFR showed superiority over the others with lower MAEs and higher percentages of predictions within ±20%. MARS showed meaningful results in the resistant sub-cohort with MAE and predictions within ±20%. CONCLUSIONS: Models generated using the RFR, MARS and SVR methods showed significantly better results in predicting warfarin doses compared to the others. Differences in model performance between patients that are normal, sensitive or resistant to warfarin were also found.

16.03.003

DEVELOP MULTISCALE COMPUTATIONAL METHOD FOR MOLECULAR MOTORS

L LI
University of Texas at El Paso

PURPOSE: Electrostatic interactions play important roles in Biology. Therefore, a lot of efforts have been made to model the electrostatic interactions in biological systems. However, it is extremely challenging to accurately calculate the electrostatic interactions in large biological systems such as dynein, a molecular motor important for cargo transportation and force generation in cells. Dysfunction of dynein is associated with many diseases, such as ciliopathies, lissencephaly and other neurodegeneration disorders.METHODS: We developed a novel multi-scale simulation approach which is used to study dynein's motion along microtubules. The multi-scale simulation approach implements a Monte-Carlo algorithm to simulate the motility of molecular motors such as dynein. Besides, the Delphi, DelPhiForce, and NAMD software tools were also utilized to study the dynein-microtubule interactions. RESULTS: The electrostatic binding funnel around microtubule is observed, which drags the dynein to the binding pocket. The electrostatic forces on dynein residues form a torsion which reorients the dynein when it is in an un-native orientation. Furthermore, the electrostatic component of the binding energy of dynein and microtubule strongly affects the velocity and run length of the dynein. CONCLUSION:These results reveal the mechanisms of dynein's motility and functions along microtubule. Understanding such fundamental mechanisms sheds light on curing many molecular motor related diseases.

16.05.001

TRANSCRIPTOMICS OF OBESE MICE LACKING SELENIUM RECYCLING

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PURPOSE: Obesity is a health disparity particularly among underserved populations, and triggered by nutritional intake. In general, Americans present high levels of circulating selenium, a dietary micronutrient found primarily in seafood, a significant source of protein among Native Hawaiians and Pacific Islanders. Selenium is utilized to produce the amino acid selenocysteine (Sec), which can be incorporated into selenoproteins, which act on redox reactions. Selenocysteine lyase (Scly) is an enzyme which decomposes Sec into selenide and alanine, releasing the selenide to be utilized in selenoprotein synthesis. Disruption of the Scly gene in mice (Scly KO) led to obesity with lipid deposition in hepatocytes, worsened by a selenium-deficient diet. Our objective was to determine differentially expressed genes in Scly KO mice livers affected by dietary selenium levels that could correlate with the observed phenotype of this mouse model. METHODS: Scly KO and wild-type mice were fed diets containing 0.08 (mildly low) or 0.25 (adequate) ppm of sodium selenite. High-quality total RNA (RIN ≥ 7) from livers was employed in RNA-sequencing. RNA-Seq data analysis performed on Partek flow software followed by pathway analysis using Ingenuity Pathway Analysis software. Real-time RT-qPCR with specific primers was used to validate RNA-Seq results. RESULTS: Hepatic RNA-Seq analysis revealed 52 genes differentially regulated in the Scly KO mice, encompassing 41 pathways, including PXR/RXR activation, LPS/IL-1-mediated inhibition of RXR function, xenobiotic metabolism signaling, nicotine degradation, adipogenesis, and acyl-CoA hydrolysis. Ten differentially expressed genes were validated by real-time RT-qPCR, including Selenbp2, Eif4ebp3, Mt1, and Mt2. CONCLUSION: We identified and validated genes and pathways in the Scly KO mouse liver that may be implicated in the metabolic phenotype displayed by this mouse model. Understanding of the crosstalk between selenium nutrition and energy metabolism may further our knowledge of hepatic physiology, and clarify the complex interconnection between selenium and metabolic disorders, particularly in populations with high selenium consumption.

| BEHAVIORAL SCIENCE |

21.05.002

FACTORS INFLUENCING PREP UPTAKE AMONG MSM IN PUERTO RICO

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PURPOSE: Men who have sex with men (MSM) are at increased risk for HIV. Pre-exposure prophylaxis (PrEP) is an effective biomedical tool to prevent HIV infection. In Puerto Rico (PR) information about acceptability and use of PrEP is scarce. The objective of this study is to describe barriers and facilitators for PrEP uptake among sexually active MSM in PR. METHODS: We administered a web-based survey to assess sexual risk practices, PrEP attitudes, awareness, and use/potential use. Qualitative interviews to explore barriers and facilitators for PrEP use among MSM are ongoing. RESULTS: A total of 209 MSM completed the survey. Mean age was 35 y/o, over 60% had an academic degree. Most identified as homosexual (88%), single (68%), HIV-negative (76%), and were aware of PrEP (91%). Most (63%) participants reported recent condomless receptive anal sex and 45.5% documented condomless sex with multiple partners of unknown HIV status. While 75% self-perceived at risk for HIV, only 13% have used PrEP. Attitudes towards PrEP were positive (i.e., 68% consider PrEP is effective), yet there were concerns about its efficacy (43%). Of n=176 with no PrEP experience, 51% were willing to use it. Qualitative interviews preliminary findings highlight side-effects as a barrier, while developing a routine to take the pill serves as a facilitator for uptake. CONCLUSIONS: Results suggest potential benefits of PrEP for at-risk MSM in PR, yet uptake remains low. Most participants expressed willingness to use PrEP. Mistrust about PrEP's efficacy and side effects are barriers for uptak

21.06.001

FAMILIALISM: ROLE ON IMMUNIZATION PRACTICES IN HISPANICS

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The University of Texas at El Paso School of Pharmacy (SN, MP, GF)

Purpose: People in the United States continue to get diseases that are vaccine preventable. The purpose of this study was to assess the impact of familism (close family relationships) on vaccination practices. Methods: A prospective observational study assessed factors that may contribute to an individual's vaccination behavior, such as the role of one's family on shaping individual behaviors. Specifically familism, is a construct commonly used to describe Hispanic family relationships. Results: A total of ninety-one participants completed two surveys The majority of respondents were women (67/91 = 73.6%), had an average age of 51, identified as Hispanic/Latino (89/91 = 97.8%), and lived in a home in which the primary language spoken is Spanish (70/91 = 76.9%).Individual values and family conversations are predictors of vaccination adherence in this predominantly Spanish-speaking Hispanic community. Conclusions: These results suggest that a large number of participants place a high importance on the beliefs of the family unit when making decisions about vaccines, indicating that familism is an important construct to assess in Hispanic populations. Future studies aim to identify other cultural components that contribute to optimal vaccination practices in Hispanic population.

22.04.004

TELOMERE LENGTH SHORTENED BY EXPOSURE TO VIOLENCE

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Violence exposure has longlasting social and biological impacts on African American (AA) health and can lead to physiological changes, including shorter telomere length (TL). While studies have investigated the relationship between TL and life stress, few focus on African American young adults and their direct nexus to violence. This study examines the effect of violence and gender on both stress biomarkers and TL in AA young adults. We examine the relationship between violence exposure, seven stress biomarkers (IgA/G/E/M, C Reactive Protein, Cortisol, Epstein Barr Virus Antigen) and TL in a cross sectional analysis of 50 buccal samples (N=50 males & 50 females) of AA 18-25years old in Washington DC who experience differential violence exposure (physical, threat, witnessed, and sexual). Average TL was measured by qPCR. Mann-Whitney tests identified differences between males and females in exposure to violence, stress biomarkers, and the measures of TL. Correlations were calculated between TLs, biomarker levels, and violence measures. Elevated sexual violence exposure was positively correlated (RRANGE= 0.22 to 0.55) with all elevated stress biomarkers except IgE. TL in the high violence exposure group was negatively correlated to all stress biomarker levels (RRANGE= 0.09 to 0.31) except for IgG. There was no significant difference in TL among females exposed and not exposed to violence. Violence exposed females had a longer TL than men (MeanF:M=1.87 v 1.62, p≤.05). Male sexual violence exposure was correlated to TL (R=0.575, p≤ 0.03). High violence levels correlate to shorter TLs and higher stress

biomarker levels in AA young adults. These findings suggest that additional focus should be placed on African American young men who have experienced sexual violence.

23.01.002

INTEGRATION OF STUDENTS AND FACULTY IN TRANSLATIONAL SCIENCE

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University of Puerto Rico, Medical Sciences Campus (RGG, EFR, ELRS, JCSS, LDJO, MIR); Universidad Central del Caribe (ERI, JRMA, MEGM, MIRV).

PURPOSE: Acknowledging the need and interest of students and faculty in their development in translational science (TS), the Title V Cooperative Project between the Medical Sciences Campus of the University of Puerto Rico and the Universidad Central del Caribe, developed and offered a series of training cycles (TCs) to integrate students and faculty Island wide in TS. METHODS: The TCs were offered in two integrated levels: Research Education Towards Opportunities (RETO I and II) and Mentorship Offering Training Opportunities for Research (MOTOR I and II), ending in the formation of the Clinical and Translational Mentoring Teams (CTMTs). Participants in CTMTs, matched by their research interests, were mentored by well-established TS researchers in their project, further developed in the Intensive Development and Experiences in Advancement of Research and Increased Opportunities (IDEARIO). RESULTS: Since 2017, 7 RETO-MOTOR I and 5 RETO-MOTOR II were offered to undergraduate students (US), graduate students (GS) and faculty (F) island wide. One hundred seventy three (173) participants were certified as follows: 94 (54.33%) US in RETO I; 47 (27.16%) GS and 32 (18.49%) F in MOTOR I, while 55 were certified in RETO MOTOR II, distributed: 32 (58.18%) US in RETO II; 11 (20.0%) GS and 12 (21.81%) F in MOTOR II. From these, 53 (96.36%) were integrated in 18 CTMTs in a variety of research areas – cancer, cardio, endocrine, exercise, glaucoma, neonatal, liver, neuro, obesity, pathogenesis, renal, Zika–. CONCLUSION: Students and faculty from academic programs island wide were trained, developed and integrated in TS.

23.03.001

SUPPORTING GENDER EQUITY IN RESEARCH CAREER ADVANCEMENT

SB FERNANDEZ; R Clarke; DM Sheehan; MJ Trepka; S Rose

Florida International University (SBF, RC, DMS, MJT, SR); Research Center in Minority institutions (SBF, RC, DMS, MJT)

PURPOSE: Despite efforts to diversify the national scientific workforce, results are still lagging. While women's representation in health-related academic positions has increased substantially, they remain underrepresented in senior leadership roles. This study was conducted to elucidate perceptual individual-, interpersonal-, and organizational- level influences that present as barriers or facilitators towards career advancement for women in order to promote and retain a more diverse leadership workforce. METHODS: We conducted 15 in-depth, semi-structured interviews with early stage, female, investigators pursuing careers in health sciences research at a large minority serving institution in South Florida. Interviews lasted one-hour and were guided by an ecological framework. Two coders independently coded all transcripts using NVivo 11 software and synthesized codes into larger themes through a conventional thematic analysis process. RESULTS: Results highlight four primary influences on career progression: a) perceptions of familial support, b) relationships with mentors, c) institutional barriers, and d) individual characteristics. Illustrative quotes surround the lack of understanding by family members of the demands of a research career, unequal distribution of familial responsibilities that compete with career advancement, the importance of female mentors, and the differing roles and expectations among female and male faculty. DISCUSSION: To achieve meaningful and pervasive change towards gender equity, solutions must be directed at transforming systems that people live and work within. Suggestions include creating support systems for women with other women, enforcing consistent policies regarding roles and distributions of expectations among faculty, and shifting family norms including educating families about demands of academic research careers.

27.02.002

DISSEMINATING RESEARCH BEYOND THE ACADEMY TO INFORM POLICY

JM HOPKINS; K Butty; AS Belton; RJ Willock; KB Holden

Morehouse School of Medicine (JMH, KB, ASB, RJW, KBH)

PURPOSE: Achieving health equity through policy change is a complex process and necessitates cooperation of stakeholders in multiple sectors. There is a paucity of literature examining the execution and impact of diverse dissemination efforts employed by research networks focused on informing policy with evidence-based science. This presentation will describe the dissemination strategies, key outcomes, and lessons learned from a NIH-funded Transdisciplinary Collaborative Center for Health Disparities Research (TCC) led by a historically minority-serving institution in Southeast US. METHODS: Since 2012, the TCC has engaged over 80 collaborative partners across several health policy research focus areas including: childhood psychosocial development, integration of behavioral

health into primary care; health information technology; health policy leadership and workforce development; LGBT health; and chronic disease control. A centralized Dissemination Core was developed to assist in synthesizing knowledge gleaned from research and strategic outreach activities, translate knowledge into high impact products, and achieve dissemination in two primary directions: targeted and broad-based dissemination. Peer reviewed publications, policy briefs, infographics, webinars, academic and community presentations, social media posts, public comments to inform federal rulemaking processes, research summits, congressional briefings, and policy forums have been employed to disseminate TCC research and stimulate crucial policy discourse. RESULTS: To date, TCC has successfully supported 64 peer-reviewed publications, 6 policy briefs, over 75 webinars and presentations, five federal public comments, 4 regional policy forums, and 2 national health policy research conferences. CONCLUSION: Key policy impacts and lessons learned from each of these dissemination channels will be described in this presentation.

28.01.001

WEIGHT LOSS TECHNOLOGY IN FAITH-BASED ORGANIZATIONS

SN BATHEJA; AA Johnson;
Howard University (SNB, AAJ)

PURPOSE: The objective of this study was to explore the attitudes and behaviors of faith-based members on overweight, obesity, and technology in a weight loss or weight maintenance program. METHODS: A qualitative cross-sectional research design was utilized including focus groups, and involving members of faith-based organizations in the Washington, DC metro area. The focus group questions were related to overweight/obesity among faith-based members, diet and exercise habits, counseling strategies for weight loss or weight maintenance, and the use of smartphone technology for weight loss. All of the sessions were audio recorded and data were transcribed. Transcripts were imported into NVivo 11 software, which allowed for ease of identification of key words and phrases. This information was then identified and coded into categories. Categories were grouped into common themes. RESULTS: Three focus groups were conducted (n=20). Results revealed seven themes and several sub-themes. The seven themes were causes of overweight/obesity, past experiences with weight loss programs, barriers to healthy eating, motivating factors to participate in a weight loss/maintenance program, scripture and health, desirable and undesirable features of technology-based weight loss/maintenance programs. DISCUSSION: The findings of this investigation suggest that faith-based members exhibit positive attitudes and behaviors towards overweight, obesity, and the use of technology in a weight loss/maintenance program. Recommendations for future research include expanding the investigation to a greater number of denominations. Future research should compare the preferences for a smartphone technology programs with traditional face-to-face programs, as well as denomination-specific versus non-denominational programs.

29.06.001

PRELIMINARY RESULTS FROM A PHYSICAL ACTIVITY STUDY IN JAIL

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Northern Arizona University, Center for Health Equity Research (RC, TAP, LLB, GP, HJW, JAB)

PURPOSE: Women are the fastest growing incarcerated population in the US. While incarcerated, they often gain weight and experience psychological distress at levels that exceed the general female population and incarcerated men. Physical activity may be a key factor to mitigate these unique experiences and needs. However, little research has been developed to understand physical activity levels in jail settings. Thus, we estimated the proportion of women in a local, rural jail who participated in recreation time; a structured time dedicated to being physically active and described their physical activity levels. METHODS: A multidisciplinary research team in collaboration with jail administrators adapted the System for Observing Play and Recreation (SOPARC) for the correctional setting. Trained observers documented the proportion of women who participated in recreation time and the adapted SOPARC tool to measure their physical activity levels (sedentary, walking, or vigorous) during 15 scheduled recreation time. RESULTS: During the 15 observed recreation times, 26% (range: 15-38%) of incarcerated women who had permission to attend recreation time attended. Those that attended recreation time were generally sedentary, with a smaller proportion choosing to walk. Very rarely did our team observe any incarcerated women engaging in vigorous exercise. CONCLUSION: Our preliminary results suggest that most incarcerated women in jail do not attend recreation time and those who attend are generally sedentary. Our team will engage in future research to determine the motivators and barriers to physical activity among incarcerated women.

29.08.004

MENTAL HEALTH DISPARITIES AMONG TRANSGENDER NATIVE HAWAIIANS

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University of Hawaii- John A. Burns School of Medicine (CB, DB, JD, EH); The Lavender Center and Clinic (SM, RR).

PURPOSE Hawaii has the largest state proportion of transgender adults in the U.S. Transgender individuals are 12 times more likely to attempt suicide than the general population in the past year, and nearly 9 times more likely in their lifetime. A longitudinal study in Europe revealed that transgender individuals were 19 times more likely to die from suicide. To date, no studies exist on the mental health of transgender individuals in Hawaii. This study aims to characterize the similarities and differences in demographic, socioeconomic, and mental health of Native Hawaiian/ Pacific People and European American transgender individuals.METHODS: The University of Hawaii Institutional Review Board approved this study. Data were obtained retrospectively from the collaborative clinic's electronic medical record system. Patients identified with gender dysphoria and at least 18 years of age, who were from Native Hawaiian, Pacific, Filipino, and European American backgrounds, were included. RESULTS / EXPECTED RESULTS: Preliminary data revealed that patients (N=98) self-reported health issues with alcoholism (5%), insomnia (9%), mental illness (14%), anxiety (35%), depression (36%), tobacco use (43%), and alcohol use (68%). Further statistical analyses will determine whether Native Hawaiian, Pacific, and Filipino transgender individuals have higher levels of anxiety, depression, and mental illness than European Americans, controlling for demographic and socioeconomic status. DISCUSSION / CONCLUSIONS: Suicide is the lead cause of fatal injuries in Hawaii: one person dies from suicide every two days. Study findings can support the development of culturally relevant and gender-affirming mental wellness and suicide intervention programs for transgender individuals.

29.12.001

MINORITY WOMEN'S SELF-MEDICATING BEHAVIORS FROM WORK STRESS

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Morgan State University

PURPOSE: Workplace-bullying research has demonstrated that abusive work conditions can lead to depression, anxiety, and post-traumatic stress. Further, stress resulting from bullying has been linked to self-medicating behaviors. However, many studies omit minority women and how workplace-bullying may cause suicidal ideation or self-medicating behaviors. Therefore, the purpose of this study was to examine how workplace-bullying may precipitate the use of substances or suicidal ideation for minority women. METHODS: The spill-over theory was applied to consider how workplace stress interferes with the private domain. Theoretically, if employees encounter stress in the work domain, the stress spills over to the personal space where substances may be sought to seek relief. Chi-square analysis was utilized to examine whether minority women (Black, Hispanic, and Native American) are more likely than white women to seek substances and consider suicide in coping with workplace-bullying. RESULTS: With a sample generated by emailing respondents a survey, n = 375 total and n = 88 minority women, the study confirmed that minority are more likely to seek substances, (X^2 (1, N= 377) =11.75 p= .001) and more likely to have suicidal ideation (X^2 (1, N=377) = 5.8 p = .016) than white women to cope with workplace-bullying. DISCUSSION: Minority women, who typically report a higher prevalence of workplace-bullying experiences, also are more likely to seek self-medicating behaviors and have suicidal ideation. This presents a significant public health concern. Culturally sensitive psychologists are recommended to help minorities cope with workplace-bullying and manage the intersecting factors of racism and sexism.

| CLINICAL SCIENCE |

31.01.001

RACIAL DISPARITIES IN KIDNEY CARCINOMA AND ITS RELATIONSHIP

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PURPOSE: Disparities in survival of patients diagnosed with kidney carcinoma may exist among racial groups. We have analyzed the survival time of patients diagnosed with kidney carcinoma in order to explore the histological differences in the survival probability of patients while controlling for gender, geographical location, race/ethnicity, and clinical variables. The results will be used to train medical and public health students in understanding the extent of health disparities in the mortality of kidney carcinoma patients. METHODS: Using National Cancer Institute data from 1975 to 2016, we modeled the impact of histological types of kidney carcinoma on the survival probability of patients taking into consideration patients' race/ethnicity, gender, tumor grade, type of surgery, geographical location of patient, and stage of disease. This study examined 85,324 males and 48,826 females. Hypertabastic survival technique was used to analyze the data. This method can accommodate different hazard shapes, which will enable researchers to better understand the role of each player in measuring the racial disparity with respect to survival time of patients.RESULTS: Results show that 13.3% were Hispanic, 5% were Asian or Pacific Islander, 11.2% African American, and 70.5% White. Age, Race, Histology, Stage, Grade, and Surgery type were found to be significant (p-value less than 0.001). Hispanics (HR = 1.079, CI: 1.032-1.129) and African Americans (HR = 1.144, CI: 1.088-1.203) had a significantly higher hazard of death due to Kidney Carcinoma when compared to Whites. Median survival times for Whites, Asians, African Americans,

and Hispanics were 56, 52, 51, and 48 months respectively. Among racial groups, African Americans had the highest percentage of Papillary Adeno (27.2%), Renal Cell Adeno (21.4%), Chromophobe Renal Cell (4.7%), Other Carcinomas (4.2%), and Adeno Carcinoma with Mixed Subtypes (4.6%). In addition, African Americans had the highest percentage of No Surgery (4.7%), Complete Nephrectomy (8.8%), Nephrectomy/Urethrectomy (1%), Poorly Differentiated (30.1%) cancer type, and Localized (81.1%) tumor stage within race. Conclusion: Overall, the results indicate that Whites had the highest probability of surviving death due to kidney carcinoma, followed by Asians, Hispanics. African Americans had the lowest overall survival probabilities.

31.01.004

GROWING INCIDENCE OF LIVER CANCER IN WASHINGTON DC

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PURPOSE: The African-American (AA) community in Washington DC is at a higher risk for hepatocellular carcinoma (HCC) than any other ethnic group. Our objective is to evaluate the incidence and diagnosis of HCC and liver metastases (LM) among AAs in DC over the past six decades and explore the underlying causes.METHODS: Electronic medical and pathology records of liver cancer patients from 1959-2013 at Howard University Hospital (HUH) were reviewed. Demographic, clinical and pathology characteristics were examined, and statistical analysis was performed using Wilcoxon rank-sum test. RESULTS / EXPECTED RESULTS: Incidence of HCC rose substantially between 1959 and 2013, increasing eight-fold from 1.05 to 8.0 per 100,000 AAs. The rate of increase in the last decade was highest at 550%. Cases were disproportionately male (67.2%), and median age at diagnosis was 57 years. Towards the last decade, the most common etiology for HCC was non-alcoholic fatty liver disease (NAFLD) followed by NAFLD/HCV combination. Liver cancer was clustered in the eastern section of DC in wards 4, 5, 7, and 8. Cases of liver metastases clinically diagnosed and confirmed by biopsies increased 96.4% from 1959-1968 to 2009-2013. DISCUSSION / CONCLUSION: This study confirms that HCC incidence is increasing (driven by HCV and NAFLD) more rapidly in DC than previously believed, highlighting the impact of case definitions in the context of changing diagnostic approaches including the revised ICD10. The rising burden, disproportionate population distribution, and low survival rate among AAs emphasize the importance of prevention and early detection as a public health imperative.

31.02.001

GENOME-WIDE ASSOCIATION STUDY OF CLOPIDOGREL IN HISPANICS

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University of Puerto Rico Medical Sciences Campus, San Juan, PR (JD,PG,KM,DFHS,ES,JYR,FMM,HN,AFG); Icahn School of Medicine at Mount Sinai, NY (SAS).

PURPOSE: High on-treatment platelet reactivity (HTPR) with clopidogrel is predictive of ischemic events in adults with coronary artery disease. Despite strong data suggesting HTPR varies with ethnicity, clinical and genetics, no pharmacogenetic studies of clopidogrel have been performed in Caribbean Hispanics. This study was aimed to identify genetic predictors of HTPR in a cohort of cardiovascular patients from Puerto Rico. METHODS: A genomewide association study (GWAS) was conducted in 334 patients on clopidogrel. Patients were separated into cases (HTPR) and controls (no-HTPR). Clinical data was obtained from medical records. Platelet function was measured by VerifyNow® P2Y12 assays and HTPR defined as P2Y12 reaction units (PRU) ≥230. Genomewide screening was performed using Illumina MEGA-chip array and further genotyping of candidate genes (e.g., CYP2C19, ABCB1, PON1) was performed by Taqman® Assays. Plink was used to test for associations and LD analyses. About 38% of patients had HTPR (PRUavg.=204±67). RESULTS: Manhattan plot showed nominal associations ($p<10^{-5}$) between CYP2C cluster at chromosome 10 and resistance in the discovery cohort. Pairwise analysis of identified variants showed strong LD of SNPs at this cluster with CYP2C19*2 allele (D'>0.9; r2>0.8). Multiple logistic regression showed that 27% of PRU variation was explained by history of diabetes mellitus (OR=3.46; CI:1.05-11.43), hematocrit (OR=0.75; CI:0.65-0.87), CYP2C19*2 (OR=4.44; CI:1.21-16.20) and PON1 Q192R alleles. CONCLUSION: This is the first GWAS report of clopidogrel pharmacogenetics in Hispanics, confirming the relevance of CYP2C cluster. Diabetes mellitus, hematocrit, CYP2C19*2 and PON1Q192R variants were associated with HTPR, which may identify Hispanic patients at higher risk for adverse events.

31.05.001

INCREASING HCV PREVALENCE IN YOUNG HIV-INFECTED MSM AND PWID

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PURPOSE: People who inject drugs (PWID) and HIV-infected men who have sex with men (MSM) are two major

high-risk groups for transmission of hepatitis C virus (HCV). This study was conducted to understand the changes in the prevalence and risk factors of HCV infection in different age and risk groups among men living with HIV in a community-based primary care setting. METHODS: We performed cross-sectional analyses of a retrospective cohort, from 2003 through 2014, of 1948 HIV-infected men receiving care at a multisite community health center in urban/suburban and rural Maryland. We used multivariate logistic regression to determine factors independently associated with HCV infection and restricted cubic spline method to model trends in HCV prevalence over time. RESULTS: The overall HCV prevalence was 24.2%. The annual prevalence continued to decline in the full cohort, from 38% in 2013 to 24% in 2014, and among those ≤40 years old, but increased/stabilized among PWID and MSM who were <40 years old. Among the younger PWID, the prevalence rose from 33% in 2003 to 79% in 2009 and then stabilized. The factors independently associated with HCV infection differed between the men with and without injection-drug use and between those <40 and ≤40 years old. Notably, an outbreak of HCV infection was observed among young PWID residing in rural areas. CONCLUSION: HCV epidemic continued unabated among high-risk individuals in this diverse population of HIV-infected men. The ongoing HCV transmission among young HIV-infected men poses a challenge to HCV eradication.

33.01.002

AN ONLINE COURSE IN PATIENT-CENTERED OUTCOMES RESEARCH

DP Landsittel; KH Kropf; DA Taira; TL Sentell; KG Martinez; JH Southerland; EJ Garcia Rivera; A Quarshie; PY Talbert; MK Norman

University of Pittsburgh (DPL, KHK, MKN); University of Hawaii (DAT, TLS); University of Puerto Rico (KGM, EJGR); University of Texas Medical Branch (JHS); Morehouse School of Medicine (AQ); Howard University (PYT)

PURPOSE: Patient-centered outcomes research (PCOR) compares the real-world effectiveness of interventions for treating outcomes that matter to patients and directly inform healthcare decisions. Conducting high-quality PCOR is critical for reducing health disparities, but methods are complex and training is often lacking, especially in lower resource settings. This limitation is particularly critical to address at Minority-Serving Institutions (MSIs) since they are best positioned to conduct PCOR in the most vulnerable populations. METHODS: The Expanding National Capacity in PCOR through Training & Collaboration (ENACT) Network is a partnership between 8 different institutions, including 6 MSIs, to build fundamental, advanced, and experiential training in PCOR. Google Drive was used to build training resources that are publicly-available and easily updated over time. RESULTS: Based on continuous input from MSI faculty, the ENACT online self-guided course was created to provide comprehensive training resources for conducting high-quality PCOR studies. The course includes modules for asking a research question, engaging stakeholders, conducting comparative effectiveness trials and observational studies, evaluating heterogeneity, and making causal inferences. The course employs best practices in online learning, uses embedded videos for a more personalized experience, and includes workbook exercises to guide trainees through all steps of developing a PCOR proposal. Over 100 participants have participated in the training and the course is being widely disseminated across MSIs. DISCUSSION:The ENACT course makes a unique contribution to the critical need for PCOR training. The course is easily adaptable for independent study by individual researchers or for institutional programs needing self-guided training resources.

34.01.003

CHARACTERISTICS OF METABOLIC SYNDROME IN CHRONIC HIV

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PURPOSE The metabolic syndrome (MetS) defines a cluster of biochemical and physiological abnormalities associated with the development of cardiovascular disease (CVD). The association of HIV-related blood immunologic biomarkers with the presence of metabolic syndrome is under-studied. METHODS: In a cohort of HIV-infected individuals >age 40 on anti-retroviral therapy, we assessed for MetS defined as having 3 or more of the following CVD risk factors [increased waist circumference, high blood pressure (BP), high triglycerides (TG), elevated fasting blood glucose, and low high-density lipoprotein cholesterol (HDL-C)]. Plasma soluble biomarkers were assayed by multiplexing and monocyte subsets, and T cell surface markers including negative checkpoint receptors (NCR) were determined by multiparametric flow cytometry. The data was analyzed utilizing Mann-Whitney U. RESULTS: Among 160 HIV+ participants (87.5% male, median age 50 yrs, 58% Caucasian, 84.4% with plasma HIV RNA <50 copies/mL), MetS was present in 23.1%. Participants with MetS had higher body mass index and HOMA-IR but did not differ from those without MetS in age, gender, ethnicity, estimated years of HIV infection, years on antiretroviral therapy, nadir CD4, current CD4 percent, CD4/CD8 ratio, or presence of plasma HIV RNA. MetS was associated with higher levels of

total and classical monocytes, higher plasma levels of PAI-1 and IL-10, and lower presence of several single and dual expression of NCR (CD8+PD-1+, CD8+PD1+TIGIT+, CD8+PD1+TIM-3+, CD8TIGIT+TIM-3+, CD4+PD1+TIM-3+, CD4+TIGIT+TIM3+) on T-cells (all p<0.05). DISCUSSION/CONCLUSION: MetS in HIV is associated with a unique immunologic signature. Its association with lower, rather than higher, frequency of T-cell NCR warrants further evaluation.

34.01.005

SOCIOEMOTIONAL DEVELOPMENT AFTER PRENATAL ZIKA EXPOSURE

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PURPOSE: A causal link has been established between in utero Zika virus (ZIKV) infection and birth defects collectively known as Congenital Zika Syndrome (CZS). The spectrum of abnormalities includes developmental and behavioral problems. Socioemotional difficulties similar to the Autism Spectrum Disorder have been described in children with congenital Zika. The persistence of socioemotional problems impedes positive social interactions and may lead to serious behavioral disturbances. Early identification reduces morbidity, especially in those at risk for health disparities. The Pediatric Outcomes of Prenatal Zika Exposure study aims to characterize the spectrum of neurologic, developmental and behavioral outcomes of these children. METHODS: Infants born to mothers with confirmed (positive Real Time-Polymerase Chain Reaction (RT-PCR)) or probable (positive Immunoglobulin M Enzyme-linked Immunosorbent Assay) ZIKV infection were enrolled. Follow-up at 18 months included administration of Ages and Stages Socio-Emotional Questionnaires (ASQ-SE2), which identify children at risk for behavioral and socioemotional abnormalities that need referral for more complex evaluations. RESULTS: Descriptive analysis revealed that of 49 participants, 22 (45%) were born to RT-PCR positive mothers. Thirty (61%) are female, two (4%) presented moderate microcephaly at birth, and one (2%) has CZS. ASQ-SE2 identified 6 (13%) children requiring monitoring and 9 (20%) needing a referral. Higher risk scores were reported in behavioral areas of self-regulation, social communication, interaction and adaptive functioning. DISCUSSION: Socioemotional abnormalities after prenatal Zika identified by parental questionnaires can be used to facilitate early intervention. Comparison with socioemotional development of unexposed children is required to assess risks for autism and other behavioral disabilities.

34.01.013

HPV16 LINEAGE B IS ASSOCIATED WITH ANAL CANCER IN AFRICAN AM

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Background: Human papillomavirus type 16 (HPV16) is one of the most common and carcinogenic HPV types associated with high risk of anal, vagina, vulva, penis and cervical neoplastic transformations. However, many genetic variants exist within this virus and not all seem to have the same carcinogenic potential. Aim: To determine HPV16 lineages and their association with risk of high-grade anal lesions in African Americans in an inner-city hospital.Methods: We reviewed medical records of 370 African Americans with anal lesions from Jan. 2007 to Dec. 2015. This study was approved by Howard University Institutional Review Board. Demographic, clinical and pathological data including HPV, HIV, HCV (hepatitis C virus), diabetes mellitus, hypertension and body mass index (BMI) were collected. DNA was extracted from a subset of HPV16-positive patients with FFPE tissue samples (72 patients, 111 samples) and used for HPV16 whole-genome sequencing. We assessed HPV16 variant lineages and associations with disease stage. Statistical analyses were performed using Chi-square tests, Student's t-tests, and logistic regression. Odds ratios (OR) and p-values were calculated for comparisons of normal/condyloma/high-grade dysplasia (HGD) vs. squamous cell carcinoma (SCC) and for normal/condyloma vs. HGD. The most common HPV16 A1 sublineage was used as a reference in these comparisons. Results: Males represented 75% of the patients (n=276), with a median age of 44 years and BMI of 25.8 kg/m2. The frequency of condyloma, high-grade dysplasia, SCC and adenocarcinoma was 191 (52%), 26 (7%), 31 (8%) and 8 (2%), respectively. The frequency of HPV, HIV, and HCV was 231 (68%), 147 (43%) and 42 (12%), respectively. HPV and HIV were risk factors for condyloma and dysplasia (P<0.05). All four main lineages of HPV16 (A,B,C,D) were detected in our specimens, with sublineage A1 most common. Lineage B, also named the African-1 HPV16 lineage because it is most common in Africa, had the strongest association with SCC (OR=10.5) whether alone or in combination with lineages A4 and D (OR=10.5), although with a lower statistical significance (0.054 vs. 0.009). As for HGD, lineage B along with A4, C and D only gave an OR of 1.4.Conclusion: We show that

the majority of patients with anal lesions are young males with HPV and HIV co-infections. HPV16 lineage B was associated with a high risk of SCC development.

34.01.018

IMPACT OF INTEGRATED ORAL AND MEDICAL CARE ON OHRQoL IN PLWH

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Introduction: Antiretroviral therapy has transformed HIV disease into a manageable chronic illness. According to the CDC, people living with HIV (PLWH) experience a high incidence of HIV-related oral pathologies (30-80%), with considerable variations depending on accessibility of care. Objective: To evaluate the impact of fully integrated oral and medical care among virally suppressed HIV-positive patients engaged in routine dental care.Methods: An independent interviewer surveyed 60 virally suppressed patients involved in a two-year multisite NIH-sponsored and IRB-approved study. Primary goal was to analyze the influence of dental care on biomarkers of HIV-1 infected patients. The survey gathered information on personal habits, lifestyle, and oral health by means of the Oral Health Impact Profile (OHIP-14 SC). We also extracted data about HIV medical care and demographics from electronic health record, CAREWare. Results: Interim analysis showed statistically significant association between, gender, alcohol, marijuana, and cigarette use, with poor OHQoL. This final analysis corroborates the interim findings and demonstrates that case management, dental clinic attendance patterns, and oral hygiene counseling influence self-perception of oral health status among PLWH. The results of this study support the full integration of oral and medical services to improve the quality-of-life of PLWH. OHIP-14 SC emphasizes psychological and behavioral outcomes as an effective intervention tool for clinicians to evaluate the impact of fully integrated oral and medical care on the quality-of-life of PLWH. Our study highlights the need to analyze the long-term health outcomes of PLWH enrolled in a fully integrated oral and medical health services program.

36.04.002

CHARACTERIZATION OF NEONATAL ABSTINENCE SYNDROME IN ARIZONA

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PURPOSE. By the end of 2017, nearly 1% of infants born in Arizona experienced Neonatal Abstinence Syndrome (NAS), a statistic that has almost tripled since 2010. Despite substantial efforts to characterize opioid overdoses in Arizona, there are major data gaps regarding the impact of the opioid epidemic on pregnant mothers and infants. In this study, we characterize disparities associated with infants who have NAS and mothers who are opioid dependent at the time of giving birth, along with co-morbidities that could be used to trigger screening. METHODS. Analysis consists of a comprehensive record review of all infants born and all mothers who gave birth in Arizona from 2010-2017. We summarized trends, demographics, and geographic hot spots for both populations, and additionally identified co-morbidities associated with Arizona infants born with NAS. RESULTS. Stratification by race and ethnicity revealed that infants born with NAS and mothers who were opiate dependent at the time of giving birth were disproportionately non-Hispanic White and covered by Medicaid and Medicare. Married women were significantly less likely than single women to be opiate dependent at the time of giving birth. Co-morbidity analysis using supervised machine learning revealed that neonatal candidiasis, diaper dermatitis, and newborn suspected to be affected by maternal infectious and parasitic diseases were better indicators than the traditional conditions of feeding difficulties, respiratory distress, and irritability. DISCUSSION. Findings have potential to contribute to better and earlier identification of co-morbid conditions for proactive treatment and that may help in the identification of a substance exposed newborn.

36.05.001

EQTL IDENTIFICATION OF GAMMA GLOBIN GENE REGULATORS IN SCD.

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Morehouse School of Medicine [RM, ANP,IP, RPS, BEG], Emory University [DRA,BEG]

PURPOSE: Investigate blood-based RNA expression changes in drug naïve sickle cell anemia patients. METHODS: Pediatric SCA and control subjects were recruited and consented for RNA sequencing (MSM and CHOA IRB approved). RNA sequencing was performed on an Ion Torrent S5 sequencer, using the Ion Total RNA-seq v2 protocol. Data were aligned to the hg19 reference genome and subjected to bioinformatics analysis. RESULTS: RNA was extracted from 30 patients with SCA and 18 Controls. Sickle cell status was confirmed by SNP analysis of the HBB gene. 557 genes were differentially expressed between SCA and controls (±1.5 fold change FDR $p<0.05$) and 590 genes show differential transcript expression (±1.5 fold FDR $p<0.05$). Differentially expressed RNA are enriched for hemoglobin associated genes and ubiquitin-proteasome pathway genes. Further analysis show higher gamma globin gene expression in SCA. eQTL analysis identified multiple SNPs in novel non-coding RNAs as having a potential regulatory role in HBG1 and HBG2 expression levels. DISCUSSION / CONCLUSION:

These data show the utility of whole blood total RNA-Seq to identify novel pathways in disease, especially when novel non-coding RNAs are included in the analysis. These studies show the potential of blood RNA-Seq approaches to identify precision medicine approaches to address health disparities.

28.01.002

MUSCLE CONTROLLED 3D PRINTED PROSTHETIC HANDS

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PURPOSE: The Biomed Innovation Center, located at Medical Sciences Campus of the University of Puerto Rico, has been involved in developing 3D printed prosthetic hands that are remotely controlled by electrical impulses from human arm muscles. This technology can serve patients who have lost their hand although retaining muscle function in their upper and lower arms. METHODS: Two models of prosthetic hands were produced with the 3D WOX Sindoh Printer. The design of the Flexi-Hand was obtained from the Internet in the form of Standard Triangle Language (STL) files. The hand elements were printed using PLA, a biodegradable polymer filament, and the joints with FilaFlexTM , a tough flexible filament. The remote control components were Myo Gestures Control Armbands containing eight (8) separate sensors that detect electrical muscle signals, and 3-axis position sensors. Each Myo unit connected via Bluetooth to an Arduino micro-computer that controlled five separate micro-servos to mechanically activate the individual fingers. Software programs were written to activate the Bluetooth connection between the Myo unit and the Arduino and control the individual servos. RESULTS: Two prosthetic hands were successfully printed and fitted with the control components. The system was calibrated to remotely mimic specific hand motions of the individual wearing the Myo unit. CONCLUSION: We have successfully demonstrated the feasibility of generating an operational remotely controlled 3D printed hand via a Myo armband unit.

POSTER ABSTRACTS

| BASIC & BEHAVIORAL SCIENCE |

11.01.001

CHARACTERIZATION OF EXTRACELLULAR VESICLES FROM H460 TUMOR

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PURPOSE: Current research is focused on the isolation and characterization of extracellular vesicles from non-small cell lung cancer (NSCLC) in order to better understand the role of EVs in cancer progression and inflammation. We evaluated the pharmacodynamic effect of Telmisartan (TLM) in combination with Docetaxel (DTX) pegylated liposomes (DTX-L) against H460 NSCLC xenografts in BALB/c nu/nu mice and further investigated the exosomes from these tumors. METHODS: In vivo antifibrotic efficacy of TLM (10mg/kg) followed by DTX-L treatment (5mg/kg) was evaluated in lung tumor xenografts. At the end of the study, tumors were excised from both groups and were evaluated for a) exosomes extraction using established procedures involving iodixanol density gradient purification technique b) western blotting to probe for Survivin, Caspase 3, Cyclin D1, P Stat -3, MMP 9 proteins c) evaluation of exosomes for their size and protein expression using NTA and westernblotting. RESULTS: In vivo studies with TLM given orally followed by DTX-L iv treatment to H-460 tumor bearing athymic nude mice revealed significant reduction in tumor size (***$p < 0.001$). Westernblot data showed significant downregulation of Survivin, Caspase 3, Cyclin D1, MMP9 (***$p < 0.001$), P Stat -3 (**$p < 0.01$) expression illustrating role of combination treatment in apoptosis. NTA of representative gradient-purified lung tumor tissue EVs showed the smallest detected particle in this sample was 89 nm, and approximately 90% of vesicles detected were 274 nm or smaller for the treatment group. Immunoblot data of extracted EVs revealed the expression of transmembrane proteins (CD71, CD63 which are enriched in exosomes), cytosolic proteins with membrane-binding capacity (TSG101, Alix which is present in EVs) and vesicles associated proteins (Flotillin-2 and syntenin-1). Further, there was significant downregulation of exosome proteins in the combination treatment in the fourth and fifth fraction suggesting the role of Telmisartan in downregulating exosomes production when used in combination with DTX liposomes. CONCLUSION: TLM in combination with DTX-L could significantly reduce the tumor burden of H460 xenotransplanted tumors which was probably due to the induction of apoptosis and downregulation of exosome proteins suggesting the role of exosomes in tumor progression.

11.01.002

IDENTIFICATION OF NOVEL CHAPERONE IN RESISTANT BREAST CANCER

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PURPOSE: The purpose of this study was to understand the contribution of cancer stem cells (CSC) on the progression of letrozole-resistant breast cancer cells. METHODS: Human long-term letrozole-treated MCF-7 were cultured two dimensionally (2D) or three dimensionally (3D) and proteomic analyses were performed. Protein expression was determined by immunoblotting and immunohistochemistry, while gene expression was determined by RT-PCR. Functional enrichment and survival analyses were performed using the DAVID tool and KMPlotter web-based curator, respectively. RESULTS: A global proteomic analysis was conducted and over 1000 proteins with quantitative abundance ratios were identified. Among those, 359 were significantly altered ($p < 0.05$); 173 were upregulated and 186 downregulated ($p < 0.05$, fold change >1.20). Midasin, a chaperone protein required for maturation and nuclear export of the pre-60S ribosome was increased 35-fold. Midasin was ubiquitously expressed in normal tissue, but overexpressed in lobular and ductal breast carcinoma as well as ER+ and ER- breast cancer cell lines. Functional enrichment analyses indicated 19 gene ontology terms and one KEGG pathway both associated with translation. Increased midasin was strongly correlated with decreased relapse free survival in hormone independent breast cancer patients. CONCLUSION: For the first time, the global proteomic signature of CSC-enriched letrozole-resistant breast cancer cells was characterized. The study implies that as cells stop responding to letrozole, they are associated with increased breast CSC and midasin, which may poise cells for drug resistance and enhanced translation. The data suggests midasin may represent a novel therapeutic target for hormone refractory breast cancers enriched with CSCs.

11.01.003

EPIGENOMIC ALTERATIONS AND PROSTATE CANCER DISPARITIES

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Prostate cancer (PCa) is a common malignancy and a leading cause of death among men in the USA. Racial disparity in PCa is well documented; the incidence and mortality rates for PCa is about twofold higher in African American (AA) versus European-American (EA) men, with AA men experiencing among the highest rates worldwide. The disparity is believed to be a complex combination of socioeconomic factors, environment and genetics. Genetic alterations in the sex steroid hormones signaling and immune/inflammatory signals has been extensively studied in PCa susceptibility. Genetic differences in mutation, loss or the amplification/fusion of genes in androgen signaling pathway including the fusion of androgen-regulated TMPRSS2 promoter and the ERG oncogene has been shown to differ in AA and EA population. In addition to the genomic defects, epigenetic DNA methylation changes and histone modifications are associated with PCa. Scientific evidence suggests that epigenetic DNA methylation affects gene expression in an age-dependent and tissue specific manner. Such age-dependent DNA methylation changes can alter cell physiology and possibly, predispose prostate cells to neoplastic transformation. The current literature suggests a complex mechanism of aberrant epigenetic changes in PCa that can lead to either gene silencing or the activation of key regulatory genes in the disease pathway. Our analysis of global and gene-specific DNA methylation has identified differential methylation changes to be associated with PCa disparity. Our observations may provide novel insights into the molecular mechanism involved in PCa disparity and lead to identification of novel biomarker and therapeutic modalities in addressing PCa disparity.

11.01.005

THE EFFECT OF ANNEXIN A6 ON TNBC METABOLIC VULNERABILITIES

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PURPOSE: The importance of annexin A6 (AnxA6) as a tumor suppressor in various cancers has been widely investigated, but the mechanisms by which AnxA6-induced basal-like triple negative breast cancer (TNBC) progression remain largely unknown. Specific changes such as hypoxia, metabolic acidosis, and oxidative stress in the tumor microenvironment (TME) during cancer progression endow cancer cells with malignant properties, ultimately leading to metastatic dissemination that remains the major cause of death in cancer patients. By linking the altered expression status of AnxA6, with changes in metabolic output of the tumor cells and the efficacy of the otherwise ineffective epidermal growth factor receptor-tyrosine kinase inhibitors (EGFR-TKIs), these metabolic vulnerabilities can be targeted to attenuate the growth and/or motility of this hard-to-treat breast cancer subtype. METHODS AND RESULTS: We demonstrate that exposure of AnxA6-high (BT-549) and AnxA6-low (MDA-468) TNBC cell lines to acute hypoxia (1% O2; ≤24 hrs.) is associated with down-regulation of AnxA6 while chronic hypoxia (1% O2; >24 hrs.) led to a consistent up-regulation of AnxA6. AnxA6, and HIF-1α downstream genes GLUT1 and PGK-1, mRNA levels were upregulated in chronic hypoxic conditions. Metabolic studies reveal that down regulation of AnxA6 in TNBC cells increased lactate production, glucose consumption, and ATP-synthesis under chronic hypoxia. In addition, chronic hypoxia sensitized TNBC cells to EGFR-TKIs. CONCLUSION: These data suggest that the transition from AnxA6-high to AnxA6-low may be dependent on hypoxia in the TME and consequently, TNBC cell survival and resistance to EGFR-targeted therapies.

11.01.006

CYTOTOXIC EFFECTS OF TUMOR SELECTIVE PIPERIDONES

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PURPOSE: To evaluate piperidone compounds for their anti-neoplastic activity. METHODS: Cytotoxicity and molecular biology assays were employed in this analysis. RESULTS/ EXPECTED RESULTS: Piperidones have potent cytotoxic activity and selectively kill cancer cells. In addition, these compounds induce cell death through apoptosis in human HL-60 leukemia cells. Apoptosis was confirmed by significant phosphatidylserine externalization and activation of the executioner caspase, caspase-3. The intrinsic pathway of apoptosis was implicated in the mechanism of action of our novel compounds as shown by depolarization of the mitochondria and generation of reactive oxygen species. Analysis of the cell cycle profile revealed that these compounds cause DNA fragmentation. Additionally, compounds P4 and P5 cause arrest at the G2/M phase of the cell cycle. Finally, we found that these compounds and other similar compounds induce apoptotic activity by proteasome inhibition as shown by accumulation of poly-ubiquitinated proteins after compound treatment. DISCUSSION/ CONCLUSION:Our results indicate that the novel piperidones cause a tumor selective cytotoxic effect that is mediated by both cell cycle arrest and protein degradation mechanisms.

11.01.007

ANTI-BREAST CANCER ACTIVITIES OF TETRAHDYROISOQUINOLINES

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PURPOSE: Breast cancer is one of the most commonly diagnosed cancers and causes the second leading cancer deaths in women. Unfortunately, the recovery rate from advanced breast cancer by current available drug treatment is still unacceptably low. Microtubule stabilizing and destabilizing agents are widely used as clinical drugs in the treatment of cancer. However, any long-term treatment is limited due to toxic side effects and drug resistance. Synthesizing new microtubule targeting small molecules, which are safer and are relatively easier to synthesize when compared to taxanes would be a very attractive option. Our target, the tetrahydroisoquoniline (THIQ) core structure is an important pharmacophore in natural products. The THIQ moieties were reported to be selective estrogen receptor modulators (SERMs) and microtubule disruptors and also possess potent cytotoxic activities such as antitumor and antimicrobial activities. METHODS: N-Amination of substituted isoquinolines by an aminating agent O-mesytelenesulfonylhydroxylamine, followed by ylide formation and reduction yielded the desired substituted tetrahydroisoquinolines in moderate to good yields. The synthesized compounds were evaluated for in vitro antiproliferative activity on MCF-7 (ER +ve), MDA-MB-231 (ER -ve) and Ishikawa (endometrial) cancer cell lines and tubulin polymerization studies. RESULTS: Among the compounds screened, the 4-Ethyl-N-(7-hydroxy-3,4-dihydroisoquinolin-2-(1H)-yl)benzamide product showed most significant IC50 values of 0.2, 0.13 and 0.08 μg/mL on MCF-7, MDA-MB-231 and Ishikawa cell lines, respectively and also showed a strong tubulin polymerization inhibition. CONCLUSION: Among hundred analogs, a dozen substituted THIQs showed significant antiproliferative activity in this study and suggested the potential of THIQ derivatives as effective anti-breast cancer agents.

11.01.009

EFFICACY OF MODIFIED-GEMCITABINE AGAINST PANCREATIC PDX.

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PURPOSE: The objective of this study was to chemically modify Gemcitabine (Gem) and evaluate its anticancer activity against pancreatic cancer cells. METHODS: Gem was modified by linking 4-amino group of Gem and stearoyl acyl derivative to form 4-(N)-stearoyl-gemcitabine (Gem-stearate). Gem-stearate nanoparticles (GSN) was developed and characterized using Nuclear Magnetic Resonance (NMR), micro-elemental analysis and particle size analyzer. Patient-derived primary pancreatic cancer cells (CMZ and G46Ca) and MiaPaCa-2 cells were treated with free Gem and GSN and percent viability determined. PDX mouse models (G46Ca) were treated with Gem and GSN to assess their efficacy. RESULTS: Analysis of the H-NMR spectra displayed an amide bond at 11ppm confirming the bond formed between 4-amino group of Gem and stearoyl derivative. Growth inhibition of GSN-treated CMZ culture (IC50 =21±5μM) was remarkably higher than free Gem treated CMZ culture (IC50 = 62±3 μM). Similar trend of higher GSN inhibitions in G46Ca and MiaPaCa-2 cultures were found (IC50 =46±16 μM; IC50 =27±4 μM) respectively compared with free Gem treated G46Ca and Mia-PaCa-2 culture (IC50 =68±26 μM; IC50 =54±5.2 μM) respectively. Altogether, the anticancer activity of GSN was significantly more effective in CMZ, G46Ca and MiaPaCa-2 cultures compared to their corresponding free Gem treated cultures. For the tumor efficacy studies, GSN exhibited significant tumor growth inhibition compared with molar equivalent dose of free Gem. Immunohistostaining showed that GSNs have significant antiproliferative activity in G46Ca tumors. CONCLUSION: This study reveals that GSN may be a novel approach in delivering an effective and stable Gem to treat pancreatic cancer.

11.01.010

APIGENIN REDUCTION OF TNFA INFLAMMATION IN TNBC CELLS

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Triple-negative breast cancer (TNBC) is an aggressive subtype of breast cancer, which is often fatally aggressive. TNBC is categorized by a lack of hormone receptors, lack of feasible chemotherapy options (e.g. anti-estrogen or aromatase inhibitor chemotherapies), greater mortality rates in African American populations, worsened by an inflammatory component. TNFα along with IL1α, and corresponding cognate receptors are ubiquitous throughout the tumor/stroma milieu of highly invasive carcinomas and correspond to larger tumor size, lymph node metastasis and overall poor prognosis . TNFα can cause sustained release of diverse chemokines (i.e. C-C motif chemokine ligand 2 (CCL2)/CCL5), which then direct mass infiltration of leukocyte sub-populations to lodge within the tumor, triggering a loss of tumor immune surveillance

(immune evasion) and subsequent rapid tumor growth. In the present study we evaluate the effect of apigenin, a dietary flavonoid found in chamomile and parsley to alter TNFα mediated inflammation in TNBC, by evaluating the entire transcriptome for mRNA and long intergenic non-coding RNA using Affymetrix HuGene-2_1-st human microarrays. Differential gene-expression analysis was conducted on 48,226 genes and the results show that TNFα caused up-regulation of 75 genes / down-regulation of 10. Of these, apigenin effectively down-regulated 35 of the 75 genes which were up-regulated by TNFα. The largest differential was evident for the TNFα evoked spike in IL1A vs. untreated controls [+21-fold change (FC), p<0.0001] being attenuated by apigenin (70% reduction). Similar trends confirm our previous reported findings where apigenin hampered TNFα up-regulated transcripts: IKBKE , CCL2 , IL6 and CSF2 . In addition, we further demonstrate greater than a 65% reduction by apigenin for the following TNF up-regulated pro-inflammatory transcripts : CTSS, C3, LAMC2, TLR2, GPRC5B, CNTNAP1, CLDN1, NFATC2, CXCL10, CXCL11, IRAK3, NR3C2, IL32, IL24, SLIT2, TMEM132A, TMEM171, STAP2, MLKL, KDR, BMPER and KLHL36. Conclusion: The findings obtained in this work suggest a possible therapeutic role for apigenin in down-regulating diverse genes associated with tumorigenic leukocyte sub-population infiltration by triple-negative breast cancer.

11.01.012

KDM5B AND SKP2 ON PROSTATE CANCER MALIGNANCY AND DISPARITIES

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Prostate cancer (PCa) is disproportionally striking African American (AA) men more than other ethnic populations in the US. Despite androgen deprivation therapy delivers the promising initial responses, most of PCa patients invariably develop castration-resistant prostate cancer (CRPC). Therefore, the novel and effective treatment strategy is needed. Literature reports that SKP2 is increased in AA PCa specimens. Our studies showed the levels of KDM5B, a member of histone demethylases, are higher in AA PCa than that in Caucasian PCa. However, the interactive mechanism and contributions of KDM5B and SKP2 to PCa malignancy and disparities are still elusive. We previously reported that SKP2 loss partially decreases the growth of prostate tumors and that KDM5B levels are reversely regulated by SKP2 in PCa cells. Here, we showed that KDM5B knockout (KO) decreased the proliferation of PCa cells, and KDM5B KO cells were more vulnerable to SKP2 inhibition. More importantly, a combined inhibition of KDM5B and SKP2 significantly blocked malignant transformation of PCa cells and prostate tumorigenesis in Pten/Trp53 mutant mice. Mechanistically, combined treatments resulted in a decrease in AKT signaling pathway and an induction of cellular senescence, along with the reduction of KDM5B and SKP2 levels in vitro and in vivo. Taken together, our results show that combined inhibition of KDM5B and SKP2 is more efficacious in inhibiting the proliferation of PCa cells and CRPC growth, and this regimen would be an ideal strategy for treating CRPC and reducing PCa disparities.

11.01.013

ENHANCEMENT OF DOCETAXEL EFFICACY IN 3D LUNG CANCER MODELS

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PURPOSE: Non-small-cell lung cancer (NSCLC) accounts for 87% of total cases of lung cancer with overall 5-year survival rate less than 18.2%. Poor penetration of drug into solid tumors due to tumor stromal barriers are serious challenges restricting the efficacy of existing chemotherapeutic agents. This study aims to determine the efficacy of the combination of Docetaxel liposome (DTXPL) and Telmisartan, a tumor stromal disrupting agent using in-vitro studies. METHODS: DTXPL was prepared using modified hydration method. Cell viability studies of DTXPL, DTXPL and Telmisartan combination and Telmisartan treatments were determined in 2D culture of H460WT and 3D systems (from Wells Biosciences and with a 3D printer using a sodium alginate-gelatin hydrogel). Hypoxic conditions in 3D spheroids were assessed using a fluorescent hypoxia reagent. The effect of Telmisartan pretreatment on drug uptake was evaluated. RESULTS: The entrapment efficiency of DTXPL was 96% and the size was 133.2±11.7nm. The increase in IC50 values in DTXPL, DTXPL+ Telmisartan and Telmisartan was approximately 2.8, 3.5 and 4.8-fold respectively in 3D culture as compared to 2D culture of H460WT (p value < 0.0001). There was a significant increase (p< 0.05) in the uptake of liposome in Telmisartan pretreated 3D culture. DTXPL and Telmisartan treatment showed a significant decrease in spheroids with hypoxic cores. CONCLUSION: Pretreatment with anti-fibrotic agent prior to the treatment of anticancer nanomedicine has a great potential as an approach to combat NSCLC. The use of 3D cultures for in-vitro drug efficacy screening are more reliable in translating to in-vivo experiments.

11.01.014

NEW CELL MODEL OF MALIGNANT PERIPHERAL NERVE SHEATH TUMOR

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Malignant peripheral never sheath tumors (MPNST) is a very aggressive Schwann cell-derived soft tissue sarcoma and account for 3-5% of sarcomas. 50% of this MPNST cases are associated with NF1 (Neurofibromatosis type 1) and are the leading cause of death of all patients with this autosomal dominant syndrome. The other 40% are sporadic and the rest 10% are considered radiation therapy induced. There is a limited availability of cell line models for MPNST and that led us to establish additional models for further study of these rare type of cancer. The in vitro tumorigenic potential of this new cell line model was assessed by performing morphology evaluation, PRC2 components expression, cell proliferation rate and clonogenicity. The in vivo tumorigenic potential was determined by subcutaneous injection into immunocompromised mice. MPNST 4970 is a new potential cell line model for the study of the mechanism of disease progression and for investigation of therapies for MPNST and will be shared with the scientific community.

11.01.015

ZB499, AN IRREVERSIBLE ESTROGEN RECEPTOR ANTAGONIST

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METHODS: To determine the binding affinity of the two porotype irreversible inhibitors to the estrogen receptor, the LanthaScreen TR-FRET assay (Life Technologies) was used in which ZB499 competed with a fluomone ligand and the percent displacement was quantitatively correlated to the fluorescence intensity from the displaced tracer. MCF-7, MCF-7/TamR, and MCF-7(Y537S) were treated with ZB499 to determine the antiproliferative activity of ZB499. ER mediated transcriptional activities were measured by the T47D-kb-Luc stably transfected human breast cancer cell reporter gene assay. To determine the in vivo efficacy of ZB499, mice bearing MCF-7 derived xenograft breast tumors and patient derived xenograft breast tumors were treated with oral doses of ZB499. RESULTS: ZB499 acted as an irreversible antiestrogen in blocking ER mediated transcriptional activities and cell proliferation of ER+ breast cancer cells including tamoxifen resistant phenotypes and those harboring mutant ER. ZB499 inhibited tumor growth in a panel of xenograft breast tumor models harboring wild type ER and Y537S mutant ER. Single dose pharmacokinetic studies demonstrate that ZB499, owing to its unique boronic acid structure, exhibits superior oral bioavailability in rodents compared to other nonsteroidal antiestrogens. DISCUSSION/CONCLUSION: Our studies demonstrate that ZB499 is a promising next generation antiestrogen that is effective in clinically relevant ER+ breast cancer models. Because ZB499 acts through covalent, irreversible binding of ER, it could lead to more durable clinical efficacy both in endocrine naïve breast cancer and in recurring disease which has often become endocrine resistant.

11.01.016

PRO-APOPTOTIC EFFECT OF PENTAGALLOYL GLUCOSE IN TNBC CELLS

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Pentagalloyl glucose (PGG) is a polyphenolic compound reported to modulate apoptosis, angiogenesis, metastasis, and signaling pathways in many cancers. PURPOSE: this study investigated PGG apoptotic effect in MDA-MB-231 (Caucasian) and MDA-MB-468 (African American) triple-negative breast cancer (TNBC) cells; recognized as the most aggressive type of breast cancer with poor prognosis. METHODS: Flow cytometry and RT-PCR were performed to investigate apoptotic action mechanisms. RESULTS: cytotoxicity assays showed that PGG was more potent in African American (IC50 35.7 μM) compared to MDA-MB-231 cells (IC50 176.1 μM). Also, PGG anti-proliferative effect was more effective in African American cells compared to Caucasians. Afterward, flow cytometry showed that PGG induced 42.3% of apoptosis in Caucasian, and 62% in African American TNBC cells in the concentration of 100 μM. In RT-PCR PGG increased the expression of several genes associated with apoptosis regulation in both cell lines, including CASP3 and CASP4, although a higher efficiency was observed in Caucasians compared to African American cells. Remarkably, the highest increase was seen in Tumor Necrosis Factor expression (TNF) with a 154.6-fold increase in MDA-MB-468 cells, compared to 14.6-fold in MDA-MB-231. TNF Receptor Superfamily Member 10a (TNFRSF10A) expression was also increased in both cell lines; however TNF Receptor Superfamily Member 9 (TNFRSF9) expression was induced exclusively in MDA-MB-231 cells. CONCLUSION: the results suggest that PGG could be a potential inducer of apoptosis in TNBC cells in Caucasian and African American women, by inducing expression of caspases, TNF and its receptors and thus offering a promising approach for cancer therapy.

11.01.017

PENTAGALLOYL GLUCOSE INHIBITS CXCL1 VIA NFκB/MAPK IN TNBC

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CXCL1 (GRO-α) is a chemokine derived from tumor-associated macrophages (TAMs), which mediates the communication between cancer cells and tumor microenvironment, inducing cancer progression and metastasis. In breast cancer cells, CXCL1 induces cancer survival and metastasis by activating calprotectin expression. PURPOSE: the current study investigated the effect of the naturally occurring polyphenol pentagalloyl glucose (PGG) in TNF-α-induced CXCL1 expression in MDA-MB-231 (Caucasian) and MDA-MB-468 (African American) triple negative breast cancer (TNBC) cells. Additionally, NFκB and MAPK signaling pathways were explored as possible mechanisms for PGG effect. METHODS: cytokine arrays, ELISA assays, RT-PCR, and Western analysis were performed. RESULTS: PGG inhibited TNF-α-stimulated CXCL1 expression in the transcription and protein level in Caucasian and African American TNBC cell lines. Through mRNA quantification analysis, data showed that PGG downregulated IKBKE (expressed in 60.4% of the breast cancer tumors) and MAPK1/ERK2 (expressed in tumor tissues with 5 to 10-fold increase) expression in both cell lines. Moreover, PGG was more effective in inhibiting IKBKE mRNA expression in MDA-MB-231 compared to MDA-MB-468 (11 and 2-fold inhibition, respectively). In addition, PGG reduced MAPK1 mRNA expression in 3-fold in Caucasian and 6-fold in African American cells. Through Western analysis PGG inhibitory effect over IKBKE and MAPK1 expression were also validated in the protein level. CONCLUSION: the data show that PGG inhibits the expression of CXCL1 through NFκB and MAPK signaling pathways, attenuating the expression of IKBKE and MAPK1 in both cell lines. The results suggest that PGG might have great potential in target therapy for TNBC.

11.01.018

LOSS OF BIT1 EXPRESSION INDUCES FOCAL ADHESION KINASE ACTIVA

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The Bcl-2 inhibitor of transcription (Bit1) protein exerts anti-tumor function in NSCLC through induction of anoikis and inhibition of EMT. As an inhibitor of anoikis resistance and EMT, Bit1 turns off the TLE1 corepressor-mediated transcription repression of the epithelial marker E-cadherin gene via the transcriptional regulator protein Amino-terminal Enhancer of Split (AES). Here, we have uncovered a novel mechanism by which Bit1 regulates the TLE1 corepressor function via the Focal Adhesion Kinase (FAK) protein, a known determinant of lung cancer cell survival. Using the human adenocarcinoma A549 cell line as a model system, we show that Bit1 functionally interacts with FAK and inhibits FAK activation. In Bit1 deficient A549 cells which exhibit enhanced FAK activation as compared to control cells, inhibition of FAK activity through specific pharmacological FAK inhibitors resulted in attenuation of their enhanced anoikis resistance and anchorage-independent growth, indicating that the increased FAK activity contributes to loss of Bit1-mediated tumorigenecity. Importantly, the FAK activation promoted transformation phenotypes of the Bit1 knockdown A549 cells by transcriptionally repressing E-cadherin expression in part via the TLE1 corepressor. Underscoring the role of FAK as a target of Bit1, the Bit1 knockdown cells exhibited enhanced resistance to the growth inhibitory and apoptosis inducing effects of the EGFR-TKI inhibitor, gefitinib, in part through FAK activation-dependent TLE1 transcriptional silencing of E-cadherin. These collective findings indicate that Bit1 may exert anti-tumor function and regulate E-cadherin expression in NSCLC cells through FAK-dependent regulation of TLE1.

11.01.019

DETERMINATION AND VALIDATION OF MYCOPHENOLIC ACID LC-MS/MS

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Mycophenolate sodium (MPS) is a prodrug of mycophenolic acid (MPA), an immunosuppressant agent, that has shown strong synergistic effect in combination with oxaliplatin (OXP) for the inhibition of dysplastic oral keratinocyte (DOK) cells. A novel patch formulation containing MPS and OXP has been developed for the treatment of oral cancer. With respect to the potential therapeutic advantages of this novel drug delivery route, there is a need for preclinical assessment for future clinical trials. The development of and validation of an analytical method is essential for the quantification of active pharmaceutical ingredients in biological samples for pharmacokinetic and tissue distribution studies. This study focuses on the LC-MS/MS method development and validation of MPS in rat plasma and tongue tissues. Blank rat plasma or tongue tissues coupled with griseofulvin, as internal standard, was used for generating standard curves ranging from 0.5 – 1000 ng/mL ($r > 0.99$) for both plasma and tongue tissues. The chromatographic separation was achieved by a reverse phase

ACE Excel 2 Super C18 (50 mm x 2.1 mm, 2 µm) column with a flow rate of 0.4 mL/min under gradient elution. Mass detection was performed under positive ionization electrospray. The calibration curves were linear over a concentration range between 0.5 – 1000 ng/mL ($r > 0.99$) in both plasma and tongue tissue homogenates. Inter- and intra-day accuracy and precision of the assay were < 10% in both plasma and tongue tissues. The matrix effect was non-significant and extraction recovery were in the range of 87.99% to 109.69%. We report a sensitive, specific and reproducible LC-MS/MS method for the quantification of MPA in rat plasma and tongue tissues. The assay was successfully used for the quantification of MPA in rat plasma for pharmacokinetic studies following intravenous administration of 0.5 mg/kg of MPS, and in rat tongue tissues for tissue distribution studies following 4 hour patch applications to the rat tongue.

11.01.020

THE EFFECTS OF GOSSYPOL ON CYTOKINE EXPRESSION

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Chronic inflammation-associated with cancer is characterized by the presence of leukocyte infiltration, prominently macrophages, which produce different types of cytokines and evolve normal cells to the neoplastic state. In cancer therapy, target many signaling pathways upregulate the expression of several cytokines is a major target. In the current study, we investigated the anticancer effects of the natural polyphenol gossypol (GOSS) in triple-negative breast cancer cells: MDA-MB-231 and MDA-MB-468. The obtained IC50s showed no significant difference between the two cell lines response to the compound. The human microarray assay for cytokine determination in TNF- α-stimulated cells indicated that GOSS causes 30% inhibition in CCL2 in MDA-MB-231 cells. Also, IL-8 expression was inhibited by 60% in MDA-MB-468 cells. ELISA assays supported the microarray data and proved that CCL2 was inhibited by 40% in MDA-MB-231 cells, and IL-8 was inhibited by 50% in MDA-MB-468 cells. In MDA-MB-231 cells, GOSS inhibited NF-κB, JAK-STAT, and p38 MAPK (ERK) signaling pathways that mediate CCL2 release through repressing the expression of three genes: IKBKE, CCL2, and MAPK1. Meanwhile, in MDA-MB-468 cells, the compound inhibited PI3K-AKT, JAK-STAT, and p38 MAPK signaling pathways and downregulated the release of IL-8 through repressing the expression of many genes, including IL-8, MAPK1, MAPK3, CCDC88A, STAT3, and PIK3CD. In conclusion, the data obtained indicate that the polyphenol compound GOSS may provide a valuable tool in TNBC therapies, which has to be proven using in vivo studies.

11.01.021

METFORMIN REGULATES AR AND CANCER CELL PROLIFERATION

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PURPOSE: The androgen receptor (AR) is a ligand-activated transcription factor expressed in prostate cancers and a subset of triple negative breast cancers (TNBCs). Currently, the role of AR in TNBC growth and progression is poorly understood. The antidiabetic medication metformin reduces growth of human breast and prostate cancers in vitro and in vivo. The goal of this study was to examine whether metformin alters AR expression and proliferation of BT-549 cells, an AR-positive TNBC cell line, and the C4-2 prostate cancer cell line. METHODS: Presto Blue viability assays were performed to measure the effect of metformin on cell proliferation. Quantitative reverse transcription-polymerase chain reaction (qRT-PCR) assays were used to measure basal AR mRNA levels as well as the effect of metformin on AR expression. RESULTS: Metformin reduced proliferation of C4-2 cells. However, it did not alter proliferation of BT-549 cells or the AR-negative PC-3 prostate cancer cells. The basal amount of AR mRNA expressed in BT549 cells was lower than that present in C4-2 cells or other AR-positive prostate cancer cell lines. Metformin did not significantly alter AR mRNA in BT549 cells. However, it did reduce the amount of AR mRNA in C4-2 cells. DISCUSSION/CONCLUSION: Previous studies suggest that wild type p53 is required for metformin-driven responses. C4-2 cells express wild type p53, while BT549 cells lack wild type p53. Therefore, the inability of metformin to regulate proliferation and AR expression in BT-549 cells may be linked to the fact these cells do not express functional p53.

11.01.022

GENOMIC ANALYSIS OF FKBP52-REGULATED AR SIGNALING

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PURPOSE: We previously demonstrated that the FKBP52 cochaperone interacts directly with β-catenin to promote β-catenin interaction with the AR BF3 surface leading to a synergistic up-regulation of AR signaling in prostate cancer cells. Previous studies also demonstrated that small molecules targeting the BF3 surface allosterically affect co-activator recruitment on AR. Thus, our current hypothesis is that the BF3 surface is a promiscuous regulatory surface capable of binding diverse regulators, which then allosterically influence co-activator recruitment to promote distinct AR-dependent gene expression profiles. METHODS: AR-dependent reporter assays and co-immunoprecipitation were used to identify novel

protein complexes that functionally interact with AR. In addition, we used CRISPR/CAS9 to delete the FKBP52 gene in 22Rv1 prostate cancer cells and assessed the AR cistrome and AR-dependent transcriptome in the presence or absence of FKBP52 and hormone by ChIP-seq and RNA-seq. RESULTS: We have identified a novel functional interaction between β-catenin and FKBP52 that is predicted to regulate AR co-activator recruitment and AR-dependent transcription. Preliminary ChIP-seq and RNA-seq findings from fkbp52-deficient (52KO) 22Rv1 cells suggest a dysregulation of AR-DNA binding in response to hormone with 52KO cells displaying approximately 14 times more global AR binding sites on the DNA. Despite the significant increase in AR binding sites, the 52KO cells display significantly reduced changes in global hormone-induced gene expression. CONCLUSION: Our preliminary data suggest that the FKBP52 cochaperone is a critical factor regulating androgen-dependent transcriptional programs, and that therapeutic targeting of FKBP52 would significantly abrogate gene expression changes in response to hormone.

11.01.023

ROLE OF NUCLEOSOME CHROMATIN REMODELING FACTOR IN PCA

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Prostate cancer (PCa) is the second-leading cause of cancer-mortality in the US and is the most commonly diagnosed malignancy in African American men. Epigenetic alterations play a crucial role in the development of human diseases and cancers. Nucleosome-remodeling factor (NURF) consisting of bromodomain-PHD finger transcription factor (BPTF), sucrose non-fermenting-2-like (SNF2L), and pRBAP46/48, controls the chromatin remodeling machinery. One of NURF's major function is to regulate histone modifications and gene expression. SNF2L serves as the energy transducing subunit in NURF. SNF2L is a ubiquitously expressed transcription activator and its elevation is associated with cancer development. However, the role of SNF2L on PCa progression is still elusive. Therefore, there are unmet needs to understand the role of SNF2L in PCa in order to develop effective therapeutic approaches. The objective of this project is to assess the impact of SNF2L loss on PCa progression. We hypothesized that SNF2L knockout (KO) will inhibit the proliferation of castration-resistant PCa cells and targeting SNF2L or SMARCA-1 gene may be beneficial for controlling cancer progression. We have generated SNF2L KO PCa cells with CRISPR-Cas9 technology. Our results showed that SNF2L deficiency resulted in a reduced proliferation and invasion of PCa cells. SNF2L KO destabilizes the NURF complex and impairs chromatin remodeling and histone modifications for cell growth and survival. Thereby, targeting SNF2L may serve as a novel therapeutic regime for PCa control.

11.01.024

IDENTIFYING ENZALUTAMIDE RESISTANCE MECHANISMS

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Prostate Cancer (PCa) disproportionately affects African American (AA) men. Compared to their Caucasian American (CA) counterparts, AA men are more likely to develop PCa and studies have suggested that AA men with metastatic castration resistant PCa (mCRPC) have shorter overall survival than CA men. Enzalutamide (ENZ) is a second-generation anti-androgen for treatment of mCPRC. It prolongs survival of CRPC patients; however, its overall benefit is modest (4.8 months) and most patients progress on in less than two years. To date, the molecular mechanism underlying ENZ resistance has not been well illustrated. Identifying molecular pathways underlying hormone therapy/ENZ resistance is critical for developing novel combinatorial therapies to inhibit resistance, prevent tumor recurrence, and extend patient survival. The primary versus mCRPC models specific to AAs were developed by subjecting primary PCa cell lines (non CRPC/AA) – RC77T, RC43T, RC165T to invasion and incremental MDV3100 selection pressure. The primary prostate tumor non CRPC/AA cell lines – RC77T, RC43T, RC165T were epithelial in appearance, while the isogenic CRPC/AA lines – RC77T-CR, RC43T-CR, RC165T-CR appeared mesenchymal. To identify transcriptomic signatures associated with acquisition of ENZ resistance, we profiled gene expression in ENZ-sensitive and -resistant mCRPC cells using RNA sequencing (RNA-seq). Analysis revealed a panel of 352 differentially expressed genes (DEG) between non CRPC/AA and CRPC/AA. Comparison of the CRPC/AA with CRPC/EA cell lines (C4-2B, PC3 and DU-145) revealed 2802 DEGs while up to 6104 DEGs were identified between EA and AA cell lines; suggesting a substantial difference between EA and AA models. Overlapping DEGs in the ENZ-sensitive and -resistant cells were ranked by Gene Set Enrichment Analysis (GSEA) and validated to correlate with gene expression. Our data showed that the cell differentiation lineage-specific gene signatures were differentially expressed in CRPC/AA compared with CRPC/EA models suggesting that molecular subtypes may play different roles in the PCa progression and treatment resistance in different ethnic groups. With IHC staining, we revealed higher expression of basal markers from AA and Nigeria patients than those in EA patients. These findings suggested that different genes are expressed between EA and AA cell lines in general and between CRPC/EA and CRPC/AA. Our results also indicated that PCa is a heterogeneous disease accompanied by differences in molecular and biological features that account for the challenge for PCa treatment and prognosis.

Poorly differentiated cancer cells may increase aggressiveness of AA tumors that in turn contribute to the disparities in disease aggressiveness. The transcriptional changes have potential for further study as predictive biomarkers and identify potential mechanisms of ENZ resistance that may serve as new targets for CRPC therapy. The molecular pathologic subtypes will be more biologically and clinically relevant to PCa aggressiveness in patients with different ancestry, especially in AA patients.

11.01.025

PYRONARIDINE; A CANDIDATE FOR A REPURPOSED ANTICANCER DRUG

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PURPOSE: To evaluate pyronaridine, for its anti-cancer activity. METHODS: Cytotoxicity and molecular biology assays as well as in-vivo studies were employed in this analysis. RESULTS/ EXPECTED RESULTS: Based on our previous work, the antimalarial drug pyronaridine (PND) was shown to exert anticancer activity. PND induces apoptosis by means of mitochondrial depolarization, alteration of cell cycle progression, and DNA intercalation. We have further investigated the mode of action of PND and have determined that it acts as a topoisomerase II inhibitor. In addition, preliminary in-vivo studies suggest that PND hinders tumor progression. In vitro combination studies of PND with known anticancer drugs such as Cisplatin and Gemcitabine, show that the combined cytotoxic effect of these drugs with PND is greater than individual administration. This results lead to the possibility of future in- vivo combination experiments that could eventually be used in human anti-cancer therapy. DISCUSSION/CONCLUSION:The findings presented in this study reconfirm and give a positive outlook to PND's potential as an anticancer drug.

11.01.026

SYNTHESIS AND ANTITUMOR ACTIVITY OF A SERIES OF NOVEL 1-OXA-

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PURPOSE: Cancer is among the leading causes of death worldwide, has a major impact on society in the United States and across the world. The main purpose of this study is to design, synthesize and evaluate novel 1-oxa-4-azaspiro[4,5]deca-6,9-diene-3,8-dione derivatives as anticancer drugs. METHOD: A series of novel 1-oxa-4-azaspiro[4.5]deca-6,9-diene-3,8-diones were designed and synthesized by using 4-aminophenol and α-glycolic acid or lactic acid as starting materials in three or four steps. The key step is the metal-catalyzed oxidative cyclization of the amide to 1-oxa-4-azaspiro[4.5]deca-6,9-diene-3,8-diones, the reaction conditions of which are investigated and optimized. The anticancer activity of 17 1-oxa-4-azaspiro[4.5] deca-6,9-diene-3,8-dione derivatives was evaluated in in vitro cytotoxicity assays. RESULTS/EXPECTED RESULTS: Preliminary results showed that 15 compounds have moderate to potent activity against human lung cancer A549, human breast cancer MDA-MB-231, and human cervical cancer HeLa cell lines. Among them, compounds 11b and 11h were the most potent against A549 cell line with 0.18 and 0.19 μM of IC50, respectively; compounds 11d, 11h, and 11k showed the most potent cytotoxicity against MDA-MB-231 cell line with 0.08, 0.08, and 0.09 μM of IC50, respectively, while the activities of 11h, 11k, and 12c against HeLa cell line were the most potent with 0.15, 0.14, and 0.14 μM of IC50, respectively. DISCUSSION/CONCLUSION: Compound 11h is a promising candidate for further development, which emerged as the most effective compound overall against the three tested cancer cell lines.

11.01.027

GLYCEOLLIN TRIGGER ANTI-PROLIFERATIVE EFFECTS IN T47D CELLS

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Aromatase inhibitors (AIs) are the standard treatment for postmenopausal women with estrogen-dependent metastatic breast cancer. Unfortunately, some patients develop resistance leading to tumor relapse, metastasis, and death. Previous research suggested that AI resistance is due to upregulation of growth factor signaling (i.e., HER2 and EGFR) and increased cellular motility. Previously, we demonstrated that a novel phytoalexin, glyceollins, inhibits proliferation, survival, and migration of hormone independent letrozole-resistant (LR) breast cancer cells (LTLT-Ca). However, many postmenopausal women with AI-resistance tumors remain hormone dependent. Therefore an understanding of distinctions between estrogen receptor (ER+) positive and ER negative (ER-) AI-resistant tumors and their response to therapy is critical. PURPOSE: We hypothesize that treating ER+ LR breast cancer cells with glyceollin and lapatinib (a dual EGFR/HER2 inhibitor) will reduce growth factor signaling and inhibit proliferation. METHODS: To test this hypothesis, T47Darom cells (T47D cells which stably overexpress the aromatase gene) and T47DaromLR cells (LR T47Darom) were treated with lapatinib and/or glyceollin. To evaluate viability and cell survival, resazurin and colony assays were performed, respectively. RESULTS/EXPECTED RESULTS: Glyceollin alone and the combination inhibited T47DaromLR

proliferation by 46% and 59%, respectively. Glyceollin caused a 33% reduction in T47Darom cell survival and the combination caused a 60% reduction in the colony formation. Interestingly, glyceollin and the combination significantly inhibited cell survival of T47Darom cells by 94% and 96%, respectively. DISCUSSION/CONCLUSION: Results suggest that using glyceollins and lapatinib in combination may have potential as a novel therapeutic approach for postmenopausal patients with hormone-dependent, LR breast tumors.

11.01.028

SPLICING FACTOR 1 DEFICIENCY REDUCES COLON TUMORIGENESIS.

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PURPOSE: Colon cancer, the third most common cancer in the US, has highest incidence and mortality rates in African Americans. Other than socioeconomic factors, it is important to consider genetic and environmental factors that could eliminate this disparity. The APC (adenomatous polyposis coli) gene is frequently mutated in colon cancers. Our laboratory utilizes mouse models to assess genetic factors that influence colon tumorigenesis. We developed a mouse strain, Sf1+/-, that expresses reduced levels of splicing factor 1 (SF1). SF1 is a widely expressed alternative splicing factor. Sf1+/- mice express reduced levels of SF1. We previously found that Sf1+/- mice had reduced incidences of testicular cancer. We therefore tested whether lower levels of SF1 could also affect colon cancer. METHODS: ApcMin/+mice carry a mutation in the APC gene and develop numerous intestinal polyps by 4 months. We collected 2 cohorts of mice, ApcMin/+and Sf1+/-;ApcMin/+ mice, in which the number and sizes of intestinal polyps were counted. RESULTS: Sf1+/-;ApcMin/+ mice had lower numbers of intestinal polyps compared to ApcMin/+. Fewer of the smaller sized polyps were detected in Sf1+/-;ApcMin/+. The numbers of larger sized polyps were similar in both cohorts. Thus, lowered SF1 led to lower number of polyps that are initiated in the intestine thus resulting in reduced incidence of colon polyps. CONCLUSION: SF1 deficiency decreased colon polyp size and numbers. It is possible that decreasing SF1 levels may also lower development of other types of cancers and SF1 could serve as potential therapeutic target in cancers.

11.01.029

ROLE OF EPRS IN REGULATING PD-L1 AND IMMUNE ENVIRONMENT IN T

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Triple negative breast cancer (TNBC) is an aggressive disease, particularly in African American patients, with limited treatment options besides chemotherapy. Evidence is accumulating that immunotherapy may represent an option for the treatment of TNBC. Immunotherapy with program death ligand (PD-L1) inhibitor, that disrupts PD-1/PD-L1 axis, has been associated with responses in patients with advanced TNBC, indicating that immune evasion contributes to the pathogenesis of this refractory disease. The mechanism of PD-L1 regulation remains largely elusive in TNBC. Glutamyl-Prolyl-TRNA Synthetase (EPRS) gene is 31% amplified in breast cancer and is overexpressed in TNBC and in BL1 subtypes. Studies have shown EPRS to be regulator of antiviral immunity and its ability to control inflammation. Our work shows that EPRS is upregulated in MDA-MB-231 cells (TNBC) as compared to hormone positive MCF-7 and T47D breast cancer cells (HPBC). EPRS-siRNA -mediated knockdown of EPRS in MDA-MB-231 breast cancer cells down regulated basal and IFN-gamma stimulated PD-L1 and ICAM-1 protein expression. Further analysis showed that EPRS knockdown also downregulated STAT3 phosphorylation in MDA-MB-231 cells while total STAT3 remains unchanged. CIBERSORT analysis of 116 TNBC patient dataset from TCGA revealed that the total abundance of all TALs was significantly higher in tumors that have high-EPRS expression ($p < 0.0001$), as compared to low-EPRS tumors. Moreover, the immunosuppressive Treg population was lower in EPRS-high as compared to EPRS-low tumors. These findings reveal that EPRS might be a critical mediator of immune microenvironment in TNBC and can be a immunotherapy target in TNBC.

11.01.030

THE BREAST CANCER SUBTYPE-SPECIFIC ROLES OF LSR

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The breast cancer (BC) mortality rate is 41% higher for Black American women (BA) than non-Hispanic White American women (WA). Our published studies established that the lipolysis stimulated lipoprotein receptor (LSR) is overexpressed in BA vs. WA BCs, and is linked with poor patient survival. LSR is also significantly overexpressed in all BC subtypes, a key aspect, as BA women have higher mortality rates within all subtypes, emphasizing a need to study disparities in all tumor types. LSR functions in lipid endocytosis and tricellular junctions. Our published studies also revealed that LSR can traffic to the nucleus. Notably, all BC patients with nuclear LSR succumbed to the disease. Our current, unpublished studies suggest the subcellular localization and functions of LSR are BC-subtype specific, and may vary by race. We are correlating LSR protein localization and expression levels with race, subtype, and other variables in over 300 patient samples. We are also

performing LSR overexpression and knockout in BA and WA BC cell models to observe proliferation, lipid-uptake, regulation of fatty acid/lipid receptors, acetyl-CoA levels/histone acetylation, and mitochondrial function. Our preliminary data suggest LSR overexpression in luminal vs. basal breast cancers is linked with distinctive cell behaviors. As LSR is significantly overexpressed in all BA tumors, the protein localization/expression of LSR, analyzed together with BC subtype, may be highly informative in directing patient treatment regimen and predicting outcome. Our goal is to develop enhanced methods to decrease BC mortality disparities, and LSR may present novel information on predicting BC behaviors.

11.01.031

SECRETORY FACTORS FROM OBESE-DERIVED OMENTUM SUPPORT OVARIAN

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PURPOSE: Ovarian cancer is the most lethal gynecological malignancy with increased risk and worse overall survival among patients with obesity. Furthermore, ovarian cancer cells preferentially metastasize to the omentum, a sheet of fatty peritoneal tissue that encloses the abdomen. Several soluble factors found in the obese ovarian microenvironment can activate the NF-kB pathway, a ubiquitous cell signaling network critical for growth, inflammation, stress response, and immune signaling that is aberrantly activated in ovarian cancer. Our goal is to understand how adipocytes in the omentum promote ovarian cancer cell metastases and growth. We hypothesize that soluble factors enriched in the obese microenvironment activate NF-kB in cancer cells to drive cell migration and proliferation. METHODS: Co-culture of primary adipocytes derived from obese omental tissue together with ovarian cancer cell lines to profile secretory factors responsible for activating NF-kB, increasing tumor initiation in vivo and clonogenicity, proliferation, and drug resistance in vitro. RNA sequencing studies are underway to elucidate other pathways that might be activated in response to adipocyte signaling. RESULTS/EXPECTED RESULTS: Obese-derived omentum significantly enhances tumorigenicity of ovarian cancer cells. We identify TWEAK, CD40, IGFBP-4, and IGF-BP6 as soluble factors that activate NF-kB to support ovarian cancer progression. Alternative signaling pathways or metabolic activities will be discovered with RNA sequencing studies. DISCUSSION/CONCLUSION: Our study uncovers the critical role of adipocytes and their secreted factors in promoting ovarian cancer progression. Ultimately, we hope to target this signaling crosstalk to inhibit disease progression and improve treatment response among patients with obesity.

11.01.032

COMPARING EFFICIENCY OF MULTIDRUG THERAPY IN GLIOBLASTOMA

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Aim: There has been increase resistance of glioblastoma to chemotherapy leading to use of combination therapy (Irinotecan-CPT11, cyclophosphamide-CTX and Temozolamide-TMZ). In this study we optimize the treatment of glioblastoma using solid lipid nanoparticle (SLN) to improve delivery of Cyclophosphamide and Irinotecan using HTB-16 and CRL-2611 cell lines. Method: Formulations were made from lecithin (40%), and variable amounts of Compritol 888 ATO, Labrafil, Poloxamer 188 prepared by hot homogenization with CPT11 dissolved in the lipid phase and CTX in the aqueous phase at 800C. Measurement of particle size, zeta potential and polydispersity index were done over 4 weeks to assure stability. HTB-16 and CRL-2611 cell lines were treated with varying concentrations of free drugs (CPT11 & CTX), individual and combined drugs entrapped into SLN for 48 hours. Viability was determined by use of automated cell counter. Results: Four formulations were retained for entrapment. Particle sized between 50-70nm (± 3.1) with zero zeta potential. Growth inhibition of combined CTX and CPT11 (IC50 = 11.1± 0.2μM) was remarkably higher than each drug entrapped in SLN CPT11 (IC50= 24.4±2 μM) and CTX (IC50=32.0±0.7 μM) for the CRL-2611 cell lines. However, we noted a significant growth inhibition by CPT-11 (IC50 =16±2 μM) entrapped compared to either CTX (IC50=44±12 μM) and both combined in SLN (IC50= 23±3 μM) when working with the HTB-16 cell lines. Conclusion: This study shows that Irinotecan may be the optimal therapy for treating glioblastoma with majority of HTB-16 cells while a combination therapy is warranted for serotypes with CRL-2611 cells.

11.01.033

MRNAS PROFILE IN RESPONSE TO STREP. VT_162 IN COLON CANCER

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Background: Streptococcus sp. VT_162 (SPV) were identified by our group showed neoplastic transformation in patients with colorectal cancer (CRC). This strain's genome contains 10 virulence factors that match S. pyogenes and 3 different strains of S. pneumomia virulence factors. Hence, we aimed to determine whether (SPV) influences the expression of carcinogenic genes in several human colon cell lines. Methods: Colon cancer cell lines (HCT116, SW480 and LoVo) were infected with SPV at a multiplicity of infection (MOI) of 10

or 50. RNA extracts were used on an Illumina sequencer and the mRNA expression profiles were compared to cells that were not exposed to SPV. Sequencing data were processed according to our previous studies. CutAdapt was used to trim Illumina adapters. Reads were aligned to the UCSC hg38 reference sequence using Bowtie2. Sequencing reads were assembled and annotated. To estimate differential expression between different samples, the count data were used in DESeq2 R package and the comparisons were performed. mRNAs with statistically significant ($p<0.05$) expression difference from untreated cell lines and log 2 FC >3 are reported and the relation to cancer of the most upregulated mRNAs was investigated. Results: An in-silico analysis of SPV genome revealed that the strain contains ten (10) putative virulence factors that match those of S. pyogenes and three (3) of different strains of S. pneumomia. At MOI of 10, a total of 427 mRNAs displayed a >3 fold upregulation of their expression. The top 20 upregulated genes were: HSPA6, CSF2, SPRR2D, SERPINB7, CXCL8, LCN2, SBSN, HSPA7, SERPINA3, SLC6A12, RSPH10B, ITGAM, BCRP3, CRYAB, GCM1, TNFRSF9, IGFN1, SNAI2, LUCAT1 and SASH3 with the following respective fold differences: 8.44, 6.75, 6.68, 6.56, 6.23, 5.91, 5.81, 5.56, 5.25, 5.21, 5.19, 5.12, 5.06, 5.03, 5.02, 5.01, 4.99, 4.97, 4.93, 4.91, most have shown involve in many other aggressive cancer, poor survival and prognosis.. Three of these mRNA HSPA6, HSPA7 and CRAB are heat shock proteins reflecting that the bacterium is perceived as a stressor to the cells. Some of the upregulated mRNA have no known roles and might correspond to novel, specifically-SPV carcinogenic pathways. Conclusion: SPV infection led to major alterations in the genome expression profiles in the colon cell lines. Many of the upregulated mRNA have known carcinogenic effects and associate with poor prognosis and survival in different organ systems. These findings increase our understanding on the targets by which SPV contributes to colorectal cancer transformation and need to be validated in clinical specimens.

11.01.034

NOVEL DRUG AGENTS FOR METASTATIC COLORECTAL CANCER THERAPY

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PURPOSE: Despite recent advances including colonoscopy in early detection of colorectal cancer (CRC), patients with K-Ras (50%) and B-Raf (10%) driven Metastatic CRC (mCRC) still do not respond to current chemotherapy and targeted therapies. The 2019 incidence and death rates of CRC in the U S are still alarming, and projections are 145,600 and 51,020, respectively. Men of African American descent are more likely to be diagnosed with CRC and equally die of it compare to other races and sex. Also, the most aggressive and deadly subtype with active mutant B-Raf is commonly diagnosed in women and patients of more advanced age. Therefore, investigating novel targeted therapy to disrupt the activities of these driving agents is a matter of urgency. We hypothesized that Polyisoprenylated cysteinyl amide inhibitors (PCAIs) would induce CRC cell death in 2D and 3D cultures by apoptosis and shrink spheroids' volume. METHODS: The effective concentration (EC50) of two PCAIs (NSL-BA-040 and NSL-BA-055) were tested for their effects on 2D and 3D cultured Caco-2 and HCT116 cells. RESULTS: NSL-BA-040 and NSL-BA-055 inhibited 2D Caco-2 cells cultured at very low concentrations of 3.8 and 1.4, respectively, and 2.2 and 1.5 μM, respectively for HCT116 cells. For the 3D cultures, NSL-BA-040 and NSL-BA-055 induced cell death of spheroids at EC50 of 20 and 5.5 μM, respectively. NSL-BA-055 induced cell death by apoptosis, blocks spheroid growth and shrinks their volumes. DISCUSSION / CONCLUSION: PCAIs were designed to target the aberrant components in the MAPK signaling pathway. PCAIs show development potentials as targeted drug for CRC therapy.

11.01.035

ZAR2 AS A MODULATOR OF CELL CYCLE VIA WEE1 IN BREAST CANCER

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Major objective of the proposed research is to evaluate the potential of a novel protein ZAR2 as a modulator of G2-M checkpoint and therapeutic target in breast cancer. ZAR2 is a novel RNA-binding C4 zinc finger containing protein, with cell cycle dependent differential nuclear/ cytosolic localization. We observed that ZAR2 expression is relatively lower in triple negative breast cancer cells (TNBC) compared to non-TNBC and forced expression in TNBC cells inhibit their growth and invasiveness. Knocking down ZAR2 in non-TNBC cells increased their growth and invasiveness. Differential RNAseq analysis with control and ZAR2 knockdown MCF7 cells revealed up regulation of several growth regulator proteins in the ZAR2 knocked down cells. Our studies showed that ZAR2, is inhibited by a c-Myc regulated miRNA, hsa-miR-130a-5p. Studies demonstrate that ZAR2 localizes in the RNA processing P-bodies and regulates the turnover of maternal WEE1 mRNA in developing oocytes. WEE1 is a tyrosine kinase, which regulates G2/M checkpoint in cell cycle, is over-expressed in various cancer types and is associated with resistance development to DNA-damaging agents. WEE1, is identified as a potential molecular target for TNBC. WEE1 inhibition is exclusively toxic for cancer cells and does not harm healthy cells. c-Myc mediated downregulation of ZAR2 expression via hsa-miR-130a-5p,

results in increased levels of WEE1 protein in breast cancer cells, increased proliferation and faster progression through cell cycle.

11.01.036

EPIGENETIC EFFECTS OF FINASTERIDE ON HUMAN LEYDIG CELLS

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Finasteride is a synthetic 4-azasteroid, used in the treatment of both androgenetic alopecia and benign prostatic hyperplasia. In some men, its use is associated with persistent erectile dysfunction, ejaculatory dysfunction, loss of libido, altered sperm counts and infertility - even after cessation of the drug. This condition has been termed "Post-finasteride Syndrome" (PFS). We want to understand the underlying biochemical mechanisms that govern the development of this condition. Therefore in this experiment we tested the effects of exposure of finasteride on human Leydig cells, the main hormone-producing cell of the testis, to identify epigenetic changes in the cells that could be at least partially responsible for PFS. We cultured human Leydig cells in the presence of 0.5 μM finasteride for 14 days and performed whole-genome DNA methylation analysis using the NimbleGen Human DNA Methylation 3x720K Promoter Plus CpG Island Array and Ingenuity Pathway Analysis. Here we describe initial identification of specific genes and pathways involved that may ultimately lead to treatments to reverse PFS.

11.01.037

MECHANISMS OF CISPLATIN-INDUCED TOXICITY TO LEUKEMIA CELLS

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PURPOSE: Cisplatin is a widely used anti-tumor drug for the treatment of a broad range of human malignancies with successful therapeutic outcomes for head and neck, ovarian, and testicular cancers. It has been found to inhibit cell cycle progression and to induce oxidative stress and apoptosis in acute promyelocytic leukemia (APL) cells. However, its mechanisms of cytotoxicity are poorly understood. We hypothesized that cisplatin induces cytotoxicity through DNA adduct formation, oxidative stress, transcriptional factors (p53 and AP-1), cell cycle regulation, stress signaling and apoptosis in APL cells. METHODS: We used the APL cell line as a model, and applied a variety of molecular tools (cytotoxicity and oxidative stress assays, western blot analysis, flow cytometry, and confocal microscopy) to elucidate the mode of action of cisplatin. RESULTS: We found that cisplatin inhibited cell proliferation by a cytotoxicity characterized by DNA-adduct formation, oxidative stress, cell cycle arrest, stress signaling and apoptosis in APL cells. Cisplatin also activated p53 and phosphorylated activator protein (AP-1) component, c-Jun at serine (63, 73) residue simultaneously leading to cell cycle arrest through stimulation of p21 and down regulation of cyclins and cyclin dependent kinases (cdks) in APL cell lines. It strongly activated the intrinsic pathway of apoptosis through alteration of the mitochondrial membrane potential, release of cytochrome C, and up regulation of caspase 3 activity.in APL cells. CONCLUSION: Overall the findings from this study provide novel targets of cisplatin mode of action that may be very useful in designing of new APL drugs.

11.01.038

SGLT2 INHIBITOR ALTERS PHOSPHORYLATION LEVELS IN CANCER

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PURPOSE: Prostate cancer is a disease that disproportionately affects African American men. To reduce the number of deaths and suffering associated with this disease, we must identify therapeutic strategies that effectively reduce prostate cancer growth and progression. Data from our laboratory and others indicate canagliflozin, an antidiabetic agent that inhibits the sodium-glucose transporter-2 (SGLT2), reduces proliferation of human prostate cancer cells. However, the mechanism by which canagliflozin decreases prostate cancer proliferation is not understood. The goal of this study was determine whether canagliflozin regulates intracellular signaling pathways that regulate the growth and progression of prostate cancer. To achieve this goal, we tested the effects of canagliflozin in the AR-positive, castration-sensitive LNCaP and AR-negative castration-resistant PC-3 prostate cancer cell lines. METHODS: Presto Blue Cell Viability Assays were used to test the effect of canagliflozin on cell proliferation. Alterations in protein expression and protein phosphorylation were detected using Western blot analysis and Human Phospho-Kinase Arrays. RESULTS: Micromolar concentrations of canagliflozin significantly reduced the proliferation of LNCaP and PC-3 cells. Data from the Human Phospho-Kinase Arrays indicated that canagliflozin also modulated the phosphorylation of several proteins. Canagliflozin induced phosphorylation of AMPK α1 and reduced phosphorylation of Akt in both cell lines. In addition, canagliflozin increased phosphorylation of the transcription factor β-Catenin in LNCaP cells. DISCUSSION/CONCLUSION: Growth inhibitory concentrations of canagliflozin altered phosphorylation of proteins that play a role in prostate cancer cell metabolism and survival. These data suggest that the anti-proliferative effect of canagliflozin may be linked to changes in protein phosphorylation.

11.01.040

IDENTIFYING SNPS IN HTR7 GENE RELATED TO BREAST CANCER

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Background: Breast cancer is the most common cancer and the second leading cause of cancer death in African American women. The annual incidence in the United States of Breast cancer is almost 178,480. Genetic variation in serotonin receptors (HTRs) has been widely implicated in a variety of health disparities including cancer. Since 5-HT has been shown to be correlated with tumor progression, loss of androgen dependence, and poor prognosis. Ethnic variations of polymorphisms should be evaluated and incorporated into investigations of susceptibility variants for common diseases. We hypothesize that minor allele frequency (MAF) distributions for HTR7 SNPs in African are significantly different from those of Caucasian-decent population. Materials and Methods: Analysis was performed using 1000 genome project to identified a total of 4129 SNPs. Also, the University of California Santa Cruz (USCS), and National Center for Biotechnology Information (NCBI), were used to narrow down the selection to five SNPs in the HTR7 gene. The selection was based on significant SNPs allele frequency differences between African and Caucasian -descent populations. Results & Discussion: Allele frequency differences were determined in the studied populations with a 20% to 60% difference for the following SNPs: rs4406742, rs34871116, rs7893260, rs12259062, rs11472590, and rs792253. All SNPS are found to be intronic and we believe they are important in alternative splicing of the mRNA which might regulate HTR7 gene expression. To our knowledge this is the first time that those SNPs have been studied in African American women breast cancer patients.

11.01.041

THE ROLE OF 5-HT2A IN MIRNA EXPRESSION IN BREAST CANCER

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Howard University (NR, AA, AA, AS, JIA, KMT, MA)

Introduction: African American women are twice as likely to be diagnosed with triple negative breast cancer (TNBC) than Caucasian women. TNBC is the most aggressive subtype of breast cancer and more difficult to treat. 5-HTR2A, a G coupled-protein serotonin receptor, was implicated in cancer progression. In this study we determined the miRNA expression profile related to 5-HTR2A biological activity in a TNBC cell line derived from an African American woman. Methods: MDA-MB-468 cell line was cultured and an MTS assay performed to identify the effective concentration of (±)-DOI hydrochloride (5-HTR2A agonist) for treatment. Following treatment with DOI, total RNA was isolated and subjected to the NanoString human v3 miRNA kit targeting 800 endogenous miRNAs using color-coded probe sets. nSolver was used for differential miRNA expression and statistical analysis. Results: Fourteen miRNAs were differentially expressed between the DOI treated and untreated breast cancer cell line (MDA-MB 468). When comparing these fourteen miRNAs to the normal breast cell line (MCF-10a), only one miRNA (hsa-miR-221-3p), was found to be significant ($p<0.05$). In DOI treated TNBC (MDA-MB 468), hsa-miR-221-3p was downregulated by 3.44 and 1.81 compared to untreated TNBC (MDA-MB 468) and normal (MCF-10a), respectively. Reportedly, hsa-miR-221-3p is associated with TNBC and acts downstream of the oncogenic RAS-RAF-MAPK pathway. Conclusion: This study elucidates miRNAs contributing to triple negative breast cancer development and progression in correlation with 5HTR2A activity. These miRNAs should be validated and further investigated in clinical specimens.

11.01.042

FIBROBLASTIC P53 MUTANT PROMOTES MAMMARY TUMOR DEVELOPMENT

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PURPOSE: The mortality rate from breast cancer is higher for African-American women than for Caucasian-American women. Breast cancer associated fibroblasts frequently contain mutants of tumor suppressor p53, the role of which remains unknown. Our goal is to investigate whether p53 mutant in stromal fibroblasts impacts breast cancer using mouse model. We hypothesize that fibroblastic p53R172H mutant accelerates mouse mammary tumor development.METHODS: A cohort of MMTV-HER2; Fsp-Cre; p53wm-R172H/+ female mice was established, which develops human-epidermal-growth-factor-receptor 2 (HER2) positive mammary carcinomas and contains p53R172H specifically in the fibroblasts. A cohort of MMTV-HER2; Fsp-Cre females was also established, where p53 remains intact in the stromal fibroblasts of HER2 tumors. Tumor development was monitored. The expression of a panel of immune-related genes in tumors was examined by immunohistochemistry/immunofluorescence, or quantitative Reverse Transcriptase PCR. Additionally, tumors and their associated fibroblasts from the above two cohorts will be isolated individually by laser capture microdissection and the mutation profiles in each compartment will be examined by exome sequencing. RESULTS/EXPECTED RESULTS: The MMTV-HER2; Fsp-Cre; p53wm-R172H/+ females exhibited a significantly shorter median tumor free survival than that of the MMTV-HER2; p53wm-R172H/+ females. Interestingly, the presence of p53R172H in fibroblasts reduced the expression of three immune-related genes that are

known to have tumor suppressive functions. Different genomic mutation profiles in tumors and their associated fibroblasts between the two cohorts are also expected. CONCLUSION/DISCUSSION: Our results show that fibroblastic mutant p53 promotes mammary tumor development, potentially through altering genomic landscapes and expression profiles in both tumor and the associated fibroblasts.

11.02.001

ATHEROSCLEROTIC MEASURES IN WOMEN WITH NO RISK FACTORS

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PURPOSE: Atherosclerotic coronary heart disease (CHD) is rising, and it disproportionally affects African American (AA) women compared to their Caucasian counterparts. The extent to which CHD risk factor differences explain the observed disparity remain unanswered beyond statistical assumptions. To rule out genetic or environmental differences as important contributors in the CHD differences, studies involving AA and Caucasian women with no CHD risk factors will need to be performed. METHODS: Sera from AA and Caucasian women with no CHD risk factors will be collected from the same location. Cholesterol efflux from macrophage foam cells and hydrogen peroxide release induced by tumor necrosis factor alpha (TNFα) will be used to measure how well the sera protect against atherosclerosis development. EXPECTED RESULTS: If genetic or environmental factors contribute to the higher CHD in AA, their sera will be less effective at promoting cholesterol efflux and suppressing hydrogen peroxide release.

11.02.002

INHIBITION OF TRANSENDOTHELIAL LDL TRANSPORT BY APOAI

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Transport of lipoproteins across endothelial cells involves membrane binding, endocytosis, and exocytosis. This study investigated the effect of apolipoprotein (apo) AI on endothelial binding, uptake and transcellular transport of apoB-carrying lipoproteins (apoB-LPs). We cultured mouse aortic endothelial cells (MAECs) in a transwell insert, and treated with apoAI and apoB-LPs in the apical side. Our data demonstrated that apoAI enhanced the amount of 125I-labeled apoB-LPs bound to the apical membrane of the MAEC monolayer by ~42%, but reduced the apical-basolateral transport of these lipoproteins by ~32%. In addition, apoAI reduced the amount of 3H-cholesterol- and 125I-labled apoB-LPs accumulated in the MAECs by ~62% and 47%, respectively. We also observed that treatment of MAECs with apoAI upregulated ATP-binding cassette transport A1 (ABCA1) expression. It has been suggested that transcytosis of apoB-LPs through endothelial cells is mediated by caveolae-associated receptors, and that ABCA1 induces redistribution of caveolae-associated proteins to the non-raft areas in the plasma membrane. We are studying whether redistribution of caveolae-associated receptors is responsible for the observed apoAI-induced changes in endothelial binding, uptake and transcytosis of apoB-LPs.

11.02.003

FORMATION OF APOE-CARRYING HDL PARTICLE IN ENDOTHELIAL CELL

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Passage of plasma triglyceride-rich lipoproteins (TRLs) and low-density lipoproteins (LDLs) through the monolayer endothelium occurs in normal and atherosclerotic arteries. The current report studied the effect of transendothelial transport on the density distribution of TRL- and LDL-associated cholesterol and apolipoproteins (apo). Our data indicated that the 3H-cholesterol and 125I-apoE in the TRLs and LDLs that were not incubated with the mouse aortic endothelial cell (MAEC) monolayer distributed primarily in the low density (LD) fractions (d: ≤1.063). In contrast, a substantial portion of the 3H-cholesterol and 125I-apoE that had passed through the MAEC monolayer were allotted into the high density (HD) (d: ≥1.063) fractions. ApoB protein was detectable only in the LD fractions before or after TRLs or LDLs were incubated with the MAEC monolayer. Inhibition of caveolae-dependent endocytosis reduced the transendothelial transport of TRLs and LDLs and its associated apoE-carrying HD particle formation. These suggest that TRLs and LDLs pass through the MAEC monolayer in the forms of apoB-carrying LD particles and apoE-carrying HD particles.

11.02.004

PPARa AND PHD2 PROTEINS WITH AKT/FOXO GENES IN HYPERTENSION

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TEXAS SOUTHERN UNIVERSITY

PURPOSE: Prolyl hydroxylase (PHD) and peroxisome proliferator activated receptor (PPAR)a, known "sensors" of cellular energy and/or oxygen and have been demonstrated to mitigate against oxidative stress, inflammation and fibrosis in cardiorenal pathologies. However, it is not fully known if any commonality exists in their mechanisms of action. This study evaluated the role of Akt/Forkhead box protein FOXO pathway as a possible common target for both PHD and PPARa. METHODS: Rats were uninephrectomized and treated with DOCA and 1% NaCl to induce hypertension.

RESULT: Hypertension was accompanied by cardiac/renal hypertrophy (P<0.05) and marked proteinuria (P<0.01). Accompanying these effects were increases in the expression of TGFb (72+/-14%), a marker of fibrosis, p65 (60+/-7%), an index of inflammation, pAkt (82+/-10%), a key signaling protein in cellular function, and PHD2 (90+/-8%), an index of hypoxia but reduced expression of FOXO1 (27+/-4%) and PPARa (27+/-6%). Clofibrate, a PPARa ligand, attenuated the hypertension (P<0.05), organ hypertrophy and proteinuria (P<0.05) and blunted the expression of PHD2 (45+6%, P<0.05), pAKt (66+/-4%, P<0.05), TGFb (P<0.05) and p65 (P<0.05) without changes in MnSOD expression. Combined administration of clofibrate and DMOG, the inhibitor of PHD, exacerbated these effects. DISCUSSION/CONCLUSION These data suggest that FOXO proteins may compliment the activities of PPARa. Moreover, PPARa activation and PHD2 inhibition resulted in similar signaling mechanisms and that combined PPARa activation and PHD2 inhibition may constitute a more effective therapeutic approach in the management of hypertension.

11.02.005

MECHANISMS OF PPARa/PHD INTERACTIONS IN RENAL FIBROSIS

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PURPOSE Peroxisome proliferator activated receptor (PPAR) and prolyl hydroxylase domain-containing protein (PHD), "sensors" of cellular energy and oxygen have protective effects in the kidney and potentially act in a complimentarily but the mechanisms involved are not fully known. This study examined PPARa and its interaction with PHD. METHODS Renal fibrosis was induced in PPARa WT and KO mice by unilateral ureteral obstruction (UUO) in the presence or absence of dimethyl oxallyl glycine (DMOG), a PHD inhibitor. RESULTS UUO increased hydroxyl proline in PPARa WT and KO kidneys (P<0.05) but to a greater extent in KO kidneys. DMOG, a PHD inhibitor, markedly blunted the effect only in WT kidneys (P<0.05). TGFb expression was also increased (~ 3-fold, P<0.05) in both WT and KO kidneys. However, DMOG blunted UUO-induced increase in TGFb expression only in WT kidneys (P<0.05). Bilirubin, an index of heme oxygenase activity, was lower in KO kidneys at basal level (P<0.05) and was reduced in WT kidneys (P<0.05) following UUO but paradoxically increased in KO kidneys (P<0.05). DMOG blunted the reduction in bilirubin in WT (P<0.05) but was without effect in KO kidneys. Serum arginase activity, an index of cellular content of L-Arginine, was increased in WT mice (P<0.05) but there was no change in KO mice following UUO. DMOG abolished the effect in WT but not KO mice. DISCUSSION/CONCLUSION These data suggest that PPARa plays a protective role against UUO that appears to be coupled to PHD proteins by mechanisms related to heme oxygenase and arginase.

11.02.006

STRUCTURAL BASIS FOR MELANOCORTIN 3-RECEPTOR FUNCTION

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PURPOSE: Hypertension is highly prevalent in African Americans and a leading cause of preventable cardiovascular and kidney diseases. Whereas many socioeconomic factors directly contribute to hypertension related health disparities, there is still a need to develop new therapies as many patients who are under treatment fail to reach safe levels of blood pressure. This study seeks to determine the molecular mechanisms of function of melanocortin 3-receptor (MC3R), which is implicated in energy metabolism and cardiovascular function. METHODS: MC3R models were generated with the software packages Modeller and I-TASSER or obtained from the databases G-protein-coupled receptors database (GPCRd) and GPCR-Sequence-Structure-Feature-Extractor (GPCR-SSFE 2.0). Ligand coordinates were generated ab initio with Spartan software. Docking was conducted with DOCK6 software. Molecular dynamics simulations were conducted with NAMD software. Molecular visualization and analysis of trajectories was conducted with the software packages UCSF-Chimera and VMD.RESULTS: DOCK6 results demonstrate the binding of melanotan II (MTII), a pharmacological MC3R agonist, in the proximity of MC3R transmembrane helices (TM) 2 and 3 and likely contacting other residues in the second and third extracellular loops. These contacts remained stable over 10 ns of molecular dynamics simulation. Interestingly, some pathological MC3R mutations map to regions in TM2 and TM3. DISCUSSION / CONCLUSION: DOCK6 simulations identified amino acid residues that likely interact with MTII and that are consistent with literature reports that used mutagenesis approaches to study MC3R-ligand interactions. The simulations identified additional residues that require further investigation. Subject to experimental validation, this approach appears feasible for optimizing ligands for MC3R.

11.03.001

GLOBAL GENE EXPRESSION OF DIABETES IN A PAKISTANI POPULATION

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PURPOSE: The epidemic of Type 2 Diabetes Mellitus (T2DM) has burdened South-East Asian populations, including Pakistan with a dramatic increase to 7.4 million cases in 2017. Little is known about the underlying gene expression of T2DM in patients from this vulnerable population. A comprehensive analysis of gene expression is therefore warranted. METHODS: Differential gene expressions (Affymetrix Array) coupled with Pathway Analysis (IPA) were performed for the TSDM group compared to healthy controls (n=3 in each group) from a previously recruited cohort from Pakistan. High-throughput qPCR Taqman Low Density Arrays (TLDA) were performed on a pre-designed array (TaqMan® Array, Human Diabetes, 96 Genes), and results were analyzed to compare these two groups. RESULTS: The pathway analysis with differentially expressed genes (N=1635, > 2 fold change: up/down-regulated) reveal B Cell Development (impaired glucose metabolism), Lipid Antigen Presentation by CD1 (cellular trafficking of lipid antigens), GADD45 Signaling (Stress), Altered T Cell and B Cell Signaling (Autoimmunity), and DNA Methylation and Transcriptional Repression Signaling (epigenetic modification) as the top canonical pathways (p value <0.0001). The diabetes profiler array shows that CSNK1A1, CSNK1D, CYP45A1, GAP43, APOE, GJB1, GSK3B, GRIN2A & 2B are the down-regulated genes, and NAE1, SLC30A3, SLC18A3, CDC2, APLP1, APBB2, IL1A are up-regulated. DISCUSSION: The pathways and the genes identified through IPA pathway analysis and profiler array may aid in developing improved biomarkers characterizing the populations developing diabetes. The outcome of the current and future results will help us to understand pathogenic mechanisms and identify future disease risks in such vulnerable populations.

11.03.002

IMPACT OF MATERNAL OVER- VS. UNDERNUTRITION ON THE OFFSPRING

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Similarities in offspring phenotype due to fetal exposure to maternal under- and over-nutrition during gestation have been observed in studies conducted at University of Wyoming utilizing sheep models of maternal nutrient restriction and obesity. In these studies, ewes either received 50% of National Research Council (NRC) requirements (nutrient-restricted, NR) from early to mid-gestation, and then 100% NRC requirements from mid-gestation to term, or were fed 150% of NRC requirements (obese, MO) from 60 days before conception and continuing through term. Fetuses were collected from some ewes of each nutritional group at mid gestation and late gestation, with the remaining ewes in each group allowed to lamb. At mid gestation, of NR fetuses were ~30% lighter than control fetuses, whereas MO fetuses were ~30% heavier than those of control ewes. By term, however, birth-weight of lambs born to NR and MO ewes were similar to that of lambs born to control ewes. This resulted from an acceleration of fetal growth from mid gestation to term in NR ewes, but a reduced rate of fetal growth over this period in MO ewes when compared to their respective control ewes. These fetal growth patterns resulted in remarkably similar effects of increased susceptibility to obesity, cardiovascular disease and glucose intolerance in offspring programmed mostly during fetal stages of development. These data provide evidence that maternal under- and /or over-nutrition can alter offspring phenotype in a similar manner, resulting in the appearance of the same cadre of physical and metabolic problems in postnatal life.

11.03.003

CENTER FOR HEALTH DISPARITIES RESEARCH (NCCU-RCHDR)

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North Carolina Central University

PURPOSE: North Carolina Central University (NCCU) established a RCMI - Center for Health Disparities Research (RCHDR) to conduct cutting edge research to address health disparities. The Center is the first and only RCMI in the state of North Carolina. METHODS: The RCHDR is a collaborative effort within multiple NCCU units and focuses on bridging basic and behavioral biomedical research. The Center leverages resources and partnerships at neighboring institutions in the Research Triangle area, community based organizations and the nationwide RTRN to advance cutting edge health disparities research at NCCU. RESULTS: (1) three innovative and significant research projects have been established with a strong focus on disparities and metabolic diseases; (2) we have developed strong research infrastructure and community engagement cores where investigators have access to cutting-edge resources for basic/biomedical and behavioral sciences; (3) to support all levels of investigators to become successful extramurally funded health disparities researchers, an Investigator Development Core has been established that has currently supported the development and funding of 5 pilot projects from early stage biomedical and behavioral researchers focused on health disparities, each supported by an experienced faculty mentor; (4) RCHDR has offered career enhancement activities, in particular, grant workshops. An annual retreat has been used as a forum to promote a collaborative environment between biomedical and behavioral scientists. DISCUSSION/CONCLUSION: Leveraging the existing biomedical commitment of NCCU and establishing an

integrated RCMI Center at NCCU is significantly enhancing the research capacity at this HBCU and driving it towards achieving its mission of addressing health disparities.

11.03.004

EPIGENETIC CHANGES IN BETA CELLS IN THE ETIOLOGY OF DIABETES

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Diabetes mellitus is a condition in which either the pancreas does not produce enough insulin, or the cells of the body do not respond properly to the insulin produced, resulting in high levels of sugar in the bloodstream. We hypothesized that epigenetic changes in pancreatic beta cells in the pancreas, the main insulin-producing cells in the body, may contribute to the etiology of diabetes. To test this hypothesis, we treated human pancreatic beta cells derived from induced pluripotent stem cells (iPSCs) with either high (30 mM) or low (2 mM) glucose for 14 days. We found epigenetic changes in over one thousand genes, including those involved in many signaling pathways, especially glucose metabolism and insulin secretion. Other pathways affected were those involved in oxytocin metabolism, gastric acid secretion, calcium signaling, and adrenergic signaling. Our study suggests that diabetes may, at least in part, be caused by epigenetic changes in pancreatic beta cells.

11.03.005

SUPPORTING NHH W/ COMMUNITY BASED SOCIAL BIOMEDICAL RESEARCH

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PURPOSE: Research indicates that Native Hawaiians have the highest rates of diabetes and obesity in the state of Hawai'i. Understanding the way epigenetics plays a role in Type 2 Diabetes (T2DM) will help us determine how environmental factors play a role in the risk of T2DM in Native Hawaiian populations. Our objectives with this study are:(1) Understand the relationship between social context and health; (2) Learn about the mechanism through which a community-based program impacted health/wellbeing of Native Hawaiians; (3) Consider a new model of community-engaged research that empowers individuals and organizations to address health disparities. METHODS: The study targeted individuals (16 years or older) in the state of Hawai'i affiliated with MA'O organic farms or connected to their social network. Stool sample kits were distributed to participants with oral and written instructions to collect their own samples at home and store them in a freezer until they can be returned via mail or collected by a community research facilitator for analysis. Stool samples were used to metagenomics analysis. Height, weight, blood pressure, pulse and A1C were measured and recorded. RESULTS: Results of this study show that main bacteria were dominant in Native Hawaiians (Bacteroidetes, Firmicutes, Proteobacteria, Actinobacteria). Actinobacteria and Proteobacteria were significantly correlated with BMI and A1c in Native Hawaiians. In the overall study population, there is a statistically significant negative correlation between A1c and the abundance of Actinobacteria (ρ= -0.169; CI = 90%) and Proteobacteria (ρ= -0.212; CI=95%). In the same group of participants, BMI is negatively correlated with the abundance of Actinobacteria (ρ= -0.222; CI=95%). The results also show the impact of social networks on the health/wellbeing of the individuals. DISCUSSION/CONCLUSION: Our project integrates social and biomedical research in evaluating a holistic community-based program on the health/wellbeing of Native Hawaiian youth and their social networks. Social networks influence individuals' choices and behaviors that either lead to unhealthy or healthy lifestyles. These networks have been shown to affect a wide range of obesity-related cardiometabolic health conditions, including Type 2 diabetes mellitus (DM), that are prevalent in Native Hawaiians. Recent studies suggest a link between social networks and health conditions that are likely mediated by biological mechanisms influencing glucose homeostasis and gut microbiome composition. Results from our study reveal insight into this mechanism that supports Native Hawaiian health in a community-based program. Our project will conclude with a description of a new model of community-engaged research that is currently being developed to facilitate the collection and sharing of social and biomedical data driven by community-based organizations to ultimately promote Native Hawaiian health.

11.03.006

DOES T.FOENUM-GRAECUM (FENUGREEK) INHIBIT ALPHA-GLUCOSIDASE

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Diabetes is a chronic, metabolic disease characterized by elevated levels of blood glucose which leads over time to serious complications. The incidence of diabetes has risen dramatically globally, and it is the 7th leading cause of death in the United States. Type 2 diabetes contributes to majority of diabetic cases. Despite the effort made with insulin and other oral hypoglycemic drugs, the search continues for newer drugs because some drugs used currently have several limitations

including Acarbose, already in the market as an antidiabetic. This drug works by competitively inhibiting alpha-glucosidase, an enzyme in the brush border of the small intestine, which delays the breakdown and absorption of complex carbohydrates. Fenugreek (T. foenum-graecum), has been reported to exhibit glucose lowering effect on type 2 diabetes. PURPOSE: The aim of this study was to examine if fenugreek produces antidiabetic activity by inhibiting alpha-glucose. METHOD: The inhibitory effect of different concentrations of the Fenugreek extract on alpha- glucosidase (from Bacillus) was examined in vitro in a 96-well micro titer plate. It was determined on a spectrophotometer at 400nm using Acarbose as the positive control. RESULTS: Acarbose produced a dose-dependent inhibition of alpha-glucosidase whereas no inhibition of alpha-glucosidase was observed with Fenugreek. DISCUSSION/CONCLUSION: Acarbose was used in its pure form. It is already marketed as an antidiabetic. Crude extract of Fenugreek was used. Further work on fenugreek will include isolation, purification and characterization of active components in order to enhance its potential as a novel agent for diabetes therapy.

11.04.001

TARGETING NONCODING RNA EXPRESSION BY CURCUMIN IN HUMAN ESCS

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PURPOSE Endometriosis is a benign estrogen dependent chronic gynecological inflammatory disorder with immune system dysregulation. Current agency-approved hormonal therapies, including synthetic progestins, GnRH-agonists, and danazol are often of limited efficacy and counterproductive to fertility, and cause systemic side effects due to suppression of endogenous steroid hormone production. Curcumin (diferuloylmethane, CUR), an anti-inflammatory Asian herb, has potential to reduce inflammation. METHODS Therefore, in the current studies we examined the effects of CUR at different doses over a time course in the regulation of proinflammatory and proangiogenic non-coding RNAs (microRNAs) in primary cultures of normal endometrial stromal cells (NESC) and cells derived from eutopic endometrium of endometriosis subjects (EESC). miRNAs are non-coding RNAs that regulate protein translation and have been shown to be involved in the pathogenesis of endometriosis. RESULTS Using semi-quantitative RT-PCR and NanoString nCounter-based assays we have identified levels of several proinflammatory and proangiogenic miRNAs that are higher in EESC compared to NESC. EESC and NESC treatment with CUR significantly reduced expression of proinflammatory and proangiogenic miRNAs in a dose- and time-dependent manner. Moreover, CUR significantly decreased phosphorylation of the AKT, ERK and prohibitin signaling pathways. CONCLUSIONS These findings demonstrate higher proinflammatory and proangiogenic miRNA production in EESC compared to NESC under basal conditions and suggest that CUR has the potential to reduce inflammation associated with endometriosis.

11.04.003

PROSTATE CANCER ADAPTATION AND SURVIVAL TO OXIDATIVE STRESS

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PURPOSE: Inadequate nutrient intake leads to oxidative stress disrupting homeostasis, activating signaling, and altering metabolism. Oxidative stress is a hallmark observed in developing prostate lesions and an aggressive cancer phenotype activating mechanisms allowing cancer cells to adapt and survive; however, it is unclear how adaptation and survival are facilitated. Literature demonstrates that quiescence and nuclear factor-kappaB (NF-κB) contribute to cancer cell survival and therapeutic resistance during oxidative stress. Our preliminary data revealed serum deprivation induced reactive oxygen species (ROS) and stressed cells displayed no significant apoptosis suggesting an adaptive mechanism to tolerate oxidative stress; therefore, we hypothesize adaptation and survival during oxidative stress is contingent upon a quiescent phenotype and NF-κB nuclear translocation. METHODS: Using DU145 prostate cancer cells as a model, we used phase-contrast microscopy and WB to examine quiescent cell characteristics. NF-κB/p65 and p27Kip1 nuclear localization were evaluated by fractionation and/or immunocytochemistry. Quiescence inhibitors targeting Mirk/Dyrk1b (AZ191 and NCGC00185981-05/ML195) were used to evaluate p27Kip1 localization via immunocytochemistry. We transiently silenced NF-κB/p65 and examined cell death via apoptosis. RESULTS: We observed DU145 cells cultured without serum and serum-deprived cells with the addition of hydrogen peroxide (H2O2) displayed a quiescent morphology accompanied by changes in the expression of quiescent markers. Furthermore, we detected nuclear accumulation of NF-κB/p65 and p27Kip1 in our samples. AZ191 and NCGC00185981-05/ML195 quiescence inhibitors prevented NF-κB/p65 localization in stressed cells and silencing NF-κB/p65 significantly increased apoptosis. DISCUSSION: Our data suggests that nutrient deprivation primes prostate cancer cells for adaptability to oxidative stress and/or a general survival mechanism to anti-tumorigenic agents.

11.04.004

YIN YANG 1 MEDIATES MANGANESE-INDUCED LRRK2 IN MICROGLIA

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PURPOSE: Chronic exposure to manganese (Mn) causes a neurological disorder similar to Parkinson's disease (PD) referred to as manganism. Mn toxicity can occur in a variety of occupational and environmental settings that are closely associated with health disparities. Leucine-rich repeat kinase 2 (LRRK2) and its genetic mutations are linked to PD and can be found in Lewy bodies, a pathogenic hallmark of PD. LRRK2 also plays a role in Mn toxicity in microglia. However, molecular mechanisms of Mn toxicity are not well understood. In this study, we aimed to test if transcription factor yin yang 1 (YY1) is critical for Mn-activated LRRK2-mediated toxicity in microglia. METHODS: Using the human microglial cells (HMC3) as a model, luciferase assay for promoter activity, qPCR for mRNA levels, Western blot for protein levels, flow cytometry for apoptosis assay, ELISA for proinflammatory cytokines. RESULTS: Mn increased LRRK2 expression in microglia. Mn activated YY1 expression, which increased LRRK2 promoter activity, mRNA and protein levels in HMC3. Several putative YY1 binding sites were identified in the LRRK2 promoter region. Mn increased YY1 via oxidative stress and NF-κB activation in microglia. These indicate that Mn increases LRRK2 via YY1, resulting in LRRK2 kinase hyperactivity leading to microglial impairment. DISCUSSION/CONCLUSION: Mn activation of LRRK2 via Mn-oxidative stress/NF-κB-YY1 signaling provides a new pathway in Mn-activated LRRK2-mediated toxicity in microglia. These suggest the interplay of environmental toxicant Mn and LRRK2, a genetic risk factor for PD, via YY1 which serves as a potential target for attenuating Mn toxicity or PD pathogenesis.

11.04.006

ROLE OF KLF6 IN THE REGULATION OF PROLIDASE TRANSCRIPTION

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Prolidase (Peptidase D), encoded by the PEPD gene, is a ubiquitously expressed cytosolic dipeptidase and a member of the matrix metalloproteinase (MMP) family. Prolidase is the only enzyme capable of cleaving imidodipeptides containing a C-terminal proline or hydroxyproline, thus playing critical roles in protein metabolism, matrix remodeling, and collagen turnover. Accordingly, prolidase is essential in several physiological and pathological processes such as carcinogenesis, inflammation, angiogenesis, cell proliferation, and wound healing. Surprisingly, little is known about the molecular and cellular regulation of PEPD gene expression. In initial studies, we carried out in silico analyses of the PEPD promoter using TRANSFAC to identify binding sites for transcription factors. Analyses identified KLF6 (Kruppel-like Factor 6) as a putative transcription factor that may be important in the transcriptional regulation of prolidase. KLF6 is regulated by TGF-β and plays an important role in collagen turnover and wound healing. To study the transcriptional regulation of prolidase, we cloned and characterized the human PEPD promoter PEPD promoter was amplified from the human genome and inserted into a luciferase reporter construct. We conducted transfection experiments using the luciferase reporter and promoter mutational studies revealed that KLF6 transcriptionally regulates PEPD transcription. These results will generate new knowledge on the molecular regulation of prolidase and aid in developing therapeutic approaches to regulate prolidase expression in various physiological and pathological conditions such as wound healing.

11.05.002

HIV-1 DNA INTEGRASE DRUG RESISTANCE MUTATIONS IN PUERTO RICO

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PURPOSE: Antiretroviral therapy (ART), including integrase strand transfer inhibitors (INSTIs), has been recommended as a first-line and as rescue therapy for HIV-1+ patients. As INSTIs have been used in Puerto Rico (PR) for several years, we aim to determine the prevalence of drug resistance mutations (DRMs) to INSTIs in PR. METHODS: Integrase sequences (n=185) comprising the period from 2016-2019 were analyzed for DRMs. HIV-1 pro-viral DNA and RNA were extracted from whole blood and plasma, respectively. The integrase gene was amplified using our WHO-accredited HIV-1 RNA genotyping protocol and a modified nested PCR for DNA. Sequences were obtained using an ABI 3730xl sequencer. We used the Stanford HIV Drug Resistance Database for genotypic resistance interpretation. RESULTS: Of the 185 DNA integrase sequences analyzed, six (3.3%) contained INSTI DRM. We detected the following major DRMs: G140S, Q148H, E138K, and R263K. No other major or accessory DRMs were detected in DNA-derived sequences. For these patients, DNA genotyping of protease and reverse transcriptase was also available. Comparing population DNA

and RNA integrase sequences (n=171), we found only 4.3% of DNA integrase sequences showed DRMs compared to 7.6% of RNA sequences from the same period (2016-2019). We did not detect accessory mutations in DNA-derived integrase sequences. CONCLUSION: Despite their low frequency, identified INSTIs DRM in the HIV-1 integrase latent reservoir are major DRMs and include some associated with intermediate resistance to Dolutegravir. This study underscores the importance of continued genotypic monitoring. The clinical significance of the resistance mutations in the latent reservoir remains unclear.

11.05.003

PROTEOMICS OF NEURONS EXPOSED TO HIV-MDM SUPERNATANTS

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PURPOSE: HIV-1 infects monocyte-derived macrophages (MDM) that cross the blood-brain barrier to the central nervous system facilitating neuronal damage and inducing HIV neurocognitive disorders (HAND). HIV-infected MDM secrete neurotoxic factors, apoptosis and neuronal damage. One of these secreted factors is Cathepsin B (CATB), a lysosomal cysteine protease that plays an important role in neurodegeneration. CATB interacts with Serum amyloid P component (SAPC) contributing to HIV-induced neurotoxicity. However, the mechanisms that trigger CATB and SAPC neuronal apoptosis remain unknown. METHODS: We aimed to elucidate changes on apoptotic intracellular pathways on neurons exposed to HIV-infected macrophage supernatants after antibody inhibition of CATB or SAPC using Tandem Mass Tag (TMT) quantitative proteomics analyses. RESULTS: Based on significant fold change (FC) ≥ |2| and p-value ≤ 0.05 criteria a total of 10 and 13 proteins were deregulated after CATB and SAPC inhibition respectively. Antibodies against CATB and SAPC downregulated two common apoptosis related proteins: Cyclophilin A (CYPA) and Tubulin alpha-1A (TUBA1). DISCUSSION: Quantitative proteomics analyses revealed that antibodies against CATB/SAPC secreted by HIV-infected MDM can reverse common and unique apoptotic pathways that deserve further studies as potential targets against HIV-induced neuronal degeneration.

11.05.004

SCREENING SMALL MOLECULE INHIBITING HIV-1 NOVEL VIF FUNCTION

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PURPOSE: Human immunodeficiency virus type 1 (HIV-1) encodes a Vif protein, which is important for virus replication and infectivity. Traditionally, it was believed that the predominant function of Vif was to counteract Apolipoprotein B mRNA-editing enzyme-catalytic polypeptide-like 3G (APOBEC3G, A3G), a potent host restriction factor that inhibits HIV-1 replication through the proteasomal degradation pathway. In our recent study, we show that Vif not only induces A3G for degradation but also directly inhibits A3G cytidine deaminase activity (CDA) in a degradation independent manner, which represents a potential target for novel anti-HIV drug development. METHODS: We developed a novel high throughput screening (HTS) assay targeting Vif's function on inhibiting A3G CDA activity. RESULTS: Subsequent high throughput screening studies selected a small molecule, Compound 5, which dramatically inhibited Vif function and restored A3G CDA. Viral infectivity assay showed that Compound 5 is a very potent HIV inhibitor with IC90 in the low micromolar range. Compound 5 also enhanced G to A hypermutation in HIV viral cDNA, which is a hallmark for A3G antiviral function. DISCUSSION/CONCLUSION: This study has not only shed light on the development of a novel anti-HIV strategy, but also proved the concept that inhibiting A3G CDA is a very important function of Vif.

11.05.005

NOVEL HIV-1 TRANSCRIPTION INHIBITORS TARGETING TAR RNA

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Current antiretroviral therapy is able to control HIV-1 infection but does not prevent HIV-1 reactivation from latent HIV-1 provirus. HIV-1 Tat protein interacts with TAR RNA and recruits CDK9/cyclin T1 and other factors to induce HIV-1 transcription. Here we searched for inhibitors of Tat-TAR RNA interaction, which is essential for HIV-1 transcription activation. A pharmacophore model was created using a crystal structure of TAR RNA with bound acetylpromazine ((PDB structure 1LVJ). Enamine database containing 1.6 million individual compounds was used to select 21,343 compounds that were docked to the pharmacophore model using QXP software. The resulting 2300 compounds were evaluated for HIV-1 transcription inhibition in 293T cells transfected with HIV-1 LTR expressing luciferase and HIV-1 Tat expressing vector. Selected 177 compounds were further tested for inhibition of one round HIV-1 infection in CEM T-cells. Top ten inhibitory compounds (IC50 < 6 μM) were further tested for toxicity and three compounds, T107 (IC50 = 4.7 μM), T48 (IC50 = 0.4 μM) and T88 (IC50 = 5.5 μM) were selected. These compounds were further tested

for HIV-1 transcription inhibition in 293T cell and showed inhibition of Tat-dependent transcription. Also compounds T48 showed significant inhibition of HIV-1 gag expression in CEM-T cells infected with HIV-1IIIB virus. None of the compounds had an effect on Tat-CDK9/cyclin T1 interaction or decreased Tat expression. Finally, compound T48 disrupted Tat-TAR RNA interaction. Taken together, our study identified novel compound T48 that targets HIV-1 transcription and may serve as a new lead for anti-HIV-1 therapeutics.

11.05.007

HEALTH DISPARITIES AMONG WOMEN LIVING WITH HIV AND DEPRESSIO

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PURPOSE: The objective is to examine the significance of prescribing antidepressant medications for HIV positive women with depressive symptoms on HIV RNA viral load. The purpose of this research is to determine if an HIV positive woman with depressive symptoms is more likely to experience virologic failure or virologic suppression if prescribed antidepressant medications. It is hypothesized that a patient is less likely to experience virologic failure if the medication regimen includes a type of antidepressant drugs and more likely to experience virologic failure if the medication regimen does not include a type of antidepressant drugs. METHODS: This study uses a descriptive methodology to compare the HIV RNA viral load to HIV positive women with depressive symptoms that are prescribed antidepressant medications, utilizing secondary data from the Women Interagency HIV Study data. The Women's Interagency HIV Study (WIHS) is an ongoing long-term observational study of 3,772 HIV positive and negative women. The inclusion criteria consist of HIV positive women with self-reported depressive symptoms, receiving clinical care at the Miami Florida clinical site during 2013-2018. An inferential statistics t-test will determine if there is a statistical significance in HIV RNA viral load and prescribing antidepressant medications. EXPECTED RESULTS: Findings can assist policy makers and stakeholders by identifying the effects of mental health treatment in HIV care that lead to increased mortality to improve health outcomes for women in the South Florida.

11.05.008

NEUROTOXICITY OF HIV-1 INTEGRASE INHIBITORS

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In spite of the success of combination antiretroviral drug therapy (cART), approximately 50% of HIV-1 infected patients continue to face a wide spectrum of behavioral, cognitive, and motor dysfunctions characterized as HIV-1-associated neurocognitive disorder (HAND). Importantly, potential toxicity of antiretroviral drugs in the central nervous system (CNS) remains remarkably underexplored and may contribute to the persistence of HAND in the cART era. Although antiviral drugs that target reverse transcription and maturation steps of the HIV-1 life cycle have been shown to cause neurotoxicity, molecular and cellular effects of integrase inhibitors on neurotoxicity are poorly understand. This is critical given that HIV-1 integration is a key barrier to develop strategies for a cure for HIV/AIDS. Viral DNA integration into the host chromosomal DNA is essential for productive infection. Integrase inhibitors, also known as integrase strand transfer inhibitors (INSTIs), are a new class of antiretroviral drugs that inhibit HIV-1 integrase, the viral enzyme that inserts the viral genome into the host chromosomes. Currently, there are three integrase inhibitors available, Raltegravir, Dolutegravir and Elvitegravir. Moreover, there is accumulating evidence that some of the new integrase inhibitors (specifically dolutegravir) cause CNS problems. The goal of this study is to understand the effects of HIV-1 integrase inhibitors on neurotoxicity. Using a differentiated neuronal cell model, we have investigated the effects of the integrase inhibitors on neuronal function. The data generated from these studies will help us better understand how these new class of anti-retrovirals affect neuronal health.

11.05.009

DISPARITIES IN HOSPITAL ADMITTANCE AMONG PERSONS LIVING WITH

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BACKGROUND: Racial/ethnic disparities have been widely documented for those receiving or accessing primary outpatient services and for persons needing inpatient care. In Florida, it is reported that nearly 30% of persons living with HIV were reported not receiving HIV related care in Florida. OBJECTIVE: The objective of this study was to determine the reasons for hospital admissions of persons living with HIV (PLWH) and the outcome of these admissions and evaluate the relative health disparities. METHODS: Retrospective review of hospital discharge data of PLWH that are admitted to the hospital in Florida from 2015-2017. Abstracted data will include age, gender, weight, presenting conditions, diagnosis, duration of hospitalization, antiretroviral treatment, and outcome. Bivariate and Multivariate analysis will be performed to determine association and disparities among race, ethnicity, age, sex and payer. Admissions will be classified as HIV- or non-HIV-related

using International Classification of Diseases, 10th revisions (ICD-10) codes. CONCLUSIONS: Findings are likely to suggest there are disparities among racial/ethnic populations that obtain care at hospitals due to barriers to medical care among minority populations in Florida.

11.05.010

CHROMATIN EPIGENETICS ALTER HIV-1 INTEGRATION TARGETING

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Productive HIV-1 infection requires integration of the viral DNA into the host genome. Accordingly, HIV-1 integration is a major target for anti-retroviral therapy. In HIV-infected cells, the preintegration complex (PIC), containing the viral DNA and viral/host proteins, carries out integration. Even though the PIC facilitates targeted integration of the viral DNA into actively transcribing genes, the underlying mechanism remains largely unclear. Here we employed a biochemical approach to assess HIV-1 PIC-mediated integration into specific target DNA substrates. We observed that chromatin is a better substrate for PIC-associated integration compared to naked genomic DNA. Since chromatin is constituted of nucleosomes, we tested if DNA associated with nucleosomes were responsible for the enhanced integration seen in chromatin. Surprisingly, PIC-mediated integration in nucleosomes was reduced, suggesting a role for epigenetic factors in facilitating integration. We tested the effects of epigenetic histone modifications on PIC-associated integration, because HIV-1 integration hotspots are associated with specific histone modifications. Upon using modified nucleosomes that contain specific histone modifications, we observed enhanced integration of HIV-1 DNA compared to unmodified nucleosomes. Further investigation supported that this enhanced integration is independent of the viral-encoded integrase. We then show that the host factor LEDGF/p75, reported to promote retroviral integration, exerts a DNA length dependent mechanism for enhanced integration in nucleosomes. Collectively, our study supports a key role of nucleosome structure in HIV-1 integration, providing novel biochemical insights into viral-host interactions.

11.05.011

ARF1 IS NOT REQUIRED FOR TETHERIN ANTI-HIV ACTIVITIES

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ADP-ribosylation factor 1 (Arf-1) regulates membrane traffic and acts as a co-factor in retrovirus assembly and release. It has been well known that innate host restriction factor tetherin inhibits HIV-1 release through a direct tethering mechanism. To understand molecular events involved in late stages of the HIV-1 life cycle, we studies the role of the Arf-1 protein in tetherin trafficking pathways as well as tetherin anti-HIV activities. Using a dominant-negative approach, we were able to impair the Arf1-mediated trafficking pathway in transformed cells. Our results showed that the disruption of the Arf-1 pathway reduced the release of VLP (virus-like-particle) derived from HIV-1 Gag, HIV-1 Gag-Pol, and HIV-1 NL4-3. However, this treatment did not alter the efficiency of HIV-1 Gag association with membrane structures. Furthermore, impaired Arf-1 function did not alter tetherin expression levels and tetherin subcellular location associated with tetherin anti-HIV activities. All these data indicate that Arf1-modulated HIV-1 assembly and release is independent of tetherin-mediated inhibition. Our studies provide new insights into host-HIV interactions involved in particle assembly and release.

11.05.012

NEW DRUG TARGETS FOR HIV DRUG DELIVERY

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Sexual transmission is the major mode of HIV infection in healthy humans. None of the vaginal microbicides and/or oral therapies has yet resulted in a complete protection from sexual transmission of HIV. Attachment of HIV to the human CD4+ T-cells, incorporation of viral enzymes and genetic material constitute the first steps of HIV sexual transmission. The purpose of the study is to screen the primary human CD4+ T-cells for the presence of prominent ABCC class of drug efflux transporters: Multi Drug Resistance Associated Proteins (MRPs), Pglycoprotein (P-gp) and Breast Cancer Resistance Protein (BCRP). Molecular screening was performed by RT-PCR gene expression followed by sequencing analysis. Functional screening was performed by 3H-Tenofovir uptake in the presence of specific MRP inhibitor (MK571), P-gp inhibitor (Pgp-4008) and BCRP inhibitor (Fumitrimorgin-C). Intracellular radio labeled drug concentrations were analyzed by liquid scintillation counter. Single specific PCR gene products corresponding to GAPDH, MRPs1-7, MRP9, BCRP and P-gp were observed in primary human T cells. Relative % drug uptake of tenofovir in primary human T cells in the presence of 50 μM MK571 was 173.9±5.8%), 100 μM MK571 (205.7±10.6%), 50μM Pgp4008 (215.4±9.2%) and 50 μM Fumitrimorgin (192.1±18.38%) compared to control (100±6.65%). The results, for the first time demonstrated the molecular and functional expression of multiple ABCC drug efflux transporters in primary human T cells.

11.06.001

ZIKA VIRUS (ZIKV) INFECTION CAUSED DYSREGULATION OF PERICENT

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The centrosome is a cytoplasmic un-enveloped organelle functioning as one of the microtubule organizing centers and composes of a centriole center surrounded by pericentriolar materials (PCM) granules. PCM consists of many different centrosomal proteins, such as PCM1 and centrosomal protein (CEP) 131 and is important in maintaining the stability of centrosome. Zika virus (ZIKV) belongs to the Spondweni serocomplex in the genus Flavivirus of the family Flaviviridae and replicates its RNA and viral particle in cytoplasm. Despite recent years of rigorous studies on ZIKV, it is not fully understood how ZIKV interacts with host cells during its productive infection. Here we report that ZIKV infection causes disruption and dispersion of the PCM granules. We demonstrated that PCM1 and CEP131 granules are dispersed in the ZIKV-infected cells while the centrioles remain intact. Cellular skeleton proteins were not seen to be significantly altered by ZIKV, and hence may not be involved in the interaction between ZIKV and centrosomal proteins. In research the mechanisms through which ZIKV modifies the PCM granules, we found that ZIKV infection decreases the production of PCM1 and CEP131 at protein levels, but not significantly at mRNA levels. We further found that MG132, a pan-inhibitor of protease, prevents the decrease of PCM1 and CEP131 and the dispersion of the centriolar satellites. Therefore, we hypothesize that ZIKV infection induces the proteasomal degradation of PCM1 and CEP131, leading to the disruption of the PCM granules. Supporting our hypothesis, we showed here that ZIKV infection increases the protein level of Mind Bomb 1 (Mib1) protein that was previously demonstrated to be an E3 ubiquitin ligase for PCM1 and CEP131 and that ZIKV infection fails to degrade and/or disperse PCM in Mib1-ko cells. Our results imply that ZIKV infection activates Mib1-mediated ubiquitination to degrade PCM1 and CEP131, leading to dispersion of PCM granules.

11.06.002

ZIKA VIRUS NON-STRUCTURAL PROTEIN 3 INTERACTS WITH SPIN2A

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PURPOSE: The Zika virus (ZIKV) epidemics in French Polynesia from 2013-2014, and in Brazil from 2015-2016 have been associated with congenital microcephaly of newborns born to the women infected during pregnancy. ZIKV was shown to negatively affect the proliferation of neural stem cells. One possible mechanism of ZIKV pathogenesis leading to microcephaly is induction of apoptosis and/or cell cycle arrest by modulation of functions of cellular pro- and anti- apoptotic proteins by ZIKV proteins. The ZIKV Non-Structural protein 3 (NS3) is responsible for proteolysis of the viral polyprotein as well as RNA unwinding during viral RNA replication. We identified an understudied protein, SPIN2A (also called SPIN2, or DXF34) as one of the host proteins that interact with NS3. SPIN2A is reportedly involved in cell cycle regulation. METHODS: Protein Macroaaray to identify host proteins that interact with NS3. PCR cloning of SPIN2A proteins. Immunofluorescence to examine subcellular localizations of SPIN2A proteins and their interactions with NS3. Quantitative RT-PCR (RT-qPCR) to determine the effect of ZIKV infection on SPIN2A expression. RESULTS: We identified 12 proteins that interact with NS3 including SPIN2A. Using RT-PCR, we identified and cloned 2 isoforms of SPIN2A (we named SPIN-2L and SPIN-2S). SPIN2A is identical to SPIN-2L. NS3 colocalizes with SPIN-2L but not with SPIN-2S. Both SPIN-2L and SPIN-2S colocalize with endoplasmic reticulum, clathrin, and histone 2B. RT-qPCR showed reduced expression of SPIN2A in ZIKV infected cells. CONCLUSION: Our results suggest that SPIN2A might be important for ZIKV replication and that the interaction between SPIN2A and NS3 may modulate its anti-apoptotic function.

11.06.003

TRYPANOSOMA CRUZI INFECTION INDUCES PHOSPHORYLATION OF CREB

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Trypanosoma cruzi, the etiological agent of Chagas Disease, is an obligate intracellular protozoan parasite. The parasite causes cardiac, neurological, esophageal and gastrointestinal disorders in afflicted individuals and remains incurable in the chronic stage despite ongoing research. The molecular mechanisms through which the parasite causes megacolon in some Chagasic patients remains to be elucidated. PURPOSE: Our goal is to identify whether T. cruzi can dysregulate phosphorylation levels of CREB and c-Jun, thereby affecting extracellular matrix. METHODS: Primary human colon epithelial cells were challenged with a pure population of invasive T. cruzi trypomastigotes for different time points. The parasites were washed off and the cells lysed in lysis buffer containing a cocktail

of protease, phosphatase inhibitors among others. The lysate was incubated with human phospho-protein array membrane according to the manufacturer instructions. Membranes were developed, scanned, and analyzed as described by the manufacturer. The normalized data was plotted as fold change increase in the level of phosphorylated protein. Phospho-protein array data was validated by western blot analysis and immunohistochemistry. RESULTS: Increased phosphorylation of CREB and c-Jun was displayed across all time points via phospho-proteome array and Western blot validation analysis. Immunohistochemistry illustrated nuclear co-localization of both p-CREB and p-c-Jun during the early phase of T. cruzi cellular infection. DISUCSSION: These findings suggest that increased activation and nuclear translocation p-CREB and p-c-Jun could potentially cause elevated deposition of extracellular matrix proteins. This could be important in the onset of Megacolon observed in Chagasic patients.

11.06.004

PH DEPENDENCY OF ESAT-6/CFP-10 IN VIRULENCE OF TUBERCULOSIS

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PURPOSE: In 2017, World Health Organization reported 10 million people fell ill with tuberculosis (TB) and 1.6 million died due to this disease. Despite existing vaccines and medications its one of the top 10 major death-causing disease worldwide. METHODS: The protonation states and net charges on the residues were obtained from DelPhiPKA web server. Visual Molecular Dynamics (VMD) was employed to prepare and Molecular Dynamics (MD) to simulate the complex at pH 7 and 4. The binding free energies were calculated via Molecular Mechanics and Poisson-Boltzmann Surface Area (MM/PBSA) analysis.RESULTS: In pH7 the net charge on each monomer is -5e, which should result in repulsive electrostatic forces between Early Secreted Antigen Target (ESAT-6) and Culture Filtrate Protein (CFP-10). Surprisingly, experiments demonstrate the complex forms a stable dimer at pH7. Our study revealed that even though the net charges on ESAT-6 and CFP-10 are repulsive, the complimentary charge distribution at the binding interface of ESAT-6/CFP-10 forms several salt bridges, which produces strong attractive binding forces and overcomes the repulsive forces generated by the overall net charges. Due to different protonation states of ionizable residues, at pH4, ESAT-6 becomes neutral and CFP-10 has a +1e charge. So, most of the salt bridges are lost resulting weaker electrostatic interaction. Interestingly, Van der Waal's energy becomes stronger, maintaining the binding energy on both the pH values almost the same, which supports experimental observations. CONCLUSION: By revealing the mechanisms of ESAT-6 and CFP-10 binding, this study sheds light on developing medications, vaccines, and early diagnosis.

11.06.005

PARKINSON'S DISEASE AND DENGUE VIRUS INFECTION COMMONALITIES

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PURPOSE: This work focus on Parkinson's Disease (PD) and Dengue virus infection (DENV) common gene expression changes. In Puerto Rico (PR) there are no official statistics on the number of PD patients living in the island, however, it is quite common to find people with relatives suffering PD. Searching for conditions that could explain why PD is common in PR, this study is looking into possible relations between PD and DENV using publicly available microarray datasets. DENV is endemic in Puerto Rico and has been present for several decades, with reported outbreaks since 1963. METHODS: The analysis of microarray datasets was modeled as a mathematical optimization problem, using multiple criteria optimization (MCO) formulation. RESULTS: Meta-analysis for PD (datasets GSE99039, GSE19587, GSE72267, and GSE7621) identified 13 significant genes: CRYAB, PTGDS, RPS4Y1, TUBB2A, HBA1/2, PTPRO, SEPP1, XIST, HBB, TUBA1A, PAQR6, RPS15, and TUBA1B. For the DENV analysis (dataset GSE51808) the solution list contains 73 genes. In DENV the list contains several genes coding for transcription factors as well as several zinc finger proteins. Two genes, RPS4Y1 and XIST, were common for both conditions. DISCUSSION: Some of the solution genes provide possible links between PD and DENV. Genes from the PD analysis are related to DENV, and genes from DENV's solution have been reported as important in PD. Currently we are working on the in-vitro validation of selected genes and are starting a dataset using PR patient's medical record information, to look for possible correlations between reported previous DENV and PD.

11.06.006

HEALTH DISPARITIES IN FOODBORNE DISEASES INCIDENCE RATES

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Foodborne illnesses are a major concern in the southern United States especially in Mississippi. These illnesses are a burden on public health and contribute significantly to the cost of health care. There is an urgent need to reduce or prevent the continuing problem of foodborne disease outbreaks and produce a safe food. Foodborne diseases rates vary considerably

by geographic region. This heterogeneity is likely in part due to differences in reporting. The southern parts of the United States is more vulnerable to increase outbreaks of foodborne illnesses due to socioeconomic status, climatic changes and agricultural practices. The objective of this study is to determine the trends and prevalence of Mississippi foodborne diseases, including Salmonella, E.coli, and Campylobacter, and to understand the attribution and risk factors for such high rates. Data of foodborne illnesses, including Salmonellosis, Campylobacter disease and E. coli, will be collected from the Mississippi state department of Health. Trend over time and regional differences in Mississippi in addition to socioeconomic and racial disparities impact will be examined. Data will be analyzed using SAS 9.4 to determine the trend of the data. Several modelling approaches will also be developed including Neural network (NN) to predict foodborne diseases rates. Results of this study will determine any variation in foodborne disease over the years and the high incidents rates based on socioeconomic status, age and racial differences. Predictive statistical modeling may help better understand these trends and forecast the occurrence of a disease whenever limited data is available.

11.06.007

THE EFFECT OF SHIFT WORK ON CHLAMYDIAL PATHOGENESIS

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PURPOSE: Shift work, performed by approximately 21 million Americans, is irregular or unusual work schedule hours occurring after 6:00 pm. Shift work has been shown to disrupt circadian rhythms and is associated with several adverse health outcomes and chronic disease such as cancer, gastrointestinal and psychiatric diseases and disorders. it is unclear if shift work influences the possible disease outcomes from chlamydia infection such as pelvic inflammatory disease, inflammation of the fallopian tubes and tubal factor infertility. METHODS: We used a validated jet lag model representing shift work in mice, where mice had a 6 hour advance in the normal light/dark cycle (LD) every week for a month. Control group were mice housed under normal 12/12 LD cycle. Our hypothesis was that mice that had their circadian rhythms disrupted in this jet lag model will have a higher bacterial burden, more pathology and decreased fertility rate. RESULTS: Results showed that mice that had their circadian rhythms disrupted (shifted) had a higher bacteria load, more pathology, with the oviduct being the most affected region of the genital tract, less TH1 cytokines, higher proinflammatory cytokines and lower fertility rate compared to mice under normal 12/12 LD cycle. DISCUSSION: These results imply that shift workers might have an increased likelihood of having more disease conditions arising from chlamydia infection. This work is groundbreaking and it highlights the need for shift workers to have more than the mandated checkup for sexually transmitted disease.

11.06.008

DETECTION OF FLAVIRUSES IN MOSQUITOES FROM PUERTO RICO

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PURPOSE: The genus Flavivirus comprises a group of viruses that use arthropods as vectors, such as the Aedes species mosquitoes, to infect the host. The dengue virus (DENV) and the Zika virus (ZIKV) are the two most widespread flaviviruses in Puerto Rico (PR). The latest DENV epidemic occurred in 2012, and the first locally transmitted case of ZIKV occurred on December 31, 2015. The objective of this study is to determine the capacity of the universal primers described in the literature to detect flaviviruses in mosquitoes collected in PR. METHODS: We captured mosquitoes from the south of the island and used microscopy to identify the species and sex. The mosquitoes were then dissected, homogenized, and viral RNA was extracted from the homogenates. The presence of DENV and ZIKV were determined by performing a reverse-transcriptase polymerase chain reaction (RT-PCR) using flavivirus-specific primers and confirmed by Sanger sequencing. RESULTS: The universal primers Flav100F/Flav200R failed to detect the flaviviruses. None of the modifications to the protocol led to the detection of the flaviviruses. A new set of primers was designed and tested. The new set of primers amplified samples of West Nile lineage 2, and the dengue virus serotypes 1 and 2. CONCLUSION: The reference sequences that were used to generate universal primers may not be representative of the virus present in Puerto Rico. This finding suggests the urgency to generate new sets of primers to detect the flaviviruses present on the island.

11.06.009

STAPHYLOCOCCUS AUREUS INFECTION DISPARITIES IN YUMA, ARIZONA

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PURPOSE Staphylococcus aureus is the most common cause of skin and soft tissue infections in the United States. Methicillin-Resistant S. aureus (MRSA), caused approximately 120,000 invasive infections and 20,000 deaths in 2017, but Methicillin-Sensitive S. aureus (MSSA) infections outnumber MRSA infections 3 to 1. Controlling the spread of S. aureus requires, in part, identifying segments of the population at greatest risk for infection. Like other infectious diseases, ethnic and socioeconomic disparities are associated with S. aureus infection rates. Compared to non-Hispanic whites, Hispanics in the US are at lower risk for skin and soft tissue infection, but more likely to be colonized with S. aureus. The opposite is true for Hispanics born in Mexico. We will test demographic-based hypotheses for the risk of infection in the large border town of Yuma, Arizona. METHODS In this work, we will analyze data from all cases involving S. aureus infections presenting at the Yuma Regional Medical Center between 2016 and 2019 by stratifying the cases and estimating the risk ratios. RESULTS / EXPECTED RESULTS Preliminary results on a subset of these data show a three-way interaction among age, sex, and ethnicity. Males are more likely to be infected than females. Although Hispanic males are at higher risk than non-Hispanic white males, the opposite is true for females. Risk of infection is highest for individuals >65 years old. DISCUSSION / CONCLUSION Elucidating the impact of ethnicity, sex, and age can help us define strategies to lower overall morbidity and reduce disparities in infection rates.

11.06.010

ASSOCIATION OF ABCG WITH ANTIMALRIAL DRUG RESISTANCE

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The subfamily G (ABCG) of the ATP-Binding Cassette transporters has been associated with sterol transport, drug resistance, and glutathione (GSH). The GSH and thioredoxin (Trx) systems in Plasmodium detoxify and prevent oxidative damage during the parasite life cycle. PURPOSE: This study aims to assess the contribution of Plasmodium berghei abcg (pbabcg) to the antioxidant response and drug sensitivity using pbabcg null mutant parasites (pbabcg-). METHODS: Expression of P. berghei genes involved in the GSH and Trx antioxidant systems, as well as membrane transporters, were assessed by quantitative real-time PCR in the pbabcg- parasite [Genes analyzed: GSH system: gamma-glutamylcysteine synthetase, glutathione-S-transferase, glutathione reductase, glutaredoxin-like protein; Trx system: thioredoxin reductase, thioredoxin 1, thioredoxin 2, and plasmoredoxin; membrane transporters: chloroquine-resistant transporter (pbcrt), multidrug-resistant 1 (pbmdr1) and multidrug resistance-associated protein (pbmrp)]. In vitro drug sensitivity to Chloroquine (CQ), Artemisinin (ART), Dihydroartemisinin (DHA), Artesunate (AS), and Atovaquone (ATQ) was determined in the pbabcg- parasites. RESULTS: Results revealed an alteration of gene expression in the GSH and Trx systems. Sensitivity assays showed a displacement of the dose-response curve for CQ, ART, AS, and DHA while no changes in ATQ. Higher EC50 values were reported in the pbabcg- parasites for four of the five antimalarial drugs tested. The pbabcg- parasites show a down-regulation of the pbcrt gene while expression levels of pbmdr1 and pbmrp remained unchanged. DISCUSSION / CONCLUSION: This study provides new insights for the role of the pbabcg gene in oxidative stress and drug resistance in Plasmodium.

11.06.011

MOSQUITO ABUNDANCE DURING HURRICANE AND NON-HURRICANE SEASON

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Mosquitoes are responsible for spreading diseases and causing over one million human losses worldwide. Aedes aegypti is the vector of dengue, chikungunya, and zika viruses, all endemic in Puerto Rico. Surveillance and control of mosquitoes are important to help control vector-borne diseases. PURPOSE: This study aims to investigated mosquito species and the seasonal abundance of the mosquito population. METHODS: Adult mosquitoes were collected using lured BG-Sentinel 2 traps from two selected sites in the metropolitan area of Puerto Rico. Mosquitoes were sampled in 2017, the year that hurricane Irma and Maria impacted PR, for a period of 8-months. Hurricane and non-hurricane seasonal groups were used to classified mosquito samples. Environmental variables including temperature, humidity, atmospheric pressure, and precipitation were recorded. Mosquitoes were identified and classified by genus, sex, and species using taxonomic keys. RESULTS: A total of 733 mosquitoes were collected belonging to four genera: Aedes spp., Culex spp., Anopheles spp., and Psorophora spp. Data analysis from hurricane and non-hurricane seasons revealed a significant increase in the total population of Aedes aegypti ($p<0.05$) and females Aedes aegypti ($p<0.05$) mosquitoes during hurricane season and a significant increase in temperature ($p<0.05$). Results revealed a positive correlation between temperature and quantity of Aedes spp. ($p<0.05$).

DISCUSSION / CONCLUSION: During hurricane season, the mosquito population increases, and Aedes aegypti was the most abundant species throughout the samplings. Understanding mosquito species composition and seasonal abundance will help to achieve efficient vector control implementation.

11.06.012

IDENTIFICATION OF NOVEL ANTIMALARIAL LEAD COMPOUNDS

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Malaria parasites are becoming increasingly drug-resistant, requiring the search for novel antimalarial drugs. The glutathione S-transferase (GST) has been proposed as an antimalarial drug target. PURPOSE: This study aims to elucidate the biological role of Plasmodium berghei glutathione S-transferase (PbGST), assess its potential as a drug target, and identify novel antimalarials. METHODS: Our approach involves reverse genetics, structure-based screening, and in vitro drug susceptibility assays. A PbGST structural model was generated and used for a structure-based screening of two libraries, the ChEMBL-NTD archive, and the ChemBridge library, to identify potential GST inhibitors. Virtual library hits were visually analyzed for binding to the PbGST binding sites. RESULTS: By using reverse genetics, we showed that PbGST is essential for survival during intra-erythrocytic stages and is a valid target for drug development. A total of 61 potential inhibitors out of 4,900,000 were identified and tested against P. berghei. Five compounds displayed P. berghei antimalarial activity (0.5-3 μM) and two of them were active against P. falciparum. Compound CB-27 showed a concentration-dependent inhibition of the PbGST without inhibiting the human ortholog. A shape similarity screening using CB-27 as a query identified 24 novel chemical scaffolds, with six of them showing antimalarial activity (0.6-4.9 μM). DISCUSSION / CONCLUSION: The identified lead compounds inhibit malaria parasite growth and represent novel leads for antimalarial drug discovery and development.

11.06.013

STAPHYLOCOCCUS AUREUS COLONIZATION, ETHNICITY, AND SES

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PURPOSE Staphylococcus aureus infections represent the most common cause of skin and soft tissue infections in the US. About 33% of Americans are asymptomatically colonized with S. aureus, but infections occur when the bacteria penetrate the outer skin layers. Infections are more likely and severe among certain ethnic groups. Compared to non-Hispanic whites, Hispanic Americans have a lower risk of infection but higher likelihood of colonization with S. aureus. Underlying causes of this disparity are not well known although socioeconomic status (SES) variables such as access to healthcare, education, and income, explain S. aureus infection disparities in other populations. Colonization of S. aureus is a risk factor and often precedes infection, yet ethnic and SES associations with colonization has not been thoroughly studied. METHODS We are currently testing the colonization status of Hispanic and non-Hispanic whites in community settings in Yuma, AZ. The association between the independent variables of ethnicity, age, SES, and education with colonization (yes or not) are being determined through logistic regression models. RESULTS / EXPECTED RESULTS Consistent with infection-based data from this area, we expect males and non-Hispanic whites to be at higher risk for colonization than females and Hispanics. We also expect colonization rates to increase with age and decrease with SES variables, consistent with infection data in other populations. DISCUSSION / CONCLUSION Understanding interactions between ethnicity, SES and colonization is the first step towards effective and targeted interventions to prevent transmission and infections.

11.06.014

PUERTO RICAN ZIKA INFECTED PLACENTA QUANTITATIVE PROTEOMICS

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PURPOSE: Zika virus (ZIKV) is a Flavivirus that evolved from a mild disease to produce significant health complications including congenital ZIKV syndrome (CZS). Our hypothesis is that ZIKV infection of placental tissue dysregulates the host proteome, facilitating vertical transmission and CZS. This study was designed to elucidate the pathways affected by ZIKV infection of the placenta in order to find targets for potential therapy. METHODS: Using nine different placental samples from Puerto Rico collected during 2016 ZIKV epidemic, we compared the proteome of five ZIKV infected samples with uninfected controls. Tandem mass tag (TMT) was performed using TMT10plex™ Isobaric Label Reagent Set and Mass Spectrometry protein quantification

was done using Q Exactive™ Hybrid Quadrupole Orbitrap Mass Spectrometer. Identification of proteins was performed by Proteome Discover 2.1, and protein fold change in both groups was compared using Limma statistics. Differentially expressed proteins were analyzed with STRING and Ingenuity Pathway. RESULTS: TMT analysis showed that ZIKV infected placentas had 94 reviewed differentially abundant proteins 32 upregulated and 62 downregulated. STRING analysis results indicate that 45 of the deregulated proteins are cellular components of the ECM and 16 play a role in its structure and organization. Some of the significantly upregulated proteins were Fibrinogen, Vitronectin and Fibronectin. DISCUSSION: Maternal infection of ZIKV results in alterations of the integrity of the placenta. Proteomics analyses may elucidate new mechanisms employed by ZIKV and uncover novel targets used to disrupt placental function.

11.06.015

ZIKA VIRUS INFECTION AND ITS EFFECT ON CREB3L1 PATHWAY

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PURPOSE: Zika virus (ZIKV) is a Flavivirus that causes congenital Zika syndrome. ZIKV preferentially infects human neural progenitor cells (hNPCs), reducing their ability to induce self-repair. Gene ontology analyses revealed the up-regulation of cAMP-responsive element binding protein 3-like 1 (CREB3L1) gene, suggesting an alteration of the CREB pathway during ZIKV infection. In this study, we wanted to assess the activation of the CREB3L1 neuroprotective pathway and its role in nerve cell survival during ZIKV infection. METHODS: SHSY-5Y neuroblastoma cells were differentiated with 10mM retinoic acid and infected with ZIKV at a multiplicity of infection of 0.1. We examined the cultures for cytopathic effects for up to 48 hours post-infection. We separated the cell nucleus and cytoplasm for protein analysis. We extracted RNA and proteins to assess gene and protein expression levels of CREB3L1 pathway target mediators using real-time polymerase chain reaction (RT-PCR), ELISA, and western blot assays.RESULTS: Preliminary analysis by RT-PCR did not reveal a difference in CREB3L1 RNA levels when comparing ZIKV-infected cells and non-infected cells. Also, analysis of the main proteins involved in the activation of the CREB3L1 pathway revealed no differences between the treatments. CONCLUSIONS: Our preliminary studies indicate that ZIKV infection does not alter CREB3L1 pathway expression levels in SHSY-5Y cells 48 hours post-infection. We will analyze RNA and protein levels at different time points to assess the alteration of the CREB3L1 mediated pathway in a time-dependent manner.

11.06.016

PLACENTAL PERICYTES AND CYTOMEGALOVIRUS PATHOBIOLOGY

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PURPOSE: Annually, about 1 out of 200 babies in the US are born with congenital Human Cytomegalovirus (HCMV) infection. This is an important health disparity in underserved communities. The placenta is an important target organ for congenital HCMV infection and this study focuses on virus-placenta interactions. Placental pericytes are pluripotent cellular components of the capillaries and post-capillary venules abluminal to microvascular endothelial cells that are essential for endothelial cell proliferation and placental microvasculature stability and integrity, but have largely been ignored in placenta biology. We hypothesize that human placental pericytes are the most permissive cell type in the placenta for HCMV infection and serve as amplification reservoirs for HCMV dissemination. METHODS: HCMV-infected placental tissue was stained by dual-labeled immunohistochemistry. Primary placental pericytes, cytotrophoblasts isolated from placenta explants, and villous fibroblasts were exposed to HCMV; and infectivity was analyzed by microscopy and immunofluorescence. Cytokine expression was examined by Luminex assay. A HCMV-GFP recombinant virus was used to examine replication kinetics. RESULTS/EXPECTED RESULTS: Immunohistochemistry showed HCMV in trophoblast and the villous core with T-cell and macrophage infiltration. Primary HCMV isolate from a patient (SBCMV)- infected pericytes showed dysregulation of proinflammatory and angiogenic cytokines when compared to control cells. A tri-cell model of the villous floor showed a unique expression profile. Finally, we show pericytes infected in vivo with HCMV in placental tissue from a congenitally infected child. DISCUSSION/CONCLUSION: Placental pericytes support HCMV lytic replication, inducing proinflammatory and angiogenic cytokines that likely contribute to viral dissemination, placenta inflammation, and dysregulation of placental angiogenesis.

11.06.017

HUMAN VAGINAL EPITHELIAL CELLS ARE SUSCEPTIBLE TO ZIKA VIRUS

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The Zika Virus (ZIKV) is an emerging flavivirus that causes congenital birth defects and neurological compilations. Although ZIKV is primarily transmitted through an infected mosquito, recent studies reveal sexual contact as a potential transmission route. In women, the vaginal epithelium

constitutes the first line of defense against viruses. Given the capacity of sexual intercourse, we hypothesize that the initial event for ZIKV vaginal transmission is the direct viral uptake at the outermost epithelial layer of the vaginal tract. We aim to test our hypothesis by (1) characterizing the replication kinetics of ZIKV in human vaginal epithelial cells (hVECs) in vitro, and (2) determining the functional role of the ZIKV entry receptor, AXL, in hVECs. The outcome of this research will provide a molecular mechanism of ZIKV vaginal transmission, which can lead to devising therapeutics aimed at interfering with the pathology caused by the virus. All performed studies use the HPV-transformed vaginal epithelial cell line VK2/E6E7. The ZIKV strains utilized in the current study were isolates from the African (MR766) and Asiatic (PRVABC59) lineage. ZIKV infection of the vaginal epithelia resulted in de novo viral replication and production, and a steady release of infectious viral particles. Additionally, the expression profile of the ZIKV entry receptor AXL was confirmed in hVECs on a protein and mRNA level. The results presented in this study provide a mechanistic perspective on the viral susceptibility and molecular mechanism of ZIKV vaginal transmission. These findings will be instrumental in developing therapeutic agents aimed to protect the human host.

11.06.018

BASIC AND TRANSLATIONAL RESEARCH IN INFECTIOUS DISEASE

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PURPOSE: This study aims to introduce a mass spectrometry (MS)-based multiomic (proteomic, glycomic, and lipidomic/metabolomic) workflow to address infectious diseases in the U.S.-Mexico border and worldwide. To that end, two model organisms were chosen: Trypanosoma cruzi and Giardia lamblia, the causative agents of Chagas disease (CD) and giardiasis, respectively. We aim to identify (1) protein and glycan biomarkers (BMKs) for diagnosis and early assessment of chemotherapy outcomes in CD; (2) glycan epitopes as vaccine candidates in CD; and (3) novel therapeutic lipid/metabolic pathway targets in Giardia. We hypothesize that MS-based multiomic approaches might advance the tempo of development of diagnostic tools and therapeutic targets in infectious organisms. METHODS :Proteomics: samples were subjected to trypsin digestion prior to high-resolution liquid chromatography-tandem MS (HR-LC-MS/MS) analysis. Glycomics: glycans were obtained from glycoproteins and analyzed by matrix-assisted laser desorption Ionization time-of-flight MS (MALDI-TOF-MS) and HR-LC-MS/MS. Lipidomics/metabolomics: samples were extracted by the Bligh-Dyer method and analyzed by HR-LC-MS/MS. RESULTS/EXPECTED RESULTS: T. cruzi: Proteomic analysis indicated the presence of potential BMKs in both infective and noninfective life-cycle stages. Glycomic analysis revealed T. cruzi cell surface glycoconjugates and glycans as novel potential vaccine targets and diagnostic/prognostic BMKs. Giardia: Lipidomics and metabolomics revealed global changes in phospholipid remodeling in the parasite, indicating potential novel therapeutic metabolic pathways. DISCUSSION/CONCLUSION: MS-based multiomic approaches provided new insights into the biology of T. cruzi and Giardia, and revealed multiple molecular targets for development of new diagnostic tools and therapeutic interventions for two major infectious diseases, which affect millions of people worldwide.

11.06.019

STRUCTURE OF HUMAN FERROPORTIN AIDED BY MS CONSTRAINTS

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Mammalian organisms require iron for red blood cell manufacture, respiration, metabolism and immunity, and as cofactor in several enzymes. Similarly, many pathogens including human immune deficiency virus require iron for transcription, replication and for their pathogenesis. Thus, there is a keen struggle for iron at the interface of host organisms and pathogens. Paradoxically, free iron is toxic from the production of reactive oxygen species which induce cellular injury and damage to DNA. It is essential that iron is tightly regulated. Ferroportin is the only known exporter of cellular iron in mammals and is crucial for maintaining iron balance. Ferroportin function and expression are tightly regulated by the antimicrobial peptide hepcidin. In spite of its importance little structural information is available on human ferroportin, and how iron is transported through ferroportin is not understood. We have built the structure of ferroportin using hybrid methods with restraints from mass spectrometry. Our model comprises 12 transmembrane helices, built in lipid bilayer and water solvent, balanced by counterions, and refined by a few hundred nanoseconds molecular dynamics simulations. The iron binding site matches remarkably with what is seen in crystal structures of distant orthologs. We are using this structure along with functional data to answer outstanding questions about the mechanism of ferroportin, iron transport and the importance of the Q248H mutation found in African and black American populations with moderately high prevalence.

11.07.001

CERVICOVAGINAL DYNAMICS ASSOCIATED TO HPV INFECTIONS AND CER

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PURPOSE: The bacterial microbiome has been extensively associated to several disease phenotypes Archaea, a major neglected component of the microbiome accounts for a relatively small percentage of the microbiota and have mostly been studied in the gastrointestinal tract. We hypothesized that dysbiosis in the genital tract included changes in both Bacterial and Archaeal organisms according to Human Papillomavirus infectios and levels of dysplasia. METHODS: We analyzed 62 patient samples from recruited patients coming for gynecology clinics, at the UPR and San Juan City clinics (Puerto Rico). From these, 52 were HPV positive and 10 were HPV-negative and were stratified according to cytology results. From genomic DNA extracted from cervical swabs, we sequenced 16S rRNA genes and selected 10 patient samples for additional shotgun metagenomics. The patients were grouped in those without epithelial lesions, CIN 1 and CIN3. DNA data analyses was done with shogun and QIIME. RESULTS: Analyses of the 16S rRNA reads revealed 16 Archaeal OTUs, revealing and abundance of Methanobrevibacter associated with CIN3 lesions. Shotgun data revealed Methanosarcina to be dominant across all samples with higher dominance in patients without lesions and an increased dominance in methanobrevibacter and methanococcus in CIN3 lesions. No archaeal significant differences were found according to HPV risk (HPV infection), however a significant decrease in Lactobacilli (bacteria) was associated with dysplasia. DISCUSSION/CONCLUSION: We found that Archaea are commensals of the cervical mucosa and may contribute to disbioses. Acetoclastic methanosarcina are dominant across samples and CIN3 lesions revealed higher dominance of hydrogenotrophic methanogens such as methanobrevibacter. The significance of these preliminary results may indicate that archaea cannot be taken out of the ecological context for future cervical cancer prevention strategies.

11.07.002

GUT MICROBIOME DYNAMICS IN RESPONSE TO DIETS

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Background: The gut microbiome is a very flexible entity within our body both in its composition and in its gene expression profile. It adapts to environmental exposures such as diet and is affected by the host's genetics and physiology as well. Aim: To assess the gut microbiome dynamics and changes in response to high and low fiber diet in obese and lean African American subjects. Methods: Four obese and four lean subjects were recruited for this study. These subjects were put on a high fiber diet for 10 days, followed by a second 10 days on low fiber diet. Stool samples were collected at baseline and after each diet regime. DNA and RNA were extracted from the stool samples to analyze the gut microbiome composition and its genes' expression changes in different hosts and under different dietary regimens. Next generation sequencing was used to generate 16S rDNA data reflective of gut microbiome composition and structure and for the metatranscriptomic analysis. Results: For 16S rDNA analysis, the generated post-diet 16S data were normalized for each subject against the pre-diet gut microbiome composition. The generated relative values were ran on a bray Curtis beta diversity and plot principal coordinate analysis. The results showed that all pre-diet points clustered together (references), the low fiber samples are clustering together, and high fiber samples are clustering together p value Permanova = 0.002 for 999 permutations. Also, high fiber diet samples are further away from the control group compared to low fiber diet, reflecting much more differences and more diversity in these high fiber diet associated gut microbiomes. The alpha rarefaction analysis after splitting the data per diet and normalize microbiota richness to 1 and express low fiber and high fiber relative to this time point was performed. There is a trend to decreased richness under low fiber diet and an increase in richness under High fiber diet. The metatranscritomic changes associated with these gut microbiome compositional charges are being analyzed within the obese and lean hosts' contexts. Conclusion: The gut microbiome shows a swift adaptation to ingested diets. High fibers were more beneficial as they increased diversity and richness in both obese and lean patients. The transcriptomic specifics that associate with these structural changes are being analyzed in the obese vs. lean subjects to assess host's impact on gene expression and energy requirement and output for the host.

11.08.001

NANOPARTICLES-MAB CONJUGATES FOR BREAST CANCER TREATMENT

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PURPOSE: To develop nanoparticle-monoclonal antibodies (mAbs) conjugates for targeted breast cancer treatment. METHOD: The power of mAbs lies in their highly specific

binding of only one antigenic determinant. MAbs may be conjugated to bioactive agents or other delivery systems such as nanoparticles to allow specific delivery to target sites. The unique properties of PEG make it suitable for many biomedical applications including PEG-monoclonal antibody conjugates. Conventional methods for covalent protein modification typically involve reacting the appropriate amino acids with reactive agents (activated PEGs). The modification methods are not site-specific and there is no control over which amino acids are modified and the resulting conjugates are often modified in positions that weaken or even abrogate the binding to the antigen, which in turn decreases the efficacy of the targeting system. The core-shell (corona) stealth polymeric nanoparticles developed in our laboratory by dispersion polymerization at ambient temperature are suitable for varied and diverse bioengineering/biopharmaceutical applications: targeted delivery of bioactive active agents such as drugs, nucleic acids and contrast agents for imaging. We developed a novel site-specific attachment of a suitably functionalized PEG to produce PEG-mAb conjugates, en route to multifunctional nanoparticles synthesis, without introducing a steric barrier into an essential binding site on the protein molecule. RESULTS: We report here our efforts for site specific conjugation of PEG-macromonomer to mAbs at the Fc region of trastuzumab and pertuzumab. CONCLUSION: The conjugation method preserved the binding (using flow-cytometry) and biological activity (cytotoxicity) of the ligands (PEG-mAbs).

11.08.002

MD SIMULATIONS ON CHIRAL DRUGS BIND IN MOLECULAR MICELLES

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Chiral separations are especially important in the medical and pharmaceutical fields because in a chiral in vivo environment, a drug's chirality often has a significant impact on its biological activity. Therefor the Food and Drug Administration mandates that the properties of each enantiomer of a chiral drug be studied separately before decisions are made to bring the drug to market as a single enantiomer or as a racemic mixture. This study is a theoretical effort to understand the mechanism of chiral recognition in capillary electrophoresis by characterizing the molecular micelle binding of chiral compounds with different geometries and charges. The result will be useful for designing new macromolecular assemblies with enhanced stereo selectivity in drug binding.

11.09.001

CANNABINOID RECEPTOR-MEDIATED MODULATION OF INTERNEURONS

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PURPOSE: In the main olfactory bulb, two populations of granule cells (GCs), GABAergic interneurons, can be distinguished based on their location in either the granule cell layer (GCL) or the mitral cell layer (MCL) where they are interspersed with mitral/tufted cells. Little is known about the properties of these two interneuron populations. METHODS: Using anatomical and functional approaches we have explored this question with respect to endocannabinoid signaling. Our understanding of the role of cannabinoid receptor type 1 (CB1R) in olfactory processing remains limited. RESULTS: Antibody staining for diacylglycerol lipase DAGLα, which is responsible for the synthesis of 2-arachidonoylglycerol (2-AG), shows prominent expression in the MCL and GCL suggesting DAGL-dependent endocannabinoid signaling in these layers. Differences in the physiology of the two GC populations were evident when we compared the responses from two metabotropic glutamate receptor (mGluR) k.o. mouse strains. MCL-GCs in slices from mGluR5 k.o. mice but not from mGluR1 k.o. mice responded to mGluR agonists, whereas GCL-GCs in slices from mGluR1 but not from mGluR5 k.o. mice were responsive to mGluR agonists suggesting different mGluR expression patterns. A CB1R agonist hyperpolarized GCs and made them less responsive to synaptic input, while a CB1R antagonist strongly excited GCs of both populations. DISCUSSION: These data indicate that the mGluR and endocannabinoid system can have different cellular and network effects and that endogenous release of endocannabinoids and glutamate prominently modulates the excitability and synaptic responsiveness of interneurons in the main olfactory bulb.

11.09.002

SIGNALING AND SYNAPTIC PLASTICITY IN CNS NEURAL CIRCUITS

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PURPOSE: The endocannabinoid (eCB) signaling system has been functionally implicated in many brain regions but our understanding of the role of cannabinoid receptor type 1 (CB1R) in olfactory processing remains limited. We study the function of the endocannabinoid system in regulating neural activity at mitral cell synapses in the olfactory bulb,

the first central relay station in the brain for the processing of olfactory information coming from the nose. METHODS: Our experimental approach uses electrophysiological recording techniques, specifically whole cell patch-clamp recordings. RESULTS: Olfactory bulb neurons express high levels of CB1R. Endocannabinoids mediate retrograde signaling at synapses in several brain regions through a form of short-term neural plasticity. Endocannabinoids are released from depolarized principal neurons and rapidly diffuse to presynaptic inhibitory interneurons to transiently reduce presynaptic firing and neurotransmitter (GABA) release. Output neurons such as mitral cells and tufted cells in the olfactory bulb are computational elements in brain circuits that integrate incoming signals with membrane properties to generate behaviorally relevant synaptic output. Our data support the notion that retrograde signaling is present in neural circuits involving mitral and tufted cells. Mitral and tufted cells release endocannabinoids and, through retrograde signaling, inhibit presynaptic periglomerular cells, which controls the GABA release of these presynaptic neurons. This, in turn, allows mitral and tufted cells to temporarily regulate their synaptic input and relieve them from synaptic inhibition. DISCUSSION: Endocannabinoids function as retrograde messengers to regulate neural signaling and mediate plasticity at olfactory bulb synapses with potential effects on olfactory threshold and behavior.

11.09.003

TLR4 CONTRIBUTES TO SEX-SPECIFIC COCAINE-INDUCED BEHAVIORS

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Purpose: Substance use disorders (SUDs) affect more than 7% (19.7 million people) of the US population. While men are twice as likely to develop SUDs, women are more sensitive to the negative consequences of drugs of abuse and have increased propensity of relapse to drug-seeking behavior. Toll-like receptor 4 (TLR4), a component of the innate immune system, is implicated in drug-related behavior. However, the contribution of TLR4 to the temporal components of cocaine experience is largely unknown. Methods: To determine the contribution of TLR4 to cocaine-induced behavior, the behavioral properties of wildtype (WT) and TLR4 knockout mice (TLR4.KO) were compared following cocaine exposure. Locomotor sensitization and place conditioning assays were used to elucidate how TLR4 modulates cocaine-induced behavior. Results: We find that TLR4 deficiency results in differential expression of cocaine-induced locomotor sensitization between males and females. While both male and female TLR4.KO mice had reduced locomotor responding during the development of cocaine sensitization, female TLR4.KO mice exhibited robust enhancement of sensitization expression following a challenge dose of cocaine. In addition, female TLR4.KO mice had prolonged retention of associative memory following cocaine exposure and displayed reinstatement following a challenge dose of cocaine. Conclusions: Taken together, these results suggest TLR4 contributes to behavioral adaptations in response to cocaine experience.

11.09.004

METHAMPHETAMINE-INDUCED TOXICITY IN RAT C6 ASTROGLIA-LIKE CE

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PURPOSE: Methamphetamine (METH) is a powerfully addictive psycho-stimulant widely abused in the US; its increased use among Afro-Americans is a growing concern for psychiatric-illness in this community. Owing to different mode of metabolism in the central nervous system (CNS), METH triggers much stronger pharmacological effect than cocaine by releasing more dopamine in the brain. Thus METH is considered dangerously addictive. Most studies with METH were focused on neuronal cell-types; since astrocytes are considerably more abundant than neurons in the CNS, it is possible that METH-induced toxic effects would first manifest in astrocytes long before they die. Present study was designed to evaluate METH-induced toxic effects in rat C6 astroglia-like cells for vacuolation, viability, reactive oxygen species (ROS), glutathione (GSH) level and cell cycle arrest. METHODS: Cells were treated with METH (0.5 – 5 mM) for 24 h, and analyzed for vacuolation by neutral red dye uptake, viability by Celltiter 96 Aqueous one solution, ROS by 2',7'-dichlorofluorescin diacetate, total GSH with Ellman's reagent and cell cycle by FACSCalibur flow cytometry. RESULTS: METH treatment showed several toxic effects in cells -like increased cellular vacuolation, decreased cell viability that reflected with increased ROS, decreased GSH level, and G0/G1 cell cycle phase inhibition. DISCUSSION / CONCLUSION: The results clearly suggest that C6 astroglia-like cells were sensitive to METH treatment. Because neurons depend on astrocytes under in vivo situation, we speculate that astrocytic dysfunction in METH addicts could result in rapid loss of neurons, a contributing factor in psychiatric illnesses.

11.09.005

EFFECTS OF MICROWAVE FIXATION ON MOUSE BRAIN METABOLITES

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PURPOSE: The study of brain metabolites is important to understand the metabolic changes in many brain diseases. In vivo animal experiments usually cannot avoid the interference caused by anesthesia, which can significantly alter the brain metabolism. Microwave fixation has previously been introduced as a viable procedure to prevent rapid degradation of the tissue for postmortem study. However, the performance of microwave fixation on the preservation of different metabolites has not been well documented. In this study, we performed proton magnetic resonance spectroscopy (1H-MRS) to compare the data acquired in vivo, after microwave fixation, and from the unfixed tissue to understand the limitations of microwave fixation. METHOD: For the microwave-fixation group, seven C57/BL6 mice were killed by a focal beam microwave irradiation system. For the no-fixation group, 16 mice were decapitated after instant isoflurane anesthesia. The heads were wrapped in Parafilm and immersed in the phosphate-buffered saline solution for 1H MRS using Bruker 9.4T spectrometer over 40 hours. For the in vivo study, 13 mice were scanned under isoflurane. Nine hippocampal metabolites were quantified by LCModel. RESULTS: The microwave-fixation group exhibited better temporal stability of Lac, tCr, tCho, Glx, mIns, GSH, and GABA, whereas the signals of NAA, Tau, and tCr of the no-fixation group were more stable and closer to those acquired in vivo. DISCUSSION/CONCLUSION: These results suggest that for the experiments that require long acquisition time, such as high spatial resolution 1H-MRS, 13C-NMR, or MRSI, appropriate fixation method should be considered according to the specific metabolites of interests.

11.09.006

THE ANTIINFLAMMATORY TARGETS OF TQ IN LPS ACTIVATED BV-2 CEL

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PURPOSE: It is widely accepted that microglial-mediated inflammation contributes to the progression of several neurodegenerative diseases such as Alzheimer's disease. Microglia are the primary immune cells of the brain, and when activated they release various pro-inflammatory cytokines. Thymoquinone (TQ), a natural compound that has an antiinflammatory, anti-oxidant, and anticancer activities may offer a promising strategy for inflammation-mediated neurodegenerative disorders involving activated microglia cells. Our previous study showed that exposure to TQ in 1μg/mL lipopolysaccharide (LPS) activated microglia reduces several cytokines/chemokines, including IL-6, IP-10, MCP-1, and MCP-5. The purpose of this study was to farther investigate the global molecular targets underlying the anti-inflammatory effects of TQ. METHODS: BV-2 microglia cells were first stimulated with 1μg/mL LPS for 1hr, then incubated for 24 hrs. in the presence or absence of 10 μM TQ. To identify the global target genes and proteins of TQ in activated BV-2 microglia cells, genomic, ELISA, and Real-time PCR technologies were used. RESULTS: Our results showed that TQ significantly decreases gene expression IL-1β by 10 folds, Il-12p40/70 by 5 folds, CCL5 by 13.2 folds, CCRL2 by 12 folds, PTGS2 (COX2) by 3.3 folds, miR-155 by 3.9 folds, and JAK2 by 2.2 folds in LPS activated BV-2 microglia cells. CONCLUSION: These findings suggest that the intervention of microglial activation process could be a promising therapeutic target for the treatment of a number of neurodegenerative diseases such as Alzheimer's disease.

11.09.007

A BABOON BRAIN ATLAS FOR ANALYSIS OF MRI AND PET SCANS

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PURPOSE: The baboon brain is one of the closest models to the human brain. Investigation into the baboon brain's metabolism and structure has shed light on the function and organization of the human brain. Metabolism has long been studied by PET imaging, but anatomical information is usually unclear in this type of scan. This study aims to create a high-resolution baboon atlas for the ease of PET imaging analysis to correlate the anatomical and metabolic data presented in MRI and PET images. METHODS: The baboon brain atlas was created based on T1 MRI images. Brain structures were manually defined based on published histological atlases and MRI atlases of other primates. The individual PET data was then normalized and registered to the MRI atlas to produce an overlay image to compare the anatomical and metabolic data. RESULTS / EXPECTED RESULTS: 35 individual structures covering the whole brain were labeled including key functional areas such as the thalamus, amygdala, insula, pallidum, and substantia nigra. Individual baboon brain PET scans were registered to the MRI atlas and segmented to allow anatomical localization of a radoligand's metabolism. Preliminary validation tests were done by dice index

and found to be 0.9378. DISCUSSION / CONCLUSION: Segmented PET-MRI images of baboon brains could facilitate analysis of metabolic structures to a higher degree of anatomical accuracy than possible before. Parallel analysis of large data sets by this method could be used to perform volumetric analysis relative to metabolism, among many other applications.

11.09.008

EFFECTS OF CLOSED HEAD INJURY ON AVOIDANCE BEHAVIOR IN RATS

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UPR Medical Sciences Campus (DSM, OMG, MCC, MRL), UPR Río Piedras (RRS, DOM, HHM), UPR Bayamón (PAF, CRS)

PURPOSE. Approximately 4 million cases of traumatic brain injury occur yearly in the United States. The most common form of brain injury, concussion, is often seen in sports and combat. The brain movement within the skull caused by concussion leads to diffuse axonal injury, which may lead to motor and cognitive dysfunction. The susceptibility of behaviors such as avoidance-reward conflict is unclear. We hypothesize that concussion will impair avoidance to an aversive stimulus in the presence of reward. METHODS. Concussion can be modeled in rodents with a closed head injury (CHI). Here, a guide tube is placed above the head of anesthetized male rats, and a weight is dropped impacting the rat's head. At impact, free rotation of the head downward occurs. RESULTS. CHI resulted in an increase in time to wake (Sham: n=11, CHI: n=11, p=0.029). To assess the effects of CHI on locomotor function, a Ladder Rung test and Rotarod were performed, which did not reveal any differences. In platform-mediated avoidance, rats were conditioned in an operant chamber to auditory tones co-terminating with a mild footshock. An acrylic platform in the opposite corner of the sucrose-delivering bar allowed rats to avoid the shocks. Our results demonstrate that CHI increased the time spent on the platform, suggesting that brain injury results in excess avoidance (p=0.0012). CONCLUSION. The translational relevance of this work suggests that brain injury may contribute to mental health disorders, since excess avoidance is characteristic of patients with fear and anxiety disorders.

11.09.009

CONTINGENT PALATABLE DIET AVAILABILITY AND ALCOHOL DRINKING

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Alcohol is unique among abused drugs in that it possesses calories and problematic alcohol consumption reduces nutrient intake and decreases the body's ability to absorb nutrients. As a result, many alcoholics are malnourished, and resultant nutritional deficiencies may contribute to the pathology of alcoholism. Furthermore, negative consequences of drinking are disproportionately higher in certain ethnic minorities. We evaluated the impact of an intermittent palatable high-fat diet (HFD) cycling on alcohol drinking and its potential neurobiological mechanisms. Male Long Evans rats, matched for body weight, water, and food intake, received intermittent (24 hrs twice a week on Tue and Thru; Int-HFD) access to HFD or normal chow (controls). Alcohol drinking was evaluated in a two-bottle choice paradigm on Mon, Wed and Friday over several weeks. Brains were isolated at the end of the study and amygdala (AD), striatum (ST), hypothalamus (HT), and ventral tegmental area (VTA) were microdissected, and 84 central neurotransmitters receptors genes expression was evaluated. Rats in the Int-HFD access group developed a binge/compensate pattern of food consumption. Alcohol intake was significantly attenuated in Int-HFD group compared to chow controls. Several genes were significantly altered in the ST and VTA whereas no changes occurred in AD and HT of Int-HFD group compared to controls, suggesting that Int-HFD cycling induced selective alterations in the brain reward circuitry compared to the brain region involved in energy homeostasis. Importantly, these findings provide mechanistic insight into a critical framework to evaluate the therapeutic potential of a nutritional contingency in the management of alcoholism.

11.09.010

NEUROMODULATION AND NEURODEGENERATIVE DISORDERS

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PURPOSE: Research on neurodegenerative and depressive disorders indicates a role of olfactory bulb neurons for propagating nerve impulses to limbic structures. The pathology of the frontal cortex in patients suffering from neurodegenerative conditions resembles closely the brains of rodent models after removal of the olfactory bulb. The olfactory bulb is a precise model to analyze cellular, molecular and neurological alterations that relate to specific patterns of behavioral modulation. Here, we determine olfactory bulb neuronal firing patterns relevant for the propagation of nerve impulses to limbic structures. METHODS: Long-lasting depolarizing activity in mitral/tufted cells (M/TCs) of the olfactory bulb is accompanied by bursts of action potentials and helps to analyze synchronization of M/TCs. Our experimental

approach involves whole-cell patch-clamp recordings from M/TCs in mouse brain slices. RESULTS: M/TCs receive input from olfactory sensory neurons and transmit signals to limbic and higher order olfactory structures. M/TCs also signal to neurons in the input layer of the olfactory bulb, specifically to GABAergic periglomerular neurons. These neurons express high levels of G-protein coupled receptors such as glutamate, dopamine, GABA-A and -B receptors. Results indicate enhanced amplitude and longer duration of long-lasting currents in M/TCs when applying a dopamine receptor antagonist and a GABA-A receptor antagonist. Both antagonists block synaptic transmission and relieve inhibition in M/TCs, thus leading to more action potentials in M/TCs. DISCUSSION: Blockade of inhibitory transmission in the olfactory bulb enhances signal output from olfactory bulb to limbic and higher order olfactory structures with potential effects for neurodegenerative pathologies.

11.09.011

EARLY-LIFE STRESS, ADOLESCENT COCAINE, AND FEAR MODULATION

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A study of a mostly African-American urban civilian population found that their levels of cocaine use highly correlated with levels of childhood abuse and PTSD symptoms. This suggests that childhood abuse, cocaine addiction, and PTSD interact in minority populations and likely contribute to worse outcomes and health disparities. The vast majority of animal models examine cocaine use and PTSD separately. However, to be able to design better treatment plans for real-life clinical scenarios, we need to understand how these two disorders interact. In this project, we propose to combine animal models of child abuse and neglect with models of cocaine abuse and PTSD to examine to what degree one condition affects the other and to examine whether exposure to cocaine at different developmental stages increases the severity of PTSD-like phenotypes. Male and female rats will be separated from their mothers for 3 hours per day from postnatal day 1-14 and then during adolescence (P35-43) rats will be given cocaine conditioned place preference. Once the rats reach adulthood (P60), they will receive fear conditioning and extinction. Comparisons will be made with groups that received different combinations of maternal separation and adolescent cocaine exposure. We are currently running our first groups of rats and anticipate that the combination of early-life stress and adolescent cocaine exposure will disrupt fear conditioning and extinction in adulthood and provide an animal model for examining the mechanisms responsible for the interactions.

11.09.012

FOODBORNE ILLNESSES AND ODOR NAVIGATION OF INSECTS

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PURPOSE: Insects contaminate food with their feces. This raises concerns about foodborne illnesses associated with microbial pathogens creating health concerns in areas of poor sanitation according to the World Health Organization. Here, we studied the olfactory system of an insect model, the house cricket Acheta domesticus, an omnivorous scavenger. House crickets use their antennae to detect mechanosensory and chemosensory information for orientation and can contaminate food with their feces. Our goal is to develop biological tools to fight insect infestations. METHODS: We used a combination of structural studies (electron microscopy) and physiological experiments (electrophysiological recordings) to determine the components of the olfactory apparatus involved in odor-mediated behavior of house crickets. In parallel behavioral studies (Y-tube bioassays), we aimed to determine the odorants that elicit positive anemotaxis (movement toward the odorant source). RESULTS: Stimulation of olfactory receptors allows house crickets to detect and identify food, find mating partners and avoid predators. These receptors are located in cuticular sensory organs (sensilla) found on their long, paired, multi-segmented antennae. Numerous small pores with underlying olfactory receptor cells, responsible for detecting odorants, pierce the cuticle of these sensilla. In behavioral experiments, we test odorants from various fruits and vegetables, as well as meat. Our data suggest that some fruit, vegetable, and meat stimuli can elicit significant positive anemotaxis which signals the presence of food to the animal. CONCLUSIONS: Data obtained in this study will be useful in suggesting possible odorant lures to trap these and possibly other insects to prevent or reduce food contamination.

11.09.013

ANTI-INFLAMMATORY EFFECTS of EGCG ON LPS ACTIVATED BV2 CELLS

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PURPOSE: Neuro-inflammation has been associated with many neurodegenerative diseases such as Alzheimer's disease. The chronic activation of microglia can cause neuronal damage through the release of pro-inflammatory cytokines and reactive oxygen mediators. Epigallocatechin-3-Gallate (EGCG) is an important bioactive polyphenol found in green tea extract. It has significant anti-inflammatory as well as neuroprotective capabilities. Our central hypothesis is that the anti-inflammatory properties of EGCG are mediated in part by inhibiting the

formation of pro-inflammatory cytokines, chemokines, and other inflammatory mediators. METHODS: To test our hypothesis, we evaluated the anti-inflammatory activity of EGCG in lipopolysaccharide (LPS) stimulated BV-2 microglia cells. BV-2 microglia cells were first stimulated with 1μg/mL of LPS for 1hr., then incubated for 24 hrs. using various concentrations of EGCG. Cell viability was assessed using resazurin (Alamar Blue) indicator dye, and nitric oxide (NO2) release was evaluated using the Griess Reagent Assay. RESULTS: Our results showed that EGCG caused concentration dependent decrease in cell viability of LPS stimulated BV-2 microglia cells for concentrations > 125 μM of EGCG. EGCG also decreases the inflammatory mediators NO2 production in LPS stimulated BV-2 cells. Conclusion: EGCG has decreased inflammatory mediator NO2 production in LPS stimulated BV-2 cells, but ongoing research into EGCG's anti-inflammatory effects has yet to be determined.

11.09.014

PROINFLAMMATORY SIGNALING MEDIATES MN-INDUCED YY1 ACTIVATION

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PURPOSE: Chronic exposure to manganese (Mn) causes a neurological disorder known as manganism, which shares pathological features of Parkinson's disease. As Mn toxicity commonly occurs via occupational exposure or contaminated drinking water, elucidating the mechanisms of Mn-induced toxicity and identifying potential therapeutic targets are crucial to reducing environmental health disparities associated with heavy metal neurotoxicity and neurodegenerative disease. METHODS: I.Reactive oxygen species (ROS) and cytokine production assays II.Promoter activity and reporter assays III.Real-time quantitative PCR (qPCR) and Western blotting. IV.Immunoprecipitation and immunocytochemistry RESULTS: Mn activates transcription factor Yin-Yang 1 (YY1), which binds to the astrocytic excitatory amino acid transporter 2 (EAAT2) promoter and represses its expression, leading to dysregulated synaptic glutamate clearance and excitotoxicity. In the present study, we found that Mn induced YY1 activation via proinflammatory nuclear factor kappa-light-chain-enhancer of activated B cells (NFkB) signaling and oxidative stress in H4 astrocytes. Accordingly, inhibition of NFkB signaling and ROS/TNF-α production abolished Mn-induced YY1 upregulation. These results indicate that Mn targets the proinflammatory NFkB pathway to activate YY1 and repress EAAT2, leading to excitotoxic neurotoxicity. DISCUSSION/CONCLUSION: Identifying therapeutic strategies to attenuate Mn neurotoxicity is crucial to alleviating disparities in toxicant exposures and increasing health equity. Here, we report that Mn activates transcription factor YY1 through proinflammatory signaling and oxidative stress in astrocytes, and treatment with anti-inflammatory and antioxidant compounds can reverse this YY1 upregulation. The NFkB-YY1-EAAT2 pathway may serve as an important mediator of Mn-induced neurotoxicity, leading to novel strategies to attenuate neurodegenerative disorders associated with excitotoxicity.

11.09.015

NEUROGENETICS AND BIOIMAGING AT THE UNIVERSITY OF PUERTO RICO

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The University of Puerto Rico Medical Sciences Campus (UPR MSC) RCMI Neurogenetics and Bioimaging Services (NBS) facility is housed at the Institute of Neurobiology, a multidisciplinary facility dedicated to the study of nervous system structure and function. The Institute is presently composed of ten laboratories that utilize a variety of model systems to address some of the most challenging issues facing modern Neuroscience – ranging from synapse development in Drosophila to the molecular basis of addiction. PURPOSE: The NBS has three objectives: 1) provide state-of-the-art neurogenetics and bioimaging services to the RCMI community and the larger biomedical research community at the University of Puerto Rico; 2) stimulate collaboration between RCMI Research Infrastructure Core (RIC) units and support initiatives for development of early-career investigators; and 3) participate in programmatic community engagement activities. METHODS: The NBS core consists of a NeuroImaging Facility (confocal, live imaging, electron microscopy), a shared Molecular Neurobiology lab, a Neurogenetics resource, and a Cell Culture lab. Support and training are provided by Dr. Mark W. Miller, Service Lead, and Mr. Luis Quiñones, Lab Technician. RESULTS: During the past year, July 2018 to June 2019, the UPR RCMI NBS facility accommodated 1,442 visits from 21 laboratories. CONCLUSION: Many of the projects conducted at the NBS address minority health and health disparities. The RCMI Neurogenetics and Bioimaging Services facility is committed to expanding its impact across all fields of biomedical research conducted at the University of Puerto Rico Medical Sciences Campus and by the greater RCMI community.

11.09.016

5-HT2A IN IMMUNOMODULATION AND STRESS IN AFRICAN AMERICANS

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Background: Serotonin is a monoamine neurotransmitter that is synthesized mainly in the brain and intestine and plays a crucial role in the regulation of several psychological functions and immune response through binding to 7 groups of receptors. Studies showed that the presence of single nucleotide polymorphism (SNP) in some serotonin receptors may associate with immune system dysregulation. Accordingly, we hypothesized that the presence of specific SNPs in serotonin receptor 2A gene (5HT2A) may modulate serotonin binding to immune cells and result in a possible higher risk of immune system dysregulation. Methods: Saliva samples were obtained from 602 young African American male and female subjects between 18-25 years followed by genotyping of four SNPs within 5HT2A which are rs6304, rs6310, rs6312 and rs4942578 using TaqMan. Genotype and haplotypes frequency, and association analysis were determined using SNPSTATS software program. Result: The C/C genotype of the coding SNP rs6304 was found to be significantly associated with elevated blood cortisol, CRP and IgM levels. The C/T genotype of rs6312 was found to be associated with elevated IgA level. Haplotype association analysis showed that CTTT haplotype is associated with elevated cortisol and IgE levels. Conclusion: Our result showed possible associations between the coding SNP rs6304 genotypes' and immune biomarker levels. These results indicate that SNPs in the 5HT2A gene might modulate serotonin binding and receptor signaling resulting in immune system dysregulation.

11.10.001

A NOVEL PEPTIDIC INHIBITOR OF PORPHYROMONAS GINGIVALIS

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Meharry Medical College

PURPOSE: Periodontitis is the 6th most common non-communicable infection worldwide, and about half of the adult population in the US suffers from periodontitis, constituting a huge economic burden. The current treatments for periodontal diseases are based on removal of dental plaque toto maintain and improve gingival and periodontal health. However, the relief is often temporary, and recurrence of the disease is common after conventional treatment, possibly due to re-emergence of periodontal pathogens, particularly P. gingivalis. METHODS/ RESULTS: Previously, we reported a peptide inhibitor of P. gingivalis (SAPP) that specifically targets P. gingivalis and reduces its virulence potential in vitro. Using a cytokine array analysis, we further found that levels of several cytokines including IL6, IL8, and MCP1 in the cultural media of human oral keratinocytes (HOKs) were significantly diminished in the presence of P. gingivalis. The levels of these cytokines were restored, at least partially, in the cultural media of HOKs exposed to P. gingivalis treated with SAPP. We also observed in an ex-vivo assay that SAPP efficiently inhibited biofilm formation of mixed species oral bacteria and significantly reverse abnormal innate immune responses induced by the mixed species oral bacteria. Convincingly, we demonstrated, using a mouse model, the role of SAPP in protection of alveolar bone loss induced by P. gingivalis. CONCLUSION: Our results suggest that SAPP specially target P. gingivalis and its associated bacterial communities and could be invisioned as an emerging therapy for periodontitis.

12.04.001

PSYCHOTROPIC MEDICATION USE ON STRESS AND METABOLIC MARKERS

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Serious mental illness (SMI) is a health disparity holding multiple associations with disproportionate lifetime morbidity and premature death. Compared to the general population, people with SMI (PWSMI) often die 26.3 years earlier due to poor cardiometabolic health and the high prevalence of psychotropic medication use (PMU) among PWSMI increases metabolic risk factors. Higher PMU (i.e. multiple drugs, high doses) is associated with unhealthy lifestyles: 1) food intake (i.e. overeating, anorexia), 2) secondary metabolic effects (i.e. dyslipidemia, cholesterolemia) and 3) altered neuroendocrine responses (i.e. elevated stress, cortisol). PURPOSE: We examined novel associations between PMU, daily meal frequency (DMF), perceived stress (PS) and secondary mediators (i.e. cortisol, lipids) among PWSMI. We hypothesized that PMU use will be inversely associated with DMF and stress markers. METHODS: In this cross-sectional pilot study, we recruited 30 outpatients receiving mental health services from the PHSU-Wellness Center before 10:00am. After informed consent, participants completed self-reported questionnaires on sociomedical history, PS Scale and DMF. Fasting blood, saliva and hair were also collected. Cortisol levels were determined by ELISA. Dataset values were group compared using Mann-Whitney U test with $p < 0.05$ being significant. RESULTS: Hair cortisol levels ($p = 0.0338$) and PMU ($p = 0.0098$) were greater in PWSMI < 3 daily meals compared to those with 3 or more. PWSMI taking 2 ≤ psychotropic medications had lower cortisol levels and less weekly vegetable intake. CONCLUSION: Results tentatively suggest that PMU and DMF affect cardiometabolic health via endogenous stress pathways and are important risk factors to curtail health disparities among PWSMI.

13.01.001

REORGANIZATION OF CCRTD RESEARCH INFRASTRUCTURE CORE IN CAU

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Clark Atlanta University (JZ, TG, VA, VO)

The Research Infrastructure Core (RIC) within the Center for Cancer Research and Therapeutic Development (CCRTD), at Clark Atlanta University (CAU) provides state-of-the-art research support including instruments, technology, education, and training for all investigators and research staffs engaged in health-related scientific research. Eight previous core facilities have recently been consolidated to five functional core laboratories, including the creation of a novel Animal Core Laboratories to support research projects and pilot projects funded by NIH/NIMHD/RCMI U54 Grant 2U54MD007590-32. With the continued support from RCMI program and Georgia Research Alliance, several cutting-edge instruments including BioRad CFX Connect Real-Time PCR Detection System, Carl Zeiss Axio Imager.Z1 microscope with Apotome, Carl Zeiss Axiovert 200M inverted microscope, Carl Zeiss LSM 700 confocal microscope, Leica LMD6000 Laser microdissection microscope, BD FACSJazz cell sorter, DAKO Autostainer, and Leica Aperio VERSA 8 were purchased for the RIC. Moreover, a web-based core facility management system, iLab Solutions, has been applied to improve RIC service and instrument management. It enabled users within CCRTD to make their reservations of special instruments and services online easily. It has also helped RIC manager and staffs in instrument usage tracking, billing and invoicing, in addition to reporting, and lab supplies requisitioning. The RIC reorganization is successfully supporting the health-related scientific research at CAU.

13.01.002

CURRICULAR INTERVENTIONS FOR ASSESSING ACEs

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Purpose: In the educational programs offered by medical schools, little time is spent on training students, who are future health care providers to offer competent care to patients with Adverse Childhood Experiences (ACEs). The purpose of this systematic review was to increase awareness of ACEs among medical students and enhance quality and frequency of ACEs assessment in medical settings. Method: To evaluate intervention studies focused on increasing awareness and enhancing ACE assessment in healthcare institutions, published articles were identified through searches of several databases using a combination of MeSH terms. Results: Out of 715 publications screened, 16 studies were identified that focused on medical education with respect to ACEs. These interventions targeted knowledge, skills, and comfort level using a variety of formats, including lectures, perspective-taking exercises, and small group discussions. Only a few articles were identified that reviewed efforts to train medical students. However, none of the interventions focused on vulnerable populations, such as migrant farmworkers, persons experiencing homelessness and LGBTQ persons, who are more likely to have been exposed to ACEs. Conclusion: While research documents a strong correlation between the number of ACE encounters experienced during childhood and adverse health outcomes of adulthood, our systematic review found little evidence to suggest medical schools are addressing ACEs in their curricula in a comprehensive manner. One of the key strategies for reducing bias is development of a curriculum that focuses not only on increasing awareness of ACEs but also allows students to practice bias reduction skills before treating patients in clinics.

13.02.001

RESEARCH INFRASTRUCTURE CORE AT XAVIER UNIVERSITY (XULA)

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Xavier University of Louisiana

The Xavier University of Louisiana (XULA) RCMI Cancer Research Center aims to enhance the quality and productivity of basic biomedical and behavioral research at XULA in the focus area of cancer and cancer-related health disparities by establishing a Research Infrastructure Core (RIC) that will have shared instrumentation, drug discovery and delivery programs, cell and molecular biology facilities, and bioinformatics services. The existing resources are built on the core laboratories that served XULA investigators and helped expand the research capacity in the last decade. Based on the assessment of strengths and weaknesses in the current research portfolio of XULA investigators, the RIC implements new rules of prioritization, revised and improved standard operation procedures, and effective management of core facilities including convergence of cross disciplinary expertise and cost recovery systems. The RIC maximally benefits XULA investigators across all health-related research areas by achieving three specific aims: Aim 1. Acquire, maintain, and operate shared analytical and bioanalytical instrumentation that will be utilized by not only the basic biomedical research projects and pilot projects to be funded by the current RCMI application, but also all XULA investigators across a broad range of health-related research areas. The RIC will provide essential instrumental and technical support for XULA's biomedical research projects that rely on the availability of functioning major equipment. Aim 2. Form a faculty expertise group (FEG) to provide faculty-level expertise in research methodology, specialized laboratory

techniques, statistics, bioinformatics and health informatics. The FEG will consist of senior faculty members with research expertise in experimental design and research strategy on drug discovery and formulation, cell and molecular biology, mechanistic investigations, and data processing using various bioinformatics and biostatistics tools drug discovery, drug delivery, cell and molecular biology, bioinformatics, and analytical instrumentation. Aim 3. Implement an effective cost recovery program for the Research Infrastructure Core. RIC will continue to use a fee charging system started in 2012. The FEG will oversee the charge back process and maintain account balance. The fees collected will continue to be used to partially defray the cost of consumable parts and unexpected repair costs needed for the core facilities. Additional measures will be implemented to increase cost recovery of core facilities by underwriting core staff efforts in external grant applications by XULA investigators.

13.03.001

OLA HAWAII PERSONALIZED TEAM-SCIENCE MENTORING PROGRAM

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University of Hawaii at Manoa (MJB, PB, GM, SO, BRJ, EKT, RY)

PURPOSE: The primary objective of the Ola HAWAII Investigator Development Core (IDC) is to grow and diversify the basic, clinical, and behavioral research workforce and thinkforce engaged in the science of minority health and health disparities. Excellence in mentoring is a key factor to career development. However, identifying mentors with the knowledge, skills and temperament best suited for individual mentees requires personalized attention. METHODS: The IDC has implemented a personalized career-development program for new and early-stage biomedical researchers. A Team-Science Mentoring Bootcamp is offered twice each year, with established investigators leading interactive sessions on career advancement, professional conduct and research resources. The IDC assists in matching mentoring teams with mentees, who jointly craft Individual Development Plans (IDP) and ensure that they are implemented for maximum career enhancement. The mentoring experience is further enriched by a complementary collection of additional faculty development opportunities provided by RTRN, IDeA-CTR and NRMN. RESULTS / EXPECTED RESULTS: Since the first Mentoring Bootcamp just over one year ago, over 90% of the mentees report new collaborations and mentoring relationships, 85% have given presentations at conferences, over 60% have new manuscripts published, over 90% have manuscripts in preparation, and 70% have submitted grant applications, with 11 awarded to date. Bootcamp participant numbers doubled from 19 in 2018 to 39 in 2019. Evaluations have provided excellent suggestions for further improvement. DISCUSSION / CONCLUSION: Our personalized team-science mentoring program has already had positive outcomes in the early stages of implementation, and we anticipate heightened research productivity and grants success.

14.01.001

GENES RELATED TO ANXIETY IN PUERTO RICANS

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PURPOSE: Anxiety is one of the most frequent psychiatric conditions which affect Puerto Ricans and contribute to a lower quality of life. The prevalence of anxiety across different ethnicities. Puerto Ricans have higher prevalence compared to other Hispanic. The goal of this study is to determine the most frequent gene variants in patients with anxiety. METHODS: We will recruit second generation of Puerto Ricans patients with a diagnostic of anxiety at the University of Puerto Rico Center for the Study and Treatment of Fear and Anxiety. After signing the written informed consent, sample for DNA extraction will be collected using buccal swabs. Variants will be determined with Infinium® Multi-Ethnic AMR/AFR Bead Chip. All the clinical data) will be collected from the health record. RESULTS / EXPECTED RESULTS: We expect to identify gene variants that can be associated with the severity of the symptoms and with the treatment durations. Also, we expect that patients with multiple variants in genes of interest will require longer treatments as compared to wild-types. DISCUSSION / CONCLUSION: The results will help to identify the genes and their variants that are present in Puerto Rican with anxiety. Also, we will develop a polygenic score of the risk factor to suffer from anxiety severe symptoms or treatment failure. This score will take into consideration the prevalence and unique variants present in Puerto Ricans. The results will give us some insight on what genes are more relevant to anxiety in our population and thus help guide future research.

14.01.002

ADRM1 IS DIFFERENCIALLY EXPRESSED IN CERVICAL CANCER

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PURPOSE: Worldwide, cervical cancer is the third most common cancer among women and the second most frequent cause of cancer-related death. The American Cancer Society's estimates for cervical cancer in the United States for 2019 indicate that Hispanic women are most likely to get cervical cancer, followed by African-Americans, Asians and Pacific Islanders, and whites. Therefore, understanding the pathways of aggression leading to health disparities is an important issue for cervical cancer. One such pathway is Ubiquitin-proteasome

pathway as cervical cancer cell lines exhibit greater sensitivity to proteasome inhibitors than HPV-negative cervical cancers or primary human keratinocytes. METHODS: We analyzed for expression of genes among the races involved in proteasome degradation pathway by using The Cancer Genome Atlas (TCGA) datasets. We performed immunohistochemistry analysis on Caucasian, African American and African clinically annotated cervical cancer patient samples. RESULTS: Our TCGA analysis results indicate that ubiquitin receptor ADRM1 is significantly elevated in the cervical tumors of African American patients. Our immunohistochemistry analysis on Caucasian, African American and African cervical cancer patient samples further confirmed the protein level difference of ADRM1 among the races. Finally our invitro studies by using ADRM1 specific inhibitor RA190, on cervical cancer cells with different race ancestry indicated differential sensitivity in IC50 values. CONCLUSION: Taken together our findings reveal that this mechanism is more likely to occur in African and African American patients. Our studies will advance our knowledge of vulnerable pathways in cervical cancer treatment.

14.01.003

SMALL MOLECULE TARGETING NLRP3 INFLAMMSOME IN MICROGLIA

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Uncontrolled CNS inflammation forms the pathophysiological basis of numerous disorders, including Alzheimer's disease (AD), a disease that affects the minority population disproportionately. Evidence strongly suggests that the inhibition of the NLRP3 inflammasome is a promising strategy for the treatment of AD. A variety of natural products including curcumin, resveratrol, and isoliquiritigenin have displayed encouraging in vitro NLRP3 inhibitory activity. These natural products, however, are reported to display low chemical and/or enzymatic stability and therefore are not considered as promising leads for drug discovery. Using computer-assisted drug design methods and classical medicinal chemistry approaches, we developed a library of tertiary sulfonylurea compounds that resembled the 3D-structure of the aforementioned natural products without the moieties responsible for the reported chemical and enzymatic instability. The compounds were synthesized, characterized, and tested for their NLRP3 inflammasome inhibitory activity. Preliminary studies indicated two of our compounds decreased the NLRP3 expression in a dose-dependent manner. These compounds reduced the production of inflammatory markers, such as, IL-1b, TNF-a, and caspase 1. MTT assays revealed that the sulfonylurea compounds did not affect the neuronal cell viability. Using computational chemistry and pharmacophore modeling, our efforts are currently focused on structural modifications to improve the biological activity of our lead molecules and penetration into the blood-brain barrier.

14.04.001

INCREASED INITIATION OF BLEBBISHIELD EMERGENCY PROGRAM SIGNA

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Hypothesis: Non-small cell lung cancer (NSCLC) accounts for 80% of all lung cancers, and is one of the most common malignant tumors worldwide. Moreover, NSCLC tumor metastasis is a leading cause of mortality and heavily driven by TGF-β mediated growth signaling. Literature has shown that these signaling pathways are involved in increased metabolism and tumor aggression which are both driving factors of drug resistance. We believe that the combination of CDODA-Me with Erlotinib will be able to overcome TGF-β induced metastasis leading to decreased tumor growth. Methods: NSCLC cell lines HCC827 spheroids (both erlotinib resistant and sensitive), were treated with CDODA-Me or Erlotinib alone and then combined. Cells were collected after 24hr and microRNA expression profiling was conducted to determine synergistic effects vs. single treatment groups. TGF-β was used to induce EMT signaling which was measured through cell invasion, migration, and spheroid formation assays.Western Blot analysis was used to confirm identified pathways as well as to quantify the effects of CDODA-Me on VEGF and TGF-β cellular release levels during treatment as well as MET and EGFR kinase activation. Samples were taken at various timepoints during ERL treatment to determine the effects of treatment on cellular metabolism. Results: When comparing spheroids (S) vs monolayer (M), erlotinib had greater cytotoxicity on monolayers.In the presence of TGF-B (10ng/ml) spheroids grew larger an observation that was overcome by combination treatment. . Western blot analysis shows that spheroid culture increased E-cadherin expression levels and the addition of TGF-B decreased these levels coupled with an increase of N-Cadherin. Combination therapy overcame the effects of TGF-B on these markers. Blebbishield transformation was confirmed through visual observation to occur at the 24hr timepoint. Western blot analysis confirmed this through increased expression of metabolic signaling proteins. Sphere reattachment was found to be dependent on the presence of growth factors VEGF and TGF-β. Media obtained after incubation in parental cells provided higher

levels of VEGF and TGF-β when compared to media obtained after 24hr treatment with (resistant to non-resistant expression ratios of 3.94 and 4.06 for HCC827 (4μM erlotinib resistant) and HCC827 Cl4 respectively). Genomic studies showed an increase in microRNAs linked to increased drug response when comparing combination therapy to ERL single treatment. Conclusions: Based on the results of these studies, CDODA-Me has been shown to inhibit NSCLC cell types from overcoming apoptosis thereby inhibiting increased drug resistance as well as tumorgenicity.

14.04.002

MICRORNA-18A AS A THERAPEUTIC TARGET IN CISPLATIN-RESISTANT

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Ovarian Cancer is the deadliest gynecological malignancy among women in the United States. Despite initial response to standard treatment of platinum and taxane-based compounds, most patients exhibit platinum resistance and eventually succumb to the disease. Strategies to overcome platinum resistance have not yielded positive outcomes yet. MicroRNAs have recently emerged as potential therapeutic targets for ovarian cancer treatment. In an expression array we found miR-18a (the 5p strand), to be significantly decreased in cisplatin-resistant ovarian cancer cells compared with cisplatin-sensitive cells. Moreover, using a miR-18a oligonucleotide mimic (miR-18a-OMM) we observed a reduction of cell growth in around 70%. Therefore, we hypothesize that upregulation of miR-18a with miR-18a-OMM will have a therapeutic effect on cisplatin-resistant ovarian cancer. To prove this hypothesis, we conducted in vivo therapeutic studies in which miR-18a-Folate-liposomal formulations were injected intraperitoneally into tumor-bearing mice (seven injections in 4 weeks). In addition, to identify miR-18a target genes we used computer tools, quantitative PCR (qPCR), and western blot analysis. Our in vivo studies showed that there was a significant decrease in tumor weight of miR-18a-OMM-treated mice compared to control mice. In our bioinformatic analysis we obtained 19 potential miR-18a-regulated genes. Following transient transfection of cisplatin-resistant ovarian cancer cells with miR-18a-OMM we isolated RNA and performed qPCR and identified seven mRNA as potential miR-18a targets. Taken together, these results demonstrate the efficacy of miR-18a-OMM as therapy for cisplatin-resistant ovarian cancer. Future experiments will perform pharmacokinetic and pharmacodynamic experiments of the miR-18a-Folate-liposomal formulation.

14.04.003

BELINOSTAT ANALOGS AS POTENT HISTONE DEACETYLASE INHIBITORS

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PURPOSE: Histone Deacetylase (HADC) is one of the most promising targets for anticancer therapy. Thus numerous HDAC inhibitors are being investigated as monotherapies or in conjunction with chemotherapy, biological therapy or radiation therapy. The main purpose of this study is to design, synthesis and evaluate new HDAC inhibitors as anticancer drugs. METHOD: A series of HDAC inhibitors based on N-hydroxycinnamamide fragment was designed as the clinically used belinostat analog using amide as the connecting unit (CU). All target compounds were evaluated for their in vitro HDAC inhibitory activities and some selected compounds were tested for their antiproliferative activities. A comprehensive understanding of the structure activity relationship was obtained. The most and the least active compounds were examined by molecular modeling studies. RESULTS/EXPECTED RESULTS: A total 19 analogs of belinostat were synthesized and studied for HDAC inhibitory activity. The results suggest that the amide moiety would be more promising as the CU compared with an ether substitution for the same. Among all, compound 7e exhibited strong HDAC inhibition. Molecular modeling studies predicted stronger binding for the most active compound (7e) than the least active compound (7b), which is in consistent with the inhibition data. DISCUSSION/CONCLUSION: Out of all the belinostat analogs, compound 7e showed an IC50 value of 11.5 nM in inhibiting the HDAC in a pan-HDAC assay, being the most active compound of the series. This study is helpful for future efforts to optimize the activity of this type (amide CU) of belinostat analogs.

14.04.004

METABOLISM AND PHARMACOKINETICS OF A BELINOSTAT PRODRUG

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PUPPOSE: ZL277 is a prodrug of belinostat with enhanced bioavailability and efficacy as a pan HDAC inhibitor. The purpose of this study is to investigate the its metabolism

and pharmacokinetics. METHOD: Liver S9 fractions, liver microsomes, liver cytosol from rats were used to study the metabolism of ZL277 in vitro. Mice were used to study the pharmacokinetics of ZL277 in vivo. The MCF-7 cells-stimulated nude mice model was used to study the metabolites of ZL277 in breast tissues. HPLC-Mass spectrometers were used to analyze samples. RESULTS: The in vitro metabolic profile of ZL277 includes ZL277-B(OH)2-452, ZL277-OH-424, belinostat, belinostat amide, belinostat acid, and methylated belinostat. Both ZL277-OH-424 and belinostat underwent further glucuronidation in liver microsome, whereas only ZL277-OH-424 but not belinostat underwent some level of sulfation in rat liver cytosols. The pharmacokinetic study of ZL277 showed the parameters of active drug belinostat with a half-life (t1/2) of 10.7 hours, the area under curve value (AUC) of 1506.9 ng/mL*h, and the maximum plasma concentration (Cmax) of 172 ng/mL reached at 3h after a single dose of 10 mg/kg. The hydrolysis product of the prodrug, ZL277-B(OH)2-452 showed exposure at AUC of 8306 ng/mL*h and Cmax of 931 ng/mL at 3h after drug administration. DICUCUSSION/CONCLUSION: ZL277 could be easily metabolized into several metabolites both in vitro and in vivo through hydrolysis, oxidation-reduction, deamination, glucuronidation, and sulfation. ZL277 showed excellent pharmacokinetics profile compared to belinostat. ZL277 was mostly excreted in feces and urine.

14.04.005

DNAJAS EXPRESSION IN TRIPLE NEGATIVE BREAST CANCER CELLS

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PURPOSE: Triple Negative Breast Cancer (TBNC) lack of biological targets results in limited therapeutic options and leads to high mortality rates. Cytotoxic chemotherapy is a last resource for which Anthracyclines (Doxorubicin) are among the most effective anti-tumor therapeutic alternatives. However, use of Anthracyclines is associated with the development of dose dependent cardiotoxicity as well as drug resistance. The objective of our research is to observe the changes in the expression levels of the DNAJA proteins exposed to cytotoxic stress and chemotherapy to determine which DNAJA (1 to 4) plays a major role in the response to Doxorubicin. In addition, we will also evaluate the relevance of the DNAJA conserved domains on the function of the DNAJA protein relative to cell survival to exposure cytotoxic chemotherapy. METHODS: Expression level changes were investigated using Real Time-PCR and Western Blots, while analysis of relevant domains were assessed from the COSMIC database. Expression levels were determined before and after treatment of heat shock and anticancer agents. RESULTS/EXPECTED RESULTS: Our results indicate a role for the heat-shock response in the cellular response to Anthracycline exposure. Specifically, the Heat-Shock protein 40 (HSP40) type I, also known as DNAJAs (1 to 4), are required for cell survival upon exposure to Doxorubicin. After analyzing the COSMIC database, it was determined that the J-Domain proved to be the location of most mutations. DISCUSSION/CONCLUSION: Modifying HSP40 function in human cancer cells may provide an alternative to hypersensitization to chemotherapy, allowing for lower dosage with concomitant less side effects.

14.04.006

IN VITRO DISSOLUTION OF PLGA NANOPARTICLES USING SOTAX® USP

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PURPOSE: The present work is the first to investigate the feasibility of SOTAX®USP apparatus 4 in studying the in vitro sustained release profile of PLGA nanoparticles. A synthetic chemotherapeutic agent AC1LPSZG , a novel mammalian target of rapamycin (mTOR) inhibitor, was chosen as a model poorly water-soluble drug. METHOD: The polymeric nanoparticles were prepared by "nanoprecipitation" technique using biocompatible polymer Poly(lactide-co-glycolide) (PLGA-50:50) and nonionic surfactant poloxamer P188. The prepared nanoparticles were characterized for particle size, size distribution, zeta potential and drug entrapment effeciency The in vitro drug release was determined in phosphate buffer pH 7.4, employing a USP-4 apparatus CE7-smart (SOTAX®) incorporated with Float-A-Lyzer dialysis cells at 300 kDa molecular weight cut–off (MWCO). The flow rate and the temperature of release medium were set at 16 mL/min at 37°C, respectively. Experiments were done in triplicate and data are presented as the mean ± SEM. RESULTS: In this study, the prepared PLGA nanoparticles were 150±7 nm in size with narrow polydispersity index (PDI) 0.193±0.05. The zeta potential value was -17±4 mV with standard deviation 7.18±1.14 mV. The drug entrapment efficiency was 60±5 %; and 40±6 % drug was released at the end of 7 days. CONCLUSION: USP-4 apparatus can serve as a potential tool for determination of in vitro drug release from PLGA nanoparticles.

15.01.001

PREVALENCE OF CHRONIC HEALTH CONDITION IN PUERTO RICAN WOMEN

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University of Puerto Rico Graduate School of Public Health, UPR Medical Sciences Campus (KPR, MP, LM, RR, KMB, GB, JB, ZYC, RH, AJM, MM, JM, KMM, DIO, IP, MP, SAP, DR, PDR, DMR, MTS, ES)

PURPOSE: Chronic health diseases (CHD) are defined as those preventable conditions whose progress is slow (WHO, 2018). In Puerto Rico (PR), six out of the ten causes of death are related to CHD (DSPR, 2016). The purpose of this study was to create a health profile of adult women living in an underserved community focusing on CHD and associated factors. METHODS: To conduct this study, a semi-structured questionnaire was administered to 282 adult women from Medianía in Loíza, PR. The instrument requested information on sociodemographic data, quality of life, access to health services, risk factors, urbanism, and chronic diseases such as asthma, Alzheimer, cancer, diabetes, cardiovascular and cerebrovascular conditions, hypertension and kidney diseases. The generated health profile was utilized to assess the prevalence of CHD and its association with socioeconomic, cultural and environmental factors. RESULTS: The median age was 56 years old and that general health ($p < 0.001$), employment status ($p < 0.001$), health insurance ($p < 0.001$), alcohol use ($p < 0.017$), tobacco habits ($p < 0.003$) and mother's family history ($p < 0.001$) were statistically associated with the prevalence of CHD. More than half (51%) of the women suffered from hypertension, 26% of diabetes and 17% of asthma. Our survey also shown that 64% of the women suffered of at least one chronic disease. CONCLUSION: Based on these results, we recommended the implementation of capacity building programs that help improve health and well-being, enhance recreation, identify infrastructure needs, and incentivize employment. Development and implementation of these programs will create healthier and sustainable communities.

16.01.001

Predicting Model for In-hospital Mortality After Transcathet

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PURPOSE: This study sought to develop and compare an array of machine learning methods to predict in-hospital mortality after transcatheter aortic valve replacement (TAVR) in the United States. METHODS: Existing risk prediction tools for in-hospital complications in patients undergoing TAVR have been designed using statistical modeling approaches and have certain limitations. Patient data were obtained from the National Inpatient Sample database from 2012 to 2015. The data were randomly divided into a development cohort (n=7,615) and a validation cohort (n=3,268). Logistic regression, artificial neural network, naive Bayes, and random forest machine learning algorithms were applied to obtain in-hospital mortality prediction models. RESULTS: A total of 10,883 TAVRs were analyzed in our study. The overall in-hospital mortality was 3.6%. Overall, prediction models' performance measured by area under the curve was good (>0.80). The best model was obtained by logistic regression (area under the curve: 0.92; 95% confidence interval: 0.89 to 0.95). Most obtained models plateaued after introducing 10 variables. Acute kidney injury was the main predictor of in-hospital mortality ranked with the highest mean importance in all the models. The National Inpatient Sample TAVR score showed the best discrimination among available TAVR prediction scores. CONCLUSIONS: Machine learning methods can generate robust models to predict in-hospital mortality for TAVR. The National Inpatient Sample TAVR score should be considered for prognosis and shared decision making in TAVR patients.

16.01.003

COMPARATIVE MACHINE LEARNING SCRIPT FOR CLINICAL APPLICATION

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PURPOSE: The main goal of this project is to develop a user friendly script which compares Machine Learning (ML) models to predict classes for clinical decision making regarding minority populations. METHODS: The script was developed in Python using Jupyter Notebook. Data imbalance issues were tackled allowing a combination of random undersampling of the majority class and random or SMOTE oversampling of the minority class. Ranking variable algorithms were incorporated for model calculated weights. Random forest, logistic regression, support vector machines, naive bayes, and multilayer perceptron ML classifiers algorithms were implemented from scikit-learn library. To evaluate the performances of the algorithms, area under the receiver operating curve, accuracy, precision, recall, and f1 metrics were computed. RESULTS: This script is created for preprocessing, visualization, feature ranking, ML algorithm training, and ML model evaluation for biomedical datasets in order to develop new clinical decision support tools focused on minority populations. The user specifies the input file, the class to predict, and the split ratio for the training

and validation datasets. Then, the script eliminates cases with missing information, assigns labels, encodes categorical data, splits the data into training and validation subsets, balances the data, and train and validates the ML algorithms. Finally, the user evaluates performance metrics and selects the best ML model. CONCLUSION: We developed a script that can be run on a web browser for easier integration into a clinical workflow, which guides the user to input a data file and predict binary classification problems regarding minority groups.

16.01.004

QUANTIFICATION OF MICROGLIAL MORPHOLOGY BY DEEP-LEARNING APP

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Howard University(YY Hsu, CH Hsu, R Syed, PC Wang, TW Tu); Fu-Jen Catholic University (YJ Lee); Children's National Medical Center (A Agaronyan)

Tracking dynamic microglia changes is critical for analyzing their role in brain disease progression. The traditional image analysis for microglial classification through manual curation has remained a challenge. In this work, we utilize the state-of-the-art automated deep learning approaches to efficiently detect and segment microglial cells from histology images and classify the morphology to a well-established categorization system according to their morphometric indices. We apply the regions with convolution neural networks (R-CNNs) and the U-shaped convolutional network (U-Net) to the microglial cells pre-defined by neuropathologist's manual annotation. Both deep learning approaches automatically determine the salient microglial features, which can effectively reduce the workload of manual detection and segmentation process. We then developed support vector machines (SVMs) to build the microglial classification model based on the extracted results of R-CNNs and U-Net. Preliminary experiments show that our proposed deep learning framework is accurate and scalable to automate the curation of large microglial image datasets and provides a direct insight for the study of microglial biology. Our proposed framework should reduce the time-consuming effort and retrieve more microglial characteristics for improving the accuracy of cell quantifications. We would like to provide this open source framework via web service and a well-established database that are accessible to all neuroscience researchers.

16.02.001

A PITFALL IN MOLECULAR RESEARCH OF PCA RELEVANT TO GS

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PURPOSE: Gleason score (GS) is among powerful prognostic factors in prostate cancer (PCa). A GS-7 tumor typically has the primary architectural pattern and secondary prevalent one being graded with 3 and 4 (or 4 and 3), respectively. Due to the well-known multifocal occurrence of different patterns, a biological sample from a GS-7 tumor used in a molecular experiment will be uncertain regarding the actually represented pattern if no special attention is given in specimen preparation. In this study, by an integrative analysis of public gene expression datasets for PCa, we demonstrate that such an uncertainty is never uncommon. METHODS: First, based on the data of paired grade-3 and grade-4 specimens of 13 GS-7 tumors, we identify 288 differentially expressed genes with respect to those two architectural patterns. Then, using the TCGA data, we evaluate the prediction strength of the transcriptomic profiling of these genes for distinguishing the GS-6 (3+3) tumors from the GS-8 (4+4) ones. The obtained AUC statistic and p-value are 0.96 and 9× ⟦10⟧ ^(-17), respectively. After that, we show that the co-expression pattern of the signature genes in the subset of the GS-7 samples resembles to that present in the aggregate of GS-6 and GS-8 samples. Finally, we verify the findings using the GSE21032 data. RESULTS: Our results suggest that the GS-7 specimens used to generate two frequently-cited genome-wide expression datasets largely are individual GP-3 or GP-4 specimens rather than the "intermediate" specimens of GP-3 and GP-4. This provides molecular evidence for the aforementioned uncertainty of GS-7 tumor samples, indicating a potential pitfall in the existing molecular and translational research of prostate tumors relevant to GS. CONCLUSION: In this study, we provide evidence for the hypothesis that the set of experimental specimens of GS-7 tumors actually used in typical genome-wide research during past years is largely composed of either GP-3 specimens or GP-4 specimens. Because the analyzed gene expression datasets include hundreds of samples and are published in top scientific journals, it is not too bold to conclude that the uncertainty of architectural patterns in GS-7 PCa samples is never uncommon in previous studies. This insight indicates a pitfall in the current molecular research of prostate cancer relevant to Gleason score.

16.02.003

NURR1 AND OVERALL SURVIVAL AMONG BREAST CANCER PATIENTS

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Our previous studies of publicly available tissue microarray data showed that suppressed expression of the orphan nuclear receptor NURR1 is associated with oncogenic transformation, and shorter relapse free survival among systemically treated breast cancer (BCa) patients. Here we interrogated the TGCA

database to determine if NURR1's prognostic value is similar among patients of different racial identity. We used KMPLOT (http://kmplot.com/analysis) to the assess overall survival of BCa patients with upper quartile (high) or lower quartile (low) expression of NURR1 based on mRNA-seq data in the TCGA PanCancer Atlas. Patient data was stratified according to racial identity (Black or White). We also investigated the occurrence of mutations, copy number variation (CNV), and tumor subtype as they each relate to NURR1 mRNA expression and race. NURR1 mRNA expression in this cohort is predictive of greater overall survival among Black, but not White BCa patients. Among Black patient's samples, 43 bore shallow deletion in NR4A2, 22 had a copy number gain (of 182 Black BCa patients). CNV overall trended toward lower NURR1 mRNA expression. Overall, Black patients expressed lower NURR1 mRNA. Within specific tumor subtypes, basal cancers showed lower expression than in luminal A tumors. We show that NURR1 may function as a biomarker with specific predictive efficacy among Black BCa patients. NURR1 could potentially be the first biomarker used for race-conscious prognostication in BCa. These studies demonstrate a clear need for greater diversity biomarker development studies in order to adequately address cancer health disparities.

16.03.001

DETECTING EPIGENETICALLY SILENCED TUMOR SUPPRESSOR GENES

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PURPOSE: Recent studies have shown that epigenetic alterations, especially the hyper-methylated promoters of tumor suppressor genes (TSGs), contribute to prostate cancer (PCa) progression and metastasis. This paper proposes a novel algorithm to identify epigenetically silenced TSGs (epi-TSGs) for PCa. METHODS: Our method is based on the perception that the promoter CpG island(s) of a typical epi-TSG has a stratified methylation profile over tumor samples. In other words, we assume that the methylation profile resembles the combination of a binary distribution of a driver mutation and a continuous distribution representing measurement noise and intra-tumor heterogeneity. RESULTS/EXPECTED RESULTS: Applying the proposed algorithm and an existing method to the Cancer Genome Atlas (TCGA) PCa data, we identify 57 candidate epi-TSGs. Over one third of these epi-TSGs have been reported to carry potential tumor suppression functions. The negative correlations between the expression levels and methylation levels of these genes are validated on external independent datasets. We further find that the expression profiling of these genes is a robust predictive signature for Gleason scores, with the AUC statistic ranging from 0.75 to 0.79. The identified signature also shows prediction strength for tumor progression stages, biochemical recurrences and metastasis events. DISCUSSION/CONCLUSION: We propose a novel method for pinpointing candidate epi-TSGs in PCa. The expression profiling of the identified epi-TSGs demonstrates significant prediction strength for tumor progression. The proposed epi-TSGs identification method can be adapted to other cancer types beyond prostate cancer. The identified clinically significant epi-TSGs would shed light on the carcinogenesis of prostate adenocarcinomas.

16.03.002

DRIVER GENE MUTATIONS BASED CLUSTERING OF TUMORS

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PURPOSE: Somatic mutations in proto-oncogenes and tumor suppressor genes constitute a major category of causal genetic abnormalities in tumor cells. The mutation spectra of thousands of tumors have been generated by The Cancer Genome Atlas (TCGA) and other whole genome (exome) sequencing projects. A promising approach to utilizing these resources for precision medicine is to identify genetic similarity-based sub-types within a cancer type and relate the pinpointed sub-types to the clinical outcomes and pathologic characteristics of patients. METHODS: We propose two novel methods, ccpwModel and xGeneModel, for mutation-based clustering of tumors. In the former, binary variables indicating the status of cancer driver genes in tumors and the genes' involvement in the core cancer pathways are treated as the features in the clustering process. In the latter, the functional similarities of putative cancer driver genes and their confidence scores as the 'true' driver genes are integrated with the mutation spectra to calculate the genetic distances between tumors. RESULTS: We apply both methods to the TCGA data of 16 cancer types. Promising results are obtained when these methods are compared to state-of-the-art approaches as to the associations between the determined tumor clusters and patient race or survival time. In particular, we find statistically significant associations between the mutation-based tumor clusters and the racial groups of patients in six cancer types. We further extend the analysis to detect mutation-characterized transcriptomic prognostic signatures, which are directly relevant to the etiology of carcinogenesis. CONCLUSION: The results obtained by the proposed methods and existing approaches collectively constitute a catalogue of tumor stratification patterns, which may represent potential cancer sub-types that warrant further investigation. This study also demonstrates a way to integrate the results of

mutations based tumor clustering with the widely available gene expression data for prognostic signature identification.

16.05.002

EXPRESSION PROFILING IDENTIFIES TWIST2 TARGET GENES IN SETLE

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Setleis Syndrome (MIM#227260) is a rate type III focal facial dermal dysplasia frequently found in Puerto Ricans, presenting with bilateral temporal skin lesions of hypoplastic dermis, eyelash abnormalities and absent meibomian glands. Setleis Syndrome is caused by homozygous mutations in the TWIST2 gene, which codes for a transcription factor of the bHLH family known to be involved in skin and facial development and control of epithelial to mesenchymal transition. PURPOSE: Identity potential TWIST2 target genes involved in development and the processes and functions under its control. METHODS: We obtained gene expression profiles by microarray and RNA Seq analyses from normal and Setleis Syndrome patient primary skin fibroblasts and lymphoblasts. RESULTS: Out of 287 differentially regulated genes in fibroblasts, 189 were down-regulated and 98 were up-regulated, while in lymphoblasts a smaller number of differentially regulated genes (145 down-regulated and 13 up-regulated) were found after microarray analysis. RNA-Seq analysis of skin fibroblasts identified 315 under-expressed vs 173 over-expressed coding, miRNAs, snoRNAs, antisense and lincRNAs genes. Real time PCR reactions confirmed altered expression of differentially regulated genes. DISCUSSION: TWIST2 is described as a repressor, but expression profiling indicates it has a role in gene activation, as evidenced by the much higher proportion of down-regulated genes in cells from Setleis Syndrome patients, including cytokine genes, as well as genes that function in Cell-To-Cell Signaling and Interaction, Cellular Movement, Hematological System Development and Function. The top gene network found by RNA Seq functions in Connective Tissue Development and Function, Tissue Morphology and Carbohydrate Metabolism.

16.05.003

VIT.D-ASSOCIATED MIRNAS IN BREAST CANCER IN AFRICAN AMERICAN

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Breast cancer (BCa) is one of the most common malignancies in women with incidence and distribution varying widely among women of different ethnic backgrounds. African American (AA) population shows the lowest level of Vitamin D (VD) and highest incidence of BCa among ethnic population. Epidemiological studies suggest a link between increased incidence of BCa and low levels of VD. VD exerts its action via binding to its ligand, Vitamin D receptor (VDR). We investigated VDR genotypes in African American women and in a TNBC cell line that was exposed to Vit D in culture media. METHODS: We analyzed the 1000Genome databases for VDR SNPs that are prevalent in African Americans and established their prevalence in a Case-Control study. An African American TNBC cell line that has 2 of the 3 significantly associated SNPs to breast cancer was used in culture media with and without VitD to assess effects on cell proliferation and miRNA expression profile. miRNA expression was determined by the Nanostring encounter. RESULTS: Five SNPs were found to be more prevalent in African American subjects from the 1000enome database. Three of these SNPs. Were strongly associated with breast cancer in the case-control study, in a statistically significant manner. Two of these significant SNPs were found in a TNBC cell line that showed a close to normal proliferation level when VitD was added in the culture media. In the presence of VitD, 6 miRNAs (4 oncogenic and two TSG) were altered (hsa-miR-200b-3p, hsa-miR-7-5p, hsa-let-7b-5p, hsa-miR-205-5p, hsa-miR-23a-3p, hsa-miR-29b-3p). Conclusion: Our results indicate that the reduction of specific cancer-related miRNAs may be used as direction for a beneficial treatment with VD to protect from breast cancer, especially in TNBC cancer types that are prevalent and aggressive in AA women.

16.06.001

DEVELOPMENT OF A WEB-BASED TOOL FOR POPULATIONAL AND LOCUS S

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PURPOSE: Ethnicity is an important factor for effective drug recommendations. Hispanic populations come mainly from three different continental ancestries, i.e. European, African and Native Americans. Although a Hispanic patient may look white, the inherited specific genes associated, for example with cardiovascular drug resistance, may come from his/her black ancestry. The main goal of this work is to develop more user-friendly tools to determine the ancestry in Hispanics populations and use this information to create personalized

treatments. METHODS: We created several tools in different environments for preprocessing data, create input files, execute the existing ancestry tools and, finally, visualize and analyze the results. Scripting and programs were developed in Python, R and Java, along with PHP, SQL and JavaScript. To test our tools, we used sample data from Puerto Rican cardiovascular patients. As reference data, we downloaded the information from 1000Genome project populations. EXPECTED RESULTS: The main result of this work is a set of in-situ tools to manipulate genetic data to compute ancestries, focused on Hispanic population. These tools ranges from functionalities related to manipulate raw genetic data files, develop quality control, format input files until visualization and statistical analysis. Using these tools, we obtain populational and locus specific ancestry distributions for the Puerto Rican patients under cardiovascular treatments. Triangle and bar plots, along with principal components and Karyograms can be visualized. CONCLUSION: Our tools provide a user-friendly, fast and accurate option for ancestry analysis that can improve drug recommendations in Hispanics.

16.06.002

RACIAL DISPARITY PATTERNS IN PCa MORTALITY

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PURPOSE: A major racial disparity in prostate cancer (PCa) is that African American (AA) patients have a higher mortality rate than European American (EA) patients. We performed an integrative analysis of the SEER data and molecular biology data to further clarify such a disparity. METHODS: We filtered the SEER 2009-2011 records and divided them into four groups regarding patient race and cancer grades. On such a partition, we performed a series of analyses using standard statistical methods. Molecular evidence for a primary result of the epidemiological analysis is obtained by using several public gene expression datasets. RESULTS: Based on the registry-specific measures, a significant linear regression of total mortality rate on the percentage of high-grade cancers (PHG) is demonstrated in EAs ($p < 0.01$) but not in AAs. PHG and its racial disparity are differentiated across ages and the groups defined by patient outcomes. For patients with cancers in the same grade category, the survival stratification between races is not significant in most geographical areas. The genes differentially expressed between AAs' and EAs' tumors of the same grade category are rare. DISCUSSION: The perception that prostate tumors are more lethal in AAs than in EAs is convincing regarding AAs' higher PHG. However, this perception is questionable when the comparison is focused on cases within the same grade category. Supporting observations for this conclusion hold a remarkable implication for erasing racial disparity in PCa. That is, "Equal grade, equal outcomes" is not only a verifiable hypothesis but also an achievable public health goal.

16.06.003

ELECTROCHEMICAL MICROARRAY SYSTEM FOR BIOMARKER DETECTION

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The research on biomarker detection has increased dramatically in recent years and many strategies has emerged. However, current methods for identifying specific biomarkers and small molecules for point of care (POC) diagnosis outcomes suffer shortcomings of limited specificity and complex procedure in the measurement and the lack of real-time analysis to establish a causal relationship between an individual's profile and impact on health. The goals of our research are 1) to provide researchers with a new tool to better assess the impacts of biomarkers and small molecules for the cancer diagnosis and treatment and 2) to provide individuals with an inexpensive benchtop device for rapid reporting of exposure data for personalized alerts and managed care services. To achieve these goals, we are exploring several key technologies and approaches that will enable implementation of a novel autonomous sensorarray microsystem for acute multi-analyte assessment, such as sulfatases, antibody/antigen and micro-RNA/RNA, with the sensitive real-time monitoring. Electrochemistry signals were classified and quantified during the bio-interactions on the designed electrode interface, exhibiting the excellent sensitivity and specificity for targeting biomarkers without adding signal media and label. In the long term, a significantly improved medical understanding of biomarkers and small molecules would allow more relevant regulation of cancer recurrence and effective personal medical management. This project would provide medical researchers and physicians with a much needed and currently non-existent tool for personal treatment assessment and decision, over fine time scales, adding revolutionary capability to the study and treatment of acute process, and leading to more relevant disease regulation, intervention for individuals diagnosis, and ultimately improvement of overall public health.

19.01.001

FBXO32 AND FOXO ARE COORDINATELY EXPRESSED IN MCI A AMERICAN

FB BEDADA; OE Ntekim; EO Nwulia; TV Fungwe; S Nadarajah; TO Obisesan

HOWARD UNIVERSITY (FBB, OEN, TVF, SN), HOWARD UNIVERSITY HOSPITAL (EON, TOO)

BACKGROUND/PURPOSE: The UPS and FOXO transcription factors play a pivotal role in maintaining the clearance system and preventing the accumulation of cells with damaged DNA and neurodegeneration. However, data are lacking regarding the role of components of UPS and FOXOs in African Americans (AA)s with MCI. It is also unknown whether fitness adaptation can alter expressions, or have downstream effects on FBXO32, TRIM63, and FOXO1. We hypothesize that exercise can enhance cellular ability to repair damaged DNA and clearance system during aging and neurodegeneration by increasing expressions of FBXO32, TRIM63, and FOXO1. METHODS: We used TaqMan gene expression analysis to investigate the component of UPS and FOXOs and provide mechanistic insight at baseline, during exercise, and in both genders. RESULTS: At baseline, only FBXO32 but not TRIM63 was expressed. A 3-month exercise intervention increased levels of FBXO32 compared with baseline. To discern gender-specific exercise-related changes, we observed that levels of FBXO32 increased in men but not in women. However, levels of FBXO32 was higher in women than in men at baseline. To gain mechanistic insight, we compared the expression level of FBXO32 to FOXO1, where both genes were coordinately expressed at baseline, during exercise, and in both genders. DISCUSSION/CONCLUSIONS: Our results demonstrate one-to-one stoichiometric expression pattern and existence of co-regulatory mechanism between FBXO32 and FOXO1. Given the significance of FBX032 and FOXO1 in neurodegeneration, our findings may explain, at least in part, the advantageous effects of exercise on memory, gait, and balance in AA MCI.

19.09.001

THE AR H1-H3 LOOP IS A PUTATIVE FKBP52 REGULATORY SURFACE

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PURPOSE: Folding of steroid hormone receptors to their functional conformation requires the assembly of three complexes which involve at least twelve proteins, many of which are potential therapeutic targets for prostate cancer treatment. The final complex in which the receptor is capable of high-affinity hormone-binding includes Hsp90, p23 and the FKBP proteins 51 or 52. FKBP52 is known for being a positive regulator of AR, PR and GR activity. Previous studies have identified the BF3 surface as an AR-specific regulatory site for FKBP52, and it is likely that there is another common regulatory surface among receptors. Furthermore, mutations within the H1-H3 loop on the GR affect FKBP52-mediated receptor activities and has been proposed as a putative regulatory surface for the FKBP proteins. Thus, our current hypothesis is that the H1-H3 loop serves as a common regulatory surface for FKBP52 among the steroid hormone receptors. METHODS: We conducted site-directed mutagenesis to identify the residues within the AR H1-H3 loop that are critical for FKBP52 regulation. Yeast-based reporter assays were performed to assess the role and relevance of those mutations in receptor signaling and FKBP52 binding affinity. RESULTS: We have identified functional mutants within the AR H1-H3 loop that show hyper-dependence on FKBP52 for normal function. CONCLUSION: Our preliminary data suggest that the H1-H3 loop is a relevant regulatory surface for the FKBP cochaperones, and that this regulatory site is likely shared by AR, GR and PR.

19.12.001

ENDOMETRIAL ORGANOIDS CAN PERSONALIZE ENDOMETRIOSIS THERAPY

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Endometriosis is an estrogen-dependent chronic gynecological inflammatory disorder in which immune system dysregulation may play a role in its initiation and progression. It is defined as the growth of endometrial tissue (specifically glands and stroma) outside the uterine cavity predominately, in the peritoneal compartment. The peritoneum is the tissue lining the abdominal wall and organs in the abdominal regions. The knowledge of molecular and cellular regulation in the endometriotic endometrium is poor. This is mainly due to multiple autocrine-paracrine hormonal signaling and lack of study models that are reliable and reproducible. Moreover, two-dimensional cell structures do not truly represent three-dimensional organ biology and functionality. Here, we have established a novel and promising organoid model from human endometrium. Organoids are small three-dimensional tissue cultures derived from stem cells that serve as replicas of the organ of interest. Dissociated human endometrial tissue was embedded in Matrigel under defined culture medium conditions. This caused a swift formation of organoid structures that showed long-term expansion capacity and reproduced the molecular and histological phenotype of the tissue's epithelium. The organoids phenocopied physiological responses of endometrial epithelium to hormones, including increased cell proliferation under estrogen and maturation upon progesterone. Together, we established an organoid culture system for endometrium, reproducing tissue epithelium physiology and allowing for long-term expansion. This novel model provides a

powerful tool for studying mechanisms underlying the biology as well as the pathology of this key reproductive organ. Future opportunities for research include utilizing organoid models to examine how reduced capacity to repair DNA affects the development of uterine fibroids.

| BEHAVIORAL SCIENCE |

21.01.001

STUDY OF CERVICAL CANCER USING A QUANTITATIVE RISK ASSEMENT

E Abdalla; T Habtemariam; S Fall; R Troy; B Tameru; D Nganwa

Tuskegee University (E Abdalla; T Habtemariam; S Fall; R Troy; D Nganwa) and U.S. Department of Agriculture, Food Safety and Inspection Service (USDA/FSIS) (B Tameru)

The objective of this study is to conduct a quantitative risk assessment (QRA) to determine factors that may explain differences in Cervical Cancer (CerCancer) outcomes between races, by locations, age groups, stages, and treatments. The data was extracted from the Alabama Cancer Registry from 2004 to 2013. The risk pathway scenario tree was developed. Monte Carlo simulations for QRA was executed with @Risk 5.70 software. Results: In rural Black Belt County, Blacks 65 to 74 years old diagnosed with regional stage of CerCancer had a high value for the likelihood of CerCancer prevalence rate ranged (from 6.598x10-6 to 2.119x108 with the mean of 1.765x106, after receiving their treatments. Sensitivity analysis along with the tornado chart was useful for identifying the key variables and uncertain parameters that were driving the result of the model by giving some measure of the input distribution's influence on the output. In urban county, Whites 75 years and older diagnosed with regional stage of CerCancer and underwent chemotherapy treatment. Similarly, in other rural county, Blacks 17- 49 years old and Whites 50 - 64 years old diagnosed with regional stage of CerCancer and underwent surgery-radiation sequence treatment. These treatments had almost the same high impact of about 81% on the likelihood of still having CerCancer in these patients, compared to any other treatments and age groups whether in Blacks or Whites. Conclusion: Treatment disparities exist between Blacks and Whites in Alabama. Differences in care may significantly contribute to racial disparities in outcomes for women with CerCancer.

21.02.001

SYNERGY ACROSS RACE, LOCATION & HEART DISEASE IN HISPANICS

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The focal points of this study are the interactions between PM2.5 exposure, genetic variants and genetic ancestry with the expression (or lack there-off) of chronic conditions (i.e. cardiovascular diseases) in Puerto Rican populations living in the island of Puerto Rico using available genetic and environmental data that is geographically bounded.The data used contains clinical and genomic information from 191 patients undergoing Warfarin and Clopidrogel treatments at the Hospital Centro Médico at San Juan, Puerto Rico. To generate a PM2.5 exposure estimate, a clustering algorithm similar to K-Nearest Neighbor (KNN) was used in conjunction with the average value for PM2.5 levels from January 2000 to January 2015 per monitoring location in Puerto Rico, these were used as the value for each starting central point (centroid) in the model. Procedures like ancestral fractions estimation with ADMIXTURE, regression, mutual information and ANOVA were used to verify if any associations exist. Results showed a significant association between pulmonary embolism and average PM2.5 exposure ($p = 0.0422$) while there is a possibility that the level of iberian ancestry might be an important factor in this outcome ($p = 0.0511$). The detection of effective interactions between the three variables might lead to the discovery of pathways that are currently unknown. Thus, this research could lead the way to better personalized treatments and drug recommendations for underrepresented cardiovascular disease patients. Moreover, it also serves to identify mechanisms by which exposure to air pollutants may influence public health.

21.05.001

USE OF SOCIAL NETWORKS FOR SEXUAL ENCOUNTERS IN PUERTO RICO

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PONCE HEALTH SCIENCES UNIVERSITY/ PONCE RESEARCH INSTITUTE (CL, KA, PL, VRA)

PURPOSE: Social network technologies have become very popular over the past years. With the internet connecting people across the globe, many social networking websites compete for consumers' attention. The increase in social networking between people has facilitated sexual encounters. The purpose of our study was to explore the role of social networking in Puerto Rico and assess the rate of using these technologies for sex-seeking and sexual risk behaviors. METHODS: We collected socio-demographic information from study participants. To assess the array of reasons to seek sexual encounters across social network technologies in Puerto Rico, we used a short anonymous questionnaire distributed through the internet. The questionnaire evaluated several relevant aspects to determinate

the risk of disease transmission, including HIV. RESULTS: We recruited 314 participants; 45% females, 49% males, and 5% missing data. Men reported using social networking technologies more frequently than women to engage in sexual encounters. The principal reason for the use of social networks is the privacy level provided by this approach. CONCLUSIONS: The privacy factor promotes the search for sexual encounters with anonymous partners, which may translate into increased risk of disease transmission. If we can see more clearly how social networks are used to establish sexual encounters, we can help to develop prevention strategies or reduce the risk of among our youth population. Measurement of these determinants over time is crucial for the evaluation of prevention programs.

21.09.001

ROLE OF NEUROKININ RECEPTORS IN THE MODULATION OF NICOTINE W

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PURPOSE: Although prevalence of cigarette and tobacco use in America's minority population is statistically lower compared to the American White population, minorities are more likely to die from smoking related diseases. The most effective way to intercept and circumvent the effects of first and second hand smoking is cessation. The emergence of nicotine withdrawal symptoms after cessation is the most challenging thing to overcome, and failure to do so often leads to relapse. The aim of this project is to measure the ability of neurokinin receptors (NKRs) to alter nicotine intake by either minimizing withdrawal symptoms or altering the rewarding properties of nicotine. METHODS: For withdrawal studies, nicotine dependence was established by treating mice with nicotine in the drinking water for a minimum of six weeks. Spontaneous withdrawal was induced by replacing the nicotine drinking water with control water for twenty-four hours. Mice received injections of NKR1 receptor antagonist before testing for increased anxiety-like, depression-like or physical withdrawal behaviors. Conditioned place preference is used to test the rewarding effects of nicotine in the presence of NKR antagonist. RESULTS / EXPECTED RESULTS: We are anticipating that NKR1 antagonism will alter nicotine CPP. In addition, given that physical signs of nicotine withdrawal are precipitated by NK1 antagonist, we anticipate changes in affective symptoms of withdrawal. DISCUSSION / CONCLUSION: The latest results of these studies will be presented. Overall our studies will provide more insight on the behavioral and biological factors that are linked to the physical and psychological manifestations of nicotine dependence as well as the positive rewarding effects of nicotine.

22.01.001

FAMILY MEMBERS IN MEANING CENTERED PSYCHOTHERAPY

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Objective: Family caregivers are a fundamental source of care for Latino cancer patients. Yet the family related psychosocial needs and perspectives of family caregiver's integration in psychological care of Latino patients with advanced cancer are not well understood. Changes in cancer care and delivery, along with the growing population of Latinos with advanced cancer and their caregivers, warrant increased attention to the roles and demands of caregiving and family needs. This presentation describes: 1) the perspective of Latino patients with advanced cancer on the role of the family in care, and 2) the correlation between family functioning and psychological symptoms (depression and anxiety). Method: Quantitative (n=79) and qualitative data (semi-structured interviews, n=24) was collected from Latino patients with advanced cancer between 2015 and 2019 from a major cancer center (n=48), and two cancer clinics, one located in New York city (n=22) and the other in Ponce, Puerto Rico (n=12). Family functioning was measured with the Family Relationship Index and depression / anxiety with the Hospital Anxiety and Depression Scale. The semi-structured interviews were transcribed, and the data was analyzed using open coding thematic analysis. Correlation between family cohesion, and psychological factors was performed. Results: Data shows that 81% of Latino advanced cancer patients reported low family functioning; and those with low family functioning had higher depression (r(75)-.27, p=.02),anxiety (r(75)-.27, p=.02), and hopelessness (r(75)-.23, p=.05) levels. Higher family functioning was also strongly associated to lower anxiety (r(75)-.39, p<.001). The themes and codes from the qualitative data revealed presumably on family relationships with emphasizes on the following themes: counseling; support; change after diagnosis; communication; conflict; sources of meaning; sources of love; sources of beauty; sources of humor; lesson of life; legacy for kids: family union; and coping mechanism. Conclusion: Correlations between family cohesiveness and psychological symptoms (depression and anxiety) suggest that these components are crucial in the adjustment and well-being of Latinos with advanced cancer. Further, it revealed presumably the impact of family relationships in cancer coping, and likelihood of integrating family members into therapy.

22.01.002

DAILY EMPLOYMENT EXPERIENCES IN AFRICAN AMERICAN LIVES

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North Carolina Central University

Balancing the demands of work and family have become increasingly complex among families with young children in recent decades. African American families are especially susceptible to the impact of work demands, as this group tends to work longer hours and are often the racial minority in the work place. Yet, there remains a wide wealth gap between African Americans and their White counterparts. Such disparities have implications for daily family dynamics and the overall quality of life in African American households. The present study explored the associations among work demands, daily hassles, depressive symptoms, and young children's behavioral outcomes among a sample of African American families. Daily diaries were utilized over a two-week period in an effort to test the proposed associations. The study results revealed negative associations among depressive symptoms, harsh and withdrawn parent-child interactions, work demands, and sleep quality. Furthermore, working a nonstandard schedule was associated with increased daily hassles and alternative child care arrangements. The findings reveal the importance of identifying mechanisms that protect and foster healthy development in African American families.

22.01.003

IMPACT OF A NATURAL DISASTER ON LATINO CANCER SURVIVORS

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Ponce Health Sciences University (MR-B, RH, ZR, CBC-E, LM, NT, ET, AM, DA, IF, EMC, GNAP), H. Lee Moffitt Cancer Center and Research Institute (JP-M, HJ)

Cancer is the leading cause of death in Puerto Rico (PR). Hurricane Maria (HM) and its aftermath lead to widespread devastation in the island, including the collapse of the healthcare system. Medically fragile populations, such as cancer survivors, were significantly affected. The goal of this study was to assess the impact of HM on barriers to care, emotional distress, and inflammatory biomarkers among cancer survivors in PR. This exploratory longitudinal study was conducted in health care facilities and community support groups from PR. Cancer survivors (n=50) and non-cancer participants (n=50) completed psychosocial questionnaires and provided blood samples that were used to assess inflammatory cytokines levels. Data were analyzed through descriptive, frequencies, correlational, and linear regression analyses. Cancer survivors that were affected by HM reported increased barriers in accessing medical care, which were directly associated with anxiety, perceived stress, and post-traumatic symptomatology. Moreover, being a cancer survivor, along with closeness in time from HM predicted more barriers to receiving health care. Several inflammatory cytokines, such as CD31, BDNF, TFF3, Serpin E-1, Vitamin D BP, VCAM-1, Osteopontin, Chitinase 3 like 1, MMP-9 and MIF were significantly upregulated in cancer survivors while BDNF, MMP9 and Osteopontin had significant positive correlations with barriers to care. HM significantly impacted Puerto Ricans psychosocial well-being. Cancer survivors had significant barriers to care and showed increased serum inflammatory cytokines, but didn't show differences in anxiety, stress and post-traumatic symptoms compared to non-cancer participants.

22.01.004

SOCIODEMOGRAPHIC DETERMINANTS AND GLYCEMIC CONTROL IN DIABET

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Ponce Health Sciences University

Diabetes mellitus is a chronic metabolic disorder of significant public health concern, linked to adverse health outcomes. Approximately 14% of Puerto Ricans living on the island have diabetes. The aim of this study was to explore the association between biopsychosocial factors and glycated hemoglobin (HbA1c), a proxy of glycemic control, among a sample of inpatients with Type 2 Diabetes Mellitus (T2DM). Secondary data analysis was conducted on biopsychosocial variables obtained from 345 inpatients admitted to a general hospital of Puerto Rico. Inpatients received psychological evaluations from the Clinical Psychology Services Program of Ponce Health Sciences University between January 2015 and December 2017. Non-parametric inferential analyses were conducted to generate a biopsychosocial profile related to glycemic control. Fifty-three percent of this sample was female, with a mean age of 63. Sixty-two percent had poor glycemic control and the average HbA1c was 8.18% (SD = 2.27). Younger patients had poorer glycemic control compared to relatively older patients (r, [345] = -.276, p = < .001). Furthermore, patients with lower monthly household incomes were more likely to show poorer glycemic control (2 (5) = 13.12, p = .022). These results suggest that sociodemographic determinants of health play an integral role in glycemic control among inpatient with T2DM. Furthermore, these findings highlight the need to implement universal clinical psychology services in general hospital settings, especially in units that serve diabetic patients. Future studies exploring the mechanisms that uniquely link sociodemographic determinants and glycemic control among hospitalized with T2DM are warranted.

22.01.005

DIGITIZING A COMMUNITY-BASED SMOKING CESSATION INTERVENTION

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PURPOSE: There is an ongoing search for cost-effective smoking cessation programs designed to help underserved populations who are most impacted by tobacco use and its negative health effects. The Communities Engaged and Advocating for a Smoke-free Environment (CEASE) initiative, an over-a-decade-long partnership between Morgan State University and neighboring communities, has developed peer-motivation community-based smoking cessation interventions for underserved communities, with promising outcomes. However, there is a need to reach a wider population given the new trending tobacco use epidemics and the popularity of electronic cigarettes, especially among younger age groups. We aim to digitize the existing CEASE peer-motivation smoking cessation intervention to curb the tobacco-use epidemic among underserved populations.METHODS: CEASE peer-motivation interventions were developed in a four-phase trial using a Community-Based Participatory Research (CBPR) approach, in which each phase had improved outcomes using lessons learned from previous phases. The four phases of CEASE recruited 1,807 participants with smoking cessation outcomes ranging from 9.4% to 30.1%. A community-based peer-motivation smoking cessation intervention was developed with an accompanying CEASE Today Tobacco Cessation Manual. A digital version comprising a mobile app and a web-based component of the CEASE curriculum with SMS options is under development. EXPECTED RESULTS: The new digitized peer-motivation intervention will be enhanced and expanded through CBPR to include modules for emerging tobacco use problems such as the use of e-cigarettes among younger age groups. CONCLUSION: Digitizing the CEASE smoking cessation intervention has the potential to increase its reach and usability for peer-motivation with promising benefits for underserved populations.

22.01.006

DEPRESSION, EXPOSURE TO TRAUMA AND BC TUMOR PROGRESSION

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Ponce Health Sciences University

Background and Purpose: There is growing evidence that highlights inflammation as a common factor in depression, chronic psychosocial stress and tumor microenvironment. However, little is known about the role of current and past exposure to social-environmental adversity (SEA; e.g., child abuse, domestic violence) in the relationship between depression and markers of inflammation in the breast cancer (BC) tumor microenvironment. Methods: Participants (n=32) were recruited before undergoing BC tumor surgery and completed a package of surveys through interviews that included the PHQ-8, Adverse Childhood Events (ACE) questionnaire and the Trauma History Questionnaire (THQ). Regarding BC tumor samples, 10x fields were quantified for CD68 (macrophages), CD19 (B cells) and CD3 (T cells). Pearson Correlation Tests are used to explore correlation between the variables of interest.Results: Preliminary findings (n=22) reveal that the most common SEA experience were general disasters and trauma (n=21), physical and sexual abuse (n=16) and, Crime-related trauma (n=13). Out of those reporting childhood abuse experiences (n=16), 6 re-ported exposure to more than 4 ACE experiences. Mean score of PHQ-8 symptoms were low (M=3.77 ± 4.19). The relationship between depression symptoms and inflammatory markers of tumor microenvironment (macrophages, B cells and T cells) was not statisti-cally significant. However, there were statistically significant relationship between B cell lymphocytes and adverse childhood events ($p < 0.05$).Conclusions : Significant correlations between ACE and B cells lymphocytes are promising considering that Lymphocytes has been recognized as a new hall mark in BC treatment prognosis and outcomes.

22.01.007

SOCIAL ADVOCACY APPROACH FOR REDUCING HIV/AIDS IN BLACK MSM

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Impulse Group Atlanta (JMH, RR, TW, JR, DM)

The factors associated with HIV/AIDS disparities among young gay men of color are complex and require holistic, innovative solutions. Impulse Group Atlanta is a chapter-based organization dedicated to the advancement of HIV education, safe sex awareness and practice among gay men. This presentation will provide an overview of the Impulse Atlanta, explore nuances of its advocacy approach, and discuss strategies to best engage young gay men of color to reduce HIV/AIDS morbidities. Impulse Atlanta strives to normalize and authenticate the Atlanta gay experience, with the overarching goal of gay men obtaining positive health outcomes in 4 areas: HIV Prevention and Care; Addressing Stigma; Substance Abuse; and Mental Health. Impulse leverages social gatherings, interactive advocacy activations, and peer-to-peer mobilization to establish rapport with gay men of color around sensitive sexual health and cultural topics; deliver risk-reduction messaging; and facilitate linkages to care. Impulse Group Atlanta has emerged as an innovative approach to engage and mobilize a high-risk demographic that is often underrepresented in more traditional harm reduction strategies (educated, employed men of color between the ages

of 18-35). Since its inception, Impulse has successfully executed over 35 events in 8 cities across the American South, and directly engaged 2700 gay and bisexual men of color. Anecdotal evidence suggests Impulse yields high event attendance and retention; increased social support for health-yielding and harm reduction behaviors; and increased HIV testing. More robust evaluation and data collection efforts are needed to assess Impulse Group Atlanta's impact on high-risk individuals' health behaviors.

22.02.001

IMPACT OF SELF-CARE TRAINING ON PROVIDER'S RESILIENCE

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PURPOSE: Resilience is a person's ability to adapt successfully to acute stress trauma or chronic forms of adversity, ie., the dynamic capacity of the individual to modify his/her modal level of ego-control as a function of the demand characteristics of the environmental context. Our main objective was to explore the impact of a self-care mindfulness workshop provided to the healthcare providers of the Puerto Rico Women, Infants and Children program (PRWIC). METHODS: An invitation was disseminated via Email, to complete the Spanish version of the Wagnild and Young Resilience Scale along with other mental health assessment instruments, to active PRWIC providers 6 months after the workshop. In the workshop providers were instructed about resilience and were also asked to practice strategies to build resilience including mindfulness strategies. RESULTS: Volunteer responder group consisted of participants (N=65) who attended said workshops (N=23) and those who completed the questionnaire and did not attend (control group N=42). Mean resilience score among participants was 145.03(±0.6) (moderate) versus 158.99 (±0.5) (moderately-high) among controls.The lower score observed among participants could be due to a higher awareness among workshop participants. A positive response to the use of these strategies (95%) was paired with documented interest in learning new tools (98%). DISCUSSION: This may lead the way to increased awareness in the need and use of self-care strategies for this population of community based service providers. CONCLUSION: The impact of the strategies learned on participant's mental health and the quality of care they provide remain areas for further study.

22.04.001

FOOD INSECURITY: A HEALTH IMPACT ASSESSMENT APPROACH

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Background: Social determinants can create health disparities and act as barriers to community health. Food security, and income are social determinants that have been linked to health outcomes and may explain why residents of some communities in the United States have high rates of chronic conditions like obesity, high cholesterol and diabetes. Purpose: The purpose of this part one health impact assessment (HIA) was to examine household food security and other social determinants of health, and their relationship to chronic disease, in Tallahassee's Highway 20 community. Method: Utilizing a quantitative design, data collection comprised a face-to-face household survey. A measure of household food security was obtained, demographic and chronic disease data were also collected. Frequencies and logistic regression was used to analyze data using the Statistical Analysis System (SAS) 9.4 software platform. Findings: 63% of the sample (n=64) is food insecure. The association between food security, prediabetes and income tested significant. Conclusion: Tallahassee's Highway 20 community struggles with household food insecurity. Disparities in income are associate with food insecurity and poorer health outcomes. Policy, resources and actions are needed to support economic development and preventative health intervention to improve community health.

22.04.002

SOCIAL RELATIONSHIPS & STAPHYLOCOCCUS AUREUS COLONIZATION

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PURPOSE The U.S. population health profile of community acquired Staphylococcus aureus establishes a general carriage rate of approximately 33% of individuals who are asymptomatically colonized with S. aureus. The basic vectors for colonization include contact with colonized individuals, shared surfaces, and pets. We hypothesize that the strength of social ties in naturally occurring groups is linked to the carriage rate of S. aureus in those groups and consequently is not randomly distributed through the population. If the hypotheses holds, we have the opportunity to create public health screening and intervention tools to better control transmission and subsequent infections. METHODS We are testing the colonization status of S. aureus in social groups in Yuma Arizona recruited at public events, public venues (parks, malls), and private spaces (homes, workplaces). Each group member completed a social network questionnaire on the social composition of the group, as well as the strength of ties within the group. We are utilizing whole and egocentric network variables, along with network visualization techniques

to establish the distribution of colonization across group types and group sizes. RESULTS / EXPECTED RESULTS We will characterize S. aureus colonization data, as well as social network data to establish comparative colonization rates in Hispanic and non-Hispanic social groups, compared with overall population health data. DISCUSSION / CONCLUSION Understanding how transmission is influenced by interactions between social contacts, strength of ties, and types of relationship in naturally occurring groups provides a potential blueprint for effective and targeted control interventions

22.04.003

SMOKE AND MIRRORS: DISPARITIES IN SMOKING CESSATION OUTCOMES

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PURPOSE: Since the first U.S. Surgeon General's report on tobacco use in 1964, use-reduction initiatives have resulted in unprecedented improvements in tobacco-related outcomes. While population level declines are laudable, minority groups have not experienced significant declines in tobacco use and continue to bear the burden of tobacco- related disease and mortality. The purpose of this study is to examine tobacco-related cessation disparities among minorities and synthesize the relevant scientific literature. METHODS: Researchers used data from 2015-2017 Florida Adult Tobacco Survey (FLATS) (n=2,188) to examine smoking and cessation rates in Florida. Trends over time were examined using a logistic trend test. Researchers then synthesized the scientific literature on cessation-related disparities to develop a conceptual framework to guide future research and policy.RESULTS: Consistent with national trends, overall adult cigarette smoking in Florida has significantly decreased. For whites, the rate decreased from 19.7% to 14.4%. However, the rate of black smokers remained consistent (13.8% to 13.1%). Furthermore, blacks were significantly more likely to report willingness to quit than whites (60.6% , 45.4% respectively) and significantly more likely to report quit attempts (67.2%, 52.5%), yet significantly less likely to successfully quitting smoking than whites. CONCLUSION: Florida is considered a state with historically stable tobacco reduction program funding with robust and successful interventions. Given the disparities in smoking behavior and cessation-related factors, future research should closely examine reasons certain minority populations are less successful at quitting smoking. Research should inform policy and programmatic efforts tailored to these populations to increase success in cessation.

22.06.001

AFRICAN AMERICANS; CHILDHOOD VICTIMIZATION & HEALTH OUTCOMES

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Howard Univesity (FS), 2MReseach (RJH), George Washington University (CD); Bureau of Justice Statistics (JB), Howard University (ER)

Some children experience multiple forms of violence and trauma, and these exposures have significant impacts on their future physical, emotional, mental health and wellbeing that can last into adulthood. These impacts vary by the type of violence or exposure. We detail the childhood and present experiences of 637 self-identified African Americans, ages 18 to 25, who lived in Washington, DC. This study examined 5 types of exposure to childhood violence (conventional crime, child maltreatment, peer/sibling victim, sexual victimizations, and witness/indirect victim), which were independently assessed for their correlations with depressive symptoms, depressive moods, trouble sleeping, current drug use, lifetime. alcohol, tobacco, and other drug (ATOD) use, and ATOD problems. Exposure to any of the 5 types of violence was shown to be a risk factor for all but one of the outcomes tested. Depressive symptoms were significantly correlated with exposure to childhood maltreatment and witness/indirect victim. Trouble sleeping was significantly correlated with exposure to childhood maltreatment. Current drug use and problems with ATOD use were significantly correlated with exposure to childhood sexual victimizations. Exposure to all types of violence was negatively correlated with lifetime ATOD use. These data show that exposure to multiple types of violence affect a range of behavior and health outcomes. Our findings highlight the importance of examining multiple forms of childhood victimization and point to the need for trauma-informed programs that are tailored to this group.

22.06.002

INTERVENTIONS TO TEACH INTERPERSONAL VIOLENCE

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Purpose: Interpersonal violence (IV) is a leading cause of morbidity, disability, adverse mental health conditions, and mortality. Beyond both acute injuries and chronic conditions arising from IV, today there is increasing recognition that IV can have long-term effects on the health and mental health of individuals due to physiological changes arising from exposure. However, without training, physicians are likely to encounter persons experiencing or at risk for interpersonal violence without recognizing or addressing it. Methods:

A systematic review of the literature was conducted using PRISMA guidelines to identify original studies that focused on how medical students are taught to address IV across the life course. An electronic search was conducted in MEDLINE/PubMed, PsycINFO, Web of Science, Scopus, Ingenta, Science Direct, and Google Scholar databases for articles in English published between March 2005 and February 2017. The search strategy cross-referenced keywords for interpersonal violence. Results: A total of 29 articles were identified that sought to teach medical students how to respond to IV at different stages of the life course. Nineteen (65.5%) of the articles addressed domestic violence/intimate partner violence, four (13.8%) of the articles targeted sexual violence, two (6.9%) addressed child abuse, three (10.3%) of the articles addressed adolescent violence, and one (3.4%) examined family violence. Conclusion: Despite its ubiquitous nature and its known effects on the health and mental health of persons who have been exposed to IV, little attention is given to teaching medical students how to address it.

22.06.003

TRENDS OF GUN VIOLENCE AGAINST WOMEN IN THE UNITED STATES

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Gun violence in the United States exceeds rates seen in other industrialized countries. Women are often the victims of firearm injuries in the United States, but little is known regarding demographic/regional variations in injuries among women. The objective of this study was to examine firearm injury trends in a nationally representative sample of US women. Data was extracted from the CDC's Web-based Injury Statistics Query and Reporting System (2001-2017) and included victims 18 years of age and older. Number of non-fatal firearm assaults per year were extracted and crude population-based injury rates were calculated. Population-based homicide rates were also determined. Sub-stratification by age-group, race/ethnicity, and urbanicity were performed. Relative trends in injury patterns were assessed.There were 1013 female victims of non-fatal firearm assault in 2001 (3.8 per 105) and 7433 by 2017 (10.0 per 105). Homicide rates among females were 1.5 per 105 in 2001 and 1.7 per 105 in 2017. Age stratification showed that non-fatal firearm assault rates were higher in 18-44 year olds compared to 45-64 year olds. Black females had the highest rates of non-fatal firearm assault (14.6 per 105 in 2001 and 13.2 per 105 in 2017). While White females had rates of non-fatal firearm assault of 0.9 per 105 in 2001 and 2.0 per 105 in 2017. Increased victimization and possible female participation in firearm violence could be causing rising numbers. Denormalizing gun violence culture could help reduce firearm injuries seen among US women.

23.01.001

HISTOPATHOLOGY RESOURCE CORE- UNIVERSITY OF HAWAII

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University of Hawaii at Manoa (KE, MB, RB, MG)

PURPOSE: The purpose of the University of Hawaii (UH) Histopathology Resource Core (http://histocore.jabsom.hawaii.edu/) is to provide education, training, service and access to equipment and consultation for histopathological techniques to users at UH and the broader research community within the State of Hawaii, as well as interested users from other institutions. The core's focus is on health disparities research studies. METHODS: The Resource Core provides general histopathology services such as tissue processing, embedding (paraffin and fresh), H&E stain, special stains, immunohistochemistry, and in situ hybridization etc. Equipment includes: automated tissue processors, cryostats, and microtomes (sliding and rotary). The core provides training in all histological techniques and equipment. Experimental design assistance is available. Investigators and users have been surveyed for customer satisfaction by Monkey Survey. RESULTS: Seventy-seven users and 46 principal investigators received service from the core from 2017-2019. The core was cited in 24 peer reviewed publications. The survey results of customer satisfaction showed an average score of 4.6 out of 5. CONCLUSIONS: The Histopathology Resource Core is a valuable resource for the biomedical health disparity research community at the University of Hawaii, University of Hilo, and University of Michigan. The core has expanded services to National Oceanic and Atmospheric Administration, Department of Land and Natural Resources, Micronesian Environmental Services and Western Pacific Regional Fishery Management Council.

23.01.003

3D PRINTING: A TOOL TO PROMOTE BIOMEDICAL RESEARCH

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PURPOSE: At the BioMedical Innovation Center (BIC), we are using 3D printing technology to create innovative educational/training tools to promote biomedical research among students. METHODS: An educational program for high-school and undergraduate students incorporating 3D printing technology was developed. The program included a summer internship (2-6 weeks) and a 3-Day workshop utilizing 3D printers and materials used to produce anatomic models. Each student was required to access the NIH anatomic model library, choose related STL file, operate a 3D printer, generate a 3D model, and present their results to other students and faculty. RESULTS: Three Summer Internships introduced 5 high-school and 10 undergraduate students to 3D printing technology. Twenty-two (22) undergraduate students participated in four 3D-Printing workshops. At the completion of the internship, students were able to generate 3D-printed models that were shared with physicians who provided feedback and valuable role-model interactions. Preliminary evaluations revealed that over 90% of the students evaluated the internships and workshops as an excellent experience. Knowledge about 3D technology increased by 20%, as evidenced by pre- and post-test evaluations. CONCLUSION: The BIC demonstrated the capacity to develop an effective program to stimulate the interest of students in developing 3D printed biomedical educational/training tools. Surveys and evaluations confirmed the positive impact of 3D printing in developing the interest of students in the biomedical sciences.

23.02.001

DEVELOPING MEANINGFUL RCMI EVALUATION METRICS

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Florida International University

The Florida International University RCMI (FIU-RCMI) has been engaged with our university research division in developing processes, data sources, and reporting channels for evaluating the impact of the FIU-RCMI. Particular attention has been devoted to metrics for evaluating (a) the impact of FIU-RCMI investigator development trainings, (b) growth in NIH grant submissions focused on health disparities and minority health, and (c) growth in scholarly productivity among early career and established FIU-RCMI researchers. Moreover, attention has been given to establishing evaluation processes and metrics that may be replicable across RCMIs. The current report describes our evaluation approach and preliminary findings as related to the expansion of health disparities research capacity at FIU. Partnering with the FIU university research division, the FIU-RCMI evaluation team developed procedures and metrics for tracking health disparity research proposals and awards by FIU-RCMI affiliated faculty. These evaluation metrics included examination of 1) the total number of grant proposals (NIH & other) submitted and awarded overall as well as by PI sex, racial/ethnic status and rank, 2) the variety of health disparity research topics covered by proposal submissions, and 3) the number and scientific impact of journal publications. The FIU-RCMI evaluation team also developed a common metric for assessing the impact of FIU-RCMI sponsored events, which is being used for ongoing strategic planning. Two future directions of the FIU-RCMI evaluation framework include 1) network analysis to assess the expansion of collaborative efforts among affiliated faculty and 2) assessing university-wide expansion of health disparity research.

23.02.002

IDENTIFYING OPPORTUNITIES FOR BUILDING A RESEARCH CENTER

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PURPOSE: The purpose of this study was to assess key stakeholders' knowledge of the San Diego State University's HealthLINK Center for Transdisciplinary Health Disparities Research (SDSU HealthLINK Center) and expectations of how it might support transdisciplinary health disparities research at SDSU and our partner organizations. These interviews are part of a larger evaluation plan, which includes biannual key stakeholder interviews, an annual Center survey, and tracking activities to assess the Center's progress towards its aims. METHODS: Key stakeholders (n = 14) were identified based on purposive sampling procedures; they included those who are directly involved with or whose work may be impacted by the Center's activities. To ensure a diversity of opinions, key stakeholders were selected from a wide variety of professional roles, including postdocs, senior faculty, administrators, and external community partners. Interviews were one-hour long and semi-structured. Once completed, interviews were transcribed verbatim and coded using grounded theory methodology. RESULTS: Analyses revealed a number of opportunities for improving SDSU's infrastructure and administrative support for transdisciplinary health disparities research. Common themes included: grant funding (e.g. limited intramural funding opportunities); physical infrastructure (e.g., lack of laboratory space); junior investigator support (e.g. insufficient grant application support); and dissemination of research results (e.g., limited funding for travel and to pay for open-access journals). Interviewees also provided recommendations for ways by which the SDSU HealthLINK Center may encourage a culture of transdisciplinary collaboration at SDSU. DISCUSSION: Results of these interviews present opportunities for SDSU HealthLINK Center to fill gaps in research infrastructure at SDSU.

23.04.001

MENTORED TEAMS TO ADDRESS HEALTH DISPARITIES IN HISPANICS

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University of Puerto Rico, Medical Sciences Campus (MIR, EFR, MCR, RGG); Universidad Central del Caribe (ERI, JRMA, MEGM, MIRV)

PURPOSE: Title V Cooperative Project between the University of Puerto Rico Medical Sciences Campus and Universidad Central del Caribe organized Clinical and Translational Mentoring Teams (CTMTs) and launched the Center for Research Education and Science Communication Opportunities (CRESCO). Both provide resources, training opportunities and mentorship to Hispanic undergraduate students (US), graduate students (GS) and faculty (F) in their development in translational science (TS) to address HD. METHODS: After completion of the training cycles (TCs) that dealt with the theory of translational science (TS), and matched by their research interests, US, GS and F, were incorporated in CTMTs under the mentorship of well-established TS researchers to address HD. Within the CTMTs, participants prepared a concept paper (CP) and a research proposal (RP) in HD. Once approved the work is developed through hands-on experiences in Intensive Development and Experiences in Advancement of Research and Increased Opportunities (IDEARIO). RESULTS: Eighteen (18) CTMTs were formed and sixteen (16) remained active, with 16 TS mentors and 53 participants, distributed 29 US (54.71%), 13 G (24.52%) and 11 F (20.75%). Eleven (11) RP addressing HD were approved in: cancer, exercise, glaucoma, liver, neuro, obesity, pathogenesis, renal, Zika, while 5 CPs, 5 RPs and 2 publications are underway in: endocrine, cardio, neonatal, neuro, renal and ZiKa. CRESCO provided meeting rooms, resources, workshops, statistical and editorial help and on line support for meetings. CONCLUSION: The CTMTs, the provided resources and support in CRESCO are effective strategies for the mentoring of Hispanics US, GS and F in TS.

23.04.002

POTENTIAL MEETS OPPORTUNITY: CAPACITY BUILDING THROUGH EXITO

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PURPOSE: Éxito! Latino Cancer Research Leadership Training program engages Latinos in academia-based cancer control research, the only Latino training program focused on doctoral-level preparation in population sciences. APPROACH-Éxito supported an alumni's Human papillomavirus (HPV)-associated cancer prevention research internship in El Paso, TX. HYPOTHESIS-Project will enhance current and future HPV prevention initiatives in the region through engagement in academia-based community cancer research (ABCCR). OBJECTIVES-(1)contribute to current initiatives of EdTech-HPV project;(2)contribute to future HPV prevention efforts as team member on U54 interdisciplinary grant submission;(3)provide research/impact report of project informed by community-based participatory research (CBPR) framework. GOALS-(1)further establish partnerships and understanding among local university students/alumni and faculty;(2)collaborate with community organizations currently engaged in cancer prevention efforts(3)lessen disparities associated with acquiring an HPV infection through ABCCR. PURPOSE-To engage in CBPR using culturally appropriate empowerment interventions targeting cancer prevention, sexual and reproductive health, and health services navigation. METHODS: Mix-methods CBPR data collected from internship (June-November 2018) through community engagement, program reporting, and translational research efforts on parent grant contributions. RESULTS: EdTech-HPV- recruitment efforts increased (141%); follow-ups increased (778%) over 3-month span. U54- submission (November 2018); grant awarded (7/2019); PhD Research Associate (2019-2024). Éxito report- completed (December 2018); doctoral application (12/2018); acceptance (2/2019). DISCUSSION: ABCCR provides a pipeline to engage students, faculty, community with similar goals to collectively engage in sustainable community health protection efforts. Results from this project are expected to enhance current capacity-building initiatives to engage and support minority researchers by illustrating possible opportunities and challenges when engaging in academia-based research.

23.05.001

STRATEGIES FOR PROMOTING COMMUNITY ENGAGEMENT IN RESEARCH

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PURPOSE: The Community Engagement Core (CEC) of the Center of Collaborative Research in Health Disparities (CCRHD) in Puerto Rico focuses on developing and implementing strategies to increase community-academic collaborations and partnerships in research activities. METHODS: We have implemented a variety of strategies in order to fulfill our objectives. To date we have: conducted

a SWOT Analysis activity, formed a Community Coalition Team (CCT), had one on one meetings with active researchers, coordinated a community engagement retreat activity, begun to establish relationships with local communities and health organizations, and begun the process to adapt and implement the Community Engagement Studio (CES). RESULTS: The SWOT Analysis activity provided important feedback from researchers and community members that was incorporated in the CEC Strategic Plan; the CCT plays an active role in the coordination of activities; researchers supported by the CCRHD were encouraged to include community outreach initiatives; the retreat served as an opportunity for CCRHD supported researchers to learn about community engagement and listen to community members who participated in research studies; a community and health organizations directory has been developed to facilitate collaborations; and we have received training to adapt and implement the CES with CCRHD supported researchers. DISCUSSION: Community engagement can enhance the recruitment and retention of study participants, provide meaningful dissemination of research findings to a broader audience and ultimately help mitigate health disparities in Puerto Rico through the development of context appropriate interventions.

23.05.002

A MODEL FOR EVALUATING RCMI CAPACITY BUILDING

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PURPOSE: The Southwest Health Equity Research Collaborative (SHERC) is funded by the National Institutes of Health Research Centers in Minority Institutions (RCMI) program. One of the primary goals of the RCMI program is to enhance institutional research capacity within the areas of basic biomedical, behavioral and/or clinical research. Toward this end, we have designed a multilayer evaluation process in order to obtain baseline data, identify weaknesses, develop targeted programming, and document the impacts SHERC has on institutional capacity. This presentation examines the evaluation constructs, indicators, and methods for measuring capacity. An examination of investigator and institutional constructs associated with each of the RCMI program cores informs how the SHERC is building sustainable research capacity. METHODS: The SHERC team designed and operationalized evaluation measures for multiple dimensions of research capacity through several evaluation instruments and processes including an institutional readiness survey, analysis of institutional grant data, NIH RePORT system, investigator interviews, and investigator development and research infrastructure needs assessments. RESULTS: Critical elements in a successful design include measurement of research productivity, institutional infrastructure, investigator readiness for research, and institutional research climate. Findings inform institutional and programmatic planning and practices to better support investigators from underrepresented groups and early stage investigators successfully engage in health research. DISCUSSION: This model provides an opportunity for synergy across the RCMI program to develop common evaluation metrics. Common metrics for key RCMI program goals have potential to strengthen the evidence to inform the NIH about the collective impact of the RCMI program.

24.01.001

BEST PRACTICES FOR BUILDING COMMUNITY TRUST IN RCMI RESEARCH

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PURPOSE: Native Hawaiian and Pacific Islander populations in Hawai'i have younger onset of chronic diseases and lower life expectancies than the dominant populations in the state. The health challenges facing these groups would benefit from intervention research to address their health disparities. However, these populations have experienced unethical research practices in the past and may be reluctant to engage in research. This paper describes community engagement strategies of RCMI programs in Hawai'i designed to help increase community participation in research. METHODS: Community engagement is a critical component of the most recent RCMI programs at the University of Hawai'i—RMATRIX (2011-2020) and Ola HAWAI'I (2017-2022). Both aim to reduce health disparities through training, mentoring, and nurturing a cadre of health disparities researchers, including researchers from underrepresented racial and ethnic groups. Strategies to engage community were documented through case study methods and assessed by our community advisory groups as to their relative effectiveness. RESULTS / EXPECTED RESULTS: The four most effective strategies were: 1) engaging community advisors in meaningfully ways, e.g., as reviewers of proposals; 2) developing researchers from the community through training and encouragement in graduate study; 3) teaching university investigators and administrators about the community, e.g., by requiring them to attend community events and to report their findings to the community; and 4) subcontracting with community groups to plan and host community research trainings and events that are responsive to community priorities. DISCUSSION / CONCLUSION: These strategies may help other research universities develop and strengthen their community engagement programs.

24.01.002

MENTAL AND CARDIOVASCULAR HEALTH IN AFRICAN AMERICAN WOMEN

SA RACHEL; A Powers; RC Hinrichs; AS Belton; MJ Kent; KB Holden

MOREHOUSE SCHOOL OF MEDICINE (SAR, ASB, KBH); EMORY UNIVERSITY SCHOOL OF MEDICINE (AP, RCH); PHOENIX VA MEDICAL SYSTEM (MJK)

PURPOSE: The purpose of the study (Project GRIT) is to examine the impact of a goal-directed resilience intervention training on mental and cardiovascular health in urban African American women with Post-Traumatic Stress Disorder (PTSD). PTSD disproportionately affects urban African American women and is associated with elevated risk for cardiovascular disease (CVD). Research suggests that goal-directed resilience skills may improve stress responses for better mental health and psychophysiological outcomes. The central hypothesis is that development of these skills will promote and sustain goal-directed engagement that replaces stimulus-based reactivity, improves PTSD symptoms, and reduces CVD risk.METHODS: African American women (n=148) will be randomized into either an 8-week culturally relevant group intervention on goal-directed resilience strategies (n=74) or a minimal attention control (n=74). Participants will complete baseline and follow-up mental health and neuropsychological tests. Specimen collection will measure CVD biomarkers. Focus groups will elicit feedback on participants' intervention experiences and application of skills learned. EXPECTED RESULTS: We predict sustained increases in resilience, psychosocial function, emotion regulation, and wellbeing, and decreases in depression, anxiety, PTSD, posttraumatic cognitions, and CVD risk measures among those who participate in the intervention group in comparison to those in the control group. CONCLUSION: A strengths-based, culturally-relevant approach to PTSD management can help mitigate stress effects on CVD risk and outcomes. This research will also address the lack of knowledge about strategies to effectively engage African American women in existing mental health and CVD treatment options and advance the science of resilience by elucidating a bio-behavioral model.

25.01.001

DEVELOPING STRATEGIES OF HEALTH EDUCATION TO YOUNG ADULTS

Torres-Cordero, J.A., Padilla-Segarra, J.E., Valentín Butter, C.E., Emmanuelli Thompson, J. Torres, J., Torres, M., Roche, S., Guzmán, A., Miro, A., Sánchez, J., Jiménez-Chávez, J. J.A Torres, J.E. Padilla, C.E. Valentín, J. Emmanuelli, J.Torres, M. Torres, S. Roche, A. Guzmán, A. Miro, J, Sánchez, J. Jiménez.

PURPOSE: It has been recognized that education is an effective strategy to reduce cancer disparities. Studies have shown that it's a priority to raise awareness of the importance of prevention from an early age. The purpose of this study is to present the creation and outcomes of a committee composed of university students, focused on disseminating cancer prevention education among young adults. METHODS: In September 2018 and framed under the Community-Based Participatory Research principles, the Interuniversity Committee for Cancer Prevention and Education was developed. A total of ten students constitute the committee, aged 18 to 25, from six universities from Ponce, Puerto Rico. The committee focuses on developing educational materials, outlining strategies and outreach activities tailored to young adults. RESULTS: An annual work plan was developed with the following objectives: a) create opportunities for cancer prevention education for young adults and b) develop and implement activities to increase awareness on cancer prevention through the reduction of risk factors. An educational event on cancer prevention was held with the participation of 106 university students (knowledge gained $z=-6.232$, $p<0.05$). DISCUSSION: The participation of young adults from the community, and strategies implemented by the committee, demonstrates the feasibility of disseminating health education information among this population. Collaborative relationships were established with six universities in the southern PR area, which support the objectives of the committee. Outreach events, managed by young adults, appear to be effective in increasing awareness on cancer prevention-education among peers, which has not been traditionally contemplated in public health education campaigns.

25.01.002

TRAINING PROGRAM TO ADVANCE COMMUNITY-ACADEMIC PARTNERSHIPS

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Ponce Health Sciences University (PHSU)

Introduction: An increasingly promising approach, known as Community-Based Participatory Research (CBPR), has been identified as a strategy for reducing health disparities in disadvantaged and increase participation in underrepresented populations. Among all the CBPR Principles, we recognize that capacity building is an instrumental component to reduce health disparities. Considering this, we created and implemented a capacity building program to better integrate community members in research projects. During Phase I (didactic), we assessed the acceptability, feasibility, and preliminary effectiveness of the CBPR training curriculum. For phase II (experiential), trained community members (TCM) continued capacity building through hands-on experience to integrate theoretical information in the research field through

research projects. Design/Methodology: Four research projects were initialized comprised by TCM and academic researchers. Group meetings were held to: a) formulate research objectives, b) design, create, or adapt instruments to be utilized, c) identify strategies for future recruitment (e.g. educational outreach activities), and d) identify resources for research. Results: TCM have been involved in all stages of the research projects; in which one has finalized and three are on-going. In addition, various activities have been realized, which include outreach educational activities (as pre-recruitment strategy), collaborations with private and public entities, training workshops, certifications (e.g. CITI), and grant applications. Discussion/Conclusion: The CBPR training program has demonstrated to be an effective strategy to promote participatory health research through the development of community and academic partnerships. Future studies will focus on the impact of the implementation of these research partnerships and community health outcomes.

25.01.003

NCCU RCHDR COMMUNITY ENGAGEMENT CORE: RURAL ASSESSMENT

KS Kimbro, L Taylor, D Grant, A Holloman, L Jones, R Gerald

North Carolina Central University (KSK, LT, DG, AH, LJ, RG)

PURPOSE: The medically underserved populations in urban and rural North Carolina continue to demonstrate unequal rates of morbidity and mortality from chronic diseases such as cardiovascular disease and cancer. NCCU through the NIH RCMI Research Center for Health Disparities Research (RCRHD) and its Community Engagement Core (CEC) is identifying community relevant health priorities, gaps, and is assisting in discovering environmental-biological interactions that could contribute to disease risks that effect health outcomes. In previous efforts, NCCU has participated in CBPR with rural North Carolina communities and conducted most of its translational work within the context of community-based partnerships. The CEC continues such collaborations which aid in understanding the needs and finding solutions for reducing health disparities in these underserved communities. METHODS: Our objectives are to: develop infrastructures to provide the priorities of the CEC that will promote health equity among the underserved in urban and rural NC; expand the priorities of current community partners to support outreach activities that will describe the health disparities in local communities to inform NCCU RCMI research; and translate findings from NCCU RCMI cancer and cardio-metabolic research into clinical and community-based practices that reduce health disparities. RESULTS: Our results show that rural communities were responsive to focus groups (age>50), and health education fairs and that those communities expressed the need for access to health facilities and choices. DISCUSSION: The findings will lend to a better understanding of the needs of a rural NC community. Future CBPR efforts will expand to younger and urban populations.

25.01.004

PARTNERING AIM TO LOWER HPV CANCERS IN AFRICAN AMERICAN MEN

J Cunningham-Erves; L Campbell; C Barlow; C Barajas

Meharry Medical College (JCE); Second Missionary Baptist Corporative Ministries (LC, CB); Vanderbilt Ingram Cancer Center (CB) (capitalized)

Introduction: African American men suffer disproportionately from HPV-related cancer health disparities. We describe a multi-pronged, community engagement (CE) approach to develop a culturally-relevant, educational intervention for African American male communities to increase cancer screening and healthy behaviors. Methods: We used three engagement approaches to develop the intervention: 1) building capacity of community-based organization (CBO) leaders as research team members, 2) conducting focus groups with community members as consultants, and 3) conducting surveys with community members as consultants. Focus group data was analyzed using an inductive, qualitative content analysis approach to identify themes. Survey data was summarized using descriptive statistics. Results: Focus group themes were: 1) Lack of awareness and/or knowledge of HPV, cancer, and vaccine; (2) Existing Barriers to engage in Preventive Behaviors; (3) Personal Experiences with Cancer; 4) Need to Address Fear and Mistrust in Medical Doctors and Researchers; (5) Multi-Modal Strategies needed to communicate about HPV and cancer; and (6) Influential sources and networks to provide education. Survey data indicated men wanted information on penile (52%) and oral cancers (48%). A symposium with many speakers on different topics was the preferred education format (96%). Post-summit, pilot testing results indicated majority of males intended to get screened (73%), eat healthier (77%), and exercise more (64%). About 40% stated they would get themselves, children, or grandchildren the HPV vaccine. Conclusions: Use of multiple CE approaches allowed for a strengthened partnership and a more culturally-appropriate intervention to improve cancer prevention behaviors among African American men.

25.01.005

MAPPING COMMUNITY WELLNESS ASSETS IN SOUTHWEST ATLANTA

JM HOPKINS; D SPEAKS

Morehouse School of Medicine (JMH, DS)

PURPOSE: Low-income populations face significant barriers to accessing nutrient-rich foods and accumulating regular physical activity. However, communities may possess viable resources and assets that, when strategically leveraged, may ameliorate barriers and promote demand for healthy alternatives. The purpose of this project was to employ a mixed methods approach to identify and map healthy eating and active living (HEAL) assets and environments in a low-income, predominantly African American community in Southwest Atlanta, GA. METHODS: Assets were identified using internet searches, windshield surveys, field visits, and word of mouth references from key community stakeholders. Local business, medical and health services, CBOs, community entrepreneurs, and physical spaces offering low-cost or free physical activity and nutrition opportunities on a regular basis were considered. Descriptive asset data was imported into Google Maps to produce a user-responsive asset map. RESULTS: To date, 145 community wellness assets have been identified across 13 city zip codes. Assets were organized into six descriptive categories on the asset map (e.g. parks, fitness, community garden, social services, nutrition, medical services). CONCLUSION: Significant community-based physical activity and healthy nutrition assets are present in Southwest Atlanta. However, the extent to which assets are utilized by high- risk groups is unclear. Systematically linking low-income, high-risk populations to robust physical activity and healthy eating resources remains a challenge for public health practitioners. Additional qualitative inquiry is necessary to determine the quality of goods and services provided by these assets, and to determine community members' attitudes, perceptions, and barriers to accessing these assets regularly.

28.02.001

PASSIVE EXERCISE ON MOOD AND MCAv IN AFRICAN AMERICANS

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Howard University

PURPOSE: Physical activity is often restricted due to varying factors such as orthopedic conditions, poor muscular conditions, excess adiposity, poor balance, and age-associated sarcopenia. This inactivity is associated with cognitive, musculoskeletal, pulmonary, and cardiovascular complications, which translate into functional disability and decreased quality of life. To counteract the effects of inactivity researchers have developed an interest in passive exercise. We hypothesize passive motorized leg-cycling exercise influence mood response and cerebral blood flow similarly to active leg-cycling exercise. The present study examined differences in baseline mood response to 30 minutes of passive motion exercise (PME) and active motion exercise (AME).METHODS: We measured total mood disturbance (tension + depression + vigor + fatigue + anger + confusion) using the Profile of Mood States – Long Form. Middle cerebral artery velocity (MCAv) was measured using an ultrasound Doppler. Oxygen uptake (V.O2) and end-tidal carbon dioxide (ETCO2) was measured using an automated metabolic cart. Total mood disturbance, MCAv, V.O2, and ETCO2 were evaluated at baseline and following 30 minutes of PME and AME on a MOTOmed ® motorized leg cycle ergometer. RESULTS: In 15 sedentary young adult African American women and men V.O2 and MCAv were significantly increased during the last minute of PME and AME compared to baseline ($P<0.05$). ETCO2 did not change during PME and AME. Total mood disturbance improved by 13% and 9% following PME and AME, respectively ($P<0.05$). CONCLUSION: Findings support passive exercise to improve mood state and increase cerebral blood flow in a similar fashion to active exercise.

29.01.001

ROLE OF SOCIAL DETERMINANTS IN ENROLLMENT TO INSURANCE PLANS

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Northern Arizona University (AK, JAB); Brown University (MR, OAP);Virginia Commonwealth University (AMK); University of Texas Medical Branch Galveston (LC, YK, KJO); University of Pennsylvania (REB).

PURPOSE: We assessed the characteristics of older Mexican American enrollees in traditional Fee-For-Service (FFS) and Medicare Advantage (MA) insurance plan and the factors associated with disenrollment from FFS and enrollment in MA plans. METHODS: This is a longitudinal study linked with Medicare claims data. Our study sample includes community-dwelling Mexican American older adults (N=1455) participating in the Hispanic Established Populations for the Epidemiologic Study of the Elderly. RESULTS: Among Mexican American older adults, FFS enrollees were more likely to be born in Mexico, speak Spanish, lower levels of education, and have more disability than MA enrollees. Older adults with a larger number of Instrumental Acitvities of Daily Limitations (IADL) odds ratio (OR); 0.50, 95% CI: 0.26 - 0.98) and more social support (OR; 0.70, 95% CI: 0.45-0.98) were less likely to switch from FFS to MA compared to older adult with no limitations and less social support. In counties with higher number of MA plans, older adults with more social support had lower odds of switching from FFS to MA (OR; 0.48, 95%CI: 0.28-0.82) compared to older adults with less social support. CONCLUSION: Compared to those enrolled in MA, older Mexican American adults enrolled in Medicare FFS are more socioeconomically disadvantaged and are more likely to demonstrate poor health status. Stronger social

support and increased physical limitations were strongly associated with less frequent switching from FFS and to MA plans. Additionally, increased availability of MA plans at the county level is a significant driver of enrollment in MA plans.

29.01.002

EXPLORING READINESS TO CARE FOR A GROWING AGING POPULATION

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San Diego State University (MY, MKS, AC), University of California San Diego (DM), Saint George's University (SS), University of California Berkeley (DM), Columbia University (AKC)

PURPOSE: Adults over 65 are the largest group of cancer survivors in the U.S. While survival has improved, they still experience more age-related risk. We are examining hospital readiness to address the unique needs of this growing population. We will explore organizational structure, and factors related to information, technology, aging and cancer. METHODS: This is a cross-sectional analysis of hospitals using the 2014 American Hospital Association (AHA) database. We defined readiness as Medicare length of stay (LOS). Independently, hospital structures, technology, and services were assessed to determine their impact on LOS. RESULTS: Among 4,963 U.S. hospitals, the majority were small (61.92%; <150 beds), urban (58.30%), and not-for-profit (60.74%) with a mean LOS of 6 days. Only 30.63% of hospitals reported certified cancer programs while 42.43% offered robotic surgery and 28.88% virtual colonoscopies. Hospitals offering geriatric services (53.15%) and psychiatric services (47.94%) were more prevalent. Multivariable analyses found smaller hospitals compared to medium (AOR 4.49; p<.0001), urban compared to rural (AOR 1.06; p=.5574), and for-profit (AOR 1.14; p=.3384) compared to not-for-profit hospitals had greater odds of a shorter LOS (<5days). Additionally, hospitals reporting virtual colonoscopies (AOR 1.28; p<.0197), robotic surgeries (AOR 1.72; p<.0001, and palliative care (AOR 1.35; p=.0036) had greater odds of a shorter LOS compared to hospitals that did not. DISCUSSION: We highlight a need for hospitals to re-assess their readiness to provide age-friendly care. Hospital services contribute to care quality and access, further analysis in variability in care provision at the population level is needed to address disparities.

29.06.002

STAFF BARRIERS TO INCARCERATED WOMEN'S PHYSICAL ACTIVITY

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Northern Arizona University, Center for Health Equity Research (RC, TAP, LB, GP, HJW, JAB)

PURPOSE: Women are the fastest growing incarcerated population in the US and often physically inactive during their incarceration. Physical inactivity is associated with increased stress, poor sleep quality, weight gain, and other health problems. These health outcomes are particularly important considerations in jail settings, where access to comprehensive healthcare is limited. Recreation-time (rec-time) is an opportunity for incarcerated women to engage in physical activity. Detention officers' behaviors and perceptions may intentionally or unintentionally inhibit or enable rec-time attendance and physical activity. METHODS: During structured observations of rec-time, a multidisciplinary team took qualitative notes of jail staff's interactions with incarcerated women before, during, and after rec-time. RESULTS: Our team observed jail staff's perceptions and behaviors that may be barriers or motivators to both incarcerated women's rec-time attendance as well as their physical activity levels. Some jail staff did not follow the established rec-time schedule, and only allowed the opportunity for rec-time according to their personal discretion. Some jail staff expressed their disinterest in whether or not women attended recreation time. Conversely, one staff member hoped the women went out to "blow off some steam". CONCLUSION: The jail setting is unique for observation-based research. Our initial observations may provide insight into the importance of perceptions and behaviors of jail staff when considering tailored physical activity interventions for incarcerated women.

29.08.001

ENGAGING TRANSGENDER PATIENTS WITH OPIOID USE DISORDER IN PR

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University of Puerto Rico Medical Sciences Campus (KM, DSQ, CERD); George Washington University – Milken Institute School of Public Health (CERD)

PURPOSE: Despite well-established disparities with regards to opioid use disorder (OUD) among Latinx, transgender individuals, their access to treatment is low. This project aims to develop an evidence-based strategy for engaging transgender patients with OUD into care. We hypothesize that integrated, gender-affirming care for OUD combined with a patient navigation approach incorporating the unique needs of Hispanic, transgender individuals can increase accessibility of and engagement with treatment. METHODS: We will conduct formative research combining qualitative interviews with transgender individuals with OUD that are not engaged in care with surveys of providers of treatment for OUD in Puerto Rico. A convergent mixed-methods design will be used to identify the needs of transgender individuals with OUD not currently

engaged in care to inform strategies to improve engagement in care and improve health outcomes. We will include ethnographic qualitative interviews with at least 24 transgender individuals and a survey with 150 physicians certified to provide treatment for OUD in Puerto Rico. These findings will be used to develop a care engagement model utilizing a combined strategy of training providers to better provide care for transgender patients and assisting transgender patients with OUD in engaging with care. A six-month pilot will be performed to test the feasibility of this model. RESULTS / EXPECTED RESULTS: This research will help us better understand the unique barriers to care for OUD for transgender individuals and the strategies needed to overcome them in Puerto Rico. DISCUSSION / CONCLUSION: Ultimately, this will lay the groundwork to engaging transgender patients with substance use disorders and moving them into care.

29.08.002

VALIDATION OF A KNOWLEDGE TEST ON TRANSGENDER PATIENTS' CARE

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University of Puerto Rico Medical Sciences Campus (JHA, KM, DSQ, JRV, EJCF, ARO)

PURPOSE: The objective of this study was to develop and validate an assessment instrument to measure the effects of a continuing education intervention on 3 domains in pharmacists' knowledge needed to provide pharmaceutical care for transgender patients: (1) foundations of gender affirming care, (2) health disparities and the specific needs of transgender patients, and (3) hormone treatments for transgender patients. METHODS: An item bank was created based on a literature review on the 3 domains of interest. The item bank was reviewed by three content experts in: (1) professional continuing education, (2) clinical practice of gender affirming care, and (3) theoretical framework on gender minorities and gender affirming care. A draft instrument was developed with 42 items covering the 3 domains. Feedback from 7 practicing pharmacists was provided for face validity to refine the instrument. A pilot test of the instrument was then conducted with 64 pharmacists to determine internal consistency and discrimination value. RESULTS / EXPECTED RESULTS: Kuder-Richardson Formula 20 (KR-20) yielded a value of 0.653. Item difficulty index ranged from 0.078 to 0.938, and 67% (28) of the items demonstrated a discrimination index value of 0.2 or more. DISCUSSION / CONCLUSION: The instrument demonstrated moderate reliability and good discrimination in the pilot group. It will be used as pre/post test to measure the effects of continuing education interventions on pharmacists' knowledge to provide pharmaceutical care for transgender patients, by assessing growth in the 3 previously mentioned domains. Further revisions of the instrument will be made based on future results.

29.08.003

STANDARDIZED PATIENTS TO ADDRESS TRANSMEN HEALTH DISPARITIES

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Ponce Health Sciences University (ER-S, AR-P, MB, LJ, PC, NT, MB) and University of Puerto Rico, Mayagüez (DM)

BACKGROUND: Trans men (TM; assigned to female gender at birth but who live as men) are at a higher risk of cervical cancer (CC). CC incidence among Latinxs is the highest among all ethnic minorities in the United States. Latino TM (LTM) are at a higher risk as they lie at the intersection of two health disparity populations with high risk for CC (gender and ethnic minorities). Despite CC being highly preventable, lack of knowledge about specific LTM health needs, misgendering and stigmatizing behaviors among providers hamper their engagement in CC care behaviors (i.e. recommend a PAP test, offer self-sampling). However, no study to date has examined providers actual behaviors in clinical interactions with LTM. PURPOSE: Examine CC preventive care behaviors in clinical interactions using Standardized Patient Simulations (SPS; recorded simulations of clinical interactions with an actor portraying a LTM patient) in a sample of medical students. METHODS: We are implementing a cross-sectional design with quantitative (Measures: Transgender Knowledge Index, Transgender Stigma Scale) and SPS techniques. Our team (researchers, medical educators and community members) developed the LTM SPS. Simple linear regression analysis will be conducted to examine how well knowledge and attitudes explain medical students CC care preventive behaviors in the SPS interactions. A total of 20 medical students have already engaged in the study. EXPECTED RESULTS: We expect participants (n=40 expected) with higher LTM knowledge and lower stigmatizing attitudes towards LTM, will manifest higher CC preventive care behaviors (i.e. recommend a PAP test, offer self-sampling).

29.10.001

EPIDEMIOLOGICAL PROFILE OF AUTISM SPECTRUM DISORDER IN SATEL

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Ponce Health Sciences University

Autism spectrum disorders (ASD) is a growing neurodevelopmental condition that affects all racial, ethnic and socioeconomic groups characterized by various degrees of

social interaction and social communication impairment, as well as stereotypic and repetitive behaviors. In USA, about 1 in 59 children are identified with ASD. Puerto Rico in 2012 reported a prevalence of 1 in 62 children. No recent data is available so far. The purpose of this study is to construct an epidemiological profile of ASD in a satellite center on the south area of Puerto Rico. An ASD secondary data base with confirmed ASD cases, containing demographics, diagnostic methods, and comorbidities was used for this study. Descriptive statistics, univariate and bivariate analyzes were performed. Analyzes by sex, and level of severity of ASD was performed. From the 292 children with ASD, 82.2% (n=240) were male and 17.8% (n= 52) female. The mean age of all cases diagnosis was 5.3 ± 3.12. The town with the most reported cases was Ponce with 33.8% (n=99). Family history of ASD was reported in 18.2% of the cases (n=53). Comorbidities presented such as speech delay was presented in at least 34% of the cases. This is the first study that we know of on autism profile data from South Puerto Rico.

29.12.003

REDUCING THE RISK OF CORONARY HEART DISEASE IN BLACK WOMEN

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FLORIDA A&M UNIVERSITY (AM, AW, RT)

PURPOSE: Coronary Heart Disease (CHD) is the leading cause of death for African-American (AA) women in the U.S. resulting in 2.5 times higher risk of mortality compared to White women. This risk does decrease as AA women age but does not reduce to the level of White women until the eighth and ninth decade of life. Sedentary lifestyles, smoking, obesity, hypertension, stress-related factors and inflammatory risk variables greatly influence a woman's risk for heart disease. Traditional modifiable risk factors for CHD include high blood pressure (HBP), high blood cholesterol, diabetes, smoking, physical inactivity, and obesity. The purpose of this study is to examine the associations between health-related risk factors and coronary heart disease in women aged 18-64 after accounting for sociodemographic factors (age, ethnicity, marital status, education, employment, and insurance status) and self-reported health status. METHODS: We used 2015 Florida Behavioral Risk Factor Surveillance System (BRFSS). The BRFSS is the nation's premier system of health-related telephone surveys that collect state data of US adults regarding their health-related risk behaviors, chronic health conditions, and use of preventive services. RESULTS: The most statistically significant factors that impact CHD in women included self-reported poor health status (AOR=8.659; 95% CI=2.982-25.142); p<.0001) after adjusting for all other health-related risk factors as well as sociodemographic and lifestyle characteristics. Other major predictors for CHD included HBP, unemployment, high cholesterol level, education, smoking, physical inactivity, and obesity. DISCUSSION: Efforts to reduce and control risk factors, including age population-specific awareness programs are crucial for limiting the incidence of CHD.

29.12.004

BLACK WOMEN'S HEALTH THROUGH YOGA: AN ETHNOGRAPHIC STUDY

BG GULLEDGE
Howard University (CCMS)

PURPOSE: This ethnographic study examines observations of a Black-yoga space in Washington, D.C. in order to explore conversations of health, wellness, and acceptance in an explicitly Black wellness space. RQ1: How do African Americans communicate about health and wellness in a Black health focused space? RQ2: How do African Americans operate in a Black-owned health focused space? METHODS: To address these research questions, it was vital for the researcher to observe a Black yoga space to understand how people operate within it and how they communicate about it. The researcher completed two 30-minute interviews with owner of the Black-owned yoga and observed four yoga classes over the course of two days. RESULTS: Through the symbolic interactionist approach, the researcher can look at the interpersonal and nonverbal communication from the yoga studio to pull out three emerging themes. In comparison to their White counterparts: 1. Black people adorn themselves with statements of identity when reclaiming their health; 2. Black people in health and wellness spaces are focused on creating interpersonal communities; 3. Black people are attracted to cultural representations of soul and trap music. DISCUSSION: Although only a few studies have examined the effectiveness of mind body therapies in minorities, evidence suggests that mind-body interventions reduce stress and improve health in African Americans. As research for the uses of yoga continue to build a foundation, there is potentially more to explore as far as how African American communities communicate about yoga as a health and wellness space. This is especially intense in highly-gentrified areas, which can often anecdotally connect yoga and coffee shops with the introduction of gentrification.

| CLINICAL SCIENCE |

31.01.002

BLOOD BASED BIOMARKERS FOR COLORECTAL CANCER DETECTION

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University of Puerto Rico-Medical Sciences Campus (EVC,SRQ,MCC); UPR-Comprehensive Cancer Center (EVC, HCG,NC,AY,LR,JPM,MGP,MCC), San Juan, PR

PURPOSE: Colorectal cancer (CRC) is the first and second leading cause of cancer death among men and women in Puerto Rico and United States, respectively. The lack of sensitivity and specificity of current CRC screening methods limits their application for early detection. This study aims to determine the diagnostic accuracy of blood based biomarkers methylated septin-9 (mSEPT-9), Insulin-like growth factor binding protein 2 (IGFBP2), Dickkopf-3 (DKK3) and Pyruvate kinase M2(PKM2) in plasma samples from Puerto Rican Hispanics CRC cases. METHODS: Using a retrospective case-control study design we evaluated plasma samples (n=248) 124 cases and 124 controls age-gender matched. Plasma samples were tested using Epi procolon test and ELISA methods (Assay Solutions; Biorbyt Inc.). Sensitivity and specificity was calculated to evaluate the performance characteristics of the methods; receiver operating characteristic (ROC) curve was plotted for the assessment of diagnostic accuracy, and for comparisons according to CRC disease stage. RESULTS: The levels of the biomarkers were significantly different ($p<0.05$) between the CRC cases and control patients except for PKM2. The diagnostic accuracy of mSEPT9, IGFBP-2, DKK3 and PKM2 for early stages compared to controls was 64% [95% CI:59 – 74%], 70% [95% CI:61-77%], 66% [95% CI:58-74%] and 56% [95% CI: 48-65%], respectively. For CRC advanced stages there is a 62%, 71% , 57% and 41% chance that the model will be able to distinguish between control and CRC cases when classifying by mSEPT9, IGFBP-2, DKK3 and PKM2, respectively. DISCUSSION : The biomarkers with the overall best performances were mSEPT9 (AUC=0.63; p=<0.001) and IGFBP-2 (AUC=0.70; p=0.033) individually and across the stage continuum. Their combination with other available tests may further improve diagnostic sensitivity especially for early stage disease, which may provide a new alternative for future CRC screening, although further investigations are needed.

31.01.003

IMPACT OF MEDICATION THERAPY MANAGEMENT ON CAPECITABINE

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Texas Southern University (VBA, TR, AM, HX); Houston Methodist Hospital (VBA, KH)

PURPOSE: Oral chemotherapy drugs have been growing in popularity due to multiple reasons. Compared to intravenous chemotherapy, patients on oral chemotherapy have reduced multidisciplinary team support due to less frequent routine visits. Hypothesis: Medication therapy management (MTM) strategies to educate cancer patients and decrease polypharmacy will increase medication adherence of capecitabine, an oral chemotherapy agent. METHOD: This is a single center chart review study to obtain data on medication adherence, pharmacist inventions, toxicity identification/management, and drug interaction screening for patients on capecitabine, an oral chemotherapy agent. Study outcomes data (primary endpoint: patient's adherence to capecitabine post-implementation of MTM service compared to pre- implementation of MTM service; secondary endpoints will include pharmacist inventions, toxicity assessment, and drug interaction screening) will be evaluated before the implementation of MTM service (MTM service for patients on oral chemotherapy was implemented in the outpatient cancer center in November 2017 as routine care) and after the implementation of MTM service by electronic medical record review, pharmacy refill report, and/or self-report medication adherence tool. EXPECTED RESULT: Twenty patients on capecitabine during the pre-MTM service implementation timeframe were identified from pre-existing data from a previously published study titled "Evaluation of the prescribing pattern, tolerability and side effects of oral chemotherapy". Patients on capecitabine during the post-MTM service implementation timeframe are currently been identified. The results from this study will remarkably contribute to the growing literature and clinical practice on oral chemotherapy. DISCUSSION: Data analysis will be completed following data collection for 40 patients in the post-MTM timeframe.

31.04.001

DAS/DADS DECREASES OXIDATIVE STRESS IN S. CEREVISIAE EXPOSED

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Florida A&M University

PURPOSE: Due to chemoprevention strategies and the development of chemotherapeutic agents like doxorubicin, cancer survival rates have increased leading to an elevated number of patients suffering from long-term adverse effects such as bone damage. Though doxorubicin's dosage is limited due to its toxicity, its use is still widespread due to its effectiveness. Doxorubicin's secondary mechanism of action, induction of oxidative stress, is thought to be the cause of its toxicity to normal tissue, however there is limited research on its effect on bone. We hypothesize, that garlic substituents diallyl sulfide/diallyl disulfide (DAS/DADS) may reduce doxorubicin's toxic effect to normal tissue through genes involved in copper transport/activation. METHODS: Using yeast survival assays, the sensitivity of oxidative stress related strains involved in copper transport, or those dependent on copper were tested against doxorubicin and menadione with and without DAS/DADS. Strains studied include wt, ccs1, sod1, atox1, and cox17.

Strains were tested against menadione, an inducer of oxidative stress to verify that doxorubicin's second mechanism of action is causing the sensitivity. Statistical significance was set at $p<0.05$. RESULTS: DAS and DADS decreased oxidative stress in the presence of doxorubicin through the antioxidant sod1, atox1, and cox17 significantly. All strains showed increased sensitivity to doxorubicin and menadione. DISCUSSION/CONCLUSION: This model reveals doxorubicin's secondary mechanism of oxidative stress induction is behind the sensitivity of selected strains to doxorubicin. Furthermore, DAS and DADS's ability to decrease the sensitivity of strains to doxorubicin validates future studies exploring DAS/DADS's protective effect against doxorubicin induced bone damage, considering copper is necessary for bone health.

31.05.002

SPATIAL ABILITIES AND HIPPOCAMPAL VOLUMES IN HIV + WOMEN

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University of Puerto Rico Rio Piedras Campus (RJR, RJRC, AJ, JH), University of Puerto Rico Medical Sciences Campus (RJR, VW), University of Puerto Rico Mayaguez (JGR)

PURPOSE: Antiretroviral therapy (cART) has increased the survival rate of HIV-seropositive (HIV+) patients. However, there is still a high prevalence of HIV-associated neurocognitive disorder (HAND) among this population. The main aim of this study was to explore the associations between spatial and learning memory, visuospatial ability, CD4 count, and hippocampal volumes in a sample of HIV+ Latina women. METHODS: We recruited 61 women: 45 HIV seropositive and 16 HIV-seronegative controls. HIV+ women were evaluated for viral-immune profiles, Navigational Memory test (MI) for spatial learning and memory, neuropsychological testing, Beck Depression Inventory (BDI-II), and magnetic resonance imaging (MRI). We determined cognitive performance using the HAND nosology criteria, dividing the HIV+ women into cognitively normal and neurocognitive impaired (stratified into asymptomatic [ANI] and mild neurocognitive impairment [MND]). A subgroup of 19 participants from the selected sample underwent MRI to determine hippocampal volumes. Non-parametric statistics were performed. RESULTS: We found that hippocampal volumes had a strong inverse correlation with current CD4 in HIV+ women ($p <0.05$), suggesting that lower levels of current CD4 where associated with higher hippocampal volumes. We also observed a significant correlation between MI memory and current CD4 ($p< 0.05$), as with visuospatial ability and spatial memory ($p< 0.05$). No significant correlation between hippocampal volume and spatial learning or spatial memory were found. CONCLUSION: The results demonstrate that current CD4 is significantly associated with hippocampal dysfunctions and memory deficits in HIV+ women with HAND.

31.09.001

DESCRIBING ANTIPSYCHOTIC PRESCRIBING PATTERNS BASED ON RACE

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Xavier University of Louisiana (TJM, TCW, DA, ME), Optum-United Healthcare

PURPOSE: Psychosocial factors including cultural beliefs and socioeconomic status can have a large impact on accessibility to treatment in mental illness. Considering the various perceptions of mental health across cultures and stigmatization of health care providers, minority populations can potentially be prone to health disparities in regard to the treatment of mental health conditions. This pilot study will provide new data regarding drug selection of antipsychotic medications based on race/ethnicity, as well as, other individual characteristics and how it relates to possible unnecessary antipsychotic exposure. METHODS: The institutional review board approved this single-centered, retrospective chart review that was conducted at the inpatient behavioral health center of an academic hospital. To be included, patients had to have been discharged with a prescription for an oral antipsychotic or had a long-acting injectable antipsychotic administered prior to discharge for a diagnosis of a formal mood or thought disorder. The study enrolled 400 patients from October 1, 2015 – December 31, 2017. Descriptive in nature, the study relates the antipsychotics prescribed at discharge to race/ethnicity of the patient. Demographical information including socioeconomic status, healthcare coverage, past psychiatric and medication history was collected. RESULTS: Patients were found to have significantly higher doses of Thorazine equivalence upon discharge when they were involuntarily admitted to the behavioral health unit ($p=0.0356$), as well as those with previous antipsychotic trials ($p=0.001$). The study found a trend towards significance in appropriateness of therapy based on race ($p=0.0468$), as African American patients were three times more likely to receive inappropriate medications compared to the White population (95% CI 1.01 – 3.25). CONCLUSION: We reported the prescribing patterns of antipsychotics based on race/ethnicity to better target health disparities in the treatment of mental illness in future studies. Also, appropriateness of antipsychotic medications was reported based on guideline recommendations in relationship to the patients' individual demographical information, socioeconomic status, psychiatric history and previous treatment approaches . Future studies with an increased sample size in all groups and increased generalizability are warranted.

31.11.001

STANDARD SCREENING FAILS TO IDENTIFY SLEEP APNEA IN AAS

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PURPOSE: Obstructive Sleep Apnea (OSA) is a common disorder known to contribute to cardiometabolic disease and cardiovascular mortality. It affects African Americans (AA) with an increased prevalence and severity relative to other populations. Early recognition could help reduce disparities in cardiovascular outcomes. Nevertheless, little data exists regarding optimal screening tools for use with African Americans. This study reviews the performance of a validated tool, the STOP-BANG questionnaire, in an AA population. METHODS: Data were from 205 patients evaluated at the Howard University Hospital Sleep Disorder Center between April 2018 and June 2019. Records were reviewed for demographic information, body mass index (BMI), neck circumference, and medical history, including the presence of snoring, tiredness/sleepiness, observed apneas, and hypertension and results of sleep study testing. Data were analyzed using SPSS software. RESULTS/EXPECTED RESULTS: In contrast to the STOP-BANG performance in other populations, it demonstrated both poor sensitivity and specificity in our AA population. Analysis of sub-measures contributing to the score revealed that age, a complaint of tiredness, and hypertension (HTN) were especially poorly correlated with the presence of OSA. Male and female patients demonstrated very different predictive associations with factors such as body mass index and HTN. DISCUSSION/CONCLUSION: A screening tool validated in other populations performs poorly in identifying OSA in our AA Sleep Clinic population. Male and female AA patients perform very differently on screening sub-measures. These data may allow us to construct a better screening too for OSA in the AA population and further research is needed.

32.01.002

IMPROVING KNOLWEDGE RETENTION WITH STANDARDIZE PATIENT.

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The opioid crisis is a national issue and increasingly relevant. It is critical that healthcare professionals are knowledgeable about the risks associated with opioid analgesics as they pertain to their patients as well as from a public health perspective. To combat the opioid crisis, several training programs have been developed and various modes of educational delivery and evaluation methods had been incorporated into pharmacy curriculum. The goal of this study is to determine the effect of a standardized patient teaching strategy as an essential tool in improving the retention of the clinical knowledge. A standardized patient was presented and interviewed at the beginning of an all-day symposium. There were a total of 7 speakers on topics related to REMS opioid and pain management strategies. Each presenter then incorporated the case into their relative topics. At the end of the symposium, a debriefing session was held and the case was fully discussed. The program was approved by the American Council on Pharmacy Education for 7 CE hours. In order to obtain the CE credit, participants must sign onto an online portal and fill out questions regarding each topic discussed and the results were compared. A total of 302 participants attended the conference. Comparing to the other 6 presentations, the standardized patient presentation has the highest overall survey rating in retention knowledge comparing to the other 6 presentations (98.85% vs. 97.94% respectively; t=0.03298). Based on this study, it is reasonable to recommend to consider using standardized patients.

32.04.001

SOCIODEMOGRAPHIC DISPARITIES IN ADOLESCENT BARIATRIC SURGERY

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PURPOSE: As obesity is disproportionately prevalent in minority racial/ethnic groups, we sought to determine if the utilization of bariatric surgery varied by socioeconomic and demographic characteristics of morbidly obese adolescent patients. METHODS: We selected adolescent patients aged 15-21 years old with diagnoses of morbid obesity (Body Mass Index ≥40) in the 2009 and 2012 Kids Inpatient Database. Socio-demographic characteristics were extracted. Comparisons were made between bariatric and non-bariatric patients. RESULTS: There were 27,403 adolescents with morbid obesity with 1,726 patients (6%) admitted for bariatric surgery. Compared to the general morbidly obese adolescent population, those receiving operations were more likely to be Non-Hispanic White (59% vs. 41%, p<0.001), female (77% vs. 72%, p<0.001), older (mean age 18.6y vs. 16.9y, p<0.001), of highest income quartile (26.5% vs. 11.9%, p<0.001), and privately insured (72% vs. 33%, p<0.001). Morbidly obese non-Hispanic Black (Odds Ratio, 95% Confidence Interval: 0.45, 0.39-0.54) patients were significantly less likely to undergo bariatric surgery compared to non-Hispanic Whites. Patients from households in the fourth (2.34, 1.99-2.75) income quartile were more likely to have bariatric surgery compared to

those in the lowest income quartile. Adolescents with private insurance were markedly more likely to have bariatric surgery when compared to adolescents with public insurance (4.73, 4.18-5.36). DISCUSSION: Obese patients who were non-Hispanic Black, from low income households and with public insurance were less likely admitted for bariatric surgery. These findings suggest an opportunity to expand access to weight loss surgery to all adolescents who may benefit from it.

33.01.001

CREATION OF OPEN-CELLED 3D PRINTED CASTS AND SPLINTS

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PURPOSE: The mission of the BioMed Innovation Center at the UPR MSC is to apply 3D Printing technologies to medical practice. 3D printing has impacted the fields of orthopedics, cardiology, surgery, and dentistry. Our objective was to create ridged open-cell splints and casts that have improved characteristics with respect to wear ability, support and comfort for the orthopedic patient. METHODS: Custom splints and casts require a full-scale model of the injured area. Such 3D models were obtained using a 3D full-color EVA® scanner with Artec Studio 12® software and exported as a STL mesh files. These mesh surfaces were imported into Rhino 6® software, converted into NURB poly-surfaces, which were offset several millimeters to provide a comfortable fit. The offset surfaces were then imported into Grasshopper® software and programmed to generate STL files with the desired open cell characteristics. The STL files were then loaded into the software of the 3D printer and converted into g.code instrument control files. The physical cast or splint was then printed in a filament or resin 3D printer using PLA and ABS materials. RESULTS: These units were of light weight, water-proof, and comfortably fit the patient, as well as, providing access to areas that may itch. CONCLUSIONS: Creation of 3D printed open-celled casts and splints appear to be a significant improvement to the classic plaster structures. These advances have the potential for better care experience and outcome for orthopedic patients.

34.01.001

BEST STRATEGIES TO RECRUIT ELDERLY BLACKS

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Background: Historically, Blacks have been disproportionately underrepresented in clinical trials. To address this gap in research participation, we analyzed our recruitment data to identify the most effective strategies for enrolling older Blacks in clinical trials.Methods: Data used in these analyses were obtained from 3,266 potential volunteers, ages 50 or older, who completed a Mini-Mental State Exam as part of recruitment and screening for various clinical studies on Alzheimer's disease. In order to determine the most effective strategies for engaging Blacks in clinical research, we used tests of proportion to assess significant differences in recruitment sources, counts, and percentages for optimal recruitment strategies by gender. Results: Of the total 3,266 screened, 2,830 Black volunteers were identified for further analysis. Overall, more women than men (73.8% vs 26.2%) participated in our recruitment activities. However, a significantly higher proportion of men than women were engaged through family (3.86% vs 1.30%, p=0.0004) and referral sources (5.89% vs 2.59%, p=0.0005). Compared to other sources for recruitment, we encountered a higher proportion of volunteers at health fairs (42.95%), and through advertisements (14.97%). Conclusion: Our findings indicate Black men and women in our sample were predominantly recruited from health fairs and through advertisements tailored to their health needs and interests. Conversely, we mostly engaged Black men through family referrals and persons known to them, indicating a need for trust in their decision to engage study personnel and/or participate in clinical trials.

34.01.002

CD112R+ CD4 T CELLS INCREASED WITH CORONARY PLAQUES IN HIV

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Background: Chronic inflammation and increased T-cell migration are associated with arterial injury in Persons Living with HIV PLWH. Our preliminary work found a link between T-cell exhaustion (defined by upregulation of negative checkpoint receptors (NCR)) and coronary artery calcium in HIV+ adults. CD112R is a novel checkpoint for T-cells, and thereby T-cell exhaustion. We assessed NCR expressing T-cells and soft coronary plaques measured by CT angiogram to evaluate their relationship to plaque development in HIV+ donors. Methods: We assessed cross-sectional analysis of HIV+ individuals (age >40 years on stable ART >3 months). CT angiogram was performed using dual source CT to evaluate

coronary plaques as measured by total plaque severity score (TPS) and total segment stenosis score (TSS). PBMC were assessed for the frequencies (%) of NCR+ (CD112R, TIGIT, TIM-3, PD-1) T-cells and T-cell activation (CD38+HLA-DR+) by flow cytometry. Non-parametric correlations were analyzed between % T-cell subsets and measures of coronary plaque. Results: Of 12 HIV+ individuals, 92% male, age: median 57.5 years (IQR 54.5, 61.5), CD4 count: 566 cells/mL (398, 690), all HIV RNA <50 copies/ mL,TPS 3.00 (0.75, 5.75) and TSS 3.00 (0.75, 7.00). CD112R+ and CD112R+TIGIT+ CD4 T cells, irrespective of TIM-3 co-expression correlated with higher TPS and TSS scores (all p< 0.05). TIM-3+ CD8 T-cells (lacking CD112R- PD1-TIGIT-) negatively correlated with TPS. Conclusion: Expanded CD112R+ and CD112R+TIGIT+ CD4 T-cells were associated with soft coronary plaques. Our results highlight a potential role for CD112R, a co-inhibitory receptor linked to the TIGIT pathway, in CVD among PLWH.

34.01.004

BIOMARKERS OF CHRONIC KIDNEY DISEASE IN SICKLE CELL ANEMIA

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Chronic kidney disease (CKD) is a major complication of sickle cell anemia (SCA) with a three-fold higher risk than general population. Urine concentration defects and increased glomerular filtration in SCA complicate early CKD detection. To identify early biomarkers of CKD progression we conducted high resolution mass spectrometry analysis of urine samples from patients without proteinuria and with hemoglobinuria shown to correlate with CKD progression. We observed increased levels of ceruloplasmin (CP) and orosomucoid (ORM), which were confirmed by ELISA and Western blot. Urinary CP, ORM and hemoglobin demonstrated positive correlations with CKD stage in 34 samples obtained from SCA patients with CKD stages ranging from 0 to 5. However transferrin and ferritin levels, while increased in SCA anemia patients, showed no correlation with CKD progression. ORM was further validated in Howard University registry study group (96 SCA patients). Urinary ORO/CRE levels demonstrates modest correlation with CKD stage (R2=0.2218). However, when stratified into no or mild inflammation group (ORE/CRE<10µg/mg) and a significant inflammation group (ORE/CRE>10 µg/mg), strong inverse correlation was observed between the percentage of samples without inflammation and CKD stage (R2=0.996). We also observed strong correlation of CDK progression among samples with significant inflammation. About 30% of patients at CKD stage 0 (no renal disease) had advanced inflammation (ORO/CRE >10 µg/mg) suggesting that these patients might be at risk for development of CKD. In conclusion, we identified urinary CP and ORM as potential non-invasive biomarkers that can predict CKD in SCD patients before the onset of proteinuria and albuminuria.

34.01.006

MONOCYTE MIGRATION IS NEGATIVELY CORRELATED WITH CIMT IN HIV

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Background: Transmigration capacity of monocytes is an important driver of atherosclerotic plaque development. The effects of HIV infection on monocyte transmigration is unknown. We assessed the relationships of monocyte transmigration and atherosclerotic plaque burden as measured by Carotid Intima-Media Thickness (CIMT). Methods: Cross-sectional analysis of HIV+ individuals (age >40 years, stable ART with HIV viral load < 50 copies/mL) compared to a similar HIV sero-negative group. High resolution B-mode ultrasound images of right common carotid artery (CCA) and carotid bifurcation (BIF) were obtained. Monocytes isolated in both groups were added to upper well of the transwell-filter system and allowed to migrate towards human MCP-1 added to lower chamber. Live transmigrated cells were quantified via flow cytometry to determine %-transmigration. Results: Of 36 subjects 19 were HIV+ (79% male, median age 60.6 yrs), and 17 were HIV- (76% male, median age 63.2 yrs). Among the HIV+ group, median CD4 count was 591 cells/mL and HIV RNA was < 50 copies/mL in 100%. MCP1-mediated monocyte transmigration between HIV+(median 1.74 (Q1:0.71, Q3:2.55) and HIV- groups (1.67 (0.52,1.80)) was not different (p=0.483), as was difference in transmigration without added MCP1 between HIV+ (0.12 (0.11,0.28)) and HIV- (0.16 (0.11,0.24)) groups. Within HIV+ group, transmigration was correlated with CCA (rho -0.46 (p=0.057)) and BIF (rho -0.50 (p=0.036)) whereas no such correlations were noted in HIV- subjects. Conclusion: Although no difference in monocyte transmigration was noted between HIV+ and HIV- groups, transmigration was negatively correlated with CIMT in HIV+ group only. The effects of HIV on monocyte transmigration warrant further investigation.

34.01.007

MUTATIONAL/ ANCESTRAL LANDSCAPE OF CHILDHOOD LEUKEMIA IN PR

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Hispanic/Latino genomes exhibit complex population structure due to the admixture of European, Native Americans,

and African individuals. US Hispanic children with acute lymphoblastic leukemia (ALL) have higher incidence and mortality rates. We have compared the age-standardized incidence and mortality rates (2010-2014) of children with ALL in Puerto Rico (PR) with US Hispanics (USH), non-Hispanic-white (NHW), and non-Hispanic-black (NHB). PR children have lower incidence and mortality than USH; lower incidence and higher mortality than NHW; and higher incidence and mortality than NHB. We expect to contribute to a better understanding of leukemogenesis, treatment response and overall survival in the PR pediatric population by first, identifying genomic alterations in newly diagnosed ALL patients and leukemic clones present at birth using the patient's newborn screening sample, in order to increase the understanding of the development of leukemia and the mutations present at birth compared to those found at diagnosis. Secondly, we will identify additional genomic alterations in drug metabolism genes that may impact treatment response. Thirdly, we will evaluate ancestral contributions to ALL in the admixed Puerto Rican patients, including locus-specific ancestry and relate them to drug metabolism gene variants, and establish associations between ancestry, genomic alterations and drug metabolism SNPs as well the correlation that these variables may have with treatment outcomes.

34.01.008

SEX, EDUCATION AND SCREENING COLONOSCOPY AMONG BLACKS.

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PURPOSE: Black men suffer the highest burden from colorectal cancer in the United States. It is generally believed that women are more health conscious than men, but it is unknown if educational status influence compliance by sex among blacks. We evaluated sex differences in compliance with scheduled screening colonoscopy appointments among underserved urban blacks and investigated the effect of the highest education attained. METHODS: A total of 399 black patients participated in a clinical trial (NCT02464618) designed to evaluate the efficacy of self-selected social contact person in improving compliance to scheduled outpatient screening colonoscopy appointments. The primary outcome of our present study was compliance with the scheduled outpatient screening colonoscopy among attendees by sex and highest education attained. We used logistic regression models to calculate odds ratios (OR) and 95% confidence intervals (CI). RESULTS: There were 188 (47.1%) black men and 211 (52.9%) black women. Overall, there was no sex difference in compliance with the scheduled colonoscopy appointments (77.3% versus 77.1%; OR=1.01; 95% CI: 0.63-1.61). However, participants with some college education were more compliant (84.1% versus 73.1%; OR=1.95; 95% CI: 1.15-3.30) compared to those with high school education or less. This improvement in compliance was more evident among men (86.2% versus 73.1%; OR=2.30; 95% CI: 0.99-5.34) when compared with women (82.2% versus 73.2%; OR=1.76; 95% CI: 0.89-3.49). CONCLUSION: Efforts to improve general and cancer specific education of black men are needed to reduce the burden of colorectal cancer among this vulnerable population.

34.01.009

GROSS MOTOR DELAY ASSOCIATED TO PRENATAL ZIKA EXPOSURE

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PURPOSE: Zika virus (ZIKV) infection during pregnancy causes neonatal microcephaly and other birth defects. Developmental delay and sensory problems have also been described in infants without brain defects at birth. Early identification and timely intervention of gross motor delay, a useful marker for brain damage, can improve outcomes over time. The Pediatric Outcomes of Prenatal Zika Exposure (POPZE) study aims to describe the full spectrum of abnormalities in ZIKV exposed children. METHODS: We enrolled infants born to mothers with confirmed (positive Real Time-Polymerase Chain Reaction (RT-PCR)) or probable (positive Immunoglobulin M (IgM)) ZIKV infection during pregnancy and obtained clinical and demographic data from birth records and developmental outcomes from follow-up visits. The Peabody Developmental Motor Scales-2 (PDMS-2) measuring gross motor development, were administered at 18 months. Descriptive statistics were used for sociodemographic and clinical variables and an independent sample t-test to compare PDMS-2 Gross Motor Quotient (GMQ) and Subtest scores by maternal diagnosis. RESULTS: From 47 infants examined, 29 (62%) were females, 22 (47%) were born to ZIKV RT-PCR positive mothers. One infant had microcephaly at birth. The GMQ total scores of 16 (34%) infants were below average as compared to age-specific means. Infants of ZIKV RT-PCR positive mothers had significantly lower GMQ and Stationary Subtest scores than infants of ZIKV IgM positive mothers. DISCUSSION: Gross motor developmental abnormalities consistent with the ZIKV neuro-pathogenesis present in infants without microcephaly. These findings underscore the importance of developmental follow-up to identify gross motor and other developmental disabilities that benefit from early intervention.

34.01.010

MEASURE OF COGNITIVE DETERIORATION IN PSYCHIATRIC PATIENTS

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PURPOSE: Cognitive deterioration is characteristic in patients with psychiatric disorders. Several deficits are recognized in patients with mood and psychotic disorders. We hypothesized that exists a difference in the level of deterioration between patients with Bipolar disorder (BD) type I, BD type II, BD-related disorder, Major Depressive Disorder, and Schizoaffective disorder. We analyzed the Mini-Mental State Examination (MMSE-2) used with a sample of patients to measure cognitive impairment. METHODS: Ninety-nine MMSE-2 were examined from a sample of psychiatric patients recruited from a clinic of a private academic institution of psychology in the San Juan area and an outpatient governmental health agency in Puerto Rico. Participants had Bipolar Disorder, Major Depressive Disorder, or Schizoaffective Disorder. Statistical analysis was done using SPSS, Version 21 Software. RESULTS: Baseline demographic measures and clinical characteristics of the subjects were taken. A Chi-square with the value of the test statistic was 21.417, with a p-value of .045 at a significance level of $\alpha = .05$. DISCUSSION: According to MMSE-2, mild cognitive deterioration was found in 63.2% for Major Depressive disorder, 60% for BD-related disorder, and 58.3% for Schizoaffective disorder. For patients with BD, type II, 20% had severe cognitive deterioration. The results are important because identify the different level of deterioration by each psychiatric group. We recommend future studies with a larger sample size for each disorder and a control group.

34.01.011

CHARACTERIZING THE EQUOL MICROBIOME IN PUERTO RICAN WOMEN

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PURPOSE: Hispanic women are more likely to die of breast cancer (BC), a health disparity attributed to environment and diet. Our studies show that the soy-isoflavone daidzein increases BC metastasis in mice. This response is mediated by the daidzein secondary metabolite, equol. The metabolite is produced by intestinal microflora from the human microbiome that are present in ~30% of the population. Hispanic women are more likely to be equol producers than Caucasians, however this information in Puerto Rican (PR) women is unknown. The purpose of this study is to characterize equol production in PR women with the goal to describe the microbiome involved in equol biosynthesis. To test the hypothesis that soy consumption contributes to efficient equol production, we initiated a cross-sectional study in a sample of premenopausal PR women.METHODS: Inclusion criteria consisted of women 25-50 years-old (n=80), with no history of cancer, hormone or oral contraceptive intake (past 2y), or antibiotic intake (past 3-mo). Women were required to live in Puerto Rico for the past 10y. Diet and lifestyle surveys were administered. We evaluated urine samples for soy metabolites including equol, and fecal gDNA to study the gut microbiome via metagenomic analysis. RESULTS: Soy consumption was reported in 41% of the subjects, while 25% were equol producers. Bacterial diversity significantly changes ($P<0.02$) with soy consumption and equol production. Equol producers displayed lower amounts of healthy bacterial biomarkers. CONCLUSIONS: PR women that are equol producers might be predisposed to chronic diseases such as cancer due to their altered microbiome.

34.01.012

PILOT PHARMACOKINETICS OF BUPRENORPHINE IN PUERTO RICO

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Purpose:To characterize the pharmacokinetics (PK) of buprenorphine (BUP) in Puerto Ricans (PRs) diagnosed with opioid use disorder (OUD). Methods:Twelve OUD-patients on maintenance dose of BUP were recruited in three clinics in PR. Blood samples were collected at 0, 0.5, 1, 2, 3, 4, 6, and 8 hours after BUP administration. Samples were centrifuged (3000 rpms; 10 mins) to obtain plasma for quantification of BUP and metabolites using UPLC-mass spectroscopy instrumentation. Non-compartmental analysis was performed to calculate PK parameters; maximum plasma concentrations (Cmax), trough BUP concentrations at time zero (C0), and time to maximum concentration (Tmax) were observed using each participant's plasma concentration-time profile. The area under the plasma concentration-time curve for the 8 hour dosing interval (AUC) was calculated using the trapezoidal rule. Results/Expected Results:Preliminary analysis identified distinct PK characteristics such as high inter-subject variability in both plasma exposure (AUC=22.41+14.33

ng h/mL;VAR=205.4) and in BUP peak concentration (Cmax=0.74+0.36 ng/mL/mg). At least two patients were below the projected effective trough levels of 1 ng/mL, and two additional patients were near these value; totaling 4 of 6. Discussion/Conclusion:Current dosing approaches for OUD in PR use standardized models developed with Whites in the US. However, the inter-patient variability observed in this study demonstrates the need for evidence-based dosing strategies in PR. These results are the first step of a research agenda aiming at developing a pharmacokinetic model to accurately dose for OUD in PR with proven efficacy.

34.01.014

ALTERED ARID1A EXPRESSION IN COLORECTAL CANCER

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Background: ARID1A has been described as a tumor suppressor gene, participating in chromatin re-modeling, epithelial-mesenchymal-transition and many other cellular and molecular processes. It has been cited as a contribute in tumorigenesis. The role of ARID1A in CRC is not yet defined. Aim: To investigate the role ARID1A methylation and CNV in its expression in CRC cell lines and to examine the relationship between ARID1A status with survival and clinicopathologic characteristics in patients with CRC. Methods: We used RT-PCR to determine both CNV and expression of ARID1A from six CRC cell lines. And used MSP to evaluate methylation of ARID1A. We used (IHC) to ARID1A protein expression, and, evaluate both MSI and EMAST status in 18 paired CRC and adjacent normal tissues. Statistical analysis was performed to establish correlations between ARID1A expression and other parameters. Results: Among the 18 CRC tumors studied, 7 (38.8 %) and 5 tumors (27.7%) showed no or low ARID1A expression, respectively. We observed no significant difference in ARID1A expression for overall patient survival, and no difference between clinicopathological parameters including MSI and EMAST. However, lymphatic invasion was more pronounced in the low/no ARID1A expression group when compared to moderate and high expression group (33% VS. 16.6% respectively. ARID1A promoter methylation was observed in 4/6 (66%) of cell lines and correlated with ARID1A mRNA expression level ranging from very low in SW48, to more pronounced in HCT116 and HT-29/219. Treatment with the methyltransferase inhibitor 5-Azacytidine (5-aza) resulted in a 25.4-fold and 6.1-fold increase in ARID1A mRNA expression in SW48 and SW742 cells, respectively, while there was no change in SW480 and LS180 cells. No ARID1A CNV was observed in the CRC cell lines.

34.01.015

RETROSPECTIVE STUDY REVEALS A CORRELATION BETWEEN SERUM CHOL

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PURPOSE: Neurotransmitter reuptake by transporters is a major mechanism for terminating synaptic transmission. The human dopamine transporter (hDAT) is critical to dopamine homeostasis and is the target responsible for euphoria experienced when abusing psychostimulants. Cholesterol enriched nanodomains on the plasma membrane serve as organizing centers to regulate different cellular processes such as neurotransmission and trafficking. Our recent studies have shown that cholesterol modulates the function of hDAT. Excess cholesterol added to the plasma membrane decreases uptake and perturbs the steady state partitioning of hDAT into nanodomains, while reduced plasma membrane cholesterol enhances hDAT uptake compared to control in HEK 293 cell lines. The same trends are observed in Dopaminergic neurons. Based on these findings we hypothesized that serum cholesterol levels correlate to methamphetamine addiction and recovery outcomes. METHODS: To explore the translational significance of our work, we observed serum cholesterol levels in patients diagnosed with drug dependence using 9th and 10th editions of the International Statistical Classification of Diseases and Related Health Problems (ICD-9 and ICD-10). We evaluated these patients for both high cholesterol and non-high cholesterol. RESULTS: We found a significant correlation between high serum cholesterol and addiction in general. We are the first to explore the interdependence of these measures in existing medical data at a minority serving health care network. We discovered that there were significant health disparities in addicted patients with high cholesterol associated with age, sex, race, and ethnicity. CONCLUSION: This and future studies may help to predict the potential for drug dependence and to improve outcomes for those in addiction treatment programs based upon lipid profiles of patients.

34.01.016

PROBIOTICS EFFECTS IN CHILDREN'S HEALTH

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PURPOSE: Childhood obesity has significantly increased, resulting in one of the most severe public health challenges of this time. Recent studies support the critical role of gut microbiota in health and disease. This study aims to assess the effects of Lactobacillus rhamnosus GG probiotics on the host response, depressive/anxiety symptoms, and gut microbiota composition. METHODS: We recruited 16 obese children aged 6 to 12 years old. The parents completed the proxy PROMIS anxiety and depression scales and provided a fecal sample of their children. The parents provided a daily probiotic tablet to the child for three months, starting at baseline. We collected a blood sample for cytokine and chemokine expression analyses to evaluate the host response. The 16S rRNA gene was used to characterize the gut microbiome by using the Illumina MiSeq platform. Study participation comprised of six months with measures taken at baseline, third and sixth months. RESULTS: Study participants that began probiotics at recruitment exhibited a significant reduction of plasma IL-1 Beta, IL-17A, and GM-SCF at the 3rd-month follow-up. However, there were no significant changes in depression or anxiety symptomatology. At baseline, the most abundant bacteria in children's gut at the genus level were Akkermansia, SMB53, Blautia, and Bacteroides. Of these, Bacteroides showed a trend to increase after probiotics. DISCUSSION: These findings support the potential effect of probiotics to improve host response after a short-time intervention, but consumption for a more extended period might be required to identify a significant change in psychological symptomatology.

34.01.017

AN ORGANOID MODEL TO STUDY MALARIA ASSOCIATED BRAIN INJURY

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PURPOSE: Human cerebral malaria (HCM), a neurological complication of malaria, results in 20-30% mortality rates in West African children and immunologically naïve adults. During HCM pathogenesis, parasites damage infected erythrocytes and release free heme and histidine rich protein II (HRPII) into serum and cerebrospinal fluid (CSF) which results in significant neuroinflammation and brain injury. Models that mimic the complexity and organization of the human brain are needed. We utilized a human cortical organoid model to test the hypothesis that heme and HRPII mediate neuroinflammation and organoid tissue injury and recapitulates the HCM phenotype. METHODS: Human induced pluripotent stem cells were used to generate forebrain organoids and assessed for effects of heme and HRPII on development, structure and function using gene expression analysis, Western Blot, IHC and flow cytometry. We determined whether Neuregulin-1 (NRG-1) attenuates the deleterious effects of heme and HRPII. RESULTS: Cortical organoids expressed Foxg1 (forebrain marker), SOX2 (neuronal stem cells), TUJ1 (neurons) and GFAP (astrocytes), NRG-1(neuronal cytoprotectant), ErbB4 (NRG-1 receptor), CXCL10 (marker of HCM severity) and its receptor, CXCR3 and BDNF at the basal level. Heme and HRPII treatment altered expression of these factors, modified organoid structures and induced inflammation and apoptosis. Exogenously augmented NRG-1 treatment attenuated the injury. CONCLUSION: Cortical organoids can be used as a model to study pathogenesis of malaria-induced brain neuroinflammation and injury as well as test NRG-1 as a cytoprotective agent. The model allows for in depth studies of HCM pathogenesis non-invasively and offers new avenues to test novel interventions.

34.01.019

DIABETES AND OFFSPRING RISK OF CONGENITAL HEART DISEASE

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BACKGROUND: Congenital heart defects (CHDs) are the most common type of birth defects among newborns. Several authors claimed some relationship between maternal pregestational diabetes mellitus (PDM) and an increased risk of CHDs. According to the Puerto Rico Congenital Defects Surveillance and Prevention System (SVPDC), congenital defects are listed as the leading cause of infant mortality. The association, between Diabetes and infants who were born with CHD's in Puerto Rico has not been explored. METHODS AND RESULTS: A secondary database analysis was performed of the information obtained from 420 mother-infant dyads incorporated to the SVPDC due to a diagnosis of a CHD during 2016-2019. Among them, 50 (11.9%) were exposed to maternal diabetes (Type 1 and 2), and 38 (9.07%) to maternal pre-gestational diabetes. Infants with CHD (n=420) were assigned to embryologically-related cardiac phenotypes. The CHD phenotype with higher prevalence in the offspring was Ventricular Septal Defects (VSD; n=275), followed by Atrial Septal Defects (ASD) secundum (n=120).

Although our analysis did not reveal that exposure to maternal diabetes played a statistically significant role as a risk factor for CHD, we did identify a significant association between the presence of serious CHD and pulse oximetry screening. CONCLUSIONS: The current data available does not suggest that maternal diabetes has a significant role in the incidence of CHD in Puerto Rico. However, we did identify that children with CHD, where being evaluated by pulse oximetry, could lead to early identification and treatment. These findings may assist developing more vigorous pulse oximetry screening policies.

34.01.020

AUTOANTIBODIES AND COMPLEMENT IN LUPUS NEPHRITIS DISPARITY

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PURPOSE: Lupus nephritis (LN) is a chronic autoimmune kidney disease, characterized by circulating autoantibodies (autoAbs), tissue-bound immune complexes and complement activation. Compared to European-Americans (EA), LN is more common and severe in African-Americans (AA), often requiring kidney transplant. Factors underlying the development, severity and racial disparities remain incompletely understood. METHODS: The titer and subclasses of circulating anti-complement IgG autoAbs were analyzed by ELISA in de-identified serum from 18 AA and 14 EA patients with biopsy-proven LN (WHO class III, IV and V). Staining of de-identified kidney biopsy paraffin sections of AA and EA patients is ongoing and will be scored for tissue bound complement proteins and IgG subclasses. RESULTS: Anti-C1q IgG autoAbs were prevalent in LN class III and IV (the most aggressive subtypes). AA had higher levels of IgG1 than EA and IgG2 was the predominant subclass of anti-C1q in EA. The levels of anti-C3b autoAbs, which were predominantly IgG1, were significantly higher in AA patients with class IV LN. Correlation of C4, C5b-9 and IgG-subclass deposition with LN severity will be presented. DISCUSSION/ CONCLUSION: Anti-C1q and C3b autoAbs of IgG1 subclass are more prevalent in AA than EA with LN. As effective activator of complement, excessive deposition of IgG1 in kidney of AA patients will exacerbate complement-activation and kidney injury. High C4 and C5b-9 deposition in kidney are indicative of complement-mediated glomerular cell death. Thus, differences in serological profiles of anti-complement autoAbs and deposition of complement and IgG1 among AA and EA may contribute to severity and racial health disparities in LN.

34.01.021

ANNEXIN2 PROTEIN EXPRESSION IS ASSOCIATED WITH BREAST CANCER

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Background: A review of literature on the expression of Annexin 2 in cancer has shown that there is very limited research work on the association of this protein with breast cancer aggressiveness in African Americans. In the present study, TMA breast tissues from African American women were stained with Annexin 2 antibody to determine the association between the molecular subtypes and Annexin 2 protein expression. Method: An annotated case series of 135 breast cancer tissues archived from 2000 to 2010 was acquired from the Howard University Tumor Registry. The association between ANX2 expression and survival by molecular subtypes (Luminal A, Luminal B, HER2, and Triple Negative (TN)was assessed using Multinomial regression, chi-square analysis, and Kaplan-Meir graphs (Stata 11). Results: Our, findings show a marked association between ANX2 protein expression in Luminal B and HER2 subtypes when unadjusted and adjusted for age. Borderline differences in tumor grade were found in TN only. Age differences (< 50, 50+ years) and metastases were highly significant for overall survival, disease-free survival and recurrence-free survival. A difference in ANX2 expression was not significant for recurrence-free survival only. Stage, tumor size, and nodal involvement were of borderline or greater significance for overall survival while stage and tumor size predicted disease-free survival. Kaplan Meir tests of ANX2 showed significant separation of overall survival by ANX2 protein expression in all breast tumor subtypes. Conclusion: ANX2 might be a biomarker of aggressiveness and a relevant candidate biomarker in high risk African American women with Luminal B and TN breast cancer.

34.01.022

SPATIAL MODEL OF LOW-LEVEL LEAD EXPOSURE IN GEORGIA CHILDREN

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Background: Lead (Pb) is a naturally occurring, highly toxic, heavy metal that has potentially adverse effects, especially neurocognitive and hematopoiesis. In 2012, the US threshold of concern for blood lead levels (BLLs) is > 5μg/dL; recognizing there is no safe Pb level of exposure in children. Associations

between sub-threshold (< 5µg/dL) BLLs and vascular dysfunction, have been reported, but underlying molecular processes are poorly understood. There is evidence Pb toxicity alters bioavailability and function of hematopoietic stem and progenitor cells (HSPC) responsible for vascular repair and regeneration, but the impact from low-level Pb exposure is undetermined. We hypothesize that BLLs < 5µg/dL augment HSPC bioavailability and are associated with specific place-based socioenvironmental risks. Methods: Using mixed-methods and geographic information systems approach, we identify risk factors for lead exposure across a wide range of detectable BLLs (> 0.2µg/dL). Data is obtained retrospectively using multi-year data from Georgia Department of Public Health and the largest pediatric healthcare system in Georgia. Spatial statistical analyses and multi-level modeling are used to determine place-based risks associated with elevated lead levels. A cross-sectional, prospective surveillance study of children (24 to 72 months) with low BLLs is conducted to assess the bioavailability and functionality of HSPC, and to identify and compare individual and neighborhood-level risk factors. Results: 44 patients from 2018-19 were found to have BLLs > 0.2µg/dL. We have enrolled 47 children with an average age of 4.85 years. Preliminary results indicate low BLLs are associated with decreased HSPC, parental income, and primary mode of transportation.

34.01.023

OBESITY PHENOTYPE AND HEPATIC STEATOSIS IN ADULT POPULATION

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PURPOSE: Hepatic steatosis (HS) is a common chronic disease of the liver. Limited research has investigated the contribution of the combination of obesity and metabolic syndrome (MetS) (obesity phenotype) as risk factor for HS. Our objective was to examine the relationship between HS and obesity phenotype. METHODS: We analyzed data from NHANES III (1988-1994) of adults ≥ 20 years old with ultrasound data. HS was diagnosed by ultrasound. We included demographics, obesity phenotype, smoking, lipid profile, glucose, liver enzymes, c-peptide, healthy eating index, exercise, and hypertension. We used multiple logistic regression in STATA V14 (considering sampling design and weight). RESULTS: Of the 13,156 participants, 36% were metabolically healthy normal weight, 4.5% were metabolically healthy obese, 15% were metabolically healthy overweight, and 19% were metabolically unhealthy obese. In the multivariable analysis, metabolically unhealthy obese, metabolically unhealthy overweight and metabolically healthy obese were more likely to have HS relative to metabolically healthy normal weight subjects (Adjusted OR [AOR]=3.5, 95% Confidence Interval [CI]=2.6-4.7; AOR=2.2, 95% CI=1.7-3.0; AOR=2.3, 95% CI=1.3-4.1, p<0.05) respectively. Those more likely to have HS were =>50 years old, male, Hispanics, former smokers, and those with pathologically elevated lipid profile, glucose, c-peptide, and liver enzymes (p<0.05). CONCLUSION: There is an independent relationship between obesity phenotype and HS. Those with obesity have a higher likelihood of HS, and MetS appears to exacerbate the chance for HS. Health care providers should be vigilant caring for both the metabolically healthy obese and the metabolically unhealthy overweight as these are independent risk factor for HS.

34.01.024

PROFILE OF HISPANIC BURN PATIENTS IN A PEDIATRIC HOSPITAL

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PURPOSE There is no evidence in the literature about pediatric burn patients admitted to a hospital in Puerto Rico. We evaluated the profile of patients admitted to the only Pediatric Burns Unit in Puerto Rico and compared it with homologous patients in the United States. METHODS A retrospective cross-sectional study was conducted on all patients (1 month to 21 years old) from 2010-2016. Patients with burn injuries were admitted. Demographics data such as age, sex, burn degree, %Total Body Surface Area (%TBSA), treatment and length of stay (LOS) were evaluated. Data was expressed as median ± SD and percentages. Logistic regression model was used to compare prolonged LOS versus age, burn degree and %TBSA. RESULTS/EXPETEC RESULTS 696 admissions were evaluated, 12.1% (84) of them were admitted to PICU. 72% were males, with a median age of 7.7 years old. 85% of injured suffered second-degree burns; being scalds the principal cause. The peak hours of injuries were between 13:00 and 17:00, mostly during summer. Prolonged LOS (20.2days) was statistically associated with younger age (4.5 yrs), %TBSA (23.45) and higher burn degree. DISCUSSION/CONCLUSION Patients younger than 5 years old were at greater risk of suffering from burn lesions. Scalds were the most common form of burns, mostly at the kitchen. None of the patient deceased, opposed to what is reported. This may response to modified clinical techniques used by the physician, such as airways management and specialized nutrition. This study aims to be the first report regarding Puerto Rican pediatric burn population.

34.01.025

OBESITY PHENOTYPE, NON-ALCOHOLIC FATTY LIVER AND STEATOHEPAT

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PURPOSE: Non-alcoholic fatty liver disease (NAFLD) and Non-alcoholic steatohepatitis (NASH) are common chronic diseases. Limited research has investigated the relationship between obesity phenotype and NAFLD and NASH. We aimed to examine obesity phenotype as a risk factor for NAFLD and NASH. METHODS: We analyzed data from NHANES III (1988-1994). NAFLD in adults was defined as hepatic steatosis by ultrasound without hepatotoxic exposures. NASH was defined using HAIR index. We included obesity phenotype (combination of metabolic syndrome and body mass index), and confounding variables. We used multiple logistic regression in STATA V14 (considering sampling design and weight). RESULTS: Of the 10,765 participants, 36% were metabolically healthy normal weight, 4.5% were metabolically healthy obese, 15% were metabolically healthy overweight, and 19% were metabolically unhealthy obese. In the analysis, relative to healthy normal subjects, metabolically unhealthy obese and overweight, and metabolically healthy obese were more likely to have NAFLD (Adjusted OR [AOR]=3.9, 95% Confidence Interval [CI]=2.8-5.4; AOR=2.5, 95% CI=1.9-3.4; AOR=2.7, 95% CI=1.5-4.8, $p<0.05$, respectively). Obesity phenotypes were not independently associated with NASH ($p>0.05$). Predictors of NAFLD were age =>50 years old, male gender, Hispanic ethnicity, former smoking, and pathologically elevated triglyceride, glucose, c-peptide, C-reactive protein, and ALT liver enzymes ($p<0.05$). Predictors of NASH were Hispanic ethnicity, age <35 years old, and pathologically elevated AST, glucose, c-peptide, and hypertension ($p<0.05$). CONCLUSIONS: There is an independent relationship between obesity phenotype and NAFLD but not NASH. Clinicians should be careful in caring for the metabolically healthy obese as it is an independent risk factor for NAFLD.

34.01.026

CURCUMIN AND HYDROQUININE AS NOVEL ANTI-TOXOPLASMA AGENTS

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Curcumin, one of the products of study, is a bioactive polyphenol compound and a major component of the spice and herb turmeric that is widely used globally as folk medicine and nutrition. Hydroquinine is a derivative of the organic compound, quinoline, which has various medicinal properties to include antiseptic and antimalarial properties. In using these two natural products, we have hypothesized that using curcumin and hydroquinine individually and in combination would be effective in inhibiting the growth of Toxoplasma gondii (T. gondii), a zoonotic parasite causing the disease toxoplasmosis. To assess the inhibition activity of the compounds against T. gondii growth, we used a cell-based and fluorescent based assay. Parasite growth was monitored using a dose dependent and time course approach. In our fluorescent assay, the RH-GFP strain of T. gondii (Type I) was used to assess compounds effectiveness using time course of 24 to 120 hours. Individually, curcumin, hydroquinine and sulfadiazine inhibits parasites growth at IC50s ranged from 6.391μM to 23.89μM, 0.5271μM to 1.610μM, and 5.655 to 0.4718 respectively. In combination, curcumin plus hydroquinine inhibits parasites growth at IC50s ranged from 6.892 to 85.48. We observed a similar pattern in the cell-based assay as shown in the fluorescent assay results above. In conclusion, parasites inhibition was based on drug concentration and time of exposure. Further studies are underway to screen these compounds against different cell lines and different strains of T. gondii in vitro and in vivo and to decipher their mechanism of action.

34.02.001

COMPLEMENTARY ALTERNATIVE MEDICINE AMONG HYPERTENSIVE BLACKS

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PURPOSE: Blacks in the United States have the highest prevalence of hypertension (HTN) in the world and are more likely to develop complications from HTN. Several clinical, sociodemographic, cultural and behavioral factors, including the use of complementary and alternative medicine (CAM) may contribute to low medication adherence and ultimately uncontrolled blood pressure (BP) and poorer health outcomes. Since the use of CAM and its contribution to disparities in HTN treatment and BP control among Blacks versus Whites and other ethnicities remain unclear, the purpose of this study was to examine the use of CAM among Black adults with HTN. METHODS: Key informant interviews were used to guide development of focus group materials. Focus group guide was informed by the Theory of Planned Behavior to elicit salient beliefs around participant's intentions, attitudes, beliefs, and actions with regard to hypertensive medication adherence and using CAM. Institutional review board approval was obtained and all participants provided informed consent prior to participation in focus groups. The 90-120 minute focus groups were facilitated by a behavioral scientist and a pharmacy faculty to examine CAM use in the management of HTN. RESULTS: Preliminary data analysis suggest that most participants reported using CAM as a complement to their prescribed medications rather than a substitute. Reasons for using CAM included: "more natural", "lack of trust of health care system", "word of mouth from friends and family members" and "spiritual and cultural influences." Disadvantages of taking BP medications as prescribed included: suffering negative side

effects such as weight gain, bloating, dizziness. Majority of participants reported not having a BP machine and not being knowledgeable about HTN. CONCLUSION: Although CAM is used complementary and not a substitute to prescribed anti-hypertension medication, not communicating CAM use with healthcare providers might potentially possess negative health outcomes to the patients.

34.04.001

GLL398 BLOCKS TUMOR GROWTH IN XENOGRAFT BREAST CANCER MODELS

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Selective estrogen receptor degrader (SERD) has proven clinically effective in treating advanced or metastatic breast cancer since the approval of fulvestrant by FDA in 2002. Recent expansion of indications as a first line monotherapy and as combination therapy with CDK4/6 inhibitors further extends its clinical utility as an efficacious breast cancer endocrine regimen. However, the poor pharmacokinetic properties of fulvestrant and its injection-only administration route has driven continued efforts to develop orally bioavailability SERD that could potentially improve clinical response to SERD treatment. GLL398, a boron-modified GW5638 analog, showed superior oral bioavailability while retaining both antiestrogenic activity and ER degrading efficacy at a potency level comparable to the more active metabolite of GW5638, GW7604. Here we report further studies on the pharmacology and metabolism of GLL398. Consistent with GLL398's robust activities in breast cancer cells that are either tamoxifen resistant or express constitutively active, mutant ESR1 (Y537S), it was found to bind the mutant ERY537S at a high affinity. Molecular modeling of the binding mode of GLL398 to ER also found its molecular interactions consistent with the experimentally determined high binding affinity towards WT ER and ERY537S. To test the in vivo efficacy of GLL398, mice bearing MCF-7 derived xenograft breast tumors and patient derived xenograft tumors harboring ERY537S were treated with GLL398 which potently inhibited tumor growth in mice. This study demonstrates GLL398 is an oral SERD that has therapeutic efficacy in clinically relevant breast tumor models.

34.04.003

PRECLINICAL EVALUATIONS OF A NOVEL ANTILEISHMANIAL AGENT

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Purpose: OJT007 is an inhibitor of Methionine Aminopeptidase 1 with potent activity against Leishmania major. The objective of this study is to characterize the pharmacokinetics of OJT007 using rat as an animal model. Methods: Crossover design was used to evaluate oral bioavailability of OJT007. Three jugular vein-cannulated male, SD rats received a 5 mg/Kg intravenous dose of OJT007 cosolvent formulation. Serial blood samples were collected before dosing, and at 0.033, 0.0833, 0.25, 0.5,1, 1.5, 2, 4, 6, 8, 10, 24 hours post dose. Following a washout period, the rats received a 10 mg/Kg oral dose of OJT007. Blood samples were collected again as described above. Urine samples were also collected for 24 hours. OJT007 concentrations in plasma and urine were quantitated using a LC-MS/MS method. The pharmacokinetic parameters were calculated with Phoenix WinNonlin 8.1 using non-compartmental model. Results: OJT007 displayed a biexponential disposition after intravenous administration. The mean area under the curve (AUC0-∞), systemic clearance (CL), volume of distribution (Vd), and terminal elimination half-life (T1/2) were 3.140 h.mg/L, 2.306 L/kg/hr, 4.926 L/Kg and 1.864 hr, respectively. After oral administration, OJT007 had limited absorption with a mean maximum plasma concentration of 92 ng/mL. Mean oral bioavailability was 8.4%. The mean percentage of OJT007 excreted unchanged in urine after 24 hours was 0.62% and 0.45%, respectively, suggesting OJT007 was extensively metabolized in vivo. Conclusion: OJT007 displayed a biexponential disposition in rats after intravenous administration. It is poorly absorbed following oral administration with limited bioavailability. The drug is extensively metabolized in rats.

34.04.004

MUSHROOM EXTRACTS: POTENTIAL INHIBITORS OF TOXOPLASMA GONDII

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Toxoplasmosis is a zoonotic disease caused by a protozoa parasite Toxoplasma gondii (T. gondii). Presently, there are few drugs available for the treatment of the acute phase of the disease. Here, we investigated the effects of two wild edible mushrooms (Ganoderma lucidum and Meripilus giganteus) extracts against Toxoplasma gondii growth in vitro using a fluorescence monitoring assay. We discovered that the mushroom extracts were effective in inhibiting T. gondii growth in vitro in a dose and time course dependent manner. The 50% effective concentrations of Ganoderma lucidum, and Meripilus giganteus extracts that inhibit the growth of the parasite in vitro were calculated to be 0.864 mg/mL and 0.163 mg/mL, respectively. Very importantly, the mushrooms extracts had minimal cytotoxicity effects on the host cells (Vero cells) used as a medium of propagation of T. gondii

tachyzoites. Our future studies will isolate and characterize the bioactive compounds found in methanolic extracts of mushrooms as well as decipher their mechanism of action.

35.01.001

THE ASSOCIATION OF PERIODONTAL INFLAMMATION AND ORAL HPV

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Introduction-Oral health can be used as a window for assessing systemic diseases. Periodontal inflammation has been statistically significant associated with for lung, kidney, pancreatic, and hematopoietic cancers (HR = 1.30, 95% CI = 1.11–1.53). Biologic mechanisms underlying associations of periodontal disease with cancers remain unknown. Chronic inflammation is a known risk factor for cancer. Hypothesis-Periodontal inflammation as measured with local and systemic measures of inflammation is associated with oral HPV infection. Methods- The NHANES database provided detailed data on periodontal probing depths, periodontal loss of attachment, tooth number, C reactive protein (CRP), white blood cell counts, demographic data, oral HPV-positive status and HPV high–risk subtypes associated with oral cancer for the years 2009-2010 from which logistic regression analysis to assess associations was performed. Results-Periodontal measures of loss of attachment were weakly associated with HPV positivity (p=0.07) and high-risk HPV positivity (using 5 subtypes 16,18,31,33,35, p=0.06, and strongly associated with high-risk HPV positive subtypes (18 subtypes, p=0.02), and deeper periodontal probe depths were associated with HPV positivity (p=0.0035). High white blood cell counts were associated with HPV positivity and high levels of CRP were associated with 5 subtypes of high-risk HPV positivity (p<0.05). Conclusions-The clinical measures of inflammation and systemic markers of inflammation appear to be associated with oral HPV infection, which can provide insight into a potential mechanism of the association periodontal disease and precancerous oral HPV infections. Future Recommendations/Insights- Oral inflammation should be evaluated in studies of oral HPV infection and HPV-associated oropharyngeal cancer.

35.01.002

US-MX BORDER HEALTH CBPR: HPV CANCER PREVENTION- EL PASO, TX

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PURPOSE: Human papillomavirus (HPV) associated cancers exhibit disparities among Hispanics, with cervical cancer rates significantly higher in this population among others. El Paso (80% Hispanic), designated Medically Underserved Area (MUA), shows high rates of HPV-associated cancers (2012-2016) compare to overall Texas and U.S. (cervical:10.4, 9.2, 8.0), (oropharyngeal:7.0, 11.0, 12.0). APPROACH-Community approach using tailored education to increase HPV vaccination Hypothesis. Latino participants exposed to culturally and demographically tailored interventions will be receptive to education regarding HPV vaccination for child(ren) in El Paso, TX. OBJECTIVES-(1)develop community-informed, bi-lingual educational tools in collaboration with community partners;(2)target parents of CDC recommended age-groups 11-17 years;(3)navigate parental decision-making in obtaining the vaccine. GOALS-(1) increase HPV awareness, its relationship to cancer, and vaccine access;(2)increase positive perceptions of vaccine among parents;(3)encourage parents to request child vaccination. PURPOSE-To cultivate an interdisciplinary team science, community-based participatory approach preventing HPV-associated cancers in El Paso. METHODS: Development of educational tools (YR1); recruitment of adult parents/caregivers (n=200) in El Paso (YR2-4). Participants receive (1)educational and baseline components on first contact,(2) receive navigation/follow-up 1-year post-baseline. RESULTS: Preliminary findings include tools and data specific to El Paso demographics. Adult low health insurance access (28%); higher access to regular care (52%) .HPV awareness among adults of Mexican-origin. Mexico refusal to administer vaccine to males. DISCUSSION: Current findings will inform policy and future prevention efforts among interdisciplinary team science approaches of effective methods to increase vaccine completion among a diverse U.S.-Mexico border region; with preceding large-scale cancer bio-genetic-behavioral U54 project launching in El Paso.

36.01.001

MACHINE LEARNING AND TRANSCATHETER MITRAL VALVE REPAIR

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PURPOSE: Transcatheter mitral valve repair (TMVR) utilization has increased significantly in the United States over the last years. Yet, a risk prediction tool for adverse events

has not been developed. We aimed to generate a machine learning-based algorithm to predict in-hospital mortality after TMVR.METHODS: Patients who underwent TMVR between 2012 and 2015 were identified using the national inpatient sample (NIS) database. The study population was randomly divided into a training set (n=636) and a testing set (n=213). Prediction models for in-hospital mortality were obtained using five supervised machine learning classifiers.RESULTS: A total of 849 TMVRs were analyzed in our study. The overall in-hospital mortality was 3.1%. A naïve Bayes (NB) model had the best discrimination for fifteen variables with an Area Under the Curve of 0.83 (95% CI, 0.80-0.87) compared to 0.77 for logistic regression (95% CI, 0.58-0.95), 0.73 for artificial neural network (95% CI, 0.55-0.91) and 0.67 for both random forest and support vector machine (95% CI, 0.47-0.87). However, both random forest and logistic regression models obtained for 10 variables were as good as the best NB model with an AUC=0.82 (95% CI, 0.79-0.86, p=0.34). History of atrial fibrillation, coronary artery disease and dyslipidemia were the three most significant predictors of in-hospital mortality. CONCLUSION: We developed a robust machine learning-derived model to predict in-hospital mortality in patients undergoing TMVR.

36.04.001

RACIAL DISPARITIES IN S AUREUS INFECTION IN NORTHERN ARIZONA

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Northern Arizona University

PURPOSE Northern Arizona is largely composed of 3 racial/ethnic groups, with non-Hispanic whites (NHW), Hispanic/Latinos (HL), and American Indians/Alaskan Natives (AI/AN) comprising the majority of the population. Previous research has shown that infectious diseases in the Southwest disproportionately contribute to hospitalizations among the AI/AN population. Skin and soft tissue infections are among the top contributors to these hospitalizations. Our primary objective in this study was to determine if there are methicillin-susceptible and methicillin-resistant Staphylococcus aureus (MSSA and MRSA, respectively)-related racial/ethnic health disparities present in Northern Arizona. METHODS We conducted a retrospective record review using the Arizona Department of Health Services Hospital Discharge Database, including all inpatient and emergency department hospitalizations within Arizona for any resident of the six counties of Northern Arizona from 2010 through 2016 to determine whether MRSA and MSSA infections disproportionately impact the local AI/AN population. The primary assessment was the difference in the proportion of cases, stratified by ethnicity, when compared to inpatient and emergency department population proportions. RESULTS / EXPECTED RESULTS There are significantly more cases of MSSA and MRSA among AI/AN than we would expect given the proportion of the population they compose. In addition, AI/AN tend to be infected at an earlier age than NHW. DISCUSSION / CONCLUSION AI/AN in Northern Arizona experience a disproportionately high rate of Staphylococcus aureus infections and this health disparity warrants further investigation.

36.07.001

PROTEOMIC STUDY OF HISPANICS WITH RESISTANCE TO CLOPIDOGREL

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PURPOSE: The resistance to clopidogrel increases the risk of ischemic events in adults with coronary artery disease. This resistance varies with ethnicity, genetic, and many other clinical variables. Proteomic data from studies on Caribbean Hispanic (CH) patients treated with clopidogrel that have developed resistance has not yet been conducted. Thus, this is the first study performed on patients from the Caribbean region that also uses a cutting-edge proteomic approach to a Precision Medicine application. METHODS: A 10-plex tandem mass tag labeling quantitative proteomic analysis was performed on plasma proteins isolated from CH patients treated with clopidogrel. Plasma samples from 6 patients were divided into two groups: non-responder (High P2Y12 reaction units (PRU) ≥230) and responder (Low PRU <230). Both groups were compared with cardiovascular patients under other treatments. RESULTS: A total of 201 proteins were identified in the plasma. For the non-responder group, 74 proteins were significantly down-regulated, and 22 proteins were up-regulated. Conversely, 55 proteins were significantly down-regulated, whereas 28 proteins were up-regulated in the responder group. Bioinformatic analysis showed that 8 of the regulated proteins were associated to the blood coagulation system pathway, and 5 proteins were associated with Intrinsic prothrombin activation pathway. Also, some of the significantly regulated proteins participate in two interaction networks associated with Acute coronary syndrome and Acute myocardial infarction. CONCLUSION: The proteomic analysis demonstrates differences in protein abundance regarding clopidogrel responses. These findings are expected to provide preliminary evidence on early expression of novel biomarkers in CH cardiovascular patients with resistance to clopidogrel.

37.02.001

IMPACT OF PRIOR AUTHORIZATIONS ON ACCESS TO BUPRENORPHINE

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PURPOSE: Buprenorphine (BUP) is used for opioid use disorder (OUD) management and has an FDA-recommended maximum dose of 24 mg/day. Interindividual genetic variations in buprenorphine metabolism may lead some patients to require BUP doses exceeding 24 mg/day to meet their OUD management goals. Our study explores the impact that health insurance prior authorization policies that restricted access to BUP doses exceeding 24 mg/day had on treatment outcomes in an OUD patient cohort. METHODS: We conducted a retrospective cohort study of OUD-managed patients in Washington D.C. from December 30, 2015 to December 31, 2016 using the electronic medical record. Study variables included patient demographic information, BUP dose, and pharmacogenomic profile, and study outcomes were based on the presence of withdrawal symptoms, instances of unauthorized substances in urine drug tests, and BUP dose. Univariate and multivariate statistical analyses were used to assess study outcomes. RESULTS: There were 113 patients in the cohort, most of which were male (n=86) and African American (n=111), with an average age of 60 years (SD=8.5 years). DC Medicaid was the predominant primary insurance (n=62). Statistically-significant predictors for lower withdrawal instances on pharmacogenomic-guided dosing were having DC Medicaid as primary insurance and cytochrome P450 (CYP) 3A4 ultrarapid metabolizers (UMs). CONCLUSION: Our research suggests that restrictive prior authorization policies led to poorer outcomes in CYP3A4 UMs and that including pharmacogenomic testing in a health insurance policy can help improve OUD management.

38.01.001

UTILIZING COPA (COPAYMENT APP) AS A MEANS OF COLLECTION

LB Eyombo; BHailemeskel; R Misra; RHollander; RM Bachmann; R khan.

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Patients and physicians face many challenges in the payment process of copayments, both in the short-term and the long-term. Physicians, specifically, face challenges with copay collections. Patient copays alone make up roughly 20% of a provider's revenue (Smith, 2016), however most physicians only collect 60% of patient copay (Schwartz, 2015). Our data surveyed 96 different physician practices and indicated that there is a low level of physician satisfaction found in the process and involvement of collection agencies within their practices. This information also indicates the additional burden of collections that many physicians must partake in order to maintain the financial standings of themselves and their patients. This has led to our team to create a layout for a mobile application which will be known as COPA. The app will implement the most up-to-date technology to ensure health data security and physician and patient user feasibility. COPA will most importantly distinguish itself in its transaction service to help clients receive and pay copayments, while also presenting an accessible network to aid patients to determine whether they may be applicable for fee-reduction and relief options stored within our database. Thus we are confident that this app will promote the quality of healthcare, by solving one of its most prominent issues. Schwartz, D. (2015, November 16). 10 Ways to Improve Your Practice's Medical Billing Collections in 2016. Retrieved from https://blog.capterra.com/10-ways-to-improve-your-practices-medical-billing-collections-in-2016/Smith, A. (2016, May 9). Billing, Reimbursement and Claims: How to Drive more Revenue. Retrieved from https://chironhealth.com/blog/billing-reimbursement-claims-drive-revenue/

38.01.002

THE CHALLENGES SURROUNDING THE COLLECTIONS OF COPAYMENT

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There are several aspects that contribute towards the weakness of the American Healthcare system. Our team collected data and information from 96 different healthcare sites and pinpointed that a recurring issue among healthcare providers was the dissatisfaction found in the collection of copayments. This issue also traverses over to the patient service sector. From 2010 to 2015, one Indiana hospital reported more than 20,000 collections against patients who failed to pay their copay on time (Kiel, 2019). It was learned that delays and accumulations of copay not only damage the physician-patient relationship but may also discourage patients from pursuing or continuing necessary treatments. As a result, the lack of a fair and methodical system for collecting copayments has produced major challenges for American Healthcare. Fortunately, with the advancement of technology we can tackle this issue by using mobile applications to create an efficient system to help both patients and healthcare providers avoid challenging ethical and financial circumstances. Kiel, P. (2019, March 9). Nonprofit Hospital Stops Suing So

Many Poor Patients: Will Others Follow? Retrieved from https://www.propublica.org/article/nonprofit-hospital-stops-suing-so-many-poor-patients-will-others-follow.

38.01.003

NEW BIOINK FOR 3D PRINTING AND ANTICANCER DRUG SCREENING

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Purpose: Constructing 3D printed tumor microenvironment helps to narrow gaps between in vitro and in vivo disease models. This study aims to introduce animal origin-free polysaccharide based VitroGel 3D®- RGD-Plus hydrogels for 3D printed tumor tissue development and anticancer drug screening. METHOD: Rheological properties, printabilities and cytocompatability of 8 hydrogel samples were evaluated and the optimized hydrogel was chosen for 3D cell printing. Characterization of cell laden scaffolds and tumor spheroid microenvironment were done with printed H4-RGD scaffolds. Live/Dead and NucBlue/ActinGreen staining was performed to determine cell viability and spheroid formation. Immuno-fluorescence staining was performed for E-cadherin, vimentin and K67 to study cell proliferation and tumor microenvironment formation. The drug response of 3D printed MDA MB 231 WT spheroids was compared with 2D culture assays.RESULTS: Ink H4-RGD was found to be the most optimized printable and cytocompatible bioink with more than 90% cell viability. The rheological evaluation demonstrates that, this optimized bioink has shear thinning flow property and is temperature independent between 20 and 37°C.Expression of E-cadherin and k-67 showed tumor microenvironment formation and cell proliferation within the 3D printed scaffolds. The IC50 values in Docetaxel, Doxorubicin and Erlotinib was approximately of 8.2,50 and 2.5-fold respectively in 3D culture as compared to 2D culture MDA MB231 WT ($p < 0.001$). Hypoxic core formation in 3D spheroid was determined using a fluorescent hypoxia reagent. CONCLUSION: Our results of rheological analysis, shape fidelity, scaffold stability and biocompatibility suggest that this new formulated bioink could be used for 3D printed culture modeling and high throughput screening of various anti-cancer drugs.

38.02.001

IMPROVEMENT OF HUMAN SPERM FREEZING WITH HYDROXYUREA

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Introduction: Semen cryopreservation is the process of cooling, freezing, and storing spermatozoa to maintain viability and function. However, there is a 50% motility loss among cryopreserved human spermatozoa during the freezing and thawing process which contributes to reduced conception post insemination. Our hypothesis is that non-motile cryopreserved human spermatozoa are not dead but metabolically exhausted and therefore, freezing spermatozoa in the presence of sperm motility activator (hydroxyurea; patent pending) can improve post-thaw motility. Objective: The objective of our study was to improve the human sperm cryopreservation process by enhancing motility prior to freezing. Methods: Normal freshly ejaculated human semen samples (based on WHO criteria) were collected from the Ovation Fertility Center, Nashville, TN. Each sample was divided into two groups to be frozen in the presence of conventional freezing medium (FB; control cryoprotectant) or one developed in our laboratory (control FB + 3.0mM hydroxyurea [HU; treatment]). Pre-freeze sperm motility was determined for each sample prior to freezing. Subsequently, sperm motility was determined before freezing, post-thaw and post swim- up procedure and acrosomal status determined. Results: Samples subjected to freezing had a mean percentage motility of 53 + 5.1%. Following 18 hour cooling samples frozen in the presence of HU demonstrated increased motility compared to their control counterparts ($P<0.05$). Semen samples frozen in the presence of HU-supplemented FB had a higher post-thaw percentage motility than their counterparts frozen in standard FB (HU = 33.4% ± 2.5 vs Control = 25.2% ± 3.0; $P<0.002$) Lastly, after swim up harvest, sperm frozen in presence of HU exhibited higher percent motility ($P<0.05$) than the control counterpart (HU 69.11% ± 5.1 vs Control = 52.89% ± 6.97) without causing any damage in the acrosome membrane. Conclusion: Our data suggest that HU-supplemented FB can increase the percentage of motile spermatozoa for effective insemination.

39.05.001

MEASURING IMPLICIT BIAS AMONG OB-GYNS IN HAWAI'I

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PURPOSE: Persistent racial/ethnic disparities in multiple health indicators have spurred research into racism and provider bias in healthcare. Micronesians living in Hawai'i are targets of discrimination across various segments of society. Research also shows higher rates of cesarean delivery among Micronesians compared to Whites, even after controlling for

known risk factors. Thus, this pilot study examined implicit racial/ethnic bias toward Micronesians among Obstetrician-Gynecologists (OB-GYNs) using four new implicit association tests (IATs). METHODS: OB-GYNs accessed the online study via a link to a secure website. All participants were asked to complete a survey, an IAT that assessed attitudes, and an IAT that assessed associations with a specific stereotype. Participants were randomly assigned to one of two comparative conditions; 1) Micronesians vs. Whites or 2) Micronesians vs. Japanese Americans. Descriptive statistics, mean IAT scores, and associations between IAT scores and covariates were analyzed. RESULTS: Forty-nine OB-GYNs completed the study. Results for the Micronesian vs. White comparison showed a slight pro-White bias as measured by the Attitude IAT (M = 0.181, SD = 0.465, N=29) and the Stereotype IAT (M = 0.197, SD = 0.427, N = 29). Age, length of residency, and number of years working in Hawai'i were significantly and positively correlated with IAT scores. The results for the Micronesians vs. Japanese Americans condition were not statistically significant. CONCLUSION: This study found a slight preference for Whites over Micronesians within this sample of OB-GYNs, which could contribute to differences in cesarean rates and other health/healthcare disparities among these Pacific Islander populations.

39.12.001

SOCIOECONOMIC DISPARITIES IN USE OF MAMMOGRAPHY IN FLORIDA

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PURPOSE: Health-Related quality of life (HRQL) refers to a multi-dimensional concept that include domains related to physical, mental, emotional, and social functioning. Little evidence is known regarding the role of HRQoL indicators on adherence to breast cancer screening in Florida. The purpose of the study is to investigate the influence of HRQL variables on the use of mammography after controlling for sociodemographic, health access, and lifestyle characteristics. METHODS: Data from the 2016 Florida Behavioral Risk Factor Surveillance System were used. The outcome variable was self-reported use of mammography. Women were considered as adherent to mammography screening if they were 40–74 years of age and reported use of a mammogram in the previous 2 years. RESULTS: Hispanic women had a greater likelihood to receive mammography than non-Hispanic white women. Access to a personal doctor was the major predictor for mammography use. Lastly, women with barriers to access to care due to cost were less likely to receive mammography than those without any access barrier due to cost. DISCUSSION: Our findings showed that one out of four American women did not receive screening for either breast cancer. Our results identified that the function of different aspects of HRQoL on the receipt of cancer screening may not be equal or through the same mechanisms. Evidence suggests that adherence to mammography is associated with early detection and mortality reduction for breast cancers. Policymakers and healthcare professionals can target women with lower HRQoL for increasing the national breast cancer screening rates.

39.12.002

MINORITY BREAST CANCER WOMEN IN A PATIENT NAVIGATION PROGRAM

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Florida A&M University (RT, MD, KS); University of Central Florida College of Medicine (SR,SR);The Florida State University College of Medicine (GT)

PURPOSE: Low-income minority women are less likely to receive recommended and timely cancer care when compared with their more affluent counterparts. Patient Navigation programs (PNP) have been used as a strategic intervention to improve the receipt and timeliness of breast cancer (BC) screening in underserved communities. However, there is a scarcity of evidence regarding whether or not PNP improve patient care and outcomes following the actual diagnosis of cancer. This pilot study sought to evaluate breast cancer patients' clinical outcomes based on evidence-based national quality measures of the American Society of Clinical Oncology/National Comprehensive Cancer Network (ASCO/NCCN). METHODS: This study retrospectively examined socio-demographic characteristics, disease characteristics, and concordance to quality measures (QM) of BC care among women diagnosed with breast cancer and who were participating in a PNP that services minority women at the Tallahassee Memorial Health Care (TMH). RESULTS: Treatment and disease stage data were available for 150 (97.4%) and 146 patients (93.6%) respectively. The guidelines indicated-care for the three quality measures (hormonal therapy, chemotherapy, and radiation therapy) for the navigated patients were significantly different ($p<0.05$) as compared to the non-navigated controls. CONCLUSIONS: By comparing the TMH breast cancer patients' clinical outcomes to the national guidelines, we believe that our findings would inform providers about the efficacy of adopting PN in their practices and would help them identify patients who might benefit the most from navigation. In addition, our results have the potential to improve the process and outcomes of patient navigation breast cancer care in underserved settings.

39.12.003

POSTPARTUM STERILIZATION DISPARITIES IN PUERTO RICAN WOMEN

NR CARDONA CORDERO; Z Quiñones Tavarez; D Morales Vasquez; J Serrano; T Panko; S Siddiqi; J Perez-Ramos; T Dye

University of Rochester (NRCC; ZQT; DMV; JS; TP; SS; JPR; TD)

Female sterilization – or Tubal Ligation (TBL) – has a controversial history as both a desired method of contraception, and a strategy to control underrepresented populations. During the first half of the twentieth century, Puerto Rico's female sterilization rates were high and often performed without consent. With historical migration of Puerto Ricans to the United States, additional work is needed to understand women's health and racial disparities patterns related to sterilization. De-identified information from the New York Statewide Perinatal Data System for 2004-2018 was released and the subset of women who self-identify as Puerto Rican (n=38,488) was used to estimate TBL rates by birth location (in Puerto Rico v. in mainland USA) and race. Odds ratios (ORs) for TBL rates by race, controlling for covariates were estimated using SPSS. Non-white Puerto Rican-born women had higher postpartum sterilization rates (12.1%) compared to white Puerto Rican-born women (4.6%) and mainland USA-born white women and non-white women (6.7%, 6.3%, respectively). After adjusting for age, parity, unintended pregnancies and other known covariates in the Puerto Rican-born subset, non-white women were more likely to have TBL (OR 2.8, 95% confidence interval [95%IC] 1.8-4.6) compared to white Puerto Rican women. Our findings among Puerto Ricans who gave birth in Upstate New York provide insight about racial disparities within underrepresented population's concerning women's health pre- and post-pregnancy. Sociocultural experiences, such as a history of involuntary sterilizations, may be relevant, and can be considered in designing effective reproductive health prevention and intervention strategies for Puerto Rican women.

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