POSTER ABSTRACTS

3rd Annual Health Equity Summit

FEBRUARY 29, 2024
8:00 AM - 3:00 PM
PURDUE MEMORIAL UNION NORTH/SOUTH BALLROOMS

Health Equity Summit

PURDUE UNIVERSITY | Health Equity Initiatives

INDIANA CTSI Clinical and Translational Sciences Institute

(Click on the Poster #)

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Poster #: 1

"Stone Soup: What to Make When Between a Rock and a Hard Place"

Meredith Addison

Occupational Medicine, Indiana State University School of Nursing, Health, and Human Services Adjunct Faculty 2005-2022

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General Category: Community

Abstract:
Upon return from Command and General Staff School at Fort Sam Houston, Texas I was alerted by leaders of the national health system that Indiana was one of six states with no statewide trauma system. I was very cordially counseled by these amazing military. leaders that "If you want to address that you will have to go to your by-God Department of Health" and so I did. NOW Indiana has "the model trauma system" and WE have wide open opportunity to have STUDENTS JOIN US in this recipe for saving our neighbors and friends!

Background:
Trauma is the identified number one killer of all age 1-44 and yet it is barely funded in last place. HUMAN RESOURCES need to live to be able to achieve their best outcomes and work well. Let's NETWORK to "ADDRESS" our best possible improvements in trauma care no matter where

Methods:
Poster and Networking! Sharing and caring! Policy and Advocacy Professional organizational meetings

Results:
Folks really and truly do want to "do the right thing" but are overwhelmed by the immensity of their day to day top ten reality of day to day life. It is just as Helen Keller stated so eloquently. "Alone we can do so little, together we can do so much."

Conclusions:
I am keenly interested in networking with the best and the brightest to bring students into this ongoing work of TRAUMA SYSTEMS DEVELOPMENT

Translational / Human Health Impact:
Trauma is the identified number one killer of all age 1-44, and WORSE in rural areas and in less developed countries. We can CHANGE this reality!

Acknowledgements/Funding Sources:
Initially funded through marketing little slogan trinkets at specialty nursing meetings "E.R. You Watch It... WE LIVE IT!!!" but now the Indiana State Trauma Care Commission is funded through the vast increase in Public Health Funding at the Indiana State Health Department and it is an opportune time for students to join us and get letters after their names with real world experience.

Poster #: 2

Addressing Hearing Health Equity in Indiana Using Precision Audiology

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Michael Heinz, Maureen Shader, Ananth Grama, Edward Bartlett, Jennifer Simpson (All Purdue)

General Category: Community

Abstract:

Hearing health equity presents a significant challenge across Indiana, particularly affecting rural, minority, and economically disadvantaged populations. In Indiana, disparities in hearing aid usage are pronounced, with non-Hispanic white adults and those with higher socioeconomic status over twice as likely to use hearing aids compared to non-Hispanic Black, Hispanic, and lower-income or less-educated individuals. Hearing impairment is linked to several comorbidities, including depression, anxiety, poorer cognition, physical health, and increased falls, leading to 46% higher healthcare costs for those with untreated hearing loss. Notably, nearly 70% of rural residents with occupational noise exposure report hearing loss, emphasizing the need for targeted interventions, given that about 50% of hearing loss cases are preventable.

These disparities contribute to underemployment, limited access to healthcare, and lower quality of care. Additionally, the high costs of hearing aids, the stigma around hearing loss, and unequal access to quality care further challenge efforts to address hearing needs in minority and underrepresented communities. The underrepresentation of diverse populations in hearing research and clinical audiology (8% URMs) further exacerbates health disparities, limits the generalizability of research findings, and hinders effective interventions.

To combat these issues, the new Accessible Precision Audiology Research Center in Indianapolis, launched from the Life and Health Sciences Summit with support from Purdue's Office of Research and Provost's Office, will engage with a diverse group of Indiana residents. The center aims to raise awareness about the impact of untreated hearing loss and available management options through community outreach, standardized audiological evaluations, and free hearing screenings. By leveraging an open-source database and AI-powered analysis tools, the center seeks to advance precision audiology, enabling more personalized and effective hearing care solutions, thus fostering a deeper understanding of hearing health across the socioeconomic spectrum.

Background:

Methods:

Results:

Conclusions:

Translational / Human Health Impact:

Acknowledgements/Funding Sources:

Purdue's Office of Research and Provost's Office

Poster #: 3

Evaluation of a Social Justice Institute for Higher Education Faculty and Staff

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General Category: Community

Abstract:

Colleges and universities across the country struggle to achieve the changes necessary for advancing equity and inclusion principles. Deficits in knowledge and self-efficacy concerning equity and inclusion topics are barriers that keeps faculty and staff from engaging in equity and inclusion activities that facilitate developing, implementing, and evaluating equitable and inclusive policies and procedures. There may be promising solutions. Our team implemented and evaluated a 7-day, 56-hour educational initiative to address faculty and staff self-efficacy for engaging equity and inclusion activities in one college of education, health, and human sciences (CEHHS). The evaluation sought to assess the associations between attending the program and self-efficacy for engaging in equity and inclusion activities. Participants completed a pre- and post-quantitative survey of their self-efficacy relative to their ability to engage in equity and inclusion activities in their respective departments/units, as well as their evaluation and impression of the SJI. Summary and descriptive statistics were calculated to describe participant's self-efficacy and assess daily content quality, space quality, and learning. Pre-and-post self-efficacy means were calculated for the full scale and for paired individual items. Paired t-tests were calculated on individual scale items and on full-scale scores to assess for change in self-efficacy. Analyses of SJI program data indicated positive associations between SJI participation and self-efficacy to engage in equity and inclusion activities. Based on our findings we contend the SJI is one means for advancing and increasing self-efficacy for engaging equity and inclusion activities in a college of education, health, and human sciences. SJI may be a promising initiative for ensuring that CEHHS are accurately educating the next generations of health and human sciences professionals in equity and inclusion topics that are vital to their professions and future work. It may also be useful for other colleagues concerned about addressing equity and inclusion.

Background:

A 7-day, 56 hour Social Justice Institute (SJI) was implemented and evaluated to address faculty and staff self-efficacy for engaging equity and inclusion activities in one college of education, health, and human sciences. The evaluation sought to assess the associations between attending the program and self-efficacy for engaging in equity and inclusion activities. Additionally, we evaluated how the program participants rated the quality of the program daily content and setting. Public health, like other disciplines often included in colleges of education, health, and human sciences, is rooted in social justice and committed to advancing equity in health, education and professional development for faculty, staff, and students. Colleges of education, health, and human sciences are not immune to being influenced by systems of oppression including racism, heterosexism, sexism, ageism, antisemitism, cissexism, ableism, classism, religious discrimination and more. Institutions, social systems, and individuals' behavior are produced, reinforced, organized, and reproduced by systems of oppression. Colleges often struggle to make changes that advance and prioritize equity, inclusion, and justice across policies, practices, procedures, and departments. Faculty and staff self-efficacy to engage equity and inclusion activities is required to support equity and inclusion in college's policies, practices, and procedures. Self-efficacy to engage in equity and inclusion activities may improve with in-depth, experiential education about systems of oppression theory and practice in equity and inclusion activities. SJI is a curriculum designed to increase the self-efficacy of university faculty and staff to develop departments, policies, practices, and curricula which produce health

services professionals who are able to address health equity in their work and combat systems of oppression as they appear in their college. Participants employed full-time as faculty, staff, or administrators in the college of education, health, and human sciences were eligible for inclusion via application process. Participants completed a pre- and post-quantitative survey of their self-efficacy relative to their ability to engage in equity and inclusion activities in their respective departments/units, as well as their evaluation and impression of the SJI.

Methods:
Self-efficacy survey questions were developed from Bandura's theory of human agency. Additional items on the post-SJI survey solicited participant perceptions of the quality of each day's content and presentation. After the SJI, participants completed a confidential, 15-item, qualitative questionnaire to evaluate the institute and their experiences. Summary and descriptive statistics were calculated to describe participant's self-efficacy ratings and ratings of daily content quality, space quality, and learning. Pre-and-post self-efficacy means were calculated for the full scale and for paired individual items. Paired t-tests were calculated on individual scale items and on full-scale scores to assess for change in self-efficacy before and after SJI participation.

Results:
Pre-SJI, average self-efficacy score was 5.84 (sd = .76) and 5.83 (sd = .37), respectively. Post-SJI, the self-efficacy average increased to 6.49 (sd = 1.19) and 6.46 (sd = .48) respectively. In Year 1, this change in self-efficacy nearly achieved the .05 level of significance ($t = -2.11$, $p = .06$) and the effect size in scores was $d = .65$, a medium effect. In Year 2, the difference between pre-and post-assessment did not reach statistical significance ($t = -1.51$, $p = .17$). The effect size, calculated following Cohen was $d = 1.45$. Participant's self-efficacy for addressing DEI issues improved in all items, but in only five items were the improvements statistically significant.

Conclusions:
Our program showed positive associations between SJI participation and self-efficacy to engage in equity and inclusion activities. We also found that participants enjoyed the substantive program content and the quality of the space. Based on our findings we contend the SJI is one means for advancing and increasing self-efficacy for engaging equity and inclusion activities in a college of education, health, and human sciences. The positive associations between SJI and self-efficacy in equity and inclusion activities highlights the promise of such programs in colleges of education, health, and human sciences. Within the U.S., there continues to be extreme pushback against equity and inclusion as pedagogical approaches and frameworks for understanding injustices and inequities in health and society.

Translational / Human Health Impact:
The SJI is a tool that can be used in any college producing health and human science professionals. Engaging faculty and staff in programmatic efforts such as SJI may be a promising strategy for ensuring that colleges of education, health, and human sciences are accurately educating the next generations of health and human sciences professionals in equity and inclusion topics that are vital to their professions and the work they will do.

Acknowledgements/Funding Sources:
Funding provided by the College of Education, Health, and Human Sciences at University of Tennessee, Knoxville

Poster #: 4

Community Health Worker

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Community Health Worker Training, Amanda Eldridge, Cody Mullen, PhD, Randy Hubach, PhD, Yumary Ruiz, PhD, Natalia Rodriguez, PhD, Purdue University

General Category: Community

Abstract:
The Community Health Worker Training project is for a HRSA grant project to recruit and train Community Health Workers (CHWs) and have them enter the public health and medical workforce.

Background:
The Health Resources and Services Administration (HRSA) is working to expand the public health workforce through recruiting and training new Community Health Workers (CHWs) and providing upskilling of current CHWs on topics consisting of public health emergency response, increasing access to care, and addressing public health needs of underserved communities.

Methods:
Recruit participants for the certification training through partnerships and social media posts. Certified CHWs attend the Advanced/Upskilling training developed by Purdue University. Students can either apply for an apprenticeship program, continue with their current employment, or apply to other CHW opportunities throughout the state.

Results:
The results show an interest in the Community Health Workers workforce in Indiana. The inability of grant funds to support certain populations.
The interest in the program was greater than expected causing a long wait list.

Conclusions:
The results show an interest in the Community Health Workers workforce in Indiana. There has been interest from various groups to train community health workers, government agencies, health departments, medical facilities, independent pharmacies, etc.

Translational / Human Health Impact:
This project will increase the number of certified CHWs in the state of Indiana. This will also allow already certified CHWs to complete Advanced/Upskilling training to expand their knowledge.

Acknowledgements/Funding Sources:
Community Health Worker Training Program (CHWTP) HRSA-22-124

Poster #: 5

Spanish-Language Resource Readability on Ophthalmology Websites

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General Category: Community

Abstract:

Purpose: Health literacy is essential for appropriate patient care. Patient health literacy is impacted by limited English proficiency (LEP). LEP patients, including Hispanic patients, often experience health disparities. Institutional health literacy includes providing adequate materials for patient education. To better understand the institutional health literacy of ophthalmology organizations in the US, this study analyzed the availability and readability of Spanish-language resources found on ophthalmology websites. Methods: Ophthalmology organization websites were identified through online searches of US state professional societies, university library searches, and the National Institute of Health Eye Care organization list. Websites were included if they had direct relation to ophthalmology and were categorized into 3 groups: patient-facing, physician-facing, or both patient/physician-facing. Websites were then reviewed for the presence of any Spanish-language resource. For those with Spanish-language resources, readability analyses were conducted with 5 different readability formulas: Crawford (CRAW), Gilliam-Peña-Mountain (GPM), Läsbarhetsindex (LIX), Rate index (RIX), and SOL formulas. Websites were assigned a reading grade level which was compared to the recommended standard of a 6th grade reading level using a one-sample t-test. Results: 121 websites were included for analysis: 27% patient-facing, 25% physician-facing, and 48% both patient/physician-facing. Only 26% (31) of all websites provided Spanish-language resources. Of these, 39% were patient-facing, 3% physician-facing, and 58% both patient/physician-facing. 4 of 5 formulas showed that Spanish-language resources from all 3 groups were significantly higher than the 6th grade reading level: Patient-facing GPM: 10.78 ± 2.91, LIX: 11.36 ± 1.36, RIX: 10.45 ± 2.34, SOL: 11.57 ± 2.41. Physician-facing GPM: 15, LIX: 13, RIX: 11, SOL: 13.3. Both patient/physician-facing GPM: 9.75 ± 2.56, LIX: 10.82 ± 1.38, RIX 9.58 ± 1.87, SOL 10.71 ± 1.85. Conclusion: Continued efforts should be made to provide adequate Spanish-language resources for Hispanic ophthalmology patients who often experience health disparities.

Background:

Health literacy is essential for appropriate patient care. Patient health literacy is impacted by limited English proficiency (LEP). LEP patients, including Hispanic patients, often experience health disparities. Institutional health literacy includes providing adequate materials for patient education. To better understand the institutional health literacy of ophthalmology organizations in the US, this study analyzed the availability and readability of Spanish-language resources found on ophthalmology websites.

Methods:

Certified CHWs attend the Advanced/Upskilling training developed by Purdue University.

Results:

The inability of grant funds to support certain populations.

Conclusions:

The institutional health literacy of ophthalmology organization websites in the US needs improvement. Given that approximately 40.7 million people in the US speak Spanish at home4, ophthalmology organizations can partially improve their health literacy by increasing the availability of Spanish-language resources for Hispanic patients online. In addition, resources should be created by professional

translators with an emphasis on a reading level of 6th grade or lower. Increasing the availability of adequate Spanish-language ophthalmology resources will improve health literacy of Hispanic patients and address some of the ocular health disparities these patients face.

Translational / Human Health Impact:
By understanding the disparities in availability and readability of Spanish-language ophthalmology resources, we can create and implement changes to these organizations and ultimately improve care for our Spanish-speaking Ophthalmology patients. Similar work can be applied to other fields of medicine as well to improve care of Spanish-speaking patients overall.

Acknowledgements/Funding Sources:

Poster #: 6

Redesigning Engagement with Communities at the Center

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Jasmine Gonzalvo, Omolola Adeoye-Olatunde, Jerome Adams, Steven Abel, Ephrem Abebe, Noll Campbell, David Foster, Gicelle Garcia, Sonak Pastakia (all affiliated with Purdue University)

General Category: Community

Abstract:

Since March 2022, through generous gifts from Jim and Jeannie Chaney, Dr. Jerome Adams, Executive Director of Health Equity Initiatives, and the Purdue University Center for Health Equity (CHEqI) awarded 16 grants to Indianapolis community-based organizations (CBOs). The focus of the funding request was to develop innovative, sustainable models that address disparities in health affecting people who have been historically marginalized and underserved. Phase One involved issuing a call for proposals to Indianapolis CBOs in September 2021 to develop innovative, sustainable models that address disparities among people who have been historically marginalized and underserved. Proposals addressing healthcare access, sustainability, minority health gaps, social determinants of health, and scalability were prioritized. Phase Two invited CBOs to submit proposals for additional funding. A mini-grant committee comprised of clinical and tenure-track faculty helped determine funding decisions. Sixteen CBOs received funding ranging from $400 to $11,000 (Total: $50,000) in Phase One. Site visits in March 2023 were conducted to see mini-grant-funded related work in action. To celebrate the work completed through CBOs and the mini-grant initiative, in May 2023, the mini-grant committee hosted a wrap-up session to provide networking and resources for grant recipients. Five CBOs received additional funding ranging from $4,000 to $8,000 (Total: $25,000) in December due to successful impact and ongoing need. Recipients included a free clinic, two neighborhood-driven nonprofit urban farms, a CHW state association, and a school-based art therapy program. Communities are central to the health equity engagement efforts, with their priorities, expertise, and needs guiding academic initiatives. Interdisciplinary faculty have significant opportunities to partner with communities to support meaningful change. Establishing bi-directional, mutually beneficial relationships between academia and communities requires dedicated time and effort.

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Conclusions:
Communities are central to the health equity engagement efforts, with their priorities, expertise, and needs guiding academic initiatives. Interdisciplinary faculty have significant opportunities to partner with communities to support meaningful change. Establishing bi-directional, mutually beneficial relationships between academia and communities requires dedicated time and effort.

Translational / Human Health Impact:
This project highlights a collaborative effort between academic institutions and community-based organizations. Innovative solutions to address health disparities can be developed and implemented effectively by leveraging community and academic expertise. Through sustained engagement and support, these initiatives can translate into improved health outcomes and wellbeing for historically marginalized and underserved populations.

Acknowledgements/Funding Sources:
We would like to thank Jim and Jeannie Chaney for there generous funding.

Poster #: 7

Pathways to Reduce COVID-19 Health Disparities with an Intermediate Evaluation Tool

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General Category: Community

Abstract:

Capacity building (CB) is necessary to induce community change that over time, can improve population health. Evaluation of capacity building activities are often missed due a lack of available tools and resources designed to capture outcomes that bridge the gap between inputs and impact.

Purdue University adapted an activity log system used to evaluate quantitatively and visually demonstrate intermediate impact within an Indiana initiative designed to reduce COVID-19 related health disparities Indiana Healthy Opportunities for People Everywhere (I-HOPE).

The activity log system described effectively demonstrated intermediate success. It also highlighted the relationship between upfront investment in intermediate community engagement activities and resulting change outcomes over time.

Background:

Purdue's Community Transformation Team (CTT) builds partnerships and capacity among communities to ultimately reduce health disparities across the state of Indiana. (Figure 1).

Funded initiatives, like I-HOPE, often encourage, if not require, impact results to be reported back to stakeholders, including funders, state health departments, academic institutions, and community participants, when long-term goals, such as changes in health status, may not be realized within one or two years. Also, the ability to maintain, sustain, or apply for new health-facing initiatives relies heavily on demonstrable success and community impact.

To fill this gap, Purdue's CTT created an activity log system, adapted from work by Chalmers et al., 2003, to track Purdue-led I-HOPE activities and associated intermediate impacts via change outcomes over a period of 3 years.

Methods:

Data were retrospectively collected by the CTT on Purdue-led I-HOPE activities and change outcome(s) from project management tools as well as team-member and partner interviews. The CTT created and defined categories for both activities and change outcomes that aligned with Figure 1.

Activities were recorded as education and training, community-engaged research, or community assistance. Change outcomes were categorized as an individual, organizational, community, or systems-level change. Activities were assigned unique identifiers that directly link each activity with the resulting change outcome(s). Cumulative totals were then calculated, recorded, and inputted into a line graph that overlays activities and associated change outcomes over time.

Results:

Analysis demonstrates that Purdue's CTT implemented a total of 687 capacity building and partnership activities that directly resulted in 1,313 changes in Indiana communities between 2021-2024, as part of the I-HOPE initiative (Figure 2).

Figure 3 demonstrates the categories in which change outcomes occurred. 182 individual changes; 101 organizational changes; 1,021 community changes; and 9 systems-level changes occurred.

Additionally, the results demonstrate achievement of intermediate goals set by the CTT.

Goal 1: Increase knowledge, skills, and abilities of healthcare professionals and community members to address social drivers of health (individual changes).

Goal 2: Improve organizational capacity of local health departments, non-profits, grass roots organizations, and critical care providers in underserved and rural areas (organizational changes).

Goal 3: Expand community access to resources, events, healthcare, and education in underserved and rural areas (community changes).

Goal 4: Strengthen systems of care and judicial systems to improve health equity among Indiana counties and communities (systems changes).

Conclusions:

Purdue's activity log system was effective in evaluating the intermediate success of partnership and capacity building activities within Purdue-led I-HOPE activities working to reduce health disparities in Indiana. The graph was used to demonstrate program fidelity without having to wait years or decades to see changes in health status. Using the graph, the CTT was able to secure funding to sustain the project for an additional 2 years.

While no change outcomes occurred during most of 2021, from 2022-2024 the number of outcomes doubled the number of activities, demonstrating the importance of upfront investment in listening, trust and relationship building, and tailored interventions to fit community needs. A logic model was used to guide the path between proposed CB activities and reduced health disparities in Indiana.

Translational / Human Health Impact:

With the increased use of public health funding for community-based health promotion, it is important to understand the impact they have on their communities. It takes time to realize an outcome such as a change in health status. However, changes within communities may precede changes in health status. The activity log process is useful for observing the changes in a community's health promotion environment and providing an intermediate measure of an initiative's success.

Acknowledgements/Funding Sources:

This poster was supported by funds made available from the Centers for Disease Control and Prevention, Center for State, Tribal, Local and Territorial Support, under NH75OT000073.

Poster #: 8

Investigating Gender-Based and Race-Based Inequalities in Death Causes

Om Patel
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Prof. David Gleich, Purdue University

General Category: Community

Abstract:
There are many factors that are linked to how different parts of our national population are affected by mortality causes, many of which show disparities linked to gender and race. Exposing potential links and trends could help to provide targets for where underlying factors that lead to these inequalities are in order to assist in addressing them and improving overall health equity. Here, we have analyzed data from the CDC Wonder database and have utilized statistical analysis and visualization (such as with Chi-Square) in order to analyze trends in how various factors affect mortality due to specific popular causes of interest (including firearm related deaths, homicides, cancer, respiratory viruses, et cetera) and have focused on how these change with age. Interestingly, we find a number of causes that show racial impacts that change with age, such as deaths due to narcotics.

Background:
It is generally recognized that gender and race are, unfortunately, correlated with inequalities in health. Among a large number of challenges with these inequities, a starting point is presenting the data on their impact. Here, we choose to focus on mortality as the impact and see to understand how inequities in mortality vary with age, race, and gender. The utility of this study is that it may prompt investigations of hypothetical factors underlying these differences in mortality. This would help identify smaller target populations for intervention that make it easier to reach certain populations that would be best aided by measures and help build effective equity in our community.

Methods:
In order to collect and analyze the data, we started by gathering compiled data from the CDC Wonder mortality database. Categorizing by simple and understandable cause of death (for example, categorizing all forms of suicide as “suicide” rather than by other specific details) allowed for separation of deaths by cause, year, race, and gender. Then, Chi-square tests of independence were used on various groups separated by age/race/gender (with categories being people in each group that had either died of a certain cause and those who had not). Compiling these findings and visualizing through tables and graphs exposes otherwise hidden subtle patterns that expose how factors (such as age) can isolate specifically affected populations that are affected by certain causes.

Results:
The peak systolic hemodynamic parameters were observed to be elevated in a regurgitant heart and lowered in a repaired heart post surgery.

Conclusions:
Although these findings themselves are not sufficient to identify direct causes of inequity, these observations do allow for motivation for investigation of potential causes of inequity, as our results highlight between what groups the greatest disparities lie. In addition, even if causes cannot be directly identified and resolved, the correlations identified by our findings allow for more specific responses and improvements to healthcare that allow for more vulnerable or afflicted populations to be targeted. For example, for causes of death that disproportionately affect Native American younger males more than any other group, this means that any efforts that are trying to deal with these mortality causes could be better designed to ensure that they can better reach this group. In addition, for causes of death that disproportionately affect women towards the end of middle age, healthcare protocols could be tailored

towards identifying individuals that are most likely to be affected and ensuring access and awareness which are critical factors to achieving health equity.

Translational / Human Health Impact:
These results can be used in order to inform future studies on what might be possible or where differences arise. For example, ensuring that awareness and risk-screening measures are made to best reach the groups that need them most will allow for more equitable ability for more people in the US to maintain their own health.

Acknowledgements/Funding Sources:
Supported by faculty mentoring Prof. David Gleich, aforementioned

Poster #: 9

Cancer Health Equity and Colorectal Cancer Awareness: A Community Health Educator Initiative

Michael Preston

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General Category: Community

Abstract:

Background: Disparities in colorectal cancer (CRC) incidence and mortality persist in rural and underserved communities. The National Outreach Network Community Health Educator (NON-CHE) project identified barriers to CRC screening and implemented the Screen 2 Save (S2S), a national initiative, to increase community knowledge, awareness, and engagement activities. In this study, we assessed the impact of this initiative in rural and underserved communities.

Methods: Descriptive and comparative analyses were used to examine the role of the NON-CHE on CRC knowledge and CRC screening intent. 170 surveys were collected. Data included demographics, participants' current CRC knowledge, awareness, and future CRC health plans. A multivariate linear regression was fit to participants' survey scores for CRC knowledge. Analyses were done in R 3.5.2.

Results: NON-CHE engaged 441 participants in rural and underserved communities. At baseline, white participants had significantly higher CRC knowledge scores, correctly answering 1.94 (p=0.007) more questions on average. After the NON-CHE intervention, this difference was not statistically significant. The difference in participants' CRC knowledge had an overall mean of 0.92, with a standard deviation of 2.56. Greater than 95% of participants agreed that S2S sessions impacted their intent to get screened for CRC.

Conclusions: The NON-CHE facilitated community connections and increased awareness of CRC risk reduction, screening, treatment, and research. Equity of access to health information and the health care system can be achieved with precision public health strategies. The NON-CHE combined with S2S is a powerful way to engage rural and underserved communities and impact participants' intent to "Get Screened".

Background:

Disparities in colorectal cancer (CRC) incidence and mortality persist in rural and underserved communities. The National Outreach Network Community Health Educator (NON-CHE) project identified barriers to CRC screening and implemented the Screen 2 Save (S2S), a national initiative, to increase community knowledge, awareness, and engagement activities. In this study, we assessed the impact of this initiative in rural and underserved communities.

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Descriptive and comparative analyses were used to examine the role of the NON-CHE on CRC knowledge and CRC screening intent. 170 surveys were collected. Data included demographics, participants' current CRC knowledge, awareness, and future CRC health plans. A multivariate linear regression was fit to participants' survey scores for CRC knowledge. Analyses were done in R 3.5.2.

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The NON-CHE facilitated community connections and increased awareness of CRC risk reduction, screening, treatment, and research. Equity of access to health information and the health care system can be achieved with precision public health strategies.

Translational / Human Health Impact:
The NON-CHE combined with S2S is a powerful way to engage rural and underserved communities and impact participants' intent to "Get Screened".

Acknowledgements/Funding Sources:
Supported by Cancer Disparities Research in Rural and Underserved Communities: RURaL [Reaching the Underserved, Rural, and Low-Income] Lab. Funding, Purdue University; Institutional Research Grant IRG-18-159-43 from the American Cancer Society; Wright Center's Clinical and Translational Science Award (CTSA), CTSA grant number: KL2TR002648; VCU Massey Cancer Center Office of Health Equity & Disparities Research, #P30CA016059.

Poster #: 10

LGBTQIA+ Affirming Practices: Evaluation of Knowledge, Attitudes, and Confidence in Future Practice of Intermediate Learners Participating in an Interprofessional Immersion Activity

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Alexandra Marshall, PhD, University of Arkansas for Medical Sciences; Clare Brown, PhD, University of Arkansas for Medical Sciences; Kathryn Neill, PharmD, University of Arkansas for Medical Sciences

General Category: Community

Abstract:

Lesbian, Gay, Bisexual, Transgender, Queer / Questioning, Intersex, Asexual, Plus (LGBTQIA+) individuals make up roughly 7% of the U.S. adult population. However, when compared to heterosexual cisgender individuals, LGBTQIA+ individuals experience greater health disparities across disciplines. A stratified convenience sample of students attending a graduate medical institution in the South was collected through the office of Interprofessional Education (IPE) to assess student Knowledge, Attitudes, and Perceived Future Practice when working with LGBTQIA+ patients or clients. Students were randomly assigned to either the intervention or the control group with the intervention group receiving a 15-minute educational module 1-week prior to an IPE Proposal Workshop. Pre-post-test were administered to both the intervention and the control group with the post-test including four open-ended questions. Students represented the college of medicine (n=29), college of nursing (n=39), college of pharmacy (n=11), college of health professions (n=41), and college of public health (n=13). Primary findings indicated a statistically significant difference occurred across all three domains indicating participation in the workshop, not the intervention, resulted in a difference in Knowledge, Attitudes, and Perceived Future Practice. College of medicine respondents showed differences in Attitudes (p=0.01) from pre- to post-survey, as well as Perceived Future Practice (p=0.03). Also, Perceived Future Practice (p=0.001) proved statistically significant overall indicating a correlation between the workshop and differences in Perceived Future Practice. Qualitative findings yielded three themes 1) Development of Knowledge Foundation and Information Sourcing, 2) Philosophy of Interpersonal Interactions, and 3) Integration of Knowledge and Attitudes to Applied Behaviors and Target Outcomes. The control group reported a desire for more education and changes to the IPE activity, while the intervention group reported more frequently increased comfort and respect for persons.

Background:

Despite its ubiquitous nature, the frequency of infections is not high, probably due to existence of non-pathogenic isolates. The pathogenesis of Acanthamoeba includes intricate interactions between the organism and the host's immune system.

Methods:

A stratified convenience sample of students attending a graduate medical institution in the South was collected through the office of Interprofessional Education (IPE) to assess student Knowledge, Attitudes, and Perceived Future Practice when working with LGBTQIA+ patients or clients. Students were randomly assigned to either the intervention or the control group with the intervention group receiving a 15-minute educational module 1-week prior to an IPE Proposal Workshop. Pre-post-test were administered to both the intervention and the control group with the post-test including four open-ended questions. Students represented the college of medicine (n=29), college of nursing (n=39), college of pharmacy (n=11), college of health professions (n=41), and college of public health (n=13).

Results:

Primary findings indicated a statistically significant difference occurred across all three domains indicating participation in the workshop, not the intervention, resulted in a difference in Knowledge,

Attitudes, and Perceived Future Practice. College of medicine respondents showed differences in Attitudes (p=0.01) from pre- to post-survey, as well as Perceived Future Practice (p=0.03). Also, Perceived Future Practice (p=0.001) proved statistically significant overall indicating a correlation between the workshop and differences in Perceived Future Practice. Qualitative findings yielded three themes 1) Development of Knowledge Foundation and Information Sourcing, 2) Philosophy of Interpersonal Interactions, and 3) Integration of Knowledge and Attitudes to Applied Behaviors and Target Outcomes. The control group reported a desire for more education and changes to the IPE activity, while the intervention group reported more frequently increased comfort and respect for persons.

Conclusions:

Translational / Human Health Impact:
Improving provider knowledge and comfort when working with LGBTQIA+ patients leads to improved health outcomes for this population.

Acknowledgements/Funding Sources:

Poster #: 11

Phonation Signal and Image Processing for Detecting and Classifying Dysphonia

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General Category: Health and Disease

Abstract:

Detecting voice – related pathologies early is challenging. Research on processing audio and high - speed video endoscopy (HSV) data reveal that recorded signals are difficult to classify. There is potential to detect dysphonia in its early stages, while it is still not apparent, in terms of visual and audio data. We aim to use signal processing techniques to 1) Delineate pathophysiological features and 2) Classify different pathologies from audio and HSV data.

Background:

Vocal communication could have a significant monetary value for many professionals. Despite the level of automation today, vocal communication is a fundamental part of society.

Changes in muscle tension, subtle swelling, onset of tumors are not visually apparent, unlike the polyps or nodules. These changes are reflected in the vibratory characteristics of vocal folds. Functional dysphonia can only be visually detected by picking out irregularities in the vibrations of the vocal folds.

We identified a need for better audio and video data analysis methods to rid the measurement chain of inter – recording variations and achieve better classification accuracy.

Methods:

Audio signal and image processing methods - including kymogram development from High speed videoendoscopy (HSV) measurements, Wavelet transform, Hilbert transform. As the project is in its early stages, one objective is to develop better data analysis methods than reported in literature.

Results:

Visually some differences can be noted among audio signals of a patient pre and post- Deep Brain Stimulation (DBS), but signal processing methods can help us better. A preliminary demonstration is shown how discrete wavelet transform (DWT)can pick out differences in seemingly similar signals, which is used for denoising and compression. We look to also utilize the continuous wavelet transform (CWT) which can reveal discontinuities in both the time and frequency space of signals.

Conclusions:

Process simultaneous HSV and audio recordings for a patient with essential tremor (left), pre and post Deep Brain Stimulation, This is a specific application yet unexplored in literature.

Scrutinize the data features (both audio and video) and look for features which can help in characterizing the changes after treatment.

Ultimately, include normophonic control data and look towards classifying voice and video into pathological and non – pathological.

Translational / Human Health Impact:

Vocal communication drives the world. Be it a valuable tool for one's profession (teacher, singer) or the simplest way to convey one's thoughts, it is apparent that one's voice is an important aspect of their personality. Which is why losing vocal function can have severe impact on the quality of human life. The direction we have identified has the potential to improve vocal fold pathology diagnosis, so that patients

could have lesser and more informative examination sessions (an endoscope in your mouth is not very comfortable) which can detect less apparent pathophysiological features of the folds.

Acknowledgements/Funding Sources:

Poster #: 12

HPV 16 DNA Detection from Endocervical Cells with Simple Visual Readout

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General Category: Health and Disease

Abstract:

Background:

Introduction: Cervical cancer is almost entirely preventable with proper screening, however around 36% of women aged 30-49 years have had a lifetime screening [1]. Molecular detection of high-risk human papillomaviruses (hrHPV) is a sensitive method to detect cervical cancers and precancers, providing the opportunity for increasingly accessible screening methods. Unlike existing point-of-care testing methods such as CareHPV which must be run in batches and take hours to yield results, a rapid test could facilitate rapid screening and follow-up care. We report a method for detecting HPV 16 on a lateral flow assay via isothermal nucleic acid amplification testing (NAAT) with an endogenous sample control, in a format amenable for rapid diagnostic testing.

This work builds upon previously published primer sets [2] by adapting them to a rapid test format that is amenable to detection of 13 hrHPV types.

Methods:

Method: Recombinase polymerase amplification kits from TwistDx were used with a primer pool for high-risk HPV from [2] at 39oC for 20 minutes in a 50 µL reaction volume. A fluorescent probe for the HPV 16 L1 gene was designed with Geneious Prime to test the primer pool's limit of detection (LoD) in a fluorescence reader. A novel probe and the primers were labelled with biotin and fluorescein to assess the NAAT's LoD on a Milenia Biotec lateral flow strip (LFS). The NAAT was evaluated on cell lysates, alongside in-house primers for ß-globin as an endogenous sample control to ensure clinical relevance. Two (2) µL of c33A endocervical cell lysate was added to a 50 µL NAAT reaction, with either ß-globin primers or HPV 16 primers and probe with spiked 1E6 copies of HPV 16 plasmid DNA. Amplicons were detected on gel and LFS. Finally, the NAAT was performed on 1E6 copies of HPV16 DNA with the reaction volume absorbed on glass fiber and polyether sulfone (PES) membranes. The amplicons were eluted with 100 µL milliQ water, and run on a gel.

Results:

Results: The NAAT demonstrated a LoD of 100 HPV 16 copies/reaction with the fluorescent probe (n=3, fig 1) and 1000 copies/reaction with the lateral flow strips (n=3, fig 2). The NAAT produced the strongest signal for spiked HPV 16 DNA and ß-globin DNA freed by cell lysis with 0.5 U/uL Achromopeptidase, 0.04 U/uL Proteinase K, 10% Triton X100, and Guanidinium chloride (GuHCl) treatments (n=2, fig 3, 4). Finally, the NAAT performed successfully on both of the paper substrates tested (fig 5, n=1).

Conclusions:

Discussion: The LoD of 1000 exceeds that achieved by CareHPV [3]. The assay performs well with equipment-free cell lysis methods and retains functionality in paper substrates. Ongoing work is integrating the assay into the µRAAD device being designed in our lab (fig 6).

Translational / Human Health Impact:

These data should allow for in-clinic testing of Human papillomavirus, facilitating follow-up care and improving retention of at-risk patients in a setting where 20% currently go without appropriate, timely treatment.

Acknowledgements/Funding Sources:
This work was funded by the NCI grant number K01CA241073, PI: Rodriguez Our thanks to the Indiana Cancer Consortium, and our community partners.

Poster #: 13

Geospatial distribution of COVID-19 related deaths among nursing home residents across the United States in each wave.

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Cody Mullen (Purdue University) , Randy Hubach (Purdue University)

General Category: Health and Disease

Abstract:
Nursing home residents experienced a much higher rate of COVID-19 related deaths throughout the pandemic compared to the general population as well as older adults not in nursing homes. In December 2020, the COVID-19 death rate for older adults in nursing homes was 9,200 per 100,000, while the rate for older adults not in nursing homes was 87 per 100,000. Despite the glaring inequities, little research has been conducted to study how the number of COVID-19 deaths in each nursing home changed as the pandemic continued and as health policies evolved. This study aimed to investigate how the number of COVID-19 deaths were geospatially distributed and which areas of the United States had significantly higher or lower numbers. The study's data was from the Centers for Medicare and Medicaid (CMS) COVID-19 Nursing Home Datasets for the years 2020 to 2023 and from the CMS Nursing Home Provider Information dataset. We conducted an optimized hot spot analysis for each wave of the COVID-19 pandemic and it was run at the facility-level to create the visual representation of statistically significant hot and cold spots at 90%, 95%, and 99% confidence intervals. In each wave, multiple significant clusters across the United States focused on specific geographic regions, usually at the state-level. States that had statistically significant hot spots in each wave included Indiana, New York, Pennsylvania, and Massachusetts. States that had statistically significant cold spots in each wave included Florida, California, and Hawaii. This study shows that more research needs to be done about the policies implemented or state-level regulations that increased or decreased the risk of COVID-19 related deaths in nursing homes.

Background:
Throughout the COVID-19 pandemic, the residents, and staff of nursing home facilities across the United States experienced higher rates of COVID-19 hospitalizations, morbidity, and mortality than the rest of the population. This is partially explained by the fact that nursing home residents are older, more likely to have multiple co-morbidities, live in close proximity to other residents, and have close interactions with staff. For example, by August 15th of 2021, there were over 600,000 COVID-19 related deaths and about 21% of those were among residents in nursing homes. By March 2023, there were over 1.5 million confirmed COVID-19 cases for residents and over 1.5 million total staff confirmed COVID-19 cases. By mid-May 2021, nursing home residents made up almost 40% of all COVID-19 deaths in the United States, even though they represented 0.4% of the population. Furthermore, almost every nursing home in the United States had at least one case of COVID-19 and more than 80% had one COVID-19 death.

Methods:
Data on nursing home locations, COVID-19 rates, and characteristics were collected from the Centers for Medicare and Medicaid Services (CMS) COVID-19 Nursing Home Datasets for the years 2020, 2021, 2022, and 2023. This dataset was stored on a weekly basis and was first collected as of May 24, 2020. Additionally, data was collected from the CMS nursing home Provider Information datasets. Both datasets were only for Medicare and Medicaid certified nursing homes. CMS COVID-19 infection files were split into three separate datasets to represent the three distinct waves of COVID-19. The three waves include cumulative data up to these dates respectively: June 27, 2021, April 10, 2022, and April 10, 2023. The final data set only included nursing homes that reported COVID-19 data at each wave and that address information that could be matched in ArcGIS (n=14,831). For each map, once the merged nursing home datasets were created, an optimized hot spot analysis was run at the facility-level using the Getis-

Ord Gi statistic to create the visual representation of statistically significant hot and cold spots at 90%, 95%, and 99% confidence intervals. Once the analysis was run for each wave, the hot spot analysis layer was spatially joined with the nursing home information layer because there was no similar attribute field that could be used. The combined final table was exported into an excel format so the characteristics of nursing homes with statistically high or low rates could be assessed.

Results:
The map for wave one makes it very clear where the hot and cold spot clusters are located across the United States. Indiana, Illinois, Ohio, South Dakota, Iowa, Missouri, Arkansas, Maryland, Pennsylvania, Connecticut, and Massachusetts are states with concentrated, well-defined clusters of hot spots. States with concentrated cold spots include Florida, California, Hawaii, Virginia, New York, and Texas. Additionally, at the intersection of Tennessee, North Carolina, and Georgia, there is a cold spot cluster. Other hot and cold spots are located sporadically around the country and not confined to one specific state. During wave two, the spread of hot spots around Indiana became less spread out and even more concentrated. The hot spots in Philadelphia, and New York became less concentrated and a new one appeared in Oklahoma. South Dakota and Iowa's hot spots largely disappeared during wave two, however one small cluster remained. Florida and parts of California remained a consistent cold spot and a new appeared in Minnesota during this time. In wave three, it is clear which states implemented or did not implement public health policies and appropriately and sufficiently distribute resources to nursing homes and their staff. Major changes in wave three include a further concentration of hot spots around Indiana, Pennsylvania, and Massachusetts. A notable change in wave three is that the previous cold spot cluster in Washington had a major increase in the COVID-19 death rate because it became a hot spot. In this most recent wave, it is interesting to see which states consistently had statistically significant higher rates of COVID-19 deaths compared to others and whether this trend continues. Based on this brief review, it appears that the traditional predictors of COVID-19 mortality do not have significant differences between the hot and cold spots. This can be partially explained to the fact that the majority of nursing home facilities score well on their quality rates, are certified by both Medicare and Medicaid, and are for profit. However, it does signal that there are more contextual and political factors that are affecting the COVID-19 death rates and that need to be identified before the next major respiratory outbreak.

Conclusions:
There is currently a critical gap in determining the characteristics of nursing homes with statistically high and low rates of COVID-19 deaths among residents. This research will help guide future resource distributions during a respiratory disease outbreak and identify areas or locations that need infectious disease reform. Additionally, it will allow researchers and practitioners to be aware that further research is needed into the risk and protective factors that led to these specific facilities having statistically higher or lower COVID-19 death rates among nursing home residents. Finally, this study has identified cluster patterns across each COVID-19 wave and will highlight where the implementation of specific public health prevention measures worked for these facilities.

Translational / Human Health Impact:
This study has indicated the importance of state and local-level policies and interventions that took place during the COVID-19 pandemic and the impact they had on he lives of nursing home residents. To better prepare for future epidemics and pandemics, more research needs to be conducted to determine best practices for preventing transmission, reducing severity, and reducing the death rate.

Acknowledgements/Funding Sources:

Poster #: 14

Impaired visual experience-dependent oscillations and underlying interareal circuit in the visual cortex of Fmr1 KO mice

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General Category: Health and Disease

Abstract:

Fragile X syndrome (FXS) is a prevalent heritable autism spectrum disorder (ASD), marked by hypersensitivity and difficulty adapting to new sensory stimuli. Individuals with FXS often face visual perception and learning impairments. Despite previous studies highlighting disruptions in 4-8 Hz oscillations, aberrant functional connectivity, and impaired short-term plasticity in Fmr1 KO mice, the model of FXS, the impact of FXS on inter-areal connectivity remains unclear. To address this gap, we introduced a novel perceptual experience paradigm inducing familiarity-specific 4-8 Hz oscillations in the primary visual cortex (V1) and the lateromedial area (LM), a component of the ventral pathway in mice. Through in vivo simultaneous silicon probe recordings and channelrhodopsin-2-assisted circuit mapping (CRACM) in acute brain slices, we examined long-range functional connections between V1 and LM in wildtype (WT) and Fmr1 KO mice pre- and post-visual experience. Our results revealed diminished 4-8 Hz oscillations in both local field potentials and single-unit activity, as well as reduced unit population firing rates in V1 and LM of Fmr1 KO mice, suggesting impaired communication between LM and V1. Additionally, CRACM indicated altered synaptic strength from V1 onto pyramidal cells in LM layers, with only mild changes in Fmr1 KO mice. Interestingly, while synaptic properties of feedback projections in Fmr1 KO mice seemed to improve following visual experience, no changes were observed in WT mice. Furthermore, visual experience induced dendritic spine morphology plasticity and increased c-Fos expression in the visual cortex of WT but not Fmr1 KO mice. These findings underscore the significance of visual training as a potential therapeutic intervention for ASD, providing insights into inter-areal synaptic connectivity alterations in FXS.

Background:

Fragile X syndrome (FXS) is the most prevalent heritable autism spectrum disorder (ASD), characterized by hypersensitivity and difficulty adapting to new sensory stimuli. Individuals with FXS often exhibit visual perception and learning impairments. Previous studies have described attenuation of 4-8 Hz oscillations, aberrant functional connectivity in Fmr1 KO mice, and impaired short-term (STP) in Fmr1 KO mice, the model of FXS. The reciprocal connections between the primary visual cortex (V1) and higher visual areas are crucial in cognitive processes. However, the impact of FXS on inter-areal connectivity remains poorly understood.

Methods:

To shed light on this phenomenon, we developed a new perceptual experience paradigm that induced familiarity-specific 4-8 Hz oscillations in V1 and the lateromedial area (LM), a part of the ventral pathway in mice. Using in vivo simultaneous silicon probes recordings and channelrhodopsin-2-assisted circuit mapping (CRACM) in acute brain slices, we investigated the strength and characteristics of long-range functional connections between V1 and LM in wildtype (WT) and Fmr1 KO mice before and after the visual experience.

Results:

Simultaneous recordings of V1 and LM showed that the 4-8 Hz visual experience-dependent oscillations of both local field potentials and single-unit activity were lower in power and shorter in duration, and unit

population firing rates were also lower in the V1 and LM of Fmr1 KO mice, which indicated deficits in communication between LM and V1. CRACM of feedforward projections revealed increased synaptic strength from V1 onto pyramidal cells (PCs) in all cortical layers of LM after visual experience in WT, while only a mild increase in the superficial layer II/III in Fmr1 KO mice. CRACM of feedback projections revealed decreased synaptic strength from LM onto PCs in layer II/III of V1 and increased strength in deep layer V after experience in WT, but no changes in Fmr1 KO mice. The visual experience also induced dendritic spine morphology plasticity we observed using super-resolution imaging and increased c-Fos expression in the visual cortex in WT but not in Fmr1 KO mice. Interestingly, some of the synaptic properties of the feedback projections in Fmr1 KO mice appeared to improve following visual experience, such as the paired-pulse ratios as a measurement of STP.

Conclusions:
Our findings provide the first measurements of the inter-areal synaptic connectivity before and after visual experience in WT and Fmr1 KO mice, along with simultaneous in vivo recordings of neural activity, and indicate that visual training may serve as a promising therapeutic intervention for ASD.

Translational / Human Health Impact:
Repetitive pattern visual training like environmental enrichment may alleviate the neural circuit anomalies in the visual cortex and serve as an option and intervention for ASD patients. Our E-I balance and STP experiments implied that visual training or visual familiarity may alleviate the atypical synaptic property and neural circuit anomalies. Plenty of previous studies reported environmental enrichment promotes behavioral and morphological recovery in FX mice and improvement in social performance and learning in ASD children. Here, we found that training repetitively with patterns of specific SF and TF could also be helpful to fragile X mice and might also have positive indications for ASD patients. More combinations of TF and SF patterns of visual training should be utilized to test which patterns have the optimal behavioral interventions in rodents in future studies. Those could be implications for a new form of visual clue therapy for ASD patients.

Acknowledgements/Funding Sources:
This work was supported by the National Institutes of Health (NIH) grant R01 MH116500

Poster #: 15

Interventions for parents to increase HPV vaccine uptake: An integrative review of randomized controlled trials

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General Category: Health and Disease

Abstract:
Purpose: This integrative review aims to synthesize findings from randomized controlled trials (RCTs) that targeted parents to increase HPV vaccine uptake in their children.
Methods: A systematic search was conducted in PubMed and CINAHL based on the keywords: HPV vaccine, parents, intervention, and vaccine uptake. The inclusion criteria are RCTs published between 2014 and 2023, focusing on parents of HPV vaccine-eligible children (boys and girls aged 9 to 17) who had not initiated or completed the vaccine series. Articles were screened in their title, abstract, and full text.
Results: A total of nine studies were included. The primary outcomes of the studies were the initiation or completion of HPV vaccination in adolescents. Seven studies were from the US, one from Israel, and one from Australia. Among them, seven studies showed statistically significant effects in improving HPV vaccine initiation or completion. Four studies utilized in-person education on the HPV vaccine and cervical cancer, using brochures or presentations. Two studies utilized mobile health to provide information on the HPV vaccine and one study utilized SMS reminders. Among them, three studies conducted post-tests twice (at 6 months, 7 months, and 1-4 months), while four studies conducted post-tests once. Two studies found no significant difference in outcomes. One utilized Facebook campaigns (Israel), and the other utilized web-based tailored education (US).
Conclusion: This study provides insights into effective intervention strategies among parents to increase HPV vaccine uptake in their adolescents. Based on the results, we recommend an in-depth literature search for each type of intervention proven effective. Additionally, future studies should explore how these interventions could be widely applied to different populations or settings. We also suggest evaluating the optimal timeframe for the post-test.
Keywords: HPV vaccine, parents, intervention, adolescents, vaccine uptake

Background:
Efforts to prevent and control HPV infections are crucial for public health, requiring increased awareness, safe behaviors, and utilization of preventive measures. Understanding the extent to which parental interventions can influence vaccine decision-making is key to designing effective strategies to elevate adolescents' HPV vaccination rates. Thus, this integrative review aims to synthesize findings from randomized controlled trials (RCTs) that targeted parents to increase HPV vaccine uptake in their children.

Methods:
A systematic search was conducted in PubMed and CINAHL based on the keywords: HPV vaccine, parents, intervention, and vaccine uptake. The inclusion criteria are RCTs published between 2014 and 2023, focusing on parents of HPV vaccine-eligible children (boys and girls aged 9 to 17) who had not initiated or completed the vaccine series. Articles were screened in their title, abstract, and full text.

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Conclusions:
This study provides insights into effective intervention strategies among parents to increase HPV vaccine uptake in their adolescents. Based on the results, we recommend an in-depth literature search for each type of intervention proven effective. Additionally, future studies should explore how these interventions could be widely applied to different populations or settings. We also suggest evaluating the optimal timeframe for the post-test.

Translational / Human Health Impact:
This integrative review aimed to synthesize findings from randomized controlled trials (RCTs) targeting parents to increase HPV vaccine uptake in their children. The translation of these findings into actionable interventions holds significant potential for improving public health outcomes related to HPV infection and associated diseases, such as cervical cancer.

Acknowledgements/Funding Sources:

Poster #: 16

Deep transfer learning reveals morphologically benign glands that are transcriptionally associated with prostate cancer progression

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General Category: Health and Disease

Abstract:

Background The field effect describes the phenomena where environmental exposures, infection, and genetic predisposition result in molecular changes in all types of cells. This expanded "field" of tissue is predisposed to developing cancer. Though this is a well-established concept in pathology, it remains underexplored in the context of high-resolution omics. Methods We utilized our Diagnostic Evidence Gauge of Single Cells (DEGAS) deep transfer learning framework to analyze prostate cancer spatial transcriptomics to identify cells and tissues that are highly associated with cancer progression. Cell type decomposition tools were used to decipher cell type and state changes associated with the high-risk glands. After identification by DEGAS, deep learning image analysis pipelines were fine-tuned to detect subtle changes in the morphology of these high-risk glands. Findings DEGAS highlighted certain morphologically benign glands that had reduced expression of MSMB, a differentiation marker that is decreased in aggressive tumors. These glands have upregulated genes associated with antigen presentation and aggressive neoplasms. Integration of single-cell transcriptomics and deep learning image analysis separately revealed altered immune-cell infiltration, suggesting a complex interplay in the tumor environment facilitating aggressiveness. Conclusion These findings challenge the traditional distinction between benign and malignant tissues, highlighting the critical role of subtle molecular changes in cancer progression and inflammation. This work underscores the potential of integrating spatial transcriptomics and deep learning to identify early markers of aggressive cancer, paving the way for novel diagnostic and therapeutic strategies.

Background:

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Methods:

Methods We utilized our Diagnostic Evidence Gauge of Single Cells (DEGAS) deep transfer learning framework to analyze prostate cancer spatial transcriptomics to identify cells and tissues that are highly associated with cancer progression. Cell type decomposition tools were used to decipher cell type and state changes associated with the high-risk glands. After identification by DEGAS, deep learning image analysis pipelines were fine-tuned to detect subtle changes in the morphology of these high-risk glands.

Results:

Findings DEGAS highlighted certain morphologically benign glands that had reduced expression of MSMB, a differentiation marker that is decreased in aggressive tumors. These glands have upregulated genes associated with antigen presentation and aggressive neoplasms. Integration of single-cell transcriptomics and deep learning image analysis separately revealed altered immune-cell infiltration, suggesting a complex interplay in the tumor environment facilitating aggressiveness.

Conclusions:

Conclusion These findings challenge the traditional distinction between benign and malignant tissues, highlighting the critical role of subtle molecular changes in cancer progression and inflammation. This work underscores the potential of integrating spatial transcriptomics and deep learning to identify early markers of aggressive cancer, paving the way for novel diagnostic and therapeutic strategies.

Translational / Human Health Impact:
Our study has identified a biomarker, a gene called MSMB, which may be very useful for predicting prostate cancer metastasis. This is a critical clinical need, because clinicians do not now have an accurate tool to predict prostate cancer spread. Prostate cancer is the most prevalent cancer in males, and it has an epithelial origin, as do the other most common cancers (i.e., breast, colon, pancreatic, and skin). Thus, we find it very likely that the field effect phenomena will be found in other cancers, with implications for better understanding the link between chronic inflammation and tumor-immune system desensitization.

Acknowledgements/Funding Sources:
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Poster #: 17

EXPANDING THERAPEUTIC POTENTIAL: ENGINEERED IL-27 VARIANTS WITH PROLONGED HALF- LIFE FOR ENHANCED ANTI-TUMOR EFFICACY

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General Category: Health and Disease

Abstract:

Interleukin-27 (IL-27) presents a promising avenue in the quest to slow down tumor progression and induce regression across various cancer models. However, the clinical translation of cytokine-based therapeutics is hindered by their inherently short half-lives, typically ranging from 1 to 5 hours. Numerous strategies, including PEGylation and lipidation, have been devised to address this limitation. Yet, most of these strategies involve post-production modifications, escalating production costs and complicating purification processes while potentially triggering immunogenic responses. In this project, our focus centers on the expression of proteins fused with a Pro-Ala-Ser (PAS) domain, which can be genetically encoded, offering a promising avenue for extending protein stability. To this end, we have designed an IL-27 variant featuring a PAS200 domain (addition of a 200 repetitions of amino acid Pro-Ala-Ser sequence to the N-terminus) aimed at prolonging the protein's half-life, alongside a non-PASylated version serving as a control. The primary objective of this phase of the project was to devise efficient expression and purification strategies for both IL-27 variants. During the course of this study, we successfully developed methods for the expression and purification of these protein variants. Notably, while IL-27 was expressed in Escherichia coli (E. coli), its expression was unattainable in mammalian cells. Conversely, the PAS200 IL-27 variant could only be expressed in mammalian cells, failing to express in E. coli. To ensure consistency in testing conditions, we elected to express the PASylated IL-27 in Expi 293FGnTI cells, a mammalian cell line which lack N-acetylglucosaminyltransferase I (GnTI) activity and therefore lack complex N-glycans. This makes the PAS 200 IL27 variant akin to the non-glycosylated IL-27 expressed in E. coli. Our expression and purification strategy revolved around affinity and size exclusion chromatography techniques. Subsequent animal studies are planned to elucidate the activity and stability of these variants further, thus paving the way for a comprehensive understanding of their therapeutic potential.

Background:

Interleukin-27 (IL-27), belonging to the Interleukin-12 (IL-12) cytokine family, emerges as a prospective therapeutic agent for impeding tumor growth and fostering tumor regression1. The field of Osteoimmune activity delves into interdisciplinary investigations exploring the nexus between the immune and skeletal systems, elucidating shared components such as ligands, receptors, signaling molecules, and transcription factors. Bones are fertile ground for tumor cell proliferation, owing to the conducive bone matrix growth factor environment. Tumor cells exploit the equilibrium between osteoclasts (bone resorption) and osteoblasts (bone formation) to bolster tumor expansion and precipitate skeletal-related events (SRE), including severe pain and fractures2. Current research surrounding IL-27 as a treatment modality targets diseases straddling the immune and skeletal systems, such as Prostate cancer, a form of tumor bone metastases that not only interfaces with the immune microenvironment but also interacts with bone cells, rendering them viable targets for therapeutics like IL-27. Improving IL-27's efficacy in cancer treatment by activating the immune system and affecting bone cells is crucial. However, its short half-life of 1 to 5 hours presents a significant challenge for clinical use. While PEGylation and lipidation have been investigated to prolong IL-27's lifespan, they often require costly post-production modifications, complicate purification, and may trigger immune reactions3. As an alternative avenue to enhance the circulation

time of IL-27, PASylation emerges as a viable strategy. By introducing a Pro-Ala-Ser domain at the N-terminus of IL-27, the hydrodynamic radius of the protein can be increased, thereby mitigating renal filtration and potentially amplifying its efficacy. This approach holds promise not only for IL-27 but also for several other secreted factors commonly employed in PEGylated clinical settings, such as granulocyte colony-stimulating factor (GCSF) and interferon alpha-2 (IFNa2)4. Moreover, it may serve as a more efficient alternative to cytokines currently undergoing gene delivery in various clinical trials and applications, including IL-12. The initiation of our project entailed the incorporation of a ~200 amino acid (aa) PAS domain at the N-terminus of IL-27. Considering the size of our protein, this domain length was deemed suitable, necessitating only one domain to validate our hypothesis6. Notably, previous endeavors with N-terminus Flex27 fusions, such as the Nanolux IL-27 fusion, have yielded functional proteins, underscoring the feasibility of this approach. The significance of PASylation is further emphasized by the hydrophobic nature of specific proteins, exemplified by IFN, exhibiting meager solubility due to the abundance of hydrophobic residues on its surface. In contrast, PAS polypeptide chains exhibit high solubility, facilitated by their propensity to form numerous hydrogen bonds with water molecules. Considering the physiological filtration thresholds in the glomeruli, proteins with molecular weights below 15 kDa are freely filtered, while those between 45 to 60 kDa face restricted filtration5. To pursue our objectives, a histidine (His) tag was incorporated for purification, facilitating streamlined isolation processes. This comprehensive approach holds promise for advancing the therapeutic potential of I -27 and other related cytokines, laying the groundwork for enhanced clinical outcomes in cancer treatment and beyond.

Methods:
Frozen cell pellets (1L) were resuspended in 20ml buffer (50mM NaP, 300mM NaCl, EDTA-free protease inhibitor) supplemented with 6M GuHCl. Sonication (59sec bursts, 30sec cool down, 45% amplitude) for 5 minutes ensured complete lysis. Subsequent centrifugation (10k xg, 30min) yielded the clarified lysate. Metal-affinity chromatography employed 100uL Biorad IMAC resin pre-equilibrated with Buffer A (50mM NaP, 300mM NaCl, 8M Urea, 2mM DTT). Lysate incubation and gravity flow-through collection captured bound protein. Elution utilized 1000uL Buffer B (high imidazole). Urea removal involved buffer exchange via Amicon Ultra centrifugal filters to achieve 1.2ml in 1XPBS. Protein presence and purity were confirmed by SDS-PAGE and Western blot using an anti-IL27 antibody. This protocol facilitates efficient IL27 purification for further analysis. Cell culture and expression of pasylated IL-27 in mammalian cells were executed employing the Expi293 GnTI cell system in conjunction with a commercial kit sourced from ThermoFisher Scientific. Adherence to ThermoFisher protocols for the Expi293 GnTI system governed cell growth and procedural steps. Following expression, supernatant retrieval was accomplished through centrifugation at 300xg for 30 minutes, succeeded by filtration utilizing a 0.22µm filter. Subsequently, a Protease cocktail devoid of EDTA was introduced to the filtered supernatant at a recommended ratio of 1 tablet per 10ml. Purification procedures entailed Ni NTA affinity chromatography, employing Buffer A (50mM NAPO4, 300mM NACL, 20mM Imidazole, pH 7.4, 0.5% CHAPS) and Buffer B (50mM NAPO4, 300mM NACL, 500mM Imidazole, pH 7.4, 0.5% CHAPS). Gel filtration followed, utilizing 20mM MOPS and 1% CHAPS. For visualization, sample preparation involved mixing 20µL of sample with 5µL of 5X SDS loading buffer, followed by heating at 95°C for 10 minutes. These treated samples were then loaded onto 10-well TGX BioRad gels and subjected to SDS-PAGE at 120V for 60-63 minutes or 200V for 30 minutes using a BioRad Transfer machine. Primary anti-IL27 antibodies were applied at dilutions ranging from 1:1000 to 1:50000, succeeded by secondary donkey anti-mouse antibodies at a dilution of 1:10000.

Results:
The benchtop experimentation for the purification of IL-27 yielded promising outcomes. Utilizing 8M Urea and 6M GuHCl proved effective for the purification process. However, subsequent dialysis of the fractions using either 1x PBS or 0.5x PBS was essential for protein refolding. The buffer set examination demonstrated that purifying the protein with 6M GuHCl and 8M Urea led to denaturation, suggesting improper folding within bacterial hosts and potential hindrance in binding to the resin via His tag. Due to precipitation challenges in SDS-PAGE caused by GuHCl and Urea, obtaining clear relative data for cell fractions, debris, lysate, flow-through, and wash fractions proved difficult. Despite this limitation, the recovered relative protein amount notably increased to approximately 11.04mg compared to alternative

methods employing different buffer compositions. These findings underscore the efficacy of the proposed purification approach in enhancing protein yield despite initial folding challenges. The expression of PAS200 IL-27 in E. coli cells posed challenges, leading us to resort to mammalian cell expression using a commercial kit. Purification optimizations mirrored those employed with E. coli cells, with the exception of employing a different detergent while adhering to similar principles. Our results revealed a low protein yield, albeit sufficient for further analyses. Utilizing PierceTM BCA Protein Assay Kits, we determined a protein concentration of 600 g/ml, indicating successful expression and purification. This concentration aligns well with our expectations, signifying the effectiveness of the mammalian cell expression system and the purification strategy employed.

Conclusions:
In conclusion, our findings underscore the successful purification of the protein, albeit with ongoing efforts to optimize purity and yield. To this end, Size Exclusion Chromatography (SEC) utilizing a buffer comprising 1xPBS, 2mM DTT, and 0.1% Triton X-100 for both IL-27 and PAS200 IL-27 samples will be employed. SEC, capitalizing on molecular size disparity, promises effective separation of target proteins from contaminants and aggregates. Through meticulous application of this technique alongside specified buffer conditions, we anticipate obtaining a final sample of unparalleled purity and maximal yield. This purified specimen will subsequently undergo rigorous assessment for its potential therapeutic utility.

Translational / Human Health Impact:
PASylation of interleukin-27 (IL-27) marks a transformative step in cancer therapy, addressing the challenge of short cytokine half-lives. By genetically encoding a Pro-Ala-Ser domain at IL-27's N-terminus, PASylation extends its circulation time, enhancing therapeutic efficacy. This innovation not only benefits IL-27 but also holds promise for other cytokines like GCSF and IFNa2. Streamlining production with a histidine tag further facilitates clinical scalability. PASylation's impact spans beyond cancer, offering potential solutions for autoimmune disorders, infections, and inflammatory conditions reliant on cytokine therapies. By overcoming clearance limitations, PASylation introduces durable treatment options, bolstering patient outcomes across diverse medical domains. In essence, PASylation of cytokines represents a pivotal translational advancement, fostering interventions with profound implications for human health and the future of cytokine-based therapy.

Acknowledgements/Funding Sources:
We would like to express our sincere gratitude to the Protein Engineering Partners Initiative (PEPI) award and the Purdue Institute of Inflammation, Immunology, and Infectious Disease (PI4D) for their generous support and the invaluable opportunity to utilize the resources of the Molecular Evolution, Protein Engineering, and Production (MEPEP) facility. Their contributions have been instrumental in advancing our research efforts, enabling us to explore new avenues in protein engineering and molecular evolution. We are truly appreciative of their ongoing commitment to fostering scientific innovation and collaboration.

Poster #: 18

Identifying the Sexual Health Needs of Formerly Incarcerated Men

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General Category: Health and Disease

Abstract:

Objective: The purpose of this study was to evaluate Pre-exposure Prophylaxis (PrEP) interest, knowledge, and utilization among recently incarcerated men. Furthermore, this study aims to identify barriers to PrEP education and access, related sexual health needs, and competing needs during re-entry, such as housing and employment, for study participants.

Methods: The study utilized semi-structured individual interviews that aimed to acquire insight into barriers and facilitators to PrEP knowledge and utilization. The interviews were transcribed and subjected to thematic coding analysis, revealing several overarching themes.

Results: The final sample consisted of 28 participants with an average age of 32.86 years and average incarceration period of 69 months. Of the 28 participants, n=24 were not prescribed PrEP and n=4 were prescribed PrEP at the time of data collection. Ultimately three primary themes were identified: 1) Perceptions of HIV risk; 2) Barriers to PrEP adoption; and 3) What men want in programming both pre-release and post-release.

Conclusion: Many participants expressed that PrEP adoption post-release was not a priority, and that issues like housing and employment took precedent over healthcare concerns. Moreover, participants faced restricted access to HIV testing both during incarceration and post-release, highlighting the imperative for greater PrEP utilization within this demographic. Participants displayed diverse views on their HIV risk, with some perceiving low susceptibility due to factors like having a single sexual partner or engaging exclusively in penile-vaginal intercourse. Post-release, inmates expressed that access to PrEP and testing was restricted due to inadequate healthcare, encompassing a lack of health insurance, difficulties in transportation, and a limited number of physicians offering PrEP to formerly incarcerated patients. Additionally, this underscores the importance of educating this community about the advantages of PrEP post-release, along with raising awareness about their potential vulnerability to acquiring HIV following incarceration.

Background:

The purpose of this study was to evaluate Pre-exposure Prophylaxis (PrEP) interest, knowledge, and utilization among recently incarcerated men. Furthermore, this study aims to identify barriers to PrEP education and access, related sexual health needs, and competing needs during re-entry, such as housing and employment, for study participants.

Methods:

The study utilized semi-structured individual interviews that aimed to acquire insight into barriers and facilitators to PrEP knowledge and utilization. The interviews were transcribed and subjected to thematic coding analysis, revealing several overarching themes.

Results:

The expression of PAS200 IL-27 in E. coli cells posed challenges, leading us to resort to mammalian cell expression using a commercial kit. Purification optimizations mirrored those employed with E. coli cells, with the exception of employing a different detergent while adhering to similar principles. Our results revealed a low protein yield, albeit sufficient for further analyses. Utilizing PierceTM BCA Protein Assay Kits, we determined a protein concentration of 600 g/ml, indicating successful expression and purification. This concentration aligns well with our expectations, signifying the effectiveness of the mammalian cell expression system and the purification strategy employed.

Conclusions:
Many participants expressed that PrEP adoption post-release was not a priority, and that issues like housing and employment took precedent over healthcare concerns. Moreover, participants faced restricted access to HIV testing both during incarceration and post-release, highlighting the imperative for greater PrEP utilization within this demographic. Participants displayed diverse views on their HIV risk, with some perceiving low susceptibility due to factors like having a single sexual partner or engaging exclusively in penile-vaginal intercourse. Post-release, inmates expressed that access to PrEP and testing was restricted due to inadequate healthcare, encompassing a lack of health insurance, difficulties in transportation, and a limited number of physicians offering PrEP to formerly incarcerated patients. Additionally, this underscores the importance of educating this community about the advantages of PrEP post-release, along with raising awareness about their potential vulnerability to acquiring HIV following incarceration.

Translational / Human Health Impact:
Increasing knowledge of PrEP among the incarcerated population, leading to the increase of PrEP utilization and reducing HIV transmission.

Acknowledgements/Funding Sources:

Poster #: 19

Identifying the Genetic Basis of Mental Disorders in Individuals of African Ancestry

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General Category: Health and Disease

Abstract:

Neuroticism is a negative personality trait that is accessed using the 12 items of the neuroticism scale from the Eysenck Personality Questionnaire-Revised Short Form (EPQ-R-S). It is genetically correlated with disorders like schizophrenia, major depressive disorder, and bipolar disorder. Given the differences in population genetic structure between European and African populations, it is imperative to investigate whether non-European populations can already start benefiting from the results uncovered in large-scale European studies. We performed a GWAS (Genome-Wide Association Study) of Neuroticism in three (3) non-European populations from the UK biobank (Africans-AFR, East-EAS, and South Asians-SAS), and identified the most significantly associated variants and genes using post-GWAS gene prioritization methods. We also conducted GWAS on 12 neuroticism items and observed replicable variations in genetic signals between items. Here, we report top signals in chromosomes 5 (rs115795374; p = 5.939e-08), 20 (rs6046438; p = 8.063e-07), and 12 (rs10492228; p = 7.123e-07) mapping to genes COL23A1, RIN2, and HAL in AFR, EAS, and SAS respectively. The COL23A1 gene has been previously reported as being significantly associated with cannabis dependence measurement as seen in the GWAS catalog. We also replicated these signals in already established large-scale GWAS for neuroticism, hence assessing the transferability of results. In the trans-ethnic meta-analysis including the largest European GWAS, we found the most significant hits in chromosome 17 corresponding to the MAPT gene. This points to the large sample size gap between European and non-European populations as driving the GWAS results, hence, begging the need for more inclusion and recruitment of underrepresented populations to boost computational power. These discoveries significantly advance the understanding of neuroticism in non-European populations and provide specific leads for functional follow-up experiments. It also aids the harnessing of diverse linkage disequilibrium structures in fine-mapping and identifying novel loci that are otherwise not discoverable in single studies.

Background:

Neuroticism is a personality trait characterized by negative emotionality and is accessed using the 12 items of the neuroticism scale from the Eysenck Personality Questionnaire-Revised Short Form (EPQ-R-S). It is genetically correlated with disorders like schizophrenia, major depressive disorder, and bipolar disorder; however, these findings are largely Eurocentric. Given the differences in population genetic structure between European and African populations, it is imperative to investigate whether non-European populations can already start benefiting from the results uncovered in large-scale European studies.

Methods:

Students can either apply for an apprenticeship program, continue with their current employment, or apply to other CHW opportunities throughout the state.

Results:

The interest in the program was greater than expected causing a long wait list.

Conclusions:

This points to the large sample size gap between European and non-European populations as driving the GWAS results, hence, begging the need for more inclusion and recruitment of underrepresented populations to boost computational power. These discoveries significantly advance the understanding of neuroticism in non-European populations and provide specific leads for functional follow-up experiments. It also aids the harnessing of diverse linkage disequilibrium structures in fine-mapping and identifying novel loci that are otherwise not discoverable in single studies.

Translational / Human Health Impact:
The translational impact of this study lies in its potential to translate genetic insights into tangible improvements in mental health outcomes for diverse populations. By identifying specific genetic markers linked to neuroticism in non-European groups, the research paves the way for developing targeted interventions, diagnostics, and therapeutic strategies tailored to the unique genetic landscapes of these populations.

Acknowledgements/Funding Sources:
Members of the Paschou Lab, Purdue University, West Lafayette, Indiana (Dr. Topaloudi Apostolia, Dr. Jain Pritesh, Yin Jin, Sudhanshu Shekhar, Yuxin Guo, Guangxin Chen, Qingyi Zhong

Poster #: 20

Characteristics associated with access to kidney transplantation services in the Ohio River Valley

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General Category: Health and Disease

Abstract:

Background:
For patients with end stage kidney disease (ESKD), demographic and socioeconomic characteristics affect access to kidney transplantation services. End stage renal disease Network 9, of the Ohio River Valley, is one of the 13 networks which had reduced waitlisting for Black patients compared to White non-Hispanic patients.1 Additional research has shown that African American patients residing in Indiana, Kentucky, and Ohio had significantly longer time on the waitlist compared to white patients, and this time was significantly longer than the U.S. overall time on the waitlist.2 Due to the known racial disparities in access, this study further investigated social disparities in access to kidney transplantation in this region. The objective of this study was to describe the medical and non-medical factors associated with referral, evaluation start, and waitlisting among patients with ESKD in the Ohio River Valley (Network 9).

Methods:
To identify patients with ESKD in Network 9, United States Renal Data System (USRDS) data were linked to referral and evaluation data from n=4 transplant centers contributing to the Early Steps to Transplant Access Registry (E-STAR), as well as neighborhood-level characteristics from the 2021 American Community Survey. Adult patients residing within Network 9 (Indiana, Kentucky, and Ohio; Figure 1) at dialysis start among n=680 dialysis facilities from January 2016-June 2020 (followed through June 2021) were assessed.

Outcomes assessed were: referral to a contributing transplant center among dialysis patients (Figure 2, step 3), transplant evaluation start among referred patients (Figure 2, step 4), and waitlisting among patients who started evaluation (Figure 2, step 6). Multivariable logistic regression models were utilized to examine the association between demographic, clinical, and socioeconomic factors and each outcome.

Results:
During the study period, there were 38,944 incident dialysis patients in Network 9, of which 8,824 were referred (4,674 [12%] referred within 1 year) to a contributing transplant center. Of the 8,824 referred patients, 3,955 started evaluation for transplant (3,265 [37%] within 6 months of referral). Of the 4,362 evaluated patients, 1,133 were waitlisted for transplant (688 [26%] waitlisted within 6 months of evaluation start). Factors contributing to increased odds of not being referred by 1 year after dialysis start, in the adjusted analysis, included patient age >70 (OR=0.53, 95% CI 0.39-0.73) vs. younger age, and patients with unknown (OR=0.49, 95% CI 0.40-0.60) or no insurance (OR=0.28, 95% CI 0.19-0.41) vs. private insurance. Factors contributing to increased odds of being referred by 1 year were Hispanic ethnicity (OR=1.42, 95% CI 1.06-1.91) vs. white race and ZIP code-level poverty >20% (OR=1.25, 95% CI 1.00-1.57) vs. <20%.

Factors contributing to increased odds of not having a transplant evaluation within 6 months of referral were age >70 (OR=0.49, 95% CI 0.36-0.68) vs. younger age; Black race (OR=0.85, 95% CI 0.74-0.98) vs white race; Medicaid (OR=0.47, 95% CI 0.38-0.59), Medicare (OR=0.73, 95% CI 0.63-0.84), unknown insurance (OR=0.78, 95% CI 0.64-0.96), or no insurance (OR=0.30, 95% CI 0.20-0.46) vs. private; and middle MHI tercile (OR=0.81, 95% CI 0.71-0.93) vs. high MHI tercile. Factors with increased odds of

starting evaluation within 6 months were residing in small rural (OR=1.41, 95% CI 1.15-1.74) or isolated rural towns (OR=1.26, 95% CI 1.05-1.51) vs. urban areas. Factors contributing to lower odds of waitlisting 6 months after evaluation start included age >70 (OR=0.45, 95% CI 0.25-0.80) vs. younger age, female vs. male sex (OR=0.74, 95% CI 0.60-0.92), and Medicaid (OR=0.39, 95% CI 0.24-0.63) or Medicare (OR=0.61, 95% CI 0.49-0.77) vs. private insurance.

Conclusions:
Among incident ESKD patients referred to a transplant center in Network 9, age, sex, race, insurance status, MHI, and rurality were associated with delayed access to kidney transplantation services. Understanding patient characteristics affecting access to transplantation is an essential step in developing tailored interventions and targeting populations for improving equity in access.

Limitations: 4 out of 14 transplant centers in Network 9 contribute to E-STAR and our analysis is reflective of those 4 centers. Further, reason for referral/no referral was not available (e.g. some patients were likely not medically eligible for referral).

Translational / Human Health Impact:
Understanding patient characteristics affecting access to transplantation is an essential step in developing tailored interventions and targeting populations for improving equity in access.

Acknowledgements/Funding Sources:
Acknowledgements: The research was supported by CK's T32 postdoctoral fellowship in the IUSM Division of Nephrology and RP's RO1, The RaDIANT National Expansion Study (U01MD010611).

Poster #: 21

Patient's Experiences of Pregnancy Loss in Indiana

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General Category: Health and Disease

Abstract:

Nearly 1 in 5 pregnancies in the United States end in miscarriage each year. Despite how common it is, there is a dearth of research, particularly in the US context that centers patients' miscarriage experiences. We aimed to address this gap. Methods: We recruited people living in Indiana who have experienced a miscarriage since 2018 and sought related medical care. Using a guide developed specifically for this study, we conducted 21 in-depth interviews. We transcribed all interviews and carried out content and thematic analysis. Findings: In general, participants reflected negatively on the care they received during their miscarriage; many participants were referred to the emergency department (ED) when they began to experience bleeding, even if it was not medically necessary. Most described their experiences at the ED as traumatic, expensive, and sometimes inhumane as their miscarriage was trivialized by providers, especially if it occurred in early pregnancy stages. Inconsistent with standard practice, most participants were not offered the complete range of options to manage their miscarriage. Despite its commonality, the vast majority of our participants described their miscarriage experience as lonely and isolating. Consistently, participants wanted providers to show more empathy and sensitivity in their communication manner in relation to the miscarriage. Additionally, participants expressed a desire for more information regarding pain management, expectations during the miscarriage process, and resources for emotional support. Recommendations: Identifying options for miscarriage care and support outside of emergency departments appears warranted, as does working with clinicians who regularly interact with pregnant people to facilitate giving patients up-to-date, evidence-based information. Training providers on the use of patient centeredness can improve patients care experiences. Normalizing conversations about pregnancy loss could be helpful.

Background:

Despite how common miscarriage is, there is a dearth of research, particularly in the US context, that centers patients' miscarriage experiences, including their experiences with the health care system.

Methods:

We recruited people living in Indiana who have experienced a miscarriage since 2018 and sought related medical care. Using a guide developed specifically for this study, we conducted 21 in-depth interviews. We transcribed all interviews and carried out content and thematic analysis.

Results:

In general, participants reflected negatively on the care they received during their miscarriage; many participants were referred to the emergency department (ED) when they began to experience bleeding, even if it was not medically necessary. Most described their experiences at the ED as traumatic, expensive, and sometimes inhumane as their miscarriage was trivialized by providers, especially if it occurred in early pregnancy stages. Inconsistent with standard practice, most participants were not offered the complete range of options to manage their miscarriage. Despite its commonality, the vast majority of our participants described their miscarriage experience as lonely and isolating. Consistently, participants wanted providers to show more empathy and sensitivity in their communication manner in relation to the miscarriage. Additionally, participants expressed a desire for more information regarding pain management, expectations during the miscarriage process, and resources for emotional support.

Conclusions:

Lack of information about miscarriage implies that many patients experiencing miscarriage are sent to the Emergency Department event when it is not necessary. This can have negative implications for people experiencing miscarriage, and for the healthcare system.

Translational / Human Health Impact:
Identifying options for miscarriage care and support outside of emergency departments appears warranted, as does working with clinicians who regularly interact with pregnant people to facilitate giving patients up-to-date, evidence-based information. Training providers on the use of patient centeredness can improve patients care experiences. Normalizing conversations about pregnancy loss could be helpful.

Acknowledgements/Funding Sources:
This project was funded with support from Dr. LaRoche's research budget, the Purdue University Women's Global Health Institute, the Indiana Clinical and Translational Sciences Institute, and by Award Number UL1TR002529 from the National Institutes of Health, National Center for Advancing Translational Sciences, Clinical and Translational Sciences Award. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

Poster #: 22

Glucose, glutamine, and fatty acids are utilized differently in breast cancer cells that preferentially metastasize to lung or liver.

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General Category: Health and Disease

Abstract:

Metastasis is the primary cause of breast cancer-related deaths. We investigated whether utilization of different energy substrates supports metastasis to specific distant sites. Utilizing a breast cancer metastatic model that either preferentially metastasizes to the lung (metM-WntLung cells; MLg) or liver (metM-WntLiver cells; MLr), we measured the uptake of radiolabeled substrates, 13C-metabolic flux, and protein expression of metabolic enzymes to compare energy metabolism between cell lines. Results show that 14C-glucose uptake is similar, but mRNA abundance of hexokinase, the initial rate-limiting step in glycolysis, was 22% higher in MLg. This is consistent with higher 13C6-glucose flux into glycolytic metabolites pyruvate and lactate in MLg. Interestingly, high glucose (25 mM) exposure reduced viability of MLr by 39% suggesting MLg's better adaptability to glucose. Also, 14C-glutamine uptake is 27% higher in MLg, consistent with increased mRNA abundance of glutamine catabolizing enzymes, glutamate synthase and dehydrogenase, and higher 13C5-glutamine flux into the tricarboxylic acid cycle as α-ketoglutarate (18%) compared to MLr. However, high glutamine (4 mM) exposure increased cell growth of MLr by 20% suggesting MLr's adaptability to glutamine. Furthermore, 14C-palmitate uptake is similar, but fatty acid synthesis utilizing both 13C6-glucose and 13C5-glutamine is higher in MLg. Inhibition of fatty acid synthesis and oxidation reduced cell growth of MLg by 11% and 21%, respectively, compared to MLr, suggesting MLg relies on increased fatty acid metabolism. Overall, we showed that breast cancer cells with preferential metastasis to lung and liver exhibit differential energy metabolism which may support their successful metastasis to these distant sites.

Background:

Metastasis is the primary cause of breast cancer-related deaths. We investigated whether utilization of different energy substrates supports metastasis to specific distant sites.

Methods:

Utilizing a breast cancer metastatic model that either preferentially metastasizes to the lung (metM-WntLung cells; MLg) or liver (metM-WntLiver cells; MLr), we measured the uptake of radiolabeled substrates, 13C-metabolic flux, and protein expression of metabolic enzymes to compare energy metabolism between cell lines.

Results:

Results show that 14C-glucose uptake is similar, but mRNA abundance of hexokinase, the initial rate-limiting step in glycolysis, was 22% higher in MLg. This is consistent with higher 13C6-glucose flux into glycolytic metabolites pyruvate and lactate in MLg. Interestingly, high glucose (25 mM) exposure reduced viability of MLr by 39% suggesting MLg's better adaptability to glucose. Also, 14C-glutamine uptake is 27% higher in MLg, consistent with increased mRNA abundance of glutamine catabolizing enzymes, glutamate synthase and dehydrogenase, and higher 13C5-glutamine flux into the tricarboxylic acid cycle as α-ketoglutarate (18%) compared to MLr. However, high glutamine (4 mM) exposure increased cell growth of MLr by 20% suggesting MLr's adaptability to glutamine. Furthermore, 14C-palmitate uptake is similar, but fatty acid synthesis utilizing both 13C6-glucose and 13C5-glutamine is higher in MLg.

Inhibition of fatty acid synthesis and oxidation reduced cell growth of MLg by 11% and 21%, respectively, compared to MLr, suggesting MLg relies on increased fatty acid metabolism.

Conclusions:
Overall, we showed that breast cancer cells with preferential metastasis to lung and liver exhibit differential energy metabolism which may support their successful metastasis to these distant sites.

Translational / Human Health Impact:
We found that metastasizing cancer cell that metastasizes to the lung and liver utilize different metabolic pathways to successfully colonize distant sites. Thus, inhibiting one pathway is not sufficient to prevent metastasis. Our work is important because it provide basis on developing agents against specific but multiple targets. Our laboratory is interested on working with Vitamin D and positive results on this would ensue reconsideration of vitamin D as a potential anti-cancer agent and not just a bone-health related vitamin.

Acknowledgements/Funding Sources:
We acknowledge the support from Purdue University Institute for Cancer Research, Women's Global Health Institute and National Institutes of Health R01CA232589 and R01A271597.

Poster #: 23

Development of a novel diagnostic method, loop-mediated isothermal amplification (LAMP), for Balamuthia mandrillaris.

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General Category: Health and Disease

Abstract:

Balamuthia mandrillaris is a free-living amoeba that can cause severe central nervous system (CNS) infection and skin lesions, leading to a high mortality rate (~90%). The current diagnostic methods for this amoeba have many limitations and are not very sensitive and specific. We developed and evaluated a novel loop-mediated isothermal amplification (LAMP) assay targeting the 18S rRNA gene for B. mandrillaris. LAMP assays detected 5 different B. mandrillaris strains, no cross-reactivity with the DNA of other free-living amoeba, selected protozoa or bacteria. The lower limit of detection for a positive signal was 10fg/µL of extracted DNA, 10 original trophozoites, or 1 heated trophozoite/100 µL of media, which showed 10~100 fold higher sensitivity than PCR. Due to its simplicity, speed, and high sensitivity, the LAMP method described here might be useful for quickly detecting and diagnosing B. mandrillaris, particularly in resource-poor areas.

Background:

B. mandrillaris is a free-living amoeba (FLA), which is most commonly isolated from soil and dust sources. It can enter through breaks or lesions in the skin or via inhalation into the lungs, from here Balamuthia then causes systematic infection. Once B. mandrillaris infects the central nervous system (CNS) and the brain, it will cause Balamuthia amebic encephalitis (BAE), then ultimately kill the patient with a mortality rate of ~90%. As a novel pathogen, B. mandrillaris is still little known, also with poor diagnostics and worse therapeutics, which all contribute to the alarmingly high mortality rate. Current diagnosis of BAE is challenging and usually postmortem, because symptoms of the early infection may be subtle or nonspecific. Hence, we aim to develop a new diagnostic method, LAMP, for B. mandrillaris, which will provide specific and timely detection to increase diagnostic accuracy and cure rate.

Methods:

Designed the primers that targeted different genes for the LAMP assay for B. mandrillaris, and then tested the specificity by amplifying the outer primers to select the primer. Then the LAMP conditions were optimized by different concentrations of primer, temperature, and incubation time, with each parameter optimized individually and rigorously repeated. Specificity testing involves comparing DNA templates from other free-living amoeba, protozoa and bacteria. To test the sensitivity, we compared the lower limit of detection using different templates of B. mandrillaris, including extracted DNA, original trophozoites and heated trophozoites in the LAMP assay and conventional PCR.

Results:

We developed a novel LAMP assay, that targeted 18S rRNA, for B. mandrillaris. The optimized condition was 1x primers (0.16 µM F3/B3, 1.28 µM FIP/BIP and 0.32 µM LF/LB) at 65°C for 30 min. This LAMP assay can detect 5 different B. mandrillaris strains, and no cross-reactivity with the DNA of other free-living amoeba, selected protozoa or bacteria, which showed the specificity. The lower limit of detection for a positive signal was 10 fg/µL of extracted DNA, 10 original trophozoites, or 1 heated trophozoite/100 µL of media, we show 10~100-fold greater sensitivity than traditional PCR method.

Conclusions:

In conclusion, we successfully developed a LAMP assay for B. mandrillaris. This assay showed good specificity and sensitivity, and it just needs a very short time to diagnose. It could be used away from the laboratory and in environments where access to expensive equipment is not possible, since it does not or

just requires minimal equipment for both DNA extraction and subsequent LAMP analysis. Such a test might help to apply the appropriate treatment in clinical practice, and increase the cure rate.

Translational / Human Health Impact:
A major problem of BAE is that symptoms of the disease are similar to and often misdiagnosed as bacterial meningoencephalitis or tumors, resulting in incorrect management. Also, there is a short time from the symptoms occurring to death, so the diagnosis of this pathogen must be accurate and rapid while patients are still alive. However, the diagnostic methods that have been used have different limitations. Our LAMP assay can diagnose B. mandrillaris rapidly, accurately and easily. So we believe the patients can get the early chemotherapeutic intervention after the correct diagnosis, which would have a significant impact on patient survivability and human health.

Acknowledgements/Funding Sources:

Poster #: 24

In-utero detection and long-term management of congenital hearts defects – bridging the expertise gap.

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General Category: Health and Disease

Abstract:

Indiana ranks 42nd in the US for infant mortality rates, with congenital heart defects (CHDs) as a significant contributor (more than 1 in 20). Despite medical advancements, detecting CHDs accurately remains challenging, especially in rural community hospitals where detection rates can be as low as 13%. Socioeconomic factors like income, education, insurance, and race exacerbate this challenge, leading to delays in diagnosis beyond 24 weeks gestational age, hindering surgical planning and long-term management. Portable handheld ultrasound (PHUS) devices, compatible with smartphones and tablets, present an opportunity to bring high-quality imaging to underserved areas. However, limited expertise and lack of analysis tools may hinder widespread adoption of this technology. To bridge this gap, we developed a novel fetal echocardiography analysis platform capable of automated CHD diagnosis and assessment during pregnancy as well as continued imaging after birth into infancy. Our platform aims to improve detection rates, especially in non-specialist settings, facilitating early intervention planning and better outcomes for infants with CHDs. Furthermore, widespread adoption of such tools could enable population-level CHD screening, reducing the burden of undiagnosed cases.

Background:

We offer fully automated tools to analyze portable handheld ultrasound (PHUS) imaging, aiming to address gaps in access to clinical-grade imaging, specialist training, and informative imaging analysis.

Methods:

This work presents two studies conducted in a clinical setting using standard echocardiogram imaging. The first study examines changes in ventricle morphology and blood flow patterns throughout the perinatal period in healthy hearts and those with single ventricle (SV) conditions. The second study focuses on differences in blood flow patterns between healthy hearts and those with tetralogy of Fallot (TOF), both involving children aged 12 years old. In both studies, we utilized our in-house developed codes for measuring ventricular volume, strain, and flow hydrodynamics.

Results:

Our findings from the perinatal period study reveal that healthy bi-ventricular hearts exhibit smoother blood flow patterns compared to SV hearts, attributed to distinct ventricle shapes. Additionally, these morphological disparities, along with increased pressure effects from systemic circulation on SV hearts, necessitate higher pressures for blood filling and ejection, leading to greater energy loss across the flow. Similar trends were observed in the study of TOF hearts, with more disrupted flow patterns associated with higher pumping pressures.

Conclusions:

Advanced echocardiography analysis tools can detect differences in congenital heart defect (CHD) hearts during pregnancy and infancy. By integrating these tools with PHUS devices, we propose a novel approach to provide clinically relevant tools in regions with limited access, empowering non-specialists to improve CHD detection and management capabilities.

Translational / Human Health Impact:

This work has the potential impact of improving diagnosis of congenital heart defects in areas with limited access to resources, improving infant mortality rates

Acknowledgements/Funding Sources:
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Poster #: 25

Novel Echocardiogram Analysis for Mortality Prediction in Pediatric Sepsis

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General Category: Health and Disease

Abstract:

Sepsis arises as a result of the body's immune system responding exaggeratedly to an infection. Annually, in the USA, severe sepsis and septic shock incidence are up to 300 cases per 100,000 people. Mortality ranges from as low as 4% to as high as 50%, depending on multiple factors. Sepsis in pediatric patients presents a significant challenge, with cardiovascular dysfunction contributing substantially to mortality. While echocardiography aids in identifying sepsis-induced myocardial dysfunction (SIMD), traditional measures have some limitations. We conducted a retrospective cohort study from 2017-2022 on 54 pediatric sepsis patients (45 recovered, 9 deceased) admitted to a PICU. We utilized semi-automated algorithms to analyze echocardiogram indices for both the left and the right heart. Our work aimed to determine if echocardiogram indices obtained using our algorithms are associated with mortality in pediatric sepsis. Strain and diastolic indices were hypothesized to have stronger associations with mortality. Our findings underscore the feasibility of using novel algorithms for clinically relevant echocardiogram analysis in pediatric sepsis. Our study revealed impaired right ventricular global longitudinal strain (RV GLS) and left ventricular (LV) GLS were significantly associated with higher in-hospital mortality. Traditional systolic indices were not associated with mortality in this cohort. Our study suggests that abnormal strain echocardiography may serve as a prognostic indicator in pediatric sepsis, aiding in risk stratification. Notably, our work provides evidence of a strong association between abnormal right ventricle function and mortality in children with sepsis. This approach holds promise in enhancing patient care and outcomes, potentially preventing fatalities.

Background:

Sepsis is a condition of inappropriate immune response to infection. This is one of the leading causes of mortality and morbidity worldwide. In the United States, about 1.7 million people get sepsis, and nearly 270,000 of them die from it.The objective of our work is to determine if echocardiogram indices obtained using our algorithms are associated with mortality in pediatric sepsis.

Methods:

A retrospective cohort study of 54 children admitted to the PICU with sepsis. Three user inputted points outlining each heart chamber were applied to existing echocardiograms. Novel algorithms then computed the relevant echocardiographic indices. We examined right and left sided indices for systolic and diastolic function as well as strain.

Results:

Echocardiogram biomarkers of right sided chambers of heart appear to be more predictive of both mortality and morbidity.

Conclusions:

1.Our novel algorithms show potential clinical utility in stratifying high-risk pediatric patients with sepsis . 2.Abnormal strain biomarkers are associated with worse survival in pediatric patients with sepsis. 3.The right ventricle showed a more robust association with mortality than the left ventricle.

Translational / Human Health Impact:

We aimed to employ our novel algorithms designed for automatically extracting echocardiographic indices from all four chambers, eliminating the need for advanced interpretation by cardiologists. Exploring the connection between sepsis and cardiovascular biomarkers offers a pathway to enhance support and rehabilitation for those affected by sepsis. We firmly believe that by effectively managing the cardiac function of sepsis patients, it is possible to achieve improvement in overall treatment results.

Acknowledgements/Funding Sources:

Poster #: 26

Prolyl Isomerase PIN1 Modulates Oncogene Induced Senescence by Regulating PML-Nuclear Body Dynamics

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General Category: Health and Disease

Abstract:

Mammalian cells have developed intrinsic mechanisms to halt their replication, and enter to a state of permanent cell cycle arrest in response to the activation of oncogenes. This process is known as Oncogene induced senescence (OIS). The OIS processes is intricate, controlled via the differential expression of a multitude of nuclear proteins, including the Prolyl isomerase Pin1 protein. Pin1 has been shown to be involved in modulating tumor-suppressor processes in cancer cells. However, the roles of driving OIS, however, are not fully understood. To study OIS, IMR90 human fibroblasts (ATCC CCL-186) were transduced with the inducible protein ER:RasG12V, shPIN1 and shScramble lentivirus. OIS was induced with 100nM (Z)-4-Hydroxytamoxifen (4-OHT) for 0, 2, 4 or 6 days, and their phosphoproteome was analyzed with the Orbitrap Fusion Lumos mass spectrometer.

Our results show that Pin1 substrate motifs were preferentially phosphorylated during OIS. Consistent with these observations, we observed a two-fold increase in Pin1 levels upon Ras activation, which led us to hypothesize that Pin1 may act as a modulator for cell senescence. Thus, we performed a Pin1 knock down (KD) in IMR90-ER:RasG12V background cells. Our results show that Pin1 knockdown leads to the bypass of senescence and loss of the OIS phenotype in IMR90 cells. We also found that Pin1 regulates the subnuclear PML-NB structures, which play important roles in tumor suppression. Furthermore, we showed that Stat3, and other PML-NB interactor proteins, was significantly upregulated in shPin1 cells during OIS, while senescence markers, such as p21, are significantly downregulated in response to Pin1 knock-down. Our study showcases a combination of proteomics, phosphoproteomics, kinomics and immunocytochemistry studies to discuss new evidences suggesting that Pin1 acts as a tumor suppressor in response to oncogenic Ras activation.

Background:

Cellular senescence can be triggered by several stressors, including DNA damage, oxidative stress, and the activation of proto-oncogenes into oncogenes. Oncogene induced senescence (OIS) is the process in which cell cycle arrest is achieved upon oncogenic signaling, leading to the activation of key tumor suppressor proteins, and activating a myriad of signaling cascades. Consequently, OIS leads to a rearrangement of the cellular proteome in a complex process, that entails the interplay of several protein regulators, most of which are still unknown. Such players include the Prolyl isomerase Pin1 protein. Pin1 acts as a cis/trans isomerase that acts as a key regulator of protein-protein interactions, localization, and function. However, the specific roles that Pin1 exerts during OIS is still unclear. In this study, we investigated the phenotypic consequences of Pin1 regulation in response to Ras activation.

Methods:

IMR90 human diploid fibroblasts (ATCC CCL-186) were transduced with ER:RasG12V, shPIN1 and shScramble lentivirus. OIS was induced via 100nM (Z)-4-Hydroxytamoxifen (4-OHT) treatment for 0, 2, 4 or 6 days. At each time point, cells were harvested, and their nuclei extracted. Nuclear proteins were digested with Trypsin (Sigma-Aldrich, USA) and peptides were desalted using C18 spin columns (Thermo Fisher Scientific, USA) before the enrichment of phosphopeptides using the PolyMaC spin tips. Samples were then analyzed with the Orbitrap Fusion Lumos mass spectrometer. Data was analyzed with the MaxQuant and Perseus software.

Results:

Our phosphoproteomics results highlighted a significant increase in protein phosphorylation at day 2 of Ras activation, and their phosphorylation levels remained relatively unchanged. Phosphosite motif analysis suggested that a majority of differentially regulated phosphosites during OIS were ERK1/2 target sites. Interestingly, phosphorylation at these motifs are recognized by the Prolyl Isomerase Pin1 protein, which isomerizes phosphorylated proteins and regulates their localization, function and interactions. Thus, to explore the roles of Pin1 in OIS, we performed a knockdown of endogenous Pin1 in senescent IMR90-ER:RasG12V background cells followed my LC-MS/MS analysis. Our results show that Pin1 acts as key regulator of cellular senescence, and it is necessary for the induction of OIS, indicated by a lack of ß-Galactose enzyme activity and downregulation of important tumor suppressor proteins, including p53, p21 and p16. Furthermore, our findings suggest that Pin1 may exert its tumor suppressor functions via the modulation of PML-nuclear bodies (PML-NBs). PML-NBs are subnuclear structures that play pivotal roles in cellular senescence. Our data show that cells depleted of Pin1 have a decreased number of PML-NBs, despite an increase in PML protein levels. Thus, our results suggest a potential mechanism by which Pin1 modulates OIS.

Conclusions:
Our data provides new evidence that Pin1 acts as a tumor suppressor in fibroblast cells during OIS.

Translational / Human Health Impact:
Our results show for the first time that Pin1 acts as a tumor suppressor in the context of OIS, thus opening new avenues for the understanding and development of new strategies to treat cancer.

Acknowledgements/Funding Sources:
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Poster #: 27

Delayed working memory paradigm in a freely moving environment shows deficits in the learning of FX mice.

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General Category: Health and Disease

Abstract:

Autism spectrum disorder (ASD) is a neurodevelopmental disorder that widely affects information processing in the brain resulting in deficits in learning and memory. One of the most prevalent forms of ASD is Fragile X Syndrome (FXS), which results from a mutation in the FMR1 protein. Previous studies have shown alterations in cell morphology, synaptic connections, and neural circuits pertaining to sensory perception in FXS model systems. Consistent with this, our lab has identified significant differences in the visual response of FX mice to a passive visual perceptual experience paradigm, specifically regarding evoked low frequency theta (4-8 Hz) oscillations in the primary visual cortex (V1). These oscillations were attenuated in duration, amplitude, and frequency, suggesting these oscillations are a possible mechanism for visual working memory, and their impairment leads to a learning disability. However, currently, there is no widely accepted working memory behavior paradigm in mice. Here, we describe a new modified working memory paradigm based on a classical go/no-go visual discrimination task in mice. We found that across the multiple behavior paradigms, both WT and FX mice were able to show proper discrimination of the visual stimuli. However, we found that the FX mice consistently required more training days and reached lower overall training scores compared to the WT. Additionally, using DeepLabCut software we discovered that FX mice demonstrated distinct movement patterns consistent with impaired memory during freely moving behavior. Our findings highlight the efficacy of this novel method for studying working memory in mice. By employing this approach, we can gain deeper insights into the specific impairments associated with FX mice, shedding light on the underlying mechanisms and potential therapeutic targets for addressing working memory deficits in this neurodevelopmental disorder.

Background:

Autism spectrum disorder (ASD) is a neurodevelopmental disorder that widely affects information processing in the brain resulting in deficits in learning and memory. One of the prevalent forms of ASD is Fragile X Syndrome (FXS), which results from a mutation in the FMR1 protein (FMRP). Previous studies have shown alterations in cell morphology, synaptic connections, and neural circuits pertaining to sensory perception in FXS model systems. Consistent with this, our lab has identified significant differences in the visual response of FX mice to a visual perceptual experience paradigm. This study looks to shed light on how these deficits translate to behavior and looks at potential avenues to rescue learning impairments.

Methods:

Mice models of Fragile X Syndrome are used to elucidate behavioral deficits in a visual working memory task using freely moving behavior chambers and GO/NO-GO operant conditioning paradigm.

Results:

Fragile X mice show significant learning deficits in a visual working memory task in several aspects of their behavior. A conditional rescue of a specific subset of neurons shows improvements in these impairments and provides a potential avenue for therapeutics.

Conclusions:

Conditionally rescuing a subset of neurons involved in the visual working memory circuit translate to behavior and show improvements in learning and memory in Fragile X mice. This study characterizes specific aspects of behavioral differences between Fragile X and WT mice, while also showing a promising method to improve the existing learning deficits.

Translational / Human Health Impact:
Improvements in the learning and memory of Fragile X mice seen in this study can be potentially translated to Fragile X syndrome and other ASDs in the human community as well. Gene therapy involving the FMR1 protein in neural circuits responsible for various learning tasks might be a potential therapeutic avenue to help aid in learning impairments seen in ASDs.

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Poster #: 28

Age-Dependent changes in mouse brain and liver Lipidomes

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General Category: Health and Disease

Abstract:

Aging is a major risk factor associated with cancer and neurological diseases, including Alzheimer's disease (AD) and Parkinson's disease (PD). However, the mechanisms that underpin the process of aging are not well understood. Like genes and proteins, lipids play key structural, regulatory, and signaling roles. Hence, profiling lipid changes in different organs due to aging process provides useful information for understanding the molecular mechanisms underlying this process and for developing treatments or cures for age-related diseases. Despite their significance, still, very little is known about the composition and age-dependent changes of lipids in the brain and liver, the two most lipid-rich organs after adipose tissues. In this study, we performed exploratory lipidomic analysis of mice brain and liver at different ages via Multiple Reaction Monitoring Mass Spectrometry (MRM-MS) to determine changes in different classes of lipids and correlate the differences in lipid profiles with the age groups. The MRM-MS analysis was performed using ion transitions based on precursor (Prec) and neutral loss (NL) scans obtained from LIPID MAPS database for screening each sample independently for 24 different classes of lipids including different phospholipid classes such as phosphatidylcholines (PCs), phosphatidylethanolamines (PEs), ceramides, di- and tri-acylglycerols, and acylcarnitine. We identified age-dependent changes in different lipids including tri- and di-acylglycerols, phospholipids and ceramides. In our presentation, we will discuss the importance of these lipids in the context of aging and age-related disorders will be discussed.

Background:

Aging is a natural, complicated, and inevitable phenomenon involving various biological mechanisms that lead to the gradual deterioration of physiological functions. Key "pillars" of aging processes have been identified, including inflammation, macromolecular damage, breakdown of proteostasis, epigenetic alterations, and senescent cell accumulation (Kennedy et al., 2014; Lopez-Otin et al., 2013). While there has been significant research on the role of RNAs and proteins in aging, little is known about the role of lipids, that are structural as well as functional moieties of the living cells. Changes in lipid metabolism play an important role in various pathophysiological conditions. Hence our focus in this study was to understand how these lipids change with age in the brain and liver. We performed mass spectrometry-based exploratory lipidomic analysis from three different age groups of mice via Multiple Reaction Monitoring (MRM-MS) and determined the differences in the abundances of different classes of lipids and then correlate these differences with the different age groups.

Methods:

The brain and liver tissues collected from three age groups of mice-young adult (3–5-month-old), middle aged (10–12-month-old) and old-aged mice (19–21-month-old) were homogenized and normalized by protein concentrations. Lipids were extracted by Bligh-Dyer method. Extracted lipids were injected directly without any chromatographic separation into the ESI-source of an Agilent QqQ 6410 mass spectrometer. Targeted analysis was performed by screening the samples for specific ion transitions corresponding to different lipid classes and fatty acid composition based on LIPID MAPS database. Each sample was evaluated for 3246 MRMs from 24 different classes of lipids, with separate injections for each class of lipids.

Results:

The exploratory MRM-MS analysis focused on specific ion transitions corresponding to different lipid classes and fatty acid composition based on LIPID MAPS database, which includes structures and annotations of thousands of biologically relevant lipids. Using MRM-MS profiling without LC, the samples were screened for 3246 MRMs comprising of 24 different lipid classes and fatty acid composition including different phospholipid classes like phosphatidylcholines (PCs), phosphatidylethanolamines (PEs), ceramides, di- and tri-acylglycerols, and acylcarnitines. We identified 576 MRMs in the brain and 1254 MRMs in the liver. Among these, five MRMs were significantly changing in the brain, and 105 MRMs were changing in the liver, across all three age groups.

In the brain, phosphatidylcholines (PCs), phosphatidylethanolamines (PEs) and free fatty acids (FFAs) were among the most abundant classes of lipids, while in the liver, tri- and di-acylglycerols were among the most abundant ones, apart from PCs and FFAs. Statistical analysis revealed age-dependent changes in sphingomyelins, TGs and FFA in the brain, and TGs, DGs, and phospholipids classes in the liver.

Conclusions:
Applying fast MRM-MS technique to screen a wide range of lipid classes, we profiled hundreds of lipids that were altered during the aging process. Given that lipids are vital for various physiological functions including energy homeostasis and cognitive processes, determining their dysregulation with age offers better understanding about age-related pathologies. Our data shed light for understanding the mechanisms underlying age-related diseases and may guide future studies for the development of novel therapeutics.

Translational / Human Health Impact:
The study reveals potential new lipid biomarkers of aging that can be targeted for developing approaches to address aging and age-related disorders, specifically neurological disorders like Alzheimer's and Parkinson's disease.

Acknowledgements/Funding Sources:
This study was supported in part by the Bindley Bioscience Center and the Purdue COVID Disruption fund to Uma K. Aryal. All the data were collected at the Metabolite Profiling Facility of Bindley Bioscience Center. For more information, contact: uaryal@purdue.edu (Uma K. Aryal).

Poster #: 29

The Impact of Neochords Surgery on Hemodynamic Parameters in Mitigating Mitral Valve Regurgitation

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General Category: Health and Disease

Abstract:

Mitral regurgitation (MR) or mitral insufficiency, is a heart valve disorder characterized by the abnormal leakage of blood from the left ventricle (LV) back into the left atrium (LA) during the systolic phase of the cardiac cycle. Mitral regurgitation (MR) leads to increased heart workload, left ventricle enlargement, pulmonary hypertension, atrial fibrillation, heart failure, reduced oxygenation, and risk of endocarditis. 1 out of 5 heart failure (HF) patients has moderate to severe or severe secondary MR. NeoChords is a device for MV repair, adding new chordae tendineae to help close the MV during systole. Among the surgical techniques available, Neochords implantation is a promising approach; however, its impact on the overall flow patterns within the heart remains insufficiently understood. The hemodynamic parameters such as the Energy Loss, Kinetic Energy and Pressure within the heart are anticipated to have significant alterations following the Neochords surgery. Our study aims to comprehensively assess the alterations in intraoperative flow patterns before and after Neochords surgery to gain insights into the efficacy and functional outcomes of this procedure.By quantifying these flow pattern changes, we can better evaluate the overall success and clinical benefits of Neochords surgery in the management of MV-related pathologies.

Background:

Methods:

An in-house developed algorithm (DoVer) was used to reconstruct flow in the Left ventricle. The velocities are reconstructed using the vorticity-streamfunction relationship. For the BC's the boundaries are segmented using an in-house developed peak-prominence-based method.

Results:

Hemodynamic parameters were evaluated in the left ventricle in a regurgitant heart and are compared pre and post surgery.

Conclusions:

Altered Hydrodynamics were observed Pre and post corrective MV surgery. The hemodynamic parameters can potentially be used as a marker of the regurgitant severity.

Translational / Human Health Impact:

Acknowledgements/Funding Sources:

Poster #: 30

Going with the Flow in Neonatal Peritoneal Dialysis: Low-Cost, Clot Resistant PD Drainage Catheter Development

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General Category: Health and Disease

Abstract:

The kidney is an essential organ for fluid metabolite balance in early life. When neonatal patients are diagnosed with Acute Kidney Injury or End Stage Renal Disease, they commonly undergo Peritoneal Dialysis (PD). PD involves the introduction of a catheter into the peritoneal space, facilitating the filtration and equilibrium of various body metabolites before draining waste as an effluent. These catheters feature a curved shape and side port holes. However, many drainage catheters suffer from occlusion which leads to decreased or blocked flow necessitating the need for extra time to troubleshoot or restart the procedure. There are a couple of reasons for this occlusion including fibrin clot formation or omentum coverage – both of which impede the ability of effluent to drain out of the body. Additionally, current drainage catheters are large and expensive, limiting their use to areas that require low-cost and small devices to be used in neonatal patients. In this work, we seek to implement a new catheter shape and side port design that limits the chance for side port and omentum occlusion – leading to optimized drainage of the peritoneal cavity. To formulate the side port design, we used computer simulations. To validate the catheter shape, we will use a simulated peritoneum and induce fibrin-like clots. This initial phase of the project aims to determine the suitability of the drainage catheter for production and application in neonatal patients requiring a cost-effective bedside peritoneal dialysis solution. Should the findings prove promising, this innovative design has the potential to enhance accessibility to peritoneal dialysis procedures for neonatal patients who are most in need. Ultimately, this work strives to address the challenges associated with occlusion, reduce procedure-related complications, and provide a more viable solution for neonatal healthcare.

Background:

Pediatric patients in low-and-middle-income countries (LMICs) with kidney disease rely on peritoneal dialysis (PD. Due to cost and availability, many patients receive treatment with off-label devices resulting in increased complications. The purpose of this project was to develop a low-cost pediatric drainage catheter for PD and to evaluate and compare the design with an existing device under common failure methods.

Methods:

Catheters were manufactured using a thermoforming method which allowed for the desired shape to be met. COMSOL, a computer simulation software, was used to evaluate the flow patterns of different side port designs. Drainage tests utilizing a false omentum model and simulated clot model were used to evaluate the catheter designs under common failure mode conditions. A control catheter and a novel helix-designed catheter were used in these tests.

Results:

Distribution patterns of flow were graphed. The drainage volume over time was graphed with the two different failure mode conditions. Comparisons were drawn over catheter performance after the devices underwent the failure condition.

Conclusions:

Varied side port diameters distribute flow more evenly and mitigate high-pressure areas, the helix design of the catheter minimizes surface contact with side ports and omentum, and the helix catheter drainage is less affected by occlusion methods. These findings show promise in the potential for a new design of drainage catheter.

Translational / Human Health Impact:
This project aimed to evaluate the viability of a change in catheter design to withstand and improve on addressing common failure modes currently existing in drainage catheters for pediatric patients. It is hoped that this project or work done because of it will positively impact low-to-middle-income countries and their pediatric population who rely on this standard of care. Additionally, if physicians in this area receive training for the use of specific catheters for on-label use, like this potential design, it may lead to fewer complications for patients. This project closely works with Dr. Mignon McCulloch, MD who trains healthcare professionals in low-to-middle-income countries which can lead to lives saved if they have access to the appropriate tools and devices.

Acknowledgements/Funding Sources:
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Poster #: 31

Wireless LED-device for photoinactivation of HT-29 cells

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General Category: Health and Disease

Abstract:

Results show that 14C-glucose uptake is similar, but mRNA abundance of hexokinase, the initial rate-limiting step in glycolysis, was 22% higher in MLg. This is consistent with higher 13C6-glucose flux into glycolytic metabolites pyruvate and lactate in MLg. Interestingly, high glucose (25 mM) exposure reduced viability of MLr by 39% suggesting MLg's better adaptability to glucose. Also, 14C-glutamine uptake is 27% higher in MLg, consistent with increased mRNA abundance of glutamine catabolizing enzymes, glutamate synthase and dehydrogenase, and higher 13C5-glutamine flux into the tricarboxylic acid cycle as α-ketoglutarate (18%) compared to MLr. However, high glutamine (4 mM) exposure increased cell growth of MLr by 20% suggesting MLr's adaptability to glutamine. Furthermore, 14C-palmitate uptake is similar, but fatty acid synthesis utilizing both 13C6-glucose and 13C5-glutamine is higher in MLg. Inhibition of fatty acid synthesis and oxidation reduced cell growth of MLg by 11% and 21%, respectively, compared to MLr, suggesting MLg relies on increased fatty acid metabolism. Overall, we showed that breast cancer cells with preferential metastasis to lung and liver exhibit differential energy metabolism which may support their successful metastasis to these distant sites.

Background:

The long term goal of this research is a new approach to neoadjuvant therapy of cancer that is based on photodynamic therapy. An implanted miniature wireless LED is used to irradiate a deep-seated primary tumor and induce an immunogenic response that will eradicate other tumors or sites of metastases. The implanted LED will be removed during the subsequent surgery. The technology can be used for cancers where neoadjuvant therapy is common, especially breast, esophageal, rectal, pancreatic, bladder, lung, and ovarian cancer.

Methods:

Results:

Conclusions:

This study tested the use of a miniature wireless LED device with a volume of 23 mm3, one of the smallest prototypes to date. The device is wireless powered with RF and emits at 573 nm which can excite Rose Bengal as an effective PS to produce singlet oxygen. Use of the device with monolayer HT-29 cells, and Rose Bengal Diacetate revealed induced cell death with observed morphological changes observed as the formation of protruding membrane bubbles. Annexin V and Propidium Iodide stains in combination with formation of membrane bubbles suggest pyroptosis as major cell death pathway.

Translational / Human Health Impact:

Acknowledgements/Funding Sources:

This work was supported by the NIH and STIR Grant.

Poster #: 32

Genomic and proteomic profiling of Acanthamoeba isolates

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General Category: Health and Disease

Abstract:

Acanthamoeba is amphizoic amoeba majorly responsible for causing Acanthamoeba keratitis (AK) and granulomatous amoebic encephalitis (GAE). The whole genome assembly along with proteomic profiling can help us better understand pathogenic and non-pathogenic Acanthamoeba isolates. Illumina and Nanopore sequencing were performed for keratitis, encephalitis, and non-pathogenic environmental isolates. A hybrid assembly was prepared for the AK and GAE isolates, while only the Illumina reads were utilized for a non-pathogenic environmental isolate. Protein coding genes were identified using the GeneMark-ES program and BLASTx module of Diamond used for gene prediction. Additionally, the Kyoto Encyclopedia of Genes and Genomes annotation and cluster of orthologous group's anno- tation using RPS-blast against the CDD database was performed. Based on the sequencing data analysis, genes including lysophospholipase, phospholipase, S8/S53 peptidase, carboxylesterase, and mannose-binding protein (MBP) were selected as probable pathogenic targets that were evaluated for their relative gene expression in the keratitis and amoebic encephalitis animal model. In addition, liquid chromatography-mass spectrometry (LC-MS/MS) was performed for keratitis, encephalitis, and non-pathogenic environmental isolate. The genome assemblies of 9.67, 8.34, and 8.89 GBs were reported for GAE, AK, and non-pathogenic isolates, respectively. The expression analysis revealed phospholipase, lysophospholipase, and MBP genes to be significantly upregulated during AK while phospholipase, lysophospholipase, S8/S53 peptidase, and carboxylesterase genes were significantly upregulated during GAE in the animal model. The proteomic data revealed differential protein expression in pathogenic versus non-pathogenic isolates. The gene expression data suggests that the selected probable markers could play a role in the contact-dependent and independent mechanisms of Acanthamoeba pathogenesis. In addition, the proteomic profiling of the 3 isolates revealed differential protein expression crucial for parasite growth, survival, and virulence. Our results provide baseline data for selecting possible pathogenic targets that could be utilized for designing knockout experiments in the future.

Background:

Acanthamoeba are amphizoic amoeba majorly responsible for causing Acanthamoeba keratitis (AK) and Granulomatous amoebic encephalitis (GAE). Despite its ubiquitous nature, the frequency of infections is not high, probably due to existence of non-pathogenic isolates. The pathogenesis of Acanthamoeba includes intricate interactions between the organism and the host's immune system. Whole-genome sequencing and an annotated genome assembly can unravel the biological functions. Gene expression and proteomic analysis can provide information on biological processes and aid in the identification of potential genes involved in pathogenicity.

Methods:

Hybrid assembly prepared for the AK (SK_2022b) and GAE (SK_2022a) isolates while only the Illumina reads were utilized for non-pathogenic isolate (SK_2022c). Based on the data analysis, lysophospholipase, phospholipase, S8/S53 peptidase, carboxylesterase, and mannose-binding protein genes were selected as probable pathogenic genes. The relative gene expression was evaluated in the keratitis and amoebic encephalitis animal model induced using keratitis (CHA5), encephalitis (CHA24) and non-pathogenic environmental isolate (CHA36). In addition, liquid chromatography-mass spectrometry (LC-MS/MS) was performed for the three Acanthamoeba isolates and proteins were identified using Proteome Discoverer

2.4. STRING version 11 network was used for the functional network construction of protein-protein interactions (PPIs).

Results:
Hybrid genome of 51MB and 54MB assembled for SK_2022a and SK_2022b. Illumina sequencing generated 59,234,380 reads accounting for a genome of 22MB for SK_2022c. Around 711 genes were exclusively present in the two pathogenic isolates and absent in the non-pathogenic isolate. The genes including phospholipase, lysophospholipase, and mannose-binding were significantly upregulated in the keratitis isolate (CHA 5) during AK in the animal model. In the case of the amoebic encephalitis model, phospholipase, lysophospholipase, S8/S53 peptidase, and carboxylesterase were significantly upregulated in the encephalitis isolate.

Conclusions:
Pathogenic isolates had proteins responsible for cellular functions, intracellular transport, and cell division. Also, cysteine and serine proteases were found upregulated in the two pathogenic isolates known for their role in the degradation of other proteins & peptides. Gene knockout-out experiments of lysophospholipase, phospholipase, S8/S53 peptidase, carboxylesterase, and mannose-binding protein along with the transcriptome data could have provided a better insight into the proteases during the pathogenesis of Acanthamoeba.

Translational / Human Health Impact:

Acknowledgements/Funding Sources:

Poster #: 33

Association between Health Insurance Coverage and Stage of Diagnosis for Cervical Cancer among Women in Indiana from 2011-2019

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General Category: Health and Disease

Abstract:

Introduction – Cervical cancer is one of the most common types of cancer among women. Women diagnosed at earlier stages for cervical cancer had higher relative survival than those diagnosed at later stages. Health insurance status is an important determinant for health outcomes for patients with cancer. This study aims to assess the extent to which health insurance coverage is a contributing factor to the stage of cervical cancer diagnosis. Methods – We examined reported cases of cervical cancer among women (N=2518) using registry data from the Indiana State Department of Health from 2011-2019. Using multinomial logistic regression model, we examined associations of both race/ethnicity and insurance status with stage of diagnosis after adjusting for age at diagnosis. Results –The multivariate analysis showed that women who are uninsured (OR = 2.475) and those who have Medicaid (OR = 2.321) were significantly more likely to be diagnosed at the regional stage than the in-situ stage compared to women with private insurance. Additionally, women who are uninsured (OR = 4.432) and those who have Medicaid (OR = 3.007) were significantly more likely to be diagnosed at the distant stage than in-situ, compared to women with private insurance. Conclusion – The findings show that insurance status is associated with the stage of diagnosis for cervical cancer and detection at regional or distant stages often leads to higher morbidity. Impact – Increased coverage for routine cervical cancer screening and preventive care services is recommended, especially for uninsured women and women with public insurance such as Medicaid or Medicare.

Background:

Whole-genome sequencing and an annotated genome assembly can unravel the biological functions. Gene expression and proteomic analysis can provide information on biological processes and aid in the identification of potential genes involved in pathogenicity.

Methods:

We examined reported cases of cervical cancer among women (N=2518) using registry data from the Indiana State Department of Health from 2011-2019. Using multinomial logistic regression model, we examined associations of both race/ethnicity and insurance status with stage of diagnosis after adjusting for age at diagnosis.

Results:

The multivariate analysis showed that women who are uninsured (OR = 2.475) and those who have Medicaid (OR = 2.321) were significantly more likely to be diagnosed at the regional stage than the in-situ stage compared to women with private insurance. Additionally, women who are uninsured (OR = 4.432) and those who have Medicaid (OR = 3.007) were significantly more likely to be diagnosed at the distant stage than in-situ, compared to women with private insurance.

Conclusions:

The findings show that insurance status is associated with the stage of diagnosis for cervical cancer and detection at regional or distant stages often leads to higher morbidity.

Translational / Human Health Impact:
Increased coverage for routine cervical cancer screening and preventive care services is recommended, especially for uninsured women and women with public insurance such as Medicaid or Medicare.

Acknowledgements/Funding Sources:
MLK has received investigator-initiated research funding for a separate project from Merck Sharp & Dohme Corp, administered through Purdue University.

Poster #: 34

Perceptions on Antimicrobial Resistance by Health Professionals

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General Category: Health and Disease

Abstract:

In the United States, there are more than 2.8 million antimicrobial resistant infections each year. These infections disproportionately affect those at higher risk of health inequity and disparity, including children, the elderly, MSM, and people of color. AMR affects many people in different ways such as healthcare-associated infections, through the food supply, or at the community level1. In order to best combat AMR and its determinants, a multisectoral approach must be taken through One Health which targets human medicine, veterinary medicine, and the environment. The purpose of this study was to understand the perceptions of allied health professionals towards antimicrobial resistance to alleviate barriers and encourage collaboration to combat antimicrobial resistance most effectively. A qualitative interview-based methodology allows for in-depth exploration of the perceptions of health professionals, including their respective concerns and barriers that affect their practices and their ability to combat antimicrobial resistance. This study found that while veterinarians and human health professionals share some common concerns with antimicrobial resistance, the professions have differing concerns for fulfillment of client needs, testing ability, and approach to therapy. There are also concerns regarding transmission, both zoonotic and in the global health sphere. These results demonstrate the need for rapport with clients to promote compliance and satisfaction, as well as the need for increased availability of testing and trend tracking for DVMs. Meeting these needs will allow these health professionals to best serve their clients and patients across communities.

Background:

In the United States, there are more than 2.8 million antimicrobial resistant infections each year. These infections disproportionately affect those at higher risk of health inequity and disparity, including children, the elderly, MSM, and people of color. AMR affects many people in different ways such as healthcare-associated infections, through the food supply, or at the community level1. In order to best combat AMR and its determinants, a multisectoral approach must be taken through One Health which targets human medicine, veterinary medicine, and the environment. The purpose of this study was to understand the perceptions of allied health professionals towards antimicrobial resistance to alleviate barriers and encourage collaboration to combat antimicrobial resistance most effectively.

Methods:

A qualitative interview-based methodology allows for in-depth exploration of the perceptions of health professionals, including their respective concerns and barriers that affect their practices and their ability to combat antimicrobial resistance. 18 interviews were thematically analyzed to derive common themes and subthemes across the professions.

Results:

This study found that while veterinarians and human health professionals share some common concerns with antimicrobial resistance, the professions have differing concerns for fulfillment of client needs, testing ability, and approach to therapy. There are also concerns regarding transmission, both zoonotic and in the global health sphere.

Conclusions:

These results demonstrate the need for rapport with clients to promote compliance and satisfaction, as well as the need for increased availability of testing and trend tracking for DVMs. Meeting these needs will allow these health professionals to best serve their clients and patients across communities.

Translational / Human Health Impact:
These findings can inform interventions targeting interprofessional education of veterinary and medical professionals. This education could encourage an exchange of knowledge between the professions, developing testing and tracking methods of AMR. It could also encourage health professionals to educate their clients or patients on the most effective ways to fight AMR on a community level.

Acknowledgements/Funding Sources:
This study was supported by a doctoral student research grant through the Department of Public Health at Purdue University.

Poster #: 35

CDHu40: a novel marker gene set of neuroendocrine prostate cancer (NEPC)

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General Category: Health and Disease

Abstract:

Prostate cancer (PCa) is the most prevalent cancer affecting American men. Castration-resistant prostate cancer (CRPC) can emerge during hormone therapy for PCa, manifesting with elevated serum prostate-specific antigen (PSA) levels, continued disease progression, and/or metastasis to the new sites, resulting in a poor prognosis. A subset of CRPC patients shows a neuroendocrine (NE) phenotype, signifying reduced or no reliance on androgen receptor (AR) signaling and a particularly unfavorable prognosis. In this study, we employed computational approaches based on gene expression profiles and protein-protein interaction (PPI) networks. We identified 500 potential marker genes, which are significantly enriched in cell cycle and neuronal processes. The top 40 candidates, collectively named as CDHu40, demonstrated superior performance in distinguishing NE prostate cancer (NEPC) and non-NEPC samples based on gene expression profiles compared to other published marker sets. Notably, some novel marker genes in CDHu40, absent in the other marker sets, have been reported to be associated with NEPC in the literature, such as DDC, FOLH1, BEX1, MAST1, and CACNA1A. Importantly, elevated CDHu40 scores derived from our predictive model showed a robust correlation with unfavorable survival outcomes in patients, indicating the potential of the CDHu40 score as a promising indicator for predicting the survival prognosis of those patients with the NE phenotype. We further highlighted markers indirectly linked to NEPC but related to neuroendocrine features, such as ALB, FGB, and FGG. Motif enrichment analysis on the top candidates suggests that REST and E2F6 may serve as key regulators in the NEPC progression. Ultimately, our study leverages the genetic diversity present in individual NEPC studies and their protein-protein interaction network to construct a thorough understanding of the disease progression and underscores the prognostic significance of CDHu40.

Background:

Prostate cancer (PCa) is the most prevalent cancer affecting American men. Castration-resistant prostate cancer (CRPC) can emerge during hormone therapy for PCa, manifesting with elevated serum prostate-specific antigen (PSA) levels, continued disease progression, and/or metastasis to the new sites, resulting in a poor prognosis. A subset of CRPC patients shows a neuroendocrine (NE) phenotype, signifying reduced or no reliance on androgen receptor (AR) signaling and a particularly unfavorable prognosis. NEPC is lack of appropriate unique identification markers. NEPC biopsy samples also often exhibit in mixed histology, further leading to diagnostic errors and inappropriate treatments.

Methods:

In this study, we employed computational approaches based on gene expression profiles and protein-protein interaction (PPI) networks to identify a novel set of NEPC marker genes and compared with other published data.

Results:

We identified 500 potential marker genes, which are significantly enriched in cell cycle and neuronal processes. The top 40 candidates, collectively named as CDHu40, demonstrated superior performance in distinguishing NE prostate cancer (NEPC) and non-NEPC samples based on gene expression profiles compared to other published marker sets. Importantly, elevated CDHu40 scores derived from our predictive model showed a robust correlation with poor survival outcomes in patients, indicating the

potential of the CDHu40 score as a promising indicator for predicting the survival prognosis of those patients with the NE phenotype. We further highlighted markers indirectly linked to NEPC but related to neuroendocrine features, such as ALB, FGB, and FGG. Motif enrichment analysis on the top candidates suggests that REST and E2F6 may serve as key regulators in the NEPC progression.

Conclusions:
Our study leverages the genetic diversity present in individual NEPC studies and their protein-protein interaction network to construct a thorough understanding of the disease progression. The CDHu40 gene set exhibits functional relations with NE features, providing further insights into the underlying NED mechanisms.

Translational / Human Health Impact:
The CDHu40 score can emerge as a better diagnostic marker for NEPC and a reliable prognostic marker for NEPC patients.

Acknowledgements/Funding Sources:
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Poster #: 36

Cannabinoid Receptor Type II Agonist LY2828360 Reverses Sciatic Nerve Injury Hypersensitivity, Prevents Morphine Tolerance, and Blocks Morphine-Seeking Behavior

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General Category: Health and Disease

Abstract:

Amid an ongoing opioid epidemic, it remains a clinical imperative to find therapeutic options for chronic pain patients that will have long-lasting efficacy with low abuse liability. The endogenous cannabinoid system is one system within our bodies that has shown promise as a therapeutic target for chronic pain patients. More specifically, upregulation of the cannabinoid type II (CB2) receptor shows promise as a therapeutic target for pain in preclinical models, and one CB2 agonist, LY2828360 has already been shown to be safe for human use in a failed trial of osteoarthritic pain. Although LY2828360 did not work in this model, other models of chronic pain should be assessed using CB2 agonist LY2828360. In this study, we assessed analgesic efficacy of CB2 agonist LY2828360 using the scatic nerve injury (SNI) rat model of neuropathic pain. We assessed both acute and chronic efficacy to assess for potential tolerance of LY2828360. Pharmacological specificity was assessed using CB2 antagonist AM630 as a pretreatment for LY2828360 to help determine CB2 receptor specificity in this model of pain. We also asked whether co-administration of LY2828360 with morphine would prevent morphine analgesic tolerance from occurring in this SNI model. Lastly, we asked whether LY2828360 would produce rewarding behavior on its own or prevent reward behavior known to occur with opioid agonist morphine, in the conditioned place preference paradigm. We found that LY2828360 effectively reversed SNI-induced mechanical hypersensitivity and that efficacy was sustained over a 10-day chronic dosing period. LY2828360's efficacy was blocked by CB2 antagonist AM630, indicating CB2 receptor specificity in the SNI model. LY282860 prevented the development of morphine tolerance in analgesic efficacy and prevented morphine reward in the CPP assay. Lastly, LY2828360 did not produce a drug-seeking effect on its own in the CPP assay, indicating low abuse liability for LY2828360.

Background:

Opioids are prescribed regularly for chronic pain patients, but often produce tolerance in analgesic efficacy with repeated use. Opioids also have high abuse liability that can often result in abuse of opioids even if initially prescribed in a clinical setting. Finding pain-relieving therapeutics that do not produce tolerance in efficacy and do not produce rewarding effects on their own remains a clinical imperative to both improve quality of life of chronic pain patients and attenuate the ongoing opioid epidemic. Activation of Cannabinoid Type II (CB2) receptors can reduce pain behavior without producing unwanted psychoactive effects (Deng et al. 2015). The CB2 receptor agonist LY2828360 suppresses persistent nociception in models of inflammatory pain and toxic neuropathy in mice (Guenther et al. 2023; Lin et al. 2018; Carey et al. 2023). Whether LY2828360 is efficacious in other models of neuropathic pain or in other species is not known. LY2828360 failed for efficacy in a clinical trial for knee pain due to osteoarthritis but was shown to be safe in humans. We should assess LY2828360's efficacy in other models of chronic pain due to its therapeutic potential alongside its low liability for side effects, low likelihood tolerance in efficacy, and low likelihood for abuse liability based on preclinical literature.

Methods:

The spared nerve injury (SNI) pain model was used to establish chronic neuropathic pain induced by injuring the sciatic nerve. More specifically, ligation of the tibial and common peroneal branch of the

sciatic nerve were injured, resulting in mechanical hypersensitivity in the paw ipsilateral to nerve injury. Ipsilateral (injury) paw and contralateral (non-injury) paw measurements were both assessed within all animals in mechanical hypersensitivity (allodynia) studies. Assessments of mechanical paw withdrawal thresholds were performed using electronic an von Frey anesthesiometer to stimulate the intraplantar region of the animal's hindpaws until a retraction response of the paw was observed. Baseline measurements were taken before any sciatic nerve injury surgeries were performed. Lower threshold (force required to elicit the retraction response) compared to initial baseline measurements reflects higher mechanical hypersensitivity. In acute studies, LY2828360 (3 or 10 mg/kg i.p.) was injected 30 minutes prior to von Frey testing following baseline measurement, and time points of 0.5, 1 , 2 , 4 and 6 hours post administration were assessed. In a pharmacological specificity study, pretreatment of CB2 antagonist AM630 (3 mg/kg i.p.) was administered 20 minutes before LY2828360 (10 mg/kg, i.p.) injection. Animals were then Von Frey tested 0.5, 1, 2, 4, and 6 hours post administration of LY2828360. In chronic studies, daily LY2828360 (3 or 10 mg/kg i.p.) was administered once daily for 10 days. Von Frey measurements were taken on injection day 1, 4, 7 and 10. An LY2828360 washout period was also performed where animals were von Frey tested on days 11, 14, and 17 (days 1, 4, and 7 after the cessation of LY2828360) after 10 days of chronic dosing. In a morphine tolerance study, once daily LY2828360 (3 mg/kg i.p.) plus morphine (6 mg/kg i.p.), morphine alone, or vehicle injections were performed for 10 days. Von Frey measurements were taken on injection day 1, 4, 7, and 10. A washout period was also measured on day 11, 14, and 17 (days 1, 4, and 7 after the cessation of LY2828360). Conditioned place preference was used to assess drug reward. Animals received VEH (on days 5, 7, 9, and 11) and drug (3 mg/kg LY2828360 i.p., 6 mg/kg morphine i.p., or LY2828360-morphine combination) (on days 4, 6, 8, and 10) in paired chambers with distinct visual contexts.

Results:
LY2828360 (10 mg/kg i.p.) effectively reversed sciatic nerve injury-induced mechanical hypersensitivity for up to 2 hours post administration. LY2828360's efficacy was blocked by CB2 receptor antagonist AM630, confirming CB2 receptor-mediated efficacy as LY2828360's mechanism of action in reversing SNI-induced mechanical hypersensitivity. Over a 10-day chronic dosing paradigm, LY2828360's efficacy was sustained in reversing SNI-induced mechanical hypersensitivity. This effect was not permanent, as cessation of LY2828360 administration resulted in the return of mechanical hypersensitivity in SNI rats. Co-administration of LY2828360 (3 mg/kg, i.p.) with morphine (6 mg/kg, i.p.) did not block morphine's ability to reverse SNI pain up to 2 hours post administration acutely. Chronic co-administration of LY2828360 plus morphine over a 10-day chronic dosing paradigm prevented morphine tolerance in analgesic efficacy from developing, whereas morphine alone developed tolerance between 7 and 10 days of chronic dosing. LY2828360 alone did not produce drug-seeking behavior in the conditioned place preference paradigm, whereas morphine alone did produce drug-seeking behavior. When LY2828360 and morphine were combined, this drug-seeking behavior was ablated, indicating that LY2828360 blocked the rewarding effects of morphine in the conditioned place preference assay.

Conclusions:
LY2828360 effectively reverses sciatic nerve injury-induced mechanical hypersensitivity through a CB2 receptor-mediated mechanism. LY2828360's analgesic efficacy is sustained over a 10-day chronic dosing paradigm unlike morphine, in which tolerance developed between 7 and 10 days of chronic administration. LY2828360 also prevented morphine tolerance from developing when co-administered with morphine. Lastly, LY2828360 did not produce drug-seeking behavior unlike morphine and blocked the drug-seeking behavior of morphine when co-administered with morphine. These findings suggest that LY2828360 may be a promising therapeutic option for sciatic nerve pain with low abuse liability due to its lack of tolerance and drug-seeking potential. In addition to this, these findings suggest that LY2828360 could be a promising combinatorial treatment with morphine due to LY2828360's ability to prevent morphine tolerance in analgesic efficacy and block morphine drug-seeking behavior.

Translational / Human Health Impact:
Sciatic nerve pain affects millions of patients worldwide. Finding safe and effective analgesics with low abuse potential remains important in the midst of an ongoing opioid epidemic. Using a preclinical model of sciatic nerve pain, we were able to show that cannabinoid type II receptor agonist LY2828360 effectively reversed sciatic nerve pain without the development of analgesic tolerance or production of drug-seeking

behavior. Through our studies, we were also able to show that LY2828360 blocked morphine drug-seeking behavior and prevented morphine analgesic tolerance when LY was co-administered with morphine. Because LY2828360 has already been shown to be safe for human use based on clinical trials and based on our findings from these studies, we believe that LY2828360 may be a promising analgesic candidate for sciatic nerve pain patients. We also believe that LY2828360 could be considered as a co-treatment option alongside prescribed opioids due to its ability to prevent morphine tolerance and reward without sacrificing morphine's analgesic efficacy in reversing sciatic nerve pain. Overall, the cannabinoid type II receptor remains a promising target for both the treatment of chronic pain, and the attenuation of opioid misuse or abuse.

Acknowledgements/Funding Sources:
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Poster #: 37

The Collaborative Core for Cancer Bioinformatics

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General Category: Research Resource

Abstract:

The Collaborative Core for Cancer Bioinformatics (C3B) is a joint bioinformatics core shared between the Indiana University Melvin and Bren Simon Comprehensive Cancer Center (IUCCC) and the Purdue University Institute for Cancer Research (PICR). The C3B performs services such as scientific consulting, training, and high-quality bioinformatics analyses. The core employs 6 full-time staff members and mentors 5 graduate research assistants and 1 undergraduate student. The core has performed numerous analyses including RNA-seq, scRNA-seq, ChIP-seq, CRISPR/Cas9, WGS, and spatial transcriptomics. Here, we highlight three projects completed by the C3B. In the first example, we performed single-cell RNA-sequencing (scRNA-seq) on canine muscle-invasive urothelial carcinoma primary tumors before and after treatment with the Cox inhibitor Piroxicam. Higher abundance and activity of tumor-infiltrating lymphocytes was found to be associated with favorable therapeutic response. These results can be extended to evaluate immunotherapies in canine clinical trials. Another example used bulk RNA-seq to investigate human cytokine-primed natural killer cell responses to adenosinergic signaling, which acts as a potent immunosuppressant in solid tumors. We found that adenosine induces upregulation of genes involved in immune responses while downregulating cellular metabolism and protein synthesis functions, thus leading to impaired anti-tumor immunity. Our results showed that adenosine acts on specific cellular pathways in NK cells rather than inducing broad inhibition of cellular functions. A third project integrated scRNA-seq, gene set enrichment analysis, and survival analysis with cutting-edge experimental methodologies in prostate cancer and found that cancer cell expression of the chromatin effector Pygo2 promotes immunotherapy resistance by restraining tumor T cell infiltration and cytotoxicity. A significant contribution of this study is the translational implications of targeting Pygo2. We synthesized JBC117 and JBC117ana as prototype Pygo2 inhibitors and showed that they largely phenocopied Pygo2 genetic deletion to generate single-agent and combinatorial efficacy with immune checkpoint blockade, including treating castration-resistant prostate cancer.

Background:

The Collaborative Core for Cancer Bioinformatics (C3B) is a joint bioinformatics core shared between the Indiana University Melvin and Bren Simon Comprehensive Cancer Center (IUCCC) and the Purdue University Institute for Cancer Research (PICR). The C3B performs services such as scientific consulting, training, and high-quality bioinformatics analyses. The core employs 6 full-time staff members and mentors 5 graduate research assistants and 1 undergraduate student.

Methods:

The core has performed numerous analyses including RNA-seq, scRNA-seq, ChIP-seq, CRISPR/Cas9, WGS, and spatial transcriptomics. Here, we highlight three projects completed by the C3B.

Results:

In the first example, we performed single-cell RNA-sequencing (scRNA-seq) on canine muscle-invasive urothelial carcinoma primary tumors before and after treatment with the Cox inhibitor Piroxicam. Higher abundance and activity of tumor-infiltrating lymphocytes was found to be associated with favorable therapeutic response. These results can be extended to evaluate immunotherapies in canine clinical trials. Another example used bulk RNA-seq to investigate human cytokine-primed natural killer cell responses to adenosinergic signaling, which acts as a potent immunosuppressant in solid tumors. We found that adenosine induces upregulation of genes involved in immune responses while downregulating cellular metabolism and protein synthesis functions, thus leading to impaired anti-tumor immunity. Our results

showed that adenosine acts on specific cellular pathways in NK cells rather than inducing broad inhibition of cellular functions. A third project integrated scRNA-seq, gene set enrichment analysis, and survival analysis with cutting-edge experimental methodologies in prostate cancer and found that cancer cell expression of the chromatin effector Pygo2 promotes immunotherapy resistance by restraining tumor T cell infiltration and cytotoxicity. A significant contribution of this study is the translational implications of targeting Pygo2. We synthesized JBC117 and JBC117ana as prototype Pygo2 inhibitors and showed that they largely phenocopied Pygo2 genetic deletion to generate single-agent and combinatorial efficacy with immune checkpoint blockade, including treating castration-resistant prostate cancer.

Conclusions:

Translational / Human Health Impact:
Our aim is to integrate and accelerate cancer discovery, drug discovery, and precision medicine to improve and save lives through joint bioinformatics, molecular genetics, and genomics research.

Acknowledgements/Funding Sources:
The C3B is supported by the Purdue Institute for Cancer Research (Grant P30CA023168), The Indiana University Melvin and Bren Comprehensive Cancer Center (Grant P30CA082709), the Hope Foundation, and The Walther Cancer Foundation.

Poster #: 38

Indiana CTSI Access Technology Program (ATP)

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General Category: Research Resource

Abstract:

The mission of the Indiana Clinical and Translational Sciences Institute's (CTSI) Access Technology Program (ATP) is to improve the impact and competitiveness of CTSI investigator research. Campus liaisons facilitate advances in translational science by connecting Indiana CTSI investigators to state-of-the-art technologies and specialized equipment located in CTSI-designated core facilities across the state. The ATP initiatives that promote the use of innovative technologies in investigator-initiated research include a user-friendly Research Cores and Resources website and a technology-based seminar series highlighting the services offered at each of the four Indiana CTSI campuses (IU-Bloomington, IU-Indianapolis, Purdue University, and the University of Notre Dame). Seminar recordings are posted online for easy access to researchers as needed. In addition, two grant programs, the Core Pilot Awards and the Postdoctoral Challenge for the Use of Core Facilities, provide funding for services provided by Indiana CTSI-designated core facilities. The ATP also manages multi-institution site licenses for two OMICS data analysis tools, Ingenuity Pathway Analysis (IPA) and MetaCore Pathway Analysis Suite, which provide CTSI investigators access to these software packages at significantly reduced prices. Another responsibility of the ATP is to manage key support cores that are vital for the Indiana CTSI mission. The Specimen Support Facility (SSF) provides a secure and affordable solution for storing local and national biobanks. The Clinical Translational Support Laboratory (CTSL) provides CTSI investigators and other collaborators with rapid sample processing, shipping, and storage for clinical specimens. Lastly, the ATP provides guidance for and review of the Indiana CTSI-designated cores to promote best practices and ensure that the core services meet the needs of the Indiana CTSI investigators. Core facilities are granted "Indiana CTSI-designated core" status if they meet the ATP Core Oversight Program's standards for scientific quality, pricing, operations, policies governing publication, payment and dispute resolution, advisory committees, and user satisfaction.

Background:

Methods:

Results:

Conclusions:

Translational / Human Health Impact:

Acknowledgements/Funding Sources:

The Access Technology Program is supported by the Indiana Clinical and Translational Sciences Institute which is funded in part by Award Number UM1TR004402 from the National Institutes of Health, National Center for Advancing Translational Sciences, Clinical and Translational Sciences Award.