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Stanley S. Scott Cancer Center

2020 Virtual Summer Research Program

Poster Abstracts

2020 Virtual Summer Research Internship Program

The Summer Research Internship Program has provided research opportunities for medical students, undergraduates, and high school students since 2003. Due to the current COVID-19 pandemic, summer 2020 research projects were performed mainly via a virtual learning model. The program directors, Dr. Paula Gregory and Dr. Fern Tsien, matched students with mentors from LSU Health Sciences Center, University Medical Center, and the Louisiana Cancer Research Center (LCRC). The Summer Research Internship Program has allowed students to cultivate their interest in pursuing careers in clinical sciences, public health, or basic sciences. Funding support for the undergraduate virtual summer program was provided by:

- **LSUHSC School of Medicine, Office of the Dean**
- **National Science Foundation (NSF) Research Experiences for Undergraduates (REU) Program**

Drs. Gregory and Tsien would like to extend their special appreciation to mentors, laboratory and administrative personnel, and poster session judges who helped make the Virtual Summer Research Internship Program a success! Their assistance with this project affords each student a chance to be part of a bigger, ongoing research project and an opportunity to pursue their career goals.

LSU Health NEW ORLEANS School of Medicine

NSF

Nikhilesh V Alahari
Undergraduate
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Mentor's Name: Dr. Yaguang Xi
LSUHSC

"Demonstration of interaction between Celecoxib and Sulindac Sulfide with COX-2 using docking approach"

Video Access Password: 5r=P6usR

Abstract

Background: Molecular docking is the mechanism of observing how certain molecules bind to one another. Through this approach, it is clear to see the precise location on the molecules where they attach to one another. Molecular docking can show the overall efficiency and strength of certain molecular bonds. There are numerous docking softwares that are available online, but they all have different advantages and drawbacks. AutoDock Vina is one docking software that has provided some of the best results. Docking methods have been used to observe the interaction between Celecoxib and COX-2, and Sulindac Sulfide and COX-2. It is shown that COX-2 is linked to tumor growth, but both Celecoxib and Sulindac Sulfide act as inhibitors against it. The two drugs act very similarly on COX-2, inhibiting the synthesis of prostaglandins, which COX-2 is responsible for. Furthermore, Clinical trials with celecoxib have shown that it can also greatly reduce the effect of rheumatoid arthritis and osteoarthritis.

Methods: I used AutoDock Vina for my study. Along with this software, I also used PyMOL, Raccoon, and AutoDockTools. I gathered the pdb files for Celecoxib, Sulindac Sulfide, and COX-2, and converted them into PDBQT format. I then proceeded to dock Celecoxib with COX-2 to view their binding interaction. I repeated this step with Sulindac Sulfide instead of Celecoxib.

Results: This study was to observe the docking mechanism between the drug celecoxib and the enzyme COX-2, and sulindac sulfide and COX-2 as well. Unfortunately, due to numerous technical problems with using the software, I was not able to dock these molecules with one another properly. However, I was able to see how the molecules bonded together. When I conducted this docking mechanism between Celecoxib and COX-2, I was able to see that they were both adjacent to one another. In the case of docking between Sulindac Sulfide and COX-2, I noticed that Sulindac Sulfide bonded at a single point on the COX-2 molecule. Although I was not able to receive the desired results, I was able to see how the two molecules interacted with one another prior to illustrating the proper docking mechanism.

Conclusion: The next steps will be to visualize and analyze my data through AutoDock Vina. I am currently exploring other options to get better data which will be presented. COX-2 was only recently discovered, so there is still a lot to study on this. The implications of these interactions can help inhibit and prevent tumor growth, finding a plausible treatment to cancer.

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"Estrogen, Protein S, and Obesity Contribute to Thrombosis in Premenopausal Obese Women Who Use Oral Contraceptives"

Blood coagulation occurs by a finely tuned cascade of enzymatic reactions that result in fibrin formation. Central to this process is a complex of a vitamin K-dependent proteases, factor IXa (FIXa), and factor VIIIa (FVIIIa), assembled on a phospholipid-containing membrane. The FXa/FVIIIa complex is the kinetically significant activator of factor X (FX). During thrombin formation by activated FX (FXa), several anticoagulant reactions prevent systemic activation of coagulation. Impairment of these anticoagulant activities increases the risk of venous thrombosis. Common causes of high-risk venous thrombosis are hereditary and acquired deficiencies of the plasma anticoagulant Protein S (PS). PS (also vitamin K-dependent) negatively regulates coagulation by inhibiting FIXa, thereby limiting factor FXa and thrombin formation.

The female hormone estrogen depresses plasma PS level. Thus, women who use estrogen-based oral contraceptive agents experience reductions in PS abundance, and these women are at higher risk for thrombosis. Estrogen suppresses PS level by inhibiting PS gene transcription; estrogen receptor α and transcription factor SP1 mediate this transcriptional inhibition. Additionally, we found that decreased plasma PS level was associated with obesity. PS is synthesized in the liver, which becomes hypoxic in obese individuals. Hypoxia causes hypoxia inducible factor 1 alpha to downregulate PS expression in obese individuals; this effect explains why obesity increases the risk of thrombosis. Importantly, the combination of obesity and estrogen-based oral contraceptives dramatically increases thrombotic risk.

In this project, we used ELISA assays to measure the amounts of total and free PS in plasma from non-obese and obese individuals (based on BMI). We also measured the free PS levels in obese individuals who used oral contraceptives. Finally, we used a specific thrombin generation assay to measure thrombin formed by these plasma samples. We observed that obesity and estrogen, individually and synergistically, were associated with lower than control levels of plasma PS. Therefore, premenopausal, obese women who use oral contraceptives have greater thrombin generation potential compared with obese women who do not use oral contraceptives.

In further research, we will focus on 1) determining the molecular mechanism by which hypoxia, associated with obesity, and estrogen, from contraceptives, affect PS level and 2) investigate therapies to elevate PS level in obese ± estrogen premenopausal women.

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Mentors: Nicolas G. Bazan, M.D., Ph.D. and Jorgelina Calandria Ph.D.
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"The Use of Imaging to Follow Astrocyte Responses to Pro-Homeostatic Elovanoids"

Parkinson's disease (PD) is the fourth most common neurological disorder. Individuals with this disease experience tremors, bradykinesia, rigidness, and instability. Although the disease is characterized by dopaminergic cell death, there are many aspects to consider. Of them, we considered the role of astrocytes. Inflammation, damage, and dysfunction of astrocytes is associated with many brain diseases, and we believe it plays a major role in PD as well.

Elovanoids (ELVs) were discovered by the N. Bazan laboratory in 2017 and have numerous effects that result in improved cell-survival. Described their bioactivity includes: a) pro-homeostatic regulation, b)modulation of senescence gene programming, including Senescence-Associated Secretory Phenotype (SASP) secretome release, c) attenuation of a form of inflammation called inflammaging, and d) targeting of key protective events in the extracellular matrix between photoreceptors and the retinal pigment epithelial cells. Senescent cells secrete inflammatory cytokines and lead to cell death. Inflammaging is a chronic inflammation that comes with age that is thought to be a catalyst for age-related diseases such as Parkinson's. By taking advantage of ELVs we hoped to reduce cell death and slow the advance of PD.

Utilizing the imaging software Imaris, we looked at the effects of ELVs on rat astrocytes in which ferroptosis had been induced via erastin. With imaging we are evaluating the possibility that morphological protection of astrocytes may occur when exposed to pathological conditions and treated with ELVs.

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Dr. Rinku Majumder, PhD:
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"The contributions of race, age, and anticoagulant Protein S in predicting COVID-19 prognosis"
Video Access Password: m9NW8*xs

The COVID-19 pandemic has caused monumental mortality, and there is, as yet, no adequate therapy. Unlike the SARS-CoV pandemic in 2003, COVID-19 is not simply a disease of the upper respiratory tract. COVID-19 patients experience hypercoagulability and increased risk of venous thromboembolism. Severe cases of COVID-19, i.e., patients who require ventilators, involve hyper-coagulability and disseminated intravascular coagulation (DIC). Moreover, several reports indicate that hypercoagulability, as measured by the D-Dimer level, is present mostly in critically ill and deceased patients. In addition to blood clots of all sizes throughout the body, doctors who treat coronavirus patients report a range of other odd and frightening syndromes, such as kidney failure, cardiac inflammation, and immune complications.

Deficiency of the plasma anticoagulant Protein S is associated with DIC and thrombosis. Ordinarily, Protein S deficiency is due either to homozygous or heterozygous genetic alteration, and Protein S deficiency can result from various pathological states and diseases. In all these cases, Protein S deficiency is associated with a high risk of venous thrombosis. Protein S limits thrombin generation by directly inhibiting Factor IXa. Thus, the high thrombotic risk associated with PS deficiency is due to failure to regulate thrombin formation.

Clinicians measure the D dimer levels of COVID-19 patients because D dimer level is indicative of hypercoagulability and DIC. A positive D-dimer result indicates the presence of an abnormally high level of fibrin degradation products; thus, high D dimer suggests substantial blood clot (thrombus) formation and consequent degradation. Interestingly, race and age affect the severity of COVID-19 and the degree of mortality. The elderly are more susceptible to contracting COVID-19, and they have a higher risk of mortality compared with younger individuals. In addition, people of African and Hispanic origin are also at higher risk of infection.

The purpose of this research was to identify factors that can predict the risk of severe COVID-19 and its prognosis. We found that age, race, and the plasma level of anticoagulant Protein S comprise a list of risk factors that lead to severity and mortality of COVID-19. However, experimental data are required to directly correlate Protein S level with severity of COVID-19 disease.

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Mentor's Name: Michael Celestin, PhD, CHES, NCTTS
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The Relationship between E-cigarette Information Seeking and Trust in Sources of Information on E-cigarettes and Respective Use

Electronic cigarette (e-cigarette) use can lead to nicotine addiction, acute lung and respiratory illness, and death. While the use of e-cigarettes as a cessation aid remains controversial, they contain toxic and potentially carcinogenic compounds and the FDA does not consider any product safe. In 2018, 3.2% of US adults reported e-cigarette use, including 7.8% of people aged 18 to 24, representing an increase from previous years. A better understanding of factors related to decisions about the use of e-cigarettes is warranted. This study examined the relationship between e-cigarette use and e-cigarette information seeking behavior and trust in sources of information on e-cigarettes.

Using a cross-sectional retrospective study design, we analyzed data from the Health Information National Trends Survey (HINTS) FDA Cycle 2 (2017). Participants included civilian, non-institutionalized, US residents aged 18 and older, surveyed using a one-time mail questionnaire. Current e-cigarettes users included individuals that reported use either somedays or every day. E-cigarette information seeking behavior included searches for health effects, quitting or reducing smoking, list of chemicals, cost/coupons, instructions/tutorials, where to buy products, and reviews/ratings of brands. Trusted sources for e-cigarette information included health care providers, family/friends, government health agencies, health organizations, religious organizations, tobacco companies, and e-cigarette companies. Frequencies identified differences in participant demographic characteristics. Chi-square and Fisher exact tests determined statistically significant differences between current electronic cigarette users and non-users.

Of the 1736 participants included in this study, majority reported as female, non-Hispanic White, college graduates, making between $100,000 and $199,999, and 2.7% identified as e-cigarette users. Chi squared analysis found that current users were more likely to search for instructions/tutorials, places to buy e-cigarettes, and cost/coupons, compared to non-users. Also, compared to non-users, e-cigarette users reported more trust in information from electronic cigarette companies and less trust in government agencies relative to non-users.

While previous research has found electronic cigarette information seeking behavior to be associated with use, these results provide greater insight into the specific types of information that users are seeking relative to nonusers. These results can inform targeted prevention and cessation interventions to discourage e-cigarette use.

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Mentor: Chindo Hicks, Ph.D.
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"Integrative Genomics Approach to Biomarker Discovery in Colorectal Cancer"

Background: Despite remarkable progress in screening and patient management, colorectal cancer (CC) remains a major public health problem. CC is the third most commonly occurring cancer in men and the second most commonly occurring cancer in women. World-wide there were over 1.8 million new cases of CC in 2018. In United States it is estimated that there will be 147,950 newly diagnosed cases of CC and an estimated 53,200 individuals will die from the disease in 2020. Therefore, a critical unmet and urgent medical need is discovery of molecular markers for early detection of the disease. The recent surge of next generation sequencing technology have enabled generation of vast amounts of gene expression and somatic mutation data on CC. These advances have enabled molecular classification of subtypes and increased our understanding of the molecular taxonomy of CC. However, gene expression has not been optimally leveraged and integrated with somatic mutation information for the discovery of diagnostic markers. The objective of this investigation was to discover clinically actionable biomarkers for diagnosis and prognosis of CC using gene expression and somatic mutation data. Our working hypothesis was that genomic alterations in individuals diagnosed with CC and control samples could lead to measurable changes distinguishing patients diagnosed with CC from controls. **Material and Methods:** We addressed this hypothesis using gene expression and somatic mutation data derived from a total of 523 samples (481 CC samples and 42 control samples) from the Cancer Genome Atlas (TCGA). The data was partitioned into two data sets tumor samples and control normal. We performed analysis comparing gene expression levels between the two sample groups to discover a signature of significantly differentially expressed genes distinguishing tumors from controls. Significantly differentially expressed genes were evaluated for the presence of somatic mutations to identify a signature of significantly differentially expressed genes which were also significantly differentially mutated distinguishing the two sample groups. **Results:** The analysis revealed a signature of 100 highly significantly ($p<1.00x10^{-7}$) differentially expressed genes distinguishing individuals with CC from controls. Evaluation of these genes for the presence of somatic mutations revealed a signature of 80 significantly differentially expressed genes which were also differentially mutated distinguishing the two sample groups. Among the top somatic mutated differentially expressed genes distinguishing the two samples groups included the genes ATP1A1, PIGR, FCGBP, MYH11, PTPRF, CDH17, MYH14, AHNAK, FLNB, and CSDE1. **Conclusion:** We discovered a signature of somatic mutated differentially expressed genes distinguishing patients diagnosed with CC from controls. Our investigation demonstrates that integrative analysis combining gene expression with somatic mutation data is a powerful approach to discovery of molecular diagnostic and prognostic markers in CC.

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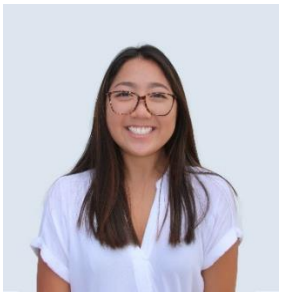
"Smartphone Technology and its Effects on Patient Education and Hydrocephalus Management Outcomes"

Video Access Password: 4r+l&!%^

Hydrocephalus is a neurological condition characterized by the buildup of cerebrospinal fluid (CSF) in the ventricles of the brain. The condition is commonly caused by CSF circulation abnormalities, absorption abnormalities, CSF overproduction, or a combination of these causes. The condition is commonly found in children and can be either congenital or acquired. The only known treatment for hydrocephalus is surgery to remove the cause of the obstruction, create an alternative pathway for CSF flow, or to place a shunt in the ventricles of the brain that will divert the excess CSF out of the brain. Most cases of hydrocephalus are lethal without treatment. The shunts that are used as the primary treatment for hydrocephalus are prone to failure and infections and can require subsequent revision surgery over the course of the patient's life. Furthermore, shunts come in a vast selection of manufacturers, models, and types. For these reasons, management of hydrocephalus can be quite complex and requires specialty care. Low health literacy in patients on both the condition and its multivariate treatment as well as complex management of these patients, which may result in transfer to tertiary care facilities, represents a costly endeavor which can be a significant burden for hydrocephalus patients and their families, both financially and otherwise.

Healthcare technology has many emerging roles in the communication and enhancement of the delivery of healthcare. Previous studies have attempted to look at more elementary ways to improve hydrocephalus patients' health literacy, but increasingly ubiquitous access to technology warrants exploration into new ways to enhance patient understanding of this condition. Our study looks to examine the role of a novel mobile application, HydroAssist®, which is the first mobile app to allow hydrocephalus patients to record and store their hydrocephalus treatment history with easy 24/7 access on their smartphone or computer. In the study, 50 pediatric hydrocephalus patients will be recruited from Children's Hospital New Orleans, and their families will be invited to use the app for approximately six months. Upon the initiation of the study, the family's baseline knowledge of their child's hydrocephalus treatment history, including shunt type and settings, will be surveyed. After utilization of the application, a similar survey will be completed by the family at the conclusion of the study. Additional questions regarding the participant's use of the app, confidence in their knowledge of the child's condition/treatment, and if the app was able to help prevent transfer to a tertiary facility for care will be included. We hypothesize that use of the HydroAssist® mobile app will increase patients' health literacy and reduce incidence of unnecessary transfer to tertiary care facilities for treatment.



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"A Novel NSC Small Molecule Inhibitor, Inhibits Proliferation of Triple-Negative Breast Cancer Cells Through Upregulation of NR4A Family Genes."

Background: Triple-negative breast cancer (TNBC) is known to be the most aggressive form of breast cancer. Challenges in treatment have occurred due to the absence of well-defined molecular targets and high invasive, proliferative capacities of these cells. Common treatments for TNBC include combinations of surgery, radiation, and chemotherapy; however, there is usually minimal success. This can be attributed to the high recurrence rate. Therefore, with the lack of success in treating patients with TNBC, novel and efficacious therapies are needed. We have found a small molecule inhibitor with potent anti-tumor activity against TNBC cells.

Methods: By using next-generation sequencing (NGS), we observed that the NR4A family genes had the largest fold change in treatment vs. control with a significant p-value, which led to us primarily focusing on these genes. A series of experiments were repeated to ensure the results remained consistent. Different dosages of the NSC small molecule inhibitor were used to treat the MDA-MB-231 cell line. Results showed that the higher dosages lead to higher expression of NR4A. Results were confirmed with the q-RT-PCR technique, done in triplicate. To further investigate, the basal expression of the NR4A family genes was measured in different cancer cell lines as well as the normal cell line. While all NR4A family genes had significant fold change, the largest fold change between the cancer cell lines and the normal cell lines was in gene NR4A2, narrowing the focus to one gene in particular. Next, we focused on comparing our results to clinical data that was available through METABRIC (Molecular Taxonomy of Breast Cancer International Consortium), using a dataset of 2,000 clinically annotated breast cancer patients. With the raw data provided, we analyzed the gene expression of NR4A2. Different subtypes of breast cancer, grade, and tumor stage were used as differentiating factors. Finally, we examined overall survival for NR4A2.

Results: Our data shows that the novel NSC small molecule inhibitor reduced the proliferation of MDA-MB-231 TNBC cells through upregulation of NR4A family genes. Analyzing the results from METABRIC, it was evident that the lowest expression of NR4A2 was shown in TNBC and grade 3, which is consistent with the hypothesis that NR4A2 is a tumor suppressor. Through the analysis of the overall survival data, it can be determined that higher expression of NR4A2 has a longer survival rate than that of lower expressing cancers.

Conclusion: In summary, our data indicated that NSC small molecule inhibitors exhibit anti-tumor activity in TNBC cells, through upregulation of the NR4A2 gene. Further investigation of the potential of NSC small molecule inhibitors as an attractive therapeutic drug for TNBC would be needed.

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Mentor: Lisa Moreno-Walton MD, MS, MSCR, FAAEM
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"Adequacy of Health Care Advance Directives in Patients Admitted to the Intensive Care Unit"

Video Access Password: 3r@!w62S

Introduction: Advance directives (AD) allow patients to state their wishes regarding medical care when unable to do so by using a living will and/or power of attorney (POA). A recent study concluded that patients who have a Do Not Resuscitate (DNR) status and are admitted to the Intensive Care Unit (ICU) have a higher mortality rate. Research indicates that care received by patients in the ICU does not always align with their wishes; one study found that 11% of healthcare providers use chest compressions if a DNR patient sustains cardiopulmonary arrest. These results indicated that in-depth analysis of the frequency, adequacy, and efficacy of ICU admission for DNR patients could potentially improve the quality and influence of ADs.

The main objectives of this study were to determine the number of patients admitted to the ICU with an AD and if they outlined specific wishes. We also observed life support measures given with regards to the AD, and if having an AD limits the number of futile procedures that the patients receive.

Methods: A retrospective chart review of 1134 patients admitted to the University Medical Center of New Orleans (UMCNO) was completed. Inclusion criteria were patients age 18 or older and treated in the UMCNO ICU between August 2015 and March 2019. We identified patients with an AD, POA, or both, demographic information, and their specific wishes in regard to life support measures. All statistical analyses were carried out in SAS 9.4. Fisher's exact and Pearson chi-square tests were used to assess the associations between categorical variables. We assessed the associations between presence of ADs and potential sociodemographic factors such as gender and race using logistic regression and calculated odds ratios (OR).

Results: Our study population consisted of 1134 patients, 697 of those males. There were 68% Black, 25% White, 4% Hispanic, <1% Asian, 3 <1% American Indian, 2.7% other, and 1.6%declined. At time of admission to the ICU, 383 had an AD and 90 had a POA; only 24 AD and 46 POA stated specific wishes. Out of 383 patients with an AD, 47 received care aligned with their wishes and 2 did not. Comparing ADs among males vs. females, the odds of having an AD were 0.742 with a CI 0.584 to 1.454, and blacks vs. whites had the odds of 0.743 with a Cl of 0.451 to 1.224. Life support measures were given to 153 patients with an AD and 188 out of 750 without an AD. Chi-squared analysis showed that the chi-square value was 26.6859; p-value was 2.39392e-7.

Conclusion: Out of the 1134 patients admitted to the ICU, 383 had an AD and 90 had a POA while only 24 AD and 46 POA stated exact wants. Almost all of the patients that required a more intense level of care received exactly as desired, with 40 ADs followed correctly. It was found that blacks were more likely to have an AD than whites, males were less likely to have an AD than females, and it was found that there is an association between having an AD and the likelihood of receiving life support measures; if a patient has an AD, they are more likely to not receive life support measures.

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Mentor: XiaoChing Li, Ph.D. Additional Affiliates: Hannah
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"How Overexpression of miR-9 in Juvenile Songbirds Affects Neural Pathway Development Within Area X"

The human basal ganglia are subcortical nuclei whose function, language development, is remarkably similar to Area X of the songbird brain. A molecular explanation of this similarity lies within FOXP2, a genetic sequence that facilitates the creation of neural pathways responsible for language development. Just prior to my arrival, my lab successfully identified specific microRNAs that directly affect the expression of the FOXP2 gene, and subsequently, language development within juvenile songbirds. Exposing juvenile Zebra Finches to overexpression of the specific microRNA, miR-9, my team discovered two findings: 1) downregulation of FOXP2 expression and 2) more variable (less effective) song production in adulthood. These findings go hand in hand as FOXP2 is responsible for the plasticity of language development that ultimately results in the quality of language understanding in adulthood. We are currently elaborating on these findings by studying the mechanism behind FOXP2's effect on the neural circuit development within Area X when overexpression of miR-9 is induced. Juvenile Zebra Finches were randomly split into two groups, experimental and control. In the experimental group, the miR-9 introduction took place via a viral injection, while the control group injections contained an empty virus. Injections occurred between the ages of 26-28 days. Half of the birds from the experimental group were sacrificed at 60 days of age while the other half at 100 days of age in order to compare results between juvenile and adult birds. The same was done within the control group. Images of medium spiny neurons (MSN), specific inhibitory cells that make up the majority of neural circuitry in Area X, were captured for dendrite and spine analysis postmortem. Specific data points such as branch point number and spine density, among others, are being collected as indicators of neural pathway development. Data analysis is still in progress, and conclusive results are currently unavailable as the blind nature of the analysis remains vital to the integrity of non-biased evaluation. The similarity between Area X and the human basal ganglia provides potential application of this study's eventual results. Understanding the structural effect that suppression of FOXP2 has on the neural pathway development could improve understanding in mild language defects, such as stuttering, and more notable language defects seen in autism spectrum disorders.

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Mentor's Name: Lisa Moreno-Walton, MD, MS
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"The Efforts to Diversify Faculty Within Their Departments: A National Survey of Emergency Medicine Department Heads"

Video Access Password: 8s#A!4%=

Background: There has been a growing amount of evidence that clinician bias, racism, inequality, stereotyping, and discrimination has indeed contributed to health inequities. These variables have been proven to have negative effects on patient care and health outcomes. Countless studies have shown that diversifying the physician workforce can produce better patient outcomes and decrease the number of health disparities. Patients are more likely to communicate a higher level of care satisfaction when treated by health professionals who share the same racial, ethnic, or cultural background as them. Although many health centers, hospitals, and divisions are determined to promote diversity among their faculty and staff, minority representation has made very little progress. This study aims to determine how diverse are Emergency Medicine departments nationwide, how is diversity being promoted, and how effective are those methods.

Methods: This is a national convenience sampling of 263 Emergency Medicine department heads including medical directors, section chiefs, and department chairs. A REDCap based questionnaire was developed and distributed to the listserv. Participation was tracked and weekly follow-up reminders were sent to participants. Interim analysis was conducted on participants. All statistical analyses were carried out in SAS 9.4. Fisher's exact tests were used to assess the associations between variables.

Results: For the interim analysis we look at the first 24 responses which consisted of 17 males (70.8%) and 7 (29.2%) females with aligning gender identity. Participants were white (91.7%), black (8.3%), and Hispanic/Latino (4.2%). Looking at suburban vs urban programs where 3 to 5, 6 to 10, and > 10 physicians of color were hired, suburban (0, 0, 0) vs urban (4, 3, 3) respectively; ($p \leq 0.0483$).

Conclusion: Upon assessing the first 24 respondents for this interim analysis, we can conclude that 66.7% of the participants classify as white males. While 66% of the leaders who were non-white hired 6 to 10 physicians of color, only 5% of white leaders hired 6 to 10 physicians of color. When asked how successful their efforts were to diversify their staff, 3 respondents reported that their efforts were very successful and 20 reported either partially or not very successful. There was an association between the type of location (suburban vs urban) and the number of physicians of color hired when looking at programs that hired 3 or more physicians of color.

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"Environmental Health Disparities and COVID-19: How air pollution is worsening outcomes for Black communities in Cancer Alley"

Coronavirus Disease 2019 (COVID-19) emerged in Wuhan city, and the outbreak has evolved rapidly worldwide. COVID-19 is caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and it has spread from person to person, mainly through respiratory droplets that can land in the mouth or nose and be inhaled by the lungs. Older adults and those with comorbidities such as hypertension, diabetes, cardiovascular disease, and respiratory system diseases tend to experience severe COVID-19 outcomes. These comorbidities are more prevalent in Black individuals. As a result, Black communities have been disproportionally affected by the virus. The health disparities in the Black population have existed prior to the pandemic and have made the Black population more vulnerable to dying from COVID-19.

Eleven Louisiana parishes along the Mississippi River, known as "Cancer Alley," comprise an 85-mile stretch of land between Baton Rouge and New Orleans. This area has a high concentration of chemical plants and is primarily Black and low income. Recent media reports indicate that within Louisiana, this area was severely impacted by the current pandemic, and past research shows an increase in long term exposure to air pollution can lead to an increase in the COVID-19 death rate. It has been proposed that the high levels of air pollution caused by chemical plants in this area contribute to the comorbidities that cause COVID-19 complications, disproportionally impacting the people who live in this area. The purpose of this study was to evaluate COVID-19 cases and deaths in the 11 Louisiana parishes along the Mississippi River. We hypothesize that these 11 parishes will have higher death rates than the entire state of Louisiana, and we believe the death rates will be higher in the Black population compared to the White population.

Data from the Louisiana Department of Health was collected for the 11 Mississippi River parishes, and infection, mortality, and case-fatality rates were calculated and compared to the entire state. Deaths and mortality rates among the Black and White population of the 11 parishes were determined and compared to those of the entire state. Relative risk ratios of cases and deaths of these parishes were calculated and compared to the remaining 53 Louisiana parishes. Additionally, the relative risk ratios of death among Blacks compared to Whites were determined for Louisiana and the 11 Mississippi River parishes.

The results of this study demonstrate that the majority of the 11 Mississippi River parishes have a higher case, death, and case-fatality rates than the state of Louisiana. The relative risk of cases and deaths in the 11 Mississippi River parishes is higher than the state of Louisiana. Also, the relative risk of deaths among Blacks compared to Whites is higher in Cancer Alley than the state of Louisiana. These results show how pre-existing health disparities, which are related to historical and current inequities and injustices in social, political, economic, and environmental factors, have worsened the effects of COVID-19 in the Black population. Further research and policy actions are required to dismantle the systems that contribute to these unequal health outcomes.

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Mentor: Dr. Donna Williams
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"Louisiana COVID-19 Risk Factor Analysis"

Novel coronavirus, commonly known as COVID-19, has become one of the largest public health crises of the century. In a mere seven months, the deadly virus has traveled across the globe, infected over eleven million people, taken over half a million lives, and caused over $3.5 trillion in economic impact. Of the afflicted countries, the United States is home to almost a third of the world's cases, with over three million infected in the U.S. as of July 2020. With such a high death toll and large economic impact, it has become increasingly imperative to identify high risk populations in order to slow the spread of disease.

The Center for Disease Control has identified gender, race, poverty, age, kidney and liver cancer, obesity, diabetes, and select heart conditions to be risk factors for expereincing severe illness from coronavirus. While these factors provide risk assessment for the general populace, this study works to analyze risk factors correlated with a higher COVID-19 death rate within Louisiana populations specifically.

The COVID-19 death rate used in this study was defined as the rate of death from COVID-19 per 100,000 people. The data for the COVID-19 death rates for each of the 64 parishes in Louisiana on each day in June was compiled from the New York Times database. These values were then average to calculate the average COVID-19 death rate in June for each parish. Race, gender, education, age, poverty, and hypertension data were compiled from the U.S. Census Bureau database while smoking, obesity, kidney cancer, liver cancer, and diabetes data were compiled from the Louisiana Department of Health database. T-tests were used to test for significant correlations between the prospective risk factor and the COVID-19 death rate.

Our findings of identifying high risk groups for coronavirus in Louisiana will provide more valuable and accurate information for health policy makers, healthcare professionals, and the general populace. Custom interventions can then be designed for the high risk groups as a method of slowing the spread of disease.

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"Assesment of Posttraumatic Stress Disorder Among Emergency Medical Services: A Survey Study Within an Urban Emergency Medical Service"
Video Access Password: 5.L#p2fo

Emergency medical service (EMS) workers, including emergency medical technicians and paramedics, are usually the first medical providers on the scene of emergencies and disaster scenarios where they often face dangerous, challenging, and traumatic events. This workplace stress and exposure is strongly associated with greater rates of post-traumatic stress disorder (PTSD) and depression than the general population. Previous research has identified increased psychological distress in a population following natural disasters, but few studies have assessed the effects of experiencing these events on EMS mental health. The severity of psychological trauma experienced from working through both Hurricane Katrina and the subsequent recovery has important mental health implications for first responders. New Orleans was hit the hardest by Hurricane Katrina 15 years ago and is currently one of the epicenters of COVID-19. This study aims to identify the prevalence of PTSD in New Orleans EMS (NOEMS) workers who participated during Hurricane Katrina and/or the COVID-19 crisis as compared to the general population and assess if those exposure to those events helped build resiliency.

This study seeks to prove three hypotheses: similar to previous findings in the literature, we believe signs and symptoms of PTSD will be higher in individuals who work in NOEMS, signs and symptoms of PTSD are higher in NOEMS workers who worked during Katrina or COVID-19, and previous experiences of traumatic events during EMS work such as Katrina build resiliency for following traumatic events. To test these, NOEMS workers who fit the study's inclusion criteria were given a questionnaire that included a validated PTSD DSM-IV assessment tool and additional demographic questions. All responses were anonymous. The results were then assessed according to each subject's characteristics and PTSD score using bio-statistical tests.

Of the total respondents (n=92), 59.8% are male, 70.7% white, 76.1% non-Hispanic, 50% have children, 84.8% of those who have children live with them, 68.1% are paramedics, 60.4% lived in New Orleans post-Katrina, 20.8% have sought therapy, 3.4% worked only during Katrina, 67.4% worked only during COVID-19, and 25% worked during both Hurricane Katrina and the pandemic. 33.7% of NOEMS personnel met PTSD diagnostic criteria which is greater than the rates of 5-10% found in the general population following natural disasters. More than half of the respondents reported moderate to severe symptoms of hyperarousal. NOEMS personnel who worked during both Hurricane Katrina and the COVID-19 pandemic have lower PCL-C severity scores as well as lower PTSD percentages. Results from this study will be used for potential future innovations to reduce PTSD in EMS.

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"Hepatitis C Among Incarcerated Patients in an Urban Emergency Department "
Video Access Password: 9d+N9^H3

In Louisiana, the incarceration rate is especially high. However, the burden of infectious diseases among the incarcerated population is even higher. Louisiana has one of the highest rates of incarceration, as well as a high prevalence of Hepatitis C. One-third of the total HCV cases in the US are among the incarcerated population. Barriers to care such as improper health insurance, delayed access, and inadequate care impair proper treatment for diseases. The Centers for Disease Control and Prevention (CDC), states that 90% of people infected with HCV are able to be cured so long as they receive proper treatment. Despite there being a cure (Harvoni) for HCV, infections continue with high rates of morbidity and mortality among the incarcerated population in Louisiana. At University Medical Center New Orleans (UMCNO), one of the first emergency department based hepatitis C Virus (HCV) testing programs was initiated in 2015. Many in-custody patients visit our ED, averaging more than 200 visits per month. This study aimed to estimate follow up rates, demographics, and prevalence rates of HCV among the prisoner population seen at UMCNO.

This was a retrospective chart review of 285 in custody patients who presented to the ED at UMCNO, March 1, 2013 to October 1, 2017. All screened positive for HCV. Review of the medical record to determine if a referral order was placed, an appointment was given, and if they attended the appointment. Those linked to care were assessed for initiation and completion of treatment. Demographic information was collected including race, gender, and age. All statistical analyses were carried out using SAS 9.4. Basic descriptives, such as mean, median, standard deviation and frequencies were calculated. Fisher's exact or Pearson's chi-square tests were used to evaluate the associations between the variables.

Analysis of our study population revealed there were 249 males (87%) and 36 (13%) females. Patients self-identified as black (172), white (97), other (15); others (included NULL, patient declined, or other). Of all patients, 87 (30.53%) were referred for follow up care, 184 (64.56%) not referred, and 14 were lost to follow up (4.91%). There were 38 (13.33%) patients who attended an appointment: 16 (42.11%) UMC, 18 (47.37%) a prison facility, and 4 (10.53%) outside facilities. There were 239 (83.86%) who did not attend an appointment, 8 we are unsure. Only 17 out of 38, (30.36%) patients that attended an appointment completed treatment.

Referral rates 30.53% compared to 70% for the general population at UMCNO. Of all incarcerated patients only 13.33% attended an appointment. While data from the prison system was limited either because of loss to follow-up, patients expired or were released, we can still make some observations. This study sheds light on the disproportionate burden of HCV among incarcerated patients. Although there were no significant differences between gender and race and receiving treatment for HCV, the rate of infection was higher among Black people than White. Even though a seemingly large portion of patients are getting diagnosed with HCV, only a small amount (30.53%) are receiving referrals and an even smaller amount are completing follow up appointments with a healthcare provider; this illuminates the pronounced disparity between rates of infection and rates of treatment among the incarcerated population in regards to HCV.

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"Impact of Chemical Exposure on Preterm Pregnancies and Low Birth Weight Outcomes"

Environmental conditions can negatively impact one's health. This can include exposure to lead, industrial emissions, and water quality. Repeated exposure to these conditions are risk factors for cancer, respiratory illness, and other diseases. In Louisiana, studies have shown that 19% of the people live in parishes that don't meet the standard for air quality. According to the Environmental Protection Agency, in Louisiana there are 560 facilities that expose residents of chemicals. In 2018, these facilities exposed residents of 150,758,424 pounds of chemicals. Of those facilities, 29 emitted 13,394,777 pounds of chemicals that affects reproductive health. Chemicals such as zinc, hydrogen cyanide, acrylamide, atrazine, and lead are the top 5 chemicals these facilities produce that negatively impacts reproductive health.

Maternal health outcomes, specifically in Louisiana, consistently have not reached the national standards. Factors such as race, gender, and age influence pregnancy outcomes. Low birth weight, weighing less than 2,500 grams, and premature pregnancy, delivering at 37 weeks, are two reproductive outcomes that this study will focus on. According to America's Health Rankings, in 2019, on average 10.7% of babies in Louisiana were low birthweight while the national average was 8.3%. In 2019, on average 12.7% of babies in Louisiana were premature while the national average was 9.9%.

This study examined the relationship between chemical plant locations and fetal health outcomes in Louisiana. Low birth weight and premature pregnancy are the two health outcomes that this study will focus on. We also examined the relationship between fetal health outcomes and demographics such as Black, White, and Hispanic in Louisiana. For each parish, the amount of chemical emissions that negatively impact maternal health was calculated per year. The percent of fetal health outcomes was also calculated per year for each parish and then broken down into separate demographics. Once the percentages were found, the significance regarding fetal health outcomes and chemical plant locations was found per parish and demographics. The association between fetal health outcomes and demographics was also found per parish.

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"Evaluation of clinical risk factors in Hepatocellular Carcinoma: A case-control study in Southeast Louisiana."

Hepatocellular Carcinoma (HCC), a prominent form of liver cancer, is one of the few cancers in which incidence has increased over the past decade in the United States. Louisiana experienced great increases in liver cancer over the past few years, making it the fastest growing cancer in state. The objective of this study is to assess the relationship between HCC and known clinical risk factors like viral hepatitis, specifically Hepatitis C (HCV), metabolic conditions such as non-alcoholic fatty liver disease, diabetes and obesity, as well as alcohol abuse.

For this study, we conducted a retrospective case-control study using data collected from the Louisiana Tumor Registry and Louisiana Public Health Institute's Research Action for Health Network (REACHnet), a clinical data research network. Cases of primary invasive HCC diagnosed 2010-2015 in patients 35 years or older were identified by LTR and linked to their medical records in REACHnet. The controls used for this research were derived from a random sample of disease-free individuals. HCC risk was modeled with logistic regression models, controlling for age, sex and race. The regression models were stratified by race and sex to control for potential confounding.

The study dataset included 758 cases and 23,270 controls. Of the cases, 80.2% were male and 62.5% were white. The most prevalent risk factor among cases was HCV (55.4%), followed by diabetes (42.2%) and alcohol use disorders (27.2%). HCV had the greatest HCC risk. Alcohol use disorders were also significantly associated with HCC, while metabolic conditions carried significant risk among white patients only.

Recently, Louisiana has experienced an influx of liver cancer diagnoses. We evaluated clinical risk factors among patients in a clinical research network in southeast Louisiana and found significant risk associated with Hepatitis C virus and alcohol use disorders. Additionally, metabolic conditions were found to have significant risk among white patients. While this epidemiological study is important in characterizing HCC in the region, these results do not provide evidence of causation and may not be generalized to racial/ethnic groups other than Black and white. Comprehensive HCC risk assessments among diverse populations in the US are important to public health efforts in cancer prevention and control.

Acknowledgements: This research was conducted in partnership with Research Action for Health Network (REACHnet). We would like to acknowledge Dr. Claudia Leonardi for her collaboration.

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"Testing the association between bone mineral density and surgical outcomes for TKA patients"
Video Access Password: 5H&A^#^U

Introduction: Osteoporosis is a disease that affects the bone quality for millions of individuals. 54% of Americans over the age of 50 suffer from osteoporosis, or low bone mineral density (BMD). Recently, we observed a lack of bone density screening in our cohort of total knee arthroplasty (TKA) patients. TKA is a deconstructive, surgical procedure which is typically used to counter osteoarthritis within the knee. The TKA procedure can be altered during surgery to account for differences in BMD, and drugs like bisphosphonates can be used to improve BMD prior to TKA. However, due to the significantly low amount of screenings for osteoporosis, low BMD goes undetected and untreated in our population. We hypothesize that patients with low bone mineral density will experience higher levels of pain and worse symptoms after a total knee arthroplasty surgery.

Methods: In order to test our hypothesis, we analyzed the correlation between surgical outcomes and BMD on 22 consented osteoarthritis patients undergoing TKA. The status of a patient's surgical outcome is determined by the Knee Osteoarthritis Outcome Scores (KOOS) survey. Each patient takes the KOOS survey before and 90 days after their TKA. In order to examine the BMD of a patient, their tibial plateau was collected during the total knee arthroplasty surgery. The central region of the tibial plateau was imaged using an ex vivo micro-computed tomography scanner (mCT). The software program, CTAn, was used to analyze the BMD from the CT scans. We outlined the regions of interest of the bone scan to include the trabecular bone while excluding the subchondral portion of the tibial plateau. BMD mean values were calculated using hydroxyapatite standards, and we used the Pearson's correlation (r) test to evaluate the strength of the correlation between bone mineral density and the patient's KOOS survey sub scores.

Results: Based on the data which was evaluated between the patient's BMD and their KOOS survey sub scores we must reject our hypothesis. There is no indication from the Pearson's correlation test (r) that patients with low amounts of bone mineral density will experience higher levels of pain or worse symptoms after TKA.

Conclusion: Although this project's data rejects the hypothesis of the connection between bone mineral density and patient pain levels, there are many ways to examine bone quality. Further analysis of a patient's bone quality can be acquired through reviewing bone turnover markers such as Sclerostin (SOST) or by inspecting a patient's trabecular architecture. Discovering the relationship between bone quality and surgical outcomes can encourage the use of certain drugs such as Bisphosphonate to increase a patient's bone mineral density before surgery or even alter TKA procedures based on the patient and their individual screening scores.

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"An Integrative Genomics Approach to Discovery of Molecular Markers in Ovarian Cancer"

Video Access Password: 7R!BJW9+

Background: Ovarian cancer (OC) is one of the most common gynecologic cancers that has the highest mortality rate. OC is the eighth most commonly occurring cancer in women and the 18th most commonly occurring cancer overall. World-wide there were nearly 300,000 new cases of OC in 2018. Within the United States an estimated 22,530 women were diagnosed with new cases of OC and an estimated 13,980 women died from the disease in 2019. Therefore, there is an urgent need for the discovery of molecular markers for early detection and prognostic prediction of the disease. Advances in next generation sequencing technology have enabled generation of vast amounts of gene expression and somatic mutation data on cancer genomes including OC. Although much progress has been made on classification of molecular subtypes of OC using transcription profiling, gene expression has not been leveraged and integrated with somatic mutations information for the discovery of diagnostic and prognostic markers. The objective of this investigation was to discover prognostic markers that are predictive of clinical outcome using gene expression and somatic mutation data. Our working hypothesis was that genomic alterations in the transcriptomes and tumor genomes of women diagnosed with OC could lead to measurable changes distinguishing patients who survived the disease from those who did not survive the disease. **Material and Methods:** We addressed this hypothesis using gene expression and somatic mutation data derived from a total of 376 samples (230 died from the disease and 146 survived the disease) from the Cancer Genome Atlas (TCGA). The data was partitioned into two patients groups, those who survived the disease and those who died from the disease. We performed analysis comparing gene expression levels between the two patient groups to discover a signature of significantly differentially expressed genes distinguishing the two patient groups. Significantly differentially expressed genes were evaluated for the presence of somatic mutations to identify a signature of significantly differentially expressed genes which were also significantly differentially mutated distinguishing the two patient groups. **Results:** The analysis revealed a signature of 130 differentially expressed genes ($P<0.005$) of which 50 were significantly ($P<0.001$) differentially expressed genes distinguishing patients who survived from patients who died. Evaluation of these genes for the presence of somatic mutations revealed a signature of 23 significantly differentially expressed genes which were also differentially mutated distinguishing the two patient groups. Among the top somatic mutated differentially expressed genes distinguishing the two patient groups included the genes: TAP1, CD79A, CD2, TAP2, EMP1, CD3E, and ITK. **Conclusion:** We discovered a signature of somatic mutated differentially expressed genes distinguishing patients who survived OC from patients who died from the disease. Our investigation demonstrates that integrative analysis combining gene expression with somatic mutation data is a powerful approach to discovery of molecular markers predictive of clinical outcomes and clinical endpoints.

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"Modulation of Glutamatergic Signaling following Adolescent Alcohol Exposure in the Hippocampus of Male and Female Mice"

Exposure to alcohol during adolescence has been proven to increase the risk of developing an alcohol abuse disorder. This increased risk is due to alcohol effects on the developing brain. One way that alcohol can produce long lasting changes within the brain is by impacting the neural mechanisms of plasticity. A key mechanism involved in the induction of plasticity is through the regulation of glutamate and its receptors (specifically AMPA and NMDA receptors). The NMDA and AMPA receptors are composed of multiple subunits and these subunit compositions contribute to their functionality. Alcohol's short-term effects on NMDARs is to inhibit receptor transmission. However, long term alcohol exposure leads to a compensatory enhancement of NMDAR in adult rodents. Unfortunately, little is known about the long-term effects of glutamatergic signaling from exposure of alcohol during adolescence. In addition, little is also known about how these effects differ between the sexes since nearly all adult work has been done on male rodents. In the Wills lab, their focus has been to look at these effects of adolescent alcohol on glutamate signaling in the bed nucleus of the stria terminalis (BNST) in male and female mice. The BNST is an important brain region because it is a crucial region for negative affect and stress regulation, which are known causes for alcohol relapse and continued alcohol use. The lab has found that adolescent alcohol exposure (AIE) causes an increase in GluN2B and GluN1 NMDAR subunits, while no changes were found in the GluA2 AMPAR subunit in male mice. In addition, it was concluded that AIE produced enhancement of NMDAR-plasticity in males. Females did not show the same response to this treatment. In my current project, our objective is to see if sex specific effects on glutamatergic signaling were found across brain regions or specific to the BNST. One brain region that projects to the BNST and has well characterized glutamatergic signaling is the hippocampus.

To do this, we used a mouse model of adolescent alcohol exposure previously used by the lab. In this model, C57 male and female mice were given two four-day cycles of alcohol vapor (14hr in, 16hr out) interspersed by three off days. Then during acute withdrawal (five hours after final vapor exposure), brains were collected and then tissue samples were taken to isolate the hippocampus. The tissue samples were analyzed using Western Blot analysis for the NMDAR subunit (GluN2B, GluN1, GluN2A) and AMPAR (GluA2) and normalized to GAPDH. I In the hippocampus, there were no changes in NMDAR subunit (GluN2B, GluN1, GluN2A) or AMPAR (GluA2) in either male or female mice. This is in contrast to from results found in the BNST where NMDAR and AMPAR were differentially affected by AIE in males and females. This it can be inferred that glutamatergic signal in BNST is more vulnerable to adolescent alcohol exposure and sex specific effects than the hippocampus. Future work will expand this analysis to other brain regions and to determine mechanisms that lead to increased vulnerability in the BNST to AIE and sex differences.

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"Using Transgenic Mouse Models to Track DNA Repeat Expansion of Friedriech's Ataxia Patients"

DNA repeat expansion disorders, also known as "trinucleotide repeat disorders," result from repeating sequences of DNA that cause disease as they progress past a threshold length. Such neurodegenerative disorders as Huntington's disease, myotonic dystrophy, and fragile X have been attributed to these expanding trinucleotide repeats. Friedriech ataxia (FRDA) is a progressive neurodegenerative disorder caused by GAA•TTC repeat expansion and specifically will be the focus of this research. Since FRDA is an autosomal recessive disorder, two inherited copies of the expanded frataxin (FXN) gene will lead to expressed symptoms of the phenotype. Patients will ordinarily exhibit a lack of reflexes and lower-body coordination, as well as speech difficulties, loss of sensation, and eventual heart disease.

Long sequences of GAA•TTC found in the first intron of the FXN gene affect proper transcription of the gene. Friedriech's patients have long repeats which hinder production of FXN. As a result, low levels of FXN mRNA transcript and frataxin proteins are characteristic of FRDA patients. Previous studies have indicated DNA mismatch repair (MMR) as a major player in repeat expansion. Sequences of repetitive nucleotide triplets are prone to forming loops by sticking to each other. Performing its usual function, MMR molecules "correct" these loops but will expand the repeating sequence in the process. While MMR is crucial for genome integrity elsewhere, the process facilitates the instability in DNA expansion. Research has identified the role of MMR molecule MLH3 in the expansion of GAA•TTC repeats in the FXN gene. Importantly, one isoform of MLH3 does not cause repeat expansion.

Of course, determining the exact location and speed of repeat expansion is a crucial step prior to any therapeutic solution. In this study, transgenic mouse models were used to track the length of repeats in the human FXN gene over time. Tissues from mice of different ages were analyzed to determine the extent of somatic expansion and to visualize the discrepancies between different tissues. As seen in these mouse models, the phenomenon of expansion is one that compounds over time, and thus an early delay or even a halt to expansion can be life changing for FRDA patients.

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Effective Patient-Provider Communication and Perceived Quality of Care among Current Smokers

Smoking tobacco ranks as the leading cause of bodily disease and the number one preventable cause of death among adults in the US. Despite medical and public health advancement, such as screening and treatment of tobacco use, disparities in the quality of health care still exist. Quality healthcare, considered the assessment and provision of effective and safe care, reflected in a culture of excellence, resulting in the attainment of optimal or desired health, improves patient trust and health outcomes. Establishing a culture of excellence includes improving patient provider communication, an important variable in patient centered care. Patients that experience effective patient-provider communication have better recovery habits, mindsets, and health outcomes. Thus, poor quality of healthcare directly can effect smoking cessation efforts. This study examined the association between measures of effective patient-provider communication and perceived quality of care among current smokers.

Using a cross-sectional study design, we examined nationally represented data from the 2017, 2018, 2019 Health Information National Trends Survey (HINTS). Perceived quality of health care was determined by respondents rating their health care in the past twelve months as excellent, very good, good, fair, or poor. Measures of patient-provider communication included how often respondents reported providers: always listened carefully, explained things, showed respect, spent enough time, and involved them in joint decision-making Current smokers were defined as participants who reported smoking 100 cigarettes in their entire life that currently smoke some days or every day. Descriptive statistics included age, gender, race, income, education, and sexual orientation. Chi-square analysis determined differences between respondents who reported excellent quality of health care and respondents who reported satisfactory or below quality of healthcare.

Among the 1,481 participants included in this study, majority reported between 51- 60 years old (30%), female (55%), heterosexual (94%), white (42%), with greater than a high school diploma (63%), and an annual income < 20K (52%). Chi square analysis revealed a statistically significant difference ($p<0.05$) between smokers who reported satisfactory healthcare quality versus unsatisfactory healthcare quality for all markers of effective patient-provider communication.

Data analysis revealed a possible relationship between patient-provider communication and effective quality of healthcare for smokers. Medical and public health policies and training related to improving quality of health care for smokers should implement effective patient-provider communication for future interventions.

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"The effect of Chronic Alcohol on CD4+ T cell Metabolic Programming"

Alcohol use is common in people living with HIV and is associated with poor disease outcomes. Previous studies by the LSU Comprehensive Alcohol Research Center showed that chronic-binge alcohol administration to simian immunodeficiency virus (SIV) infected rhesus macaques increased CD4 T cell proliferation and activation in the intestinal tract. Further, after SIV infection, plasma viral loads were higher than in non CBA SIV-infected macaques. However, the physiological mechanisms associated with T cell proliferation are incompletely understood. During activation, CD4 T cells, the primary target of HIV, undergo a metabolic switch from oxidative phosphorylation to glycolysis to maintain adequate energy production. This metabolic switch is essential to efficiently differentiate into effector T cells. Naïve T cells maintain energy homeostasis using oxidative phosphorylation due to its high efficiency, making up to 15 times as much ATP as glycolysis. However, when CD4 T cells are activated, the switch to glycolysis is beneficial because of the increased rate of ATP production, which is used in cellular processes required for T cell proliferation and differentiation. We propose a conceptual model in which ethanol exposure dysregulates expression of regulators of the metabolic switch from oxidative phosphorylation to glycolysis, impairing normal CD4+ differentiation. Specifically, we hypothesized that ethanol exposure alters peripheral blood mononuclear cell (PBMC) expression of genes regulating the metabolic switch from oxidative phosphorylation to glycolysis.

Methods: Human PBMCs were cultured *in vitro* with 0 mM, 25 mM, or 50 mM ethanol for 24 hours (acute exposure) or 7 days (chronic exposure) (n= 4-6/group). After the exposure time, PBMCs are stimulated with phorbol myristate acetate (PMA) and ionomycin for 4 hours followed by RNA isolation using the RNeasy Mini Kit. cDNA was generated by reverse transcription using the iScript cDNA Synthesis kit. Real time PCR was performed on a Bio-Rad Thermal Cycler using SSO Advanced Universal SYBR Green supermix for the following genes: Raptor, Rictor, B-cell lymphoma 6 (BCL-6), activated protein kinase (AMPK), Pyruvate Dehydrogenase, Hexokinase, peroxisome proliferator-activated receptor gamma coactivator (PGC)1-alpha, and PGC1-beta. Results were analyzed using Excel. An alpha error less than 0.05 was considered statistically significant.

Results & Discussion: Preliminary analysis of cells incubated for 24-hour in 50 mM ethanol and controls showed that the PMA and Ionomycin stimulated cells incubated with 50 mM ethanol, show a trend for increased expression of Raptor, a component of the mammalian target of rapamycin (mTOR) pathway, and a decreased expression of BCL-6, a marker for follicular helper cells. No significant differences were seen in expression of other genes. Raptor expression trended higher in the ethanol-treated cells as compared to the control groups, suggesting an increase in mTORC1 expression and, therefore, glycolysis. BCL-6 expression decreased (p=NS) in ethanol versus control in the stimulated groups, suggesting that follicular helper cell differentiation is impaired or reduced in the presence of acute ethanol exposure. Additional experiments are in progress.

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"Racial Disparities in Associations of Stress with Increased Risk of Coronary Heart Disease: A Survey Study within an Urban Emergency Department"

Coronary heart disease (CHD) is a malfunction of the heart arteries to deliver oxygenated blood to the heart. This disease is a result of artery plaque buildup, and is worsened by co-existing health conditions and other risk factors. Stress is one of the risk factors to developing CHD. Psychosocial stress, perceived stress, work-stress and other social factors play a role in predisposing individuals to the development of CHD, especially in minorities. In the United States, African Americans are more frequently exposed to those stressors because of their social and economic background. Though multiple studies have assessed work-related or occupational stress during emergency care, empirical data linking stress and increased CHD risks amongst patients and medical staff within the Emergency Department is limited. This study aimed to identify the association between stress and CHD and to determine if race and other risk factors are modifiers of stress related to increased risk of developing CHD reported in the Emergency Department.

This study is a cross-sectional survey study administered to patients and their families, ancillary staff, nurses, medical students, residents, and physicians in the Emergency Department of University Medical Center New Orleans to assess their levels of stress and the impact it has on cardiovascular health. Surveys consisted of 70-85 questions constructed from validated surveys and required 10 to 15 minutes to complete online via RedCap or pen and paper. Data points included demographic information, personal and family medical history, and experiences of stress and discrimination. SAS 9.4 was used to carry out all statistical data analysis. Fisher's exact tests were used to assess the associations between CHD and discrimination, as well as to assess the associations between perceived stress and discrimination. We also used linear regression modeling to assess potential risk factors affecting CHD scores. The risk factors we included in our model were age, gender, race and perceived stress.

Our study population consisted of 73 subjects, Females (56.2%), Whites (63.0%), Blacks (30.1%), more than one race (1.4%), Asian (2.7%), and unknown (2.7%). 35% of the population were patients, and the remainder consisted of ancillary staff, nurses, medical students, residents, and physicians. Of minority participants, 61.5% reported moderate perceived stress; however, PSS scores were not statistically significant. Though 52% reported high scores for risk of CHD in reference to discrimination as a risk factor, these findings were also not statistically significant. The insignificance may be due to the small sample size. Linear regression showed age to be statistically significant ($p=0.0031$) and being black as a risk factor ($p=0.0214$) to developing CHD. Since this is an interim analysis, further exploration is necessary to determine if the validated tools fully reflect overall stress. In addition, we will need to assess what role resilience plays in one's self reported level of perceived stress.

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Prevalence of COVID-19 in Louisiana and Its Association with Race, Concentrated Disadvantage, Chronic Disease Prevalence and other Social Determinants of Health
Video Access Password: 0C@.q@$R

The novel Coronavirus (COVID-19), caused by the severe acute respiratory syndrome coronavirus 2 (SARS-COV-2), was first identified in Wuhan, China and has globally infected over 11 million people. Those most vulnerable to the devastating effects of COVID-19 are the socioeconomically disadvantaged, elderly, homeless, and racial/ethnic minorities. In the United States, Black people are the largest demographic being disproportionately affected by COVID-19. This is also evident in the racial breakdown of COVID-19 cases and mortality in Louisiana, whereby Blacks represent a third of the state population, but account for over half of those infected and deaths. In addition, individuals with a history of underlying health conditions and chronic illnesses such as coronary heart disease (CHD), hypertension (HTN) and diabetes are associated with a greater risk of suffering severe complications if infected with COVID-19.The objective of this study was to evaluate and compare the association between social determinants of health and concentrated disadvantage, incorporating race and rates of CHD, HTN, and diabetes with the prevalence and mortality of COVID-19 in Louisiana and Orleans Parish.

The sample population was from the 1,148 census tracts in the state of Louisiana, composed of 4.6 million residents. Data sources included the 2018 American Community Survey, the United States Census Bureau, the Center for Disease Control and Prevention and Louisiana COVID-19 infection and mortality cases were from the Louisiana Department of Health. Negative binomial regression was performed to evaluate the association between prevalence of COVID-19 and concentrated disadvantage, rates of chronic disease, and other housing and socioeconomic variables. The models for concentrated disadvantage index (CDI) were further adjusted for HTN, CHD, and diabetes. As of June 29, 2020, there has been 57,081 prevalent COVID-19 cases within the included 1,105 Louisiana census tracts and 7,796 in 133 tracks in Orleans Parish. In Louisiana, the mean prevalence of COVID-19 was 11.21 (STD ±8.65) per 1,000 cases and in Orleans parish the mean prevalence was 17.06 (STD ± 7.43) per 1,000 cases. Being a renter in Orleans Parish had a negative correlation with prevalence of COVID-19 (r=-0.47). In Orleans parish, there was an 11% increased risk of COVID-19 associated with CDI at the census track level; percent Black, percent female headed-households, and percent below poverty had the highest association at the census track level. Considering all of the Louisiana census tracts, CDI had a relatively high prediction of COVID-19 with a risk ratio of 1.09 (Cl 95% 1.08,1.10). When considering the prevalence of HTN, CHD, and Diabetes, the association of CDI with increased risk of COVID-19 was reduced.

Our preliminary ecological analysis of concentrated disadvantage in Louisiana and Orleans parish demonstrate an increased risk of prevalence in census tracts with higher proportions of Black residents. We also found that the association of HTN and COVID-19 prevalence was independent of CDI. We are continuing to complete further analysis of additional measures of social determinants of health including insurance status, housing and service industry employment.

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Mentor: Dean Smith Ph.D.
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"The Effects of Risk Management Practices and Legislative Reform on Medical Malpractice Lawsuits"

Medical malpractice is when a healthcare provider deviates from the standards of practice and causes harm to a patient. When harm occurs, the provider may be found responsible under medical liability, tort law as applied to applied to healthcare patients. Risk management (RM) in the medical field has two distinct yet related roles: reducing the occurrence or severity of injuries and accidents and minimizing financial loss when harm occurs.

The two research questions of this study are: (1) what have been the trends in medical malpractice cases and insurance costs in Louisiana, also compared to the entire United States, and (2) how have the reforms to medical tort law and practices in risk management affected the trends in Louisiana. The researcher used analyses of peer reviewed journal articles, data from the Louisiana Patient's Compensation Fund (PCF), and an interview with a risk management executive in New Orleans. These research questions are relevant because instability in the malpractice insurance marketplace can lead to price increases and exits by insurers. Also, medical malpractice is a serious matter that harms patients and should be prevented with the utmost caution, and proper compensation is appropriate for patients.

In Louisiana, in response to concerns about rising medical malpractice claims, increasing insurance premiums, and exits from the marketplace by healthcare providers and insurers, the state adopted medical malpractice reform. The Medical Malpractice Act of 1975 capped total malpractice damages at $500,000. The provider is only personally liable for up to $100,000. The rest comes out of the state Patient's Compensation Fund (PCF), created by the law to compensate patients who are victims of medical malpractice. The PCF is funded by the malpractice insurance premiums paid by healthcare providers that chose to participate. The only category of damage excluded from the cap is future medical costs (1984 amendment).

Louisiana ranks high among the 50 states and District of Columbia for average annual per capita malpractice costs and average annual malpractice claims per million, 11.99 (rank of 13) and 65.23 claims per million (rank of 4), respectively. For all paid claims, Louisiana has remained fairly constant, with periodic increases and decreases. In contrast, over the same time period, the US experienced a general trend of decline. The literature suggests that reform has decreased the likelihood of a potential plaintiff taking the matter to court and that premium increases were stabilized as a result. The literature leaves unexplained the remaining high levels of claims and cost and lack of a downward trend.

In contrast to the plethora about legislative reform, little research has been published about risk management in Louisiana hospitals. The RM executive said that there is now a strong focus on eliminating preventable accidents by track and trend and by root cause analysis with input from the front line staff. We still need to learn more about how medical liability and risk management affect patient well being and compensation.